



Full wwPDB EM Validation Report ⓘ

Jul 3, 2024 – 11:47 pm BST

PDB ID : 6ZSB
EMDB ID : EMD-11392
Title : Human mitochondrial ribosome in complex with mRNA and P-site tRNA
Authors : Aibara, S.; Singh, V.; Modelska, A.; Amunts, A.
Deposited on : 2020-07-15
Resolution : 4.50 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev92
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

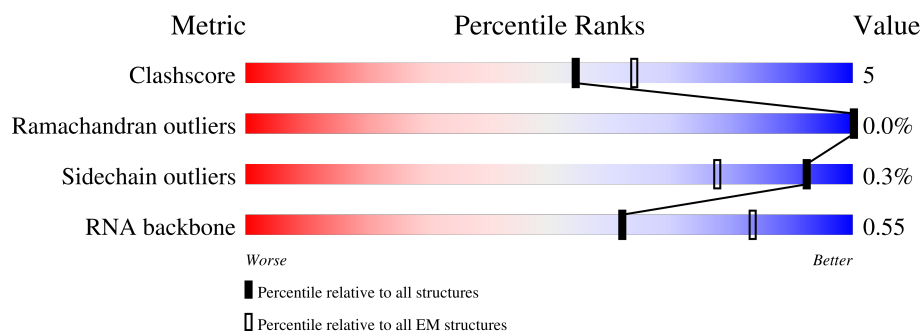
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.50 Å.

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








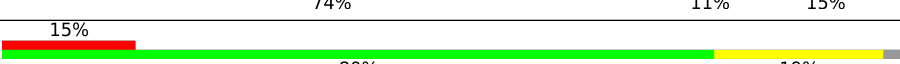
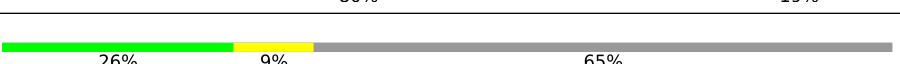
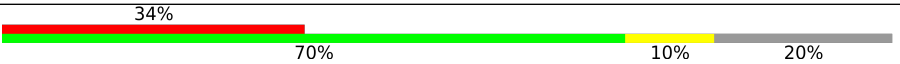


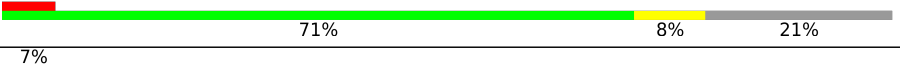
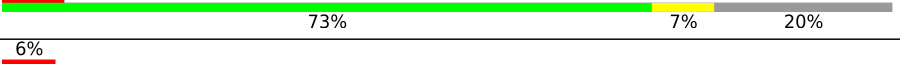

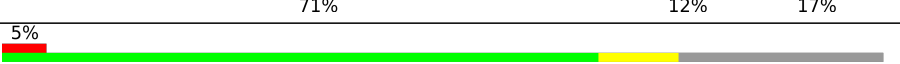
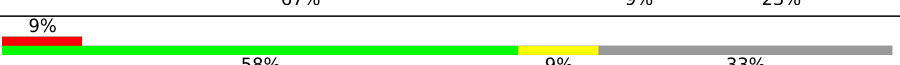










Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	0	188	
2	1	65	
3	2	92	
4	3	188	
5	4	103	
6	5	423	
7	6	380	

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Mol	Chain	Length	Quality of chain
8	7	338	
9	8	206	
10	9	137	
11	XA	1561	
12	A0	218	
13	A1	323	
14	A2	118	
15	A3	199	
16	A4	689	
17	AA	954	
18	AB	296	
19	AC	167	
20	AD	430	
21	AE	125	
22	AF	242	
23	AG	396	
24	AH	201	
25	AI	194	
26	AJ	138	
27	AK	128	
28	AL	257	
29	AM	137	
30	AN	130	
31	AO	258	
32	AP	142	


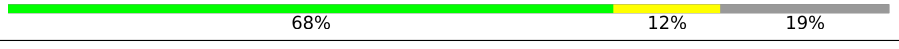
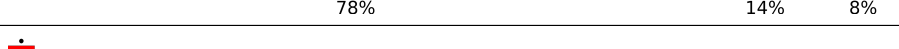
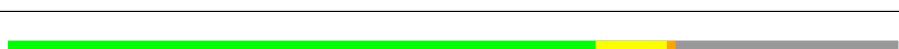



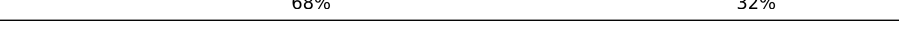



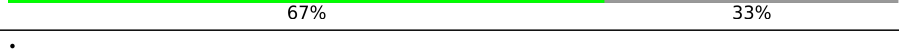

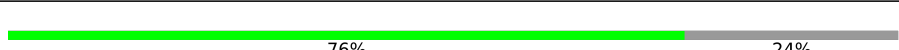


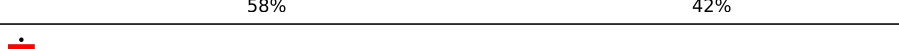







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Mol	Chain	Length	Quality of chain
33	AQ	87	
34	AR	360	
35	AS	190	
36	AT	173	
37	AU	205	
38	AV	414	
39	AW	187	
40	AX	398	
41	AY	395	
42	AZ	106	
43	XB	72	
44	XD	305	
45	XE	348	
46	XF	311	
47	XH	267	
48	XI	261	
49	XJ	192	
50	XK	178	
51	XL	145	
52	XM	296	
53	XN	251	
54	XO	175	
55	XP	180	
56	XQ	292	
57	XR	149	

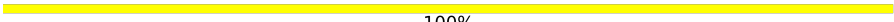
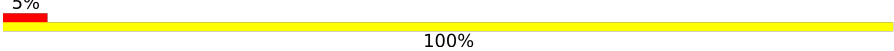








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Mol	Chain	Length	Quality of chain
58	XS	205	
59	XT	206	
60	XU	153	
61	XV	216	
62	XW	148	
63	XX	256	
64	XY	250	
65	XZ	161	
66	a	142	
67	b	215	
68	c	332	
69	d	306	
70	e	279	
71	f	212	
72	g	166	
73	h	158	
74	i	128	
75	j	123	
76	k	112	
77	l	138	
78	m	128	
79	o	102	
80	p	206	
81	q	222	
82	r	196	

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Mol	Chain	Length	Quality of chain
83	r1	4	 100%
84	r3	75	 5% 100%
85	s	439	 84% 16%
86	t1	198	 19% 23% 77%
86	t2	198	 14% 15% 85%
86	t3	198	 15% 15% 85%
86	t4	198	 15% 15% 85%
86	t5	198	 15% 15% 85%
86	t6	198	 14% 14% 86%
87	A	8	 12% 38% 38% 12%

2 Entry composition

There are 91 unique types of molecules in this entry. The entry contains 312076 atoms, of which 143042 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 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	0	108	Total	C	H	N	O	S	0	0
			1783	545	903	172	157	6		

- Molecule 2 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	1	53	Total	C	H	N	O	S	0	0
			919	281	480	84	72	2		

- Molecule 3 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	2	46	Total	C	H	N	O	S	0	0
			782	233	406	83	59	1		

- Molecule 4 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	3	95	Total	C	H	N	O	S	0	0
			1714	539	883	162	127	3		

- Molecule 5 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	4	38	Total	C	H	N	O	S	0	0
			703	217	362	72	48	4		

- Molecule 6 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	5	393	Total	C	H	N	O	S	0	0
			6404	2070	3200	559	564	11		

- Molecule 7 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	6	354	Total	C	H	N	O	S	0	0
			5786	1881	2839	525	532	9		

- Molecule 8 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	291	Total	C	H	N	O	S	0	0
			4738	1514	2373	401	432	18		

- Molecule 9 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	8	139	Total	C	H	N	O	S	0	0
			2377	747	1202	208	218	2		

- Molecule 10 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	9	124	Total	C	H	N	O	S	0	0
			1983	644	987	170	180	2		

- Molecule 11 is a RNA chain called 16S mitochondrial rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	XA	1499	Total	C	H	N	O	P	0	0
			47993	14284	16160	5756	10294	1499		

- Molecule 12 is a protein called 28S ribosomal protein S34, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	A0	201	Total	C	H	N	O	S	0	0
			3369	1065	1685	322	292	5		

- Molecule 13 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	A1	275	Total	C	H	N	O	S	0	0
			4491	1414	2261	380	425	11		

- Molecule 14 is a protein called Coiled-coil-helix-coiled-coil-helix domain-containing protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	A2	116	Total	C	H	N	O	S	0	0
			1889	574	964	181	162	8		

- Molecule 15 is a protein called Aurora kinase A-interacting protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	A3	69	Total	C	H	N	O	S	0	0
			1292	393	682	130	86	1		

- Molecule 16 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	A4	552	Total	C	H	N	O	S	0	0
			8955	2866	4485	756	820	28		

- Molecule 17 is a RNA chain called 12S mitochondrial rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	AA	924	Total	C	H	N	O	P	0	0
			29592	8800	9964	3540	6364	924		

- Molecule 18 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	AB	218	Total	C	H	N	O	S	0	0
			3545	1135	1769	322	309	10		

- Molecule 19 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	AC	132	Total	C	H	N	O	S	0	0
			2170	699	1088	195	184	4		

- Molecule 20 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	AD	343	Total	C	H	N	O	S	0	0
			5501	1706	2785	515	482	13		

- Molecule 21 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	AE	122	Total	C	H	N	O	S	0	0
			1973	614	1001	177	177	4		

- Molecule 22 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	AF	201	Total	C	H	N	O	S	0	0
			3383	1069	1715	305	283	11		

- Molecule 23 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	AG	304	Total	C	H	N	O	S	0	0
			4996	1593	2491	444	454	14		

- Molecule 24 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	AH	135	Total	C	H	N	O	S	0	0
			2241	712	1136	187	203	3		

- Molecule 25 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	AI	136	Total	C	H	N	O	S	0	0
			2063	637	1052	192	178	4		

- Molecule 26 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	AJ	108	Total	C	H	N	O	S	0	0
			1725	521	887	169	142	6		

- Molecule 27 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	AK	101	Total	C	H	N	O	S	0	0
			1746	537	885	179	140	5		

- Molecule 28 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	AL	164	Total	C	H	N	O	S	0	0
			2854	883	1472	257	235	7		

- Molecule 29 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	AM	116	Total	C	H	N	O	S	0	0
			1871	582	951	182	150	6		

- Molecule 30 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	AN	107	Total	C	H	N	O	S	0	0
			1754	549	908	153	141	3		

- Molecule 31 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	AO	185	Total	C	H	N	O	S	0	0
			3018	970	1490	285	267	6		

- Molecule 32 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	AP	95	Total	C	H	N	O	S	0	0
			1561	493	796	132	132	8		

- Molecule 33 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	AQ	85	Total	C	H	N	O	S	0	0
			1483	455	749	149	123	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AQ	50	ARG	CYS	conflict	UNP P82921

- Molecule 34 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	AR	250	Total	C	H	N	O	S	0	0
			4134	1314	2074	353	385	8		

- Molecule 35 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	AS	133	Total	C	H	N	O	S	0	0
			2203	709	1103	196	194	1		

- Molecule 36 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	AT	162	Total	C	H	N	O	S	0	0
			2673	850	1343	231	238	11		

- Molecule 37 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	AU	173	Total	C	H	N	O	S	0	0
			2932	900	1471	294	263	4		

- Molecule 38 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	AV	349	Total	C	H	N	O	S	0	0
			5729	1841	2862	478	536	12		

- Molecule 39 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	AW	97	Total	C	H	N	O	S	0	0
			1551	486	785	137	139	4		

- Molecule 40 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	AX	348	Total	C	H	N	O	S	0	0
			5619	1802	2805	491	510	11		

- Molecule 41 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	AY	113	Total	C	H	N	O	S	0	0
			1868	621	912	157	176	2		

- Molecule 42 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	AZ	86	Total	C	H	N	O	S	0	0
			1465	467	734	131	129	4		

- Molecule 43 is a RNA chain called mitochondrial tRNA^{Val}.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	XB	59	Total	C	H	N	O	P	0	0
			1890	563	635	227	406	59		

- Molecule 44 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	XD	236	Total	C	H	N	O	S	0	0
			3738	1145	1896	373	315	9		

- Molecule 45 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	XE	304	Total	C	H	N	O	S	0	0
			4798	1539	2402	416	430	11		

- Molecule 46 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	XF	250	Total	C	H	N	O	S	0	0
			4058	1294	2045	365	348	6		

- Molecule 47 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	XH	95	Total	C	H	N	O		0	0
			1616	498	832	152	134			

- Molecule 48 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	XI	211	Total	C	H	N	O	S	0	0
			3474	1086	1783	303	291	11		

- Molecule 49 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	XJ	170	Total	C	H	N	O	S	0	0
			2658	825	1367	230	234	2		

- Molecule 50 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	XK	177	Total	C	H	N	O	S	0	0
			2899	934	1448	259	251	7		

- Molecule 51 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	XL	115	Total	C	H	N	O	S	0	0
			1830	559	941	171	154	5		

- Molecule 52 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	XM	287	Total	C	H	N	O	S	0	0
			4683	1472	2378	425	402	6		

- Molecule 53 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	XN	221	Total	C	H	N	O	S	0	0
			3586	1138	1808	325	305	10		

- Molecule 54 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	XO	152	Total	C	H	N	O	S	0	0
			2528	784	1283	239	215	7		

- Molecule 55 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
55	XP	143	Total	C	H	N	O	S	0	0
			2326	729	1162	223	207	5		

- Molecule 56 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	XQ	238	Total	C	H	N	O	S	0	0
			4000	1268	2022	352	349	9		

- Molecule 57 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
57	XR	140	Total	C	H	N	O	S	0	0
			2367	732	1214	231	186	4		

- Molecule 58 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	XS	160	Total	C	H	N	O	S	0	0
			2638	829	1354	226	225	4		

- Molecule 59 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	XT	166	Total	C	H	N	O	S	0	0
			2778	875	1410	254	232	7		

- Molecule 60 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	XU	141	Total	C	H	N	O	S	0	0
			2335	743	1164	222	203	3		

- Molecule 61 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	XV	202	Total	C	H	N	O	S	0	0
			3304	1051	1656	294	295	8		

- Molecule 62 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	XW	111	Total	C	H	N	O	S	0	0
			1769	558	898	164	146	3		

- Molecule 63 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	XX	243	Total	C	H	N	O	S	0	0
			4089	1317	2054	351	362	5		

- Molecule 64 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	XY	178	Total	C	H	N	O	S	0	0
			3109	981	1575	295	254	4		

- Molecule 65 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	XZ	120	Total	C	H	N	O	S	0	0
			2008	626	1030	183	166	3		

- Molecule 66 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
66	a	97	Total	C	H	N	O	S	0	0
			1590	512	777	145	151	5		

- Molecule 67 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
67	b	148	Total	C	H	N	O	S	0	0
			2358	733	1180	229	213	3		

- Molecule 68 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
68	c	275	Total	C	H	N	O	S	0	0
			4437	1415	2220	383	410	9		

- Molecule 69 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
69	d	216	Total	C	H	N	O	S	0	0
			3501	1125	1743	305	315	13		

- Molecule 70 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
70	e	217	Total	C	H	N	O	S	0	0
			3529	1124	1767	310	323	5		

- Molecule 71 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
71	f	143	Total	C	H	N	O	S	0	0
			2314	737	1165	187	221	4		

- Molecule 72 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
72	g	132	Total	C	H	N	O	S	0	0
			2183	710	1086	191	194	2		

- Molecule 73 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
73	h	108	Total	C	H	N	O	S	0	0
			1748	560	866	154	165	3		

- Molecule 74 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
74	i	97	Total	C	H	N	O	S	0	0
			1684	532	857	165	126	4		

- Molecule 75 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
75	j	86	Total	C	H	N	O	S	0	0
			1367	426	678	134	127	2		

- Molecule 76 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
76	k	95	Total	C	H	N	O	S	0	0
			1477	456	745	139	132	5		

- Molecule 77 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
77	l	80	Total	C	H	N	O	S	0	0
			1327	427	654	118	125	3		

- Molecule 78 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
78	m	60	Total	C	H	N	O	S	0	0
			1025	309	525	104	85	2		

- Molecule 79 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
79	o	94	Total	C	H	N	O	S	0	0
			1601	501	804	165	128	3		

- Molecule 80 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
80	p	127	Total	C	H	N	O	S	0	0
			2141	661	1083	201	192	4		

- Molecule 81 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
81	q	164	Total	C	H	N	O	S	0	0
			2737	858	1358	267	249	5		

- Molecule 82 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
82	r	152	Total	C	H	N	O	S	0	0
			2514	792	1267	239	208	8		

- Molecule 83 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	r1	4	Total	C	N	O	P	0	0
			72	36	8	24	4		

- Molecule 84 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	r3	75	Total	C	N	O	P	0	0
			1459	711	222	451	75		

- Molecule 85 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
85	s	370	Total	C	H	N	O	S	0	0
			6058	1946	3022	542	534	14		

- Molecule 86 is a protein called 39S ribosomal protein L12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	t1	46	Total	C	H	N	O	2	0
			733	228	379	56	70		
86	t2	30	Total	C	H	N	O	0	0
			506	154	268	38	46		
86	t3	30	Total	C	H	N	O	0	0
			506	154	268	38	46		
86	t4	29	Total	C	H	N	O	0	0
			484	148	255	36	45		
86	t5	29	Total	C	H	N	O	0	0
			484	148	255	36	45		
86	t6	27	Total	C	H	N	O	0	0
			450	137	236	34	43		

- Molecule 87 is a protein called Quinupristin.

Mol	Chain	Residues	Atoms						AltConf	Trace
87	A	8	Total	C	H	N	O	S	0	0
			140	53	67	9	10	1		

- Molecule 88 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
88	0	1	Total	Zn	0
			1	1	

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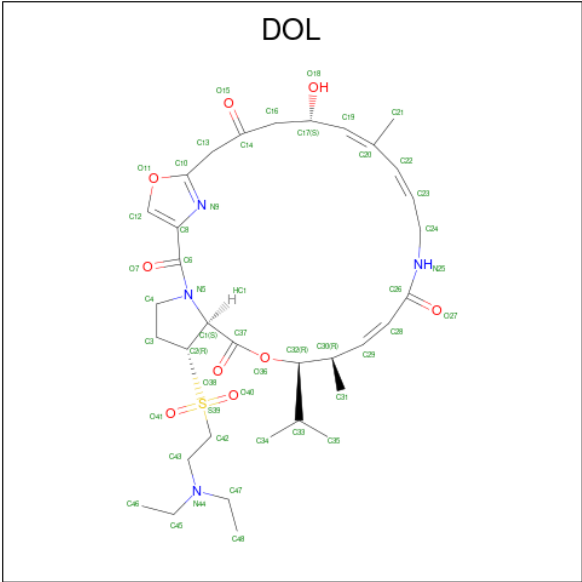
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Mol	Chain	Residues	Atoms		AltConf
88	4	1	Total 1	Zn 1	0
88	AB	1	Total 1	Zn 1	0
88	AO	1	Total 1	Zn 1	0
88	AP	1	Total 1	Zn 1	0
88	AT	1	Total 1	Zn 1	0
88	r	1	Total 1	Zn 1	0

- Molecule 89 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

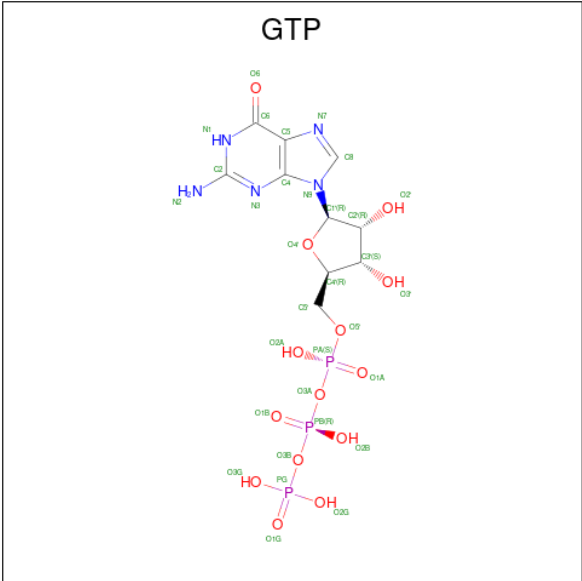
Mol	Chain	Residues	Atoms		AltConf
89	9	1	Total 1	Mg 1	0
89	XA	142	Total 142	Mg 142	0
89	A2	1	Total 1	Mg 1	0
89	AA	45	Total 45	Mg 45	0
89	XD	1	Total 1	Mg 1	0
89	XE	1	Total 1	Mg 1	0
89	XM	2	Total 2	Mg 2	0
89	XW	1	Total 1	Mg 1	0
89	g	1	Total 1	Mg 1	0

- Molecule 90 is 5-(2-DIETHYLAMINO-ETHANESULFONYL)-21-HYDROXY-10-ISOPROPYL-11,19-DIMETHYL-9,26-DIOXA-3,15,28-TRIAZA-TRICYCLO[23.2.1.00,255]OCTACOSA-1(27),12,17,19,25(28)-PENTAENE-2,8,14,23-TETRAONE (three-letter code: DOL) (formula: C₃₄H₅₀N₄O₉S).



Mol	Chain	Residues	Atoms						AltConf
90	XA	1	Total	C	H	N	O	S	0
			98	34	50	4	9	1	

- Molecule 91 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

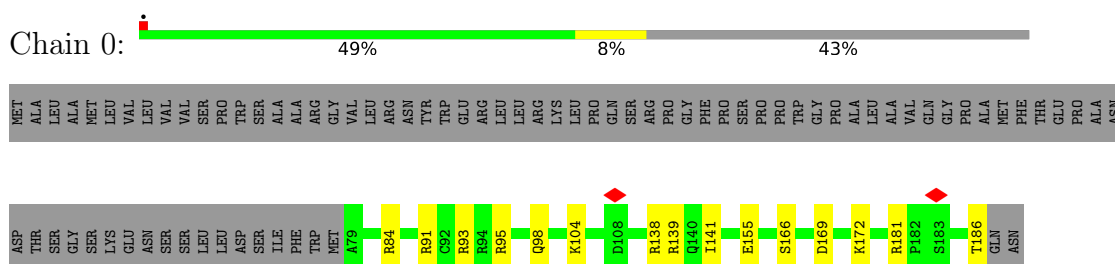


Mol	Chain	Residues	Atoms						AltConf
91	AX	1	Total	C	H	N	O	P	0
			42	10	10	5	14	3	

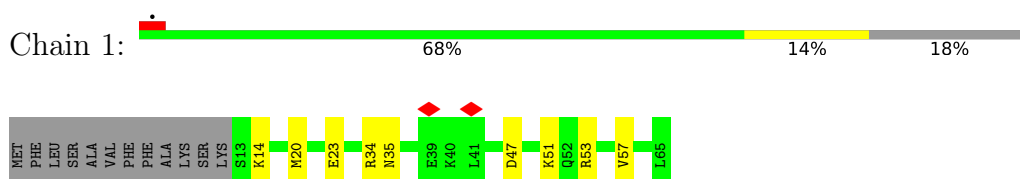
3 Residue-property plots [i](#)

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

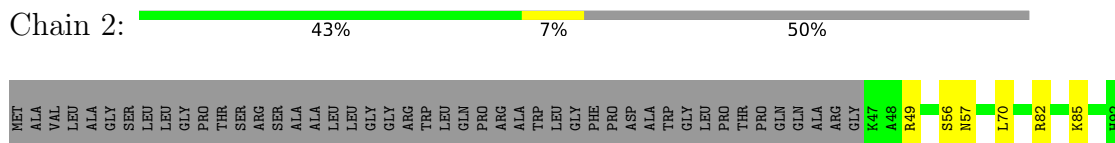
- Molecule 1: 39S ribosomal protein L32, mitochondrial



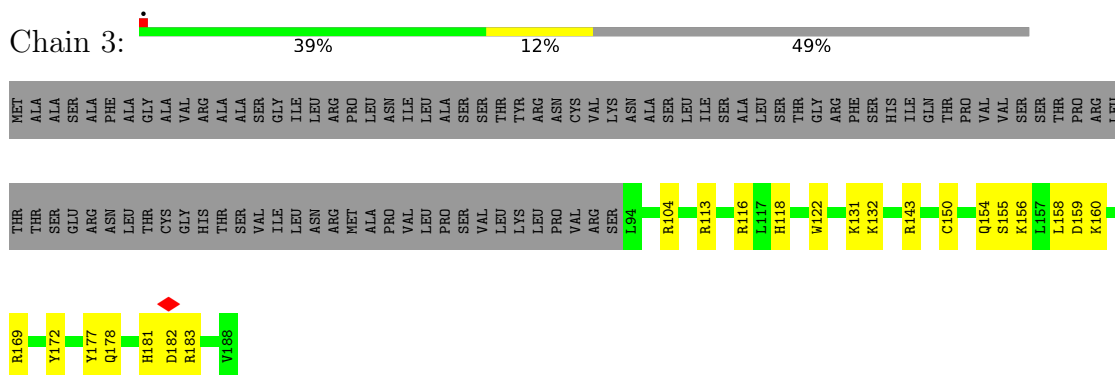
- Molecule 2: 39S ribosomal protein L33, mitochondrial



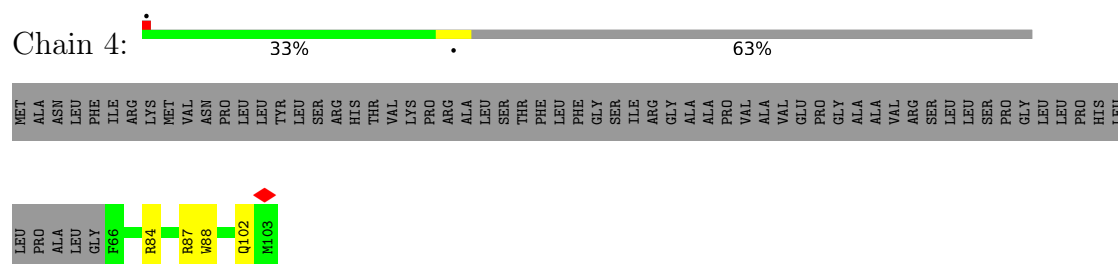
- Molecule 3: 39S ribosomal protein L34, mitochondrial



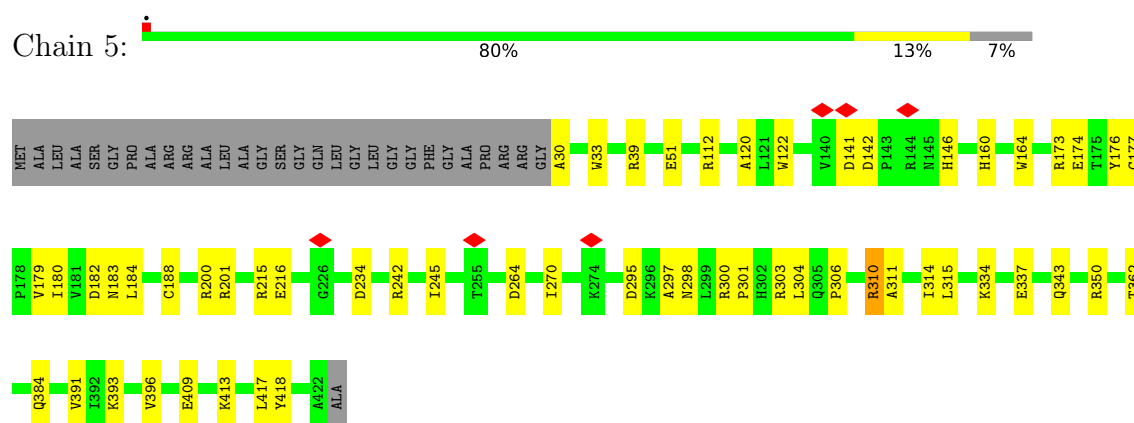
- Molecule 4: 39S ribosomal protein L35, mitochondrial



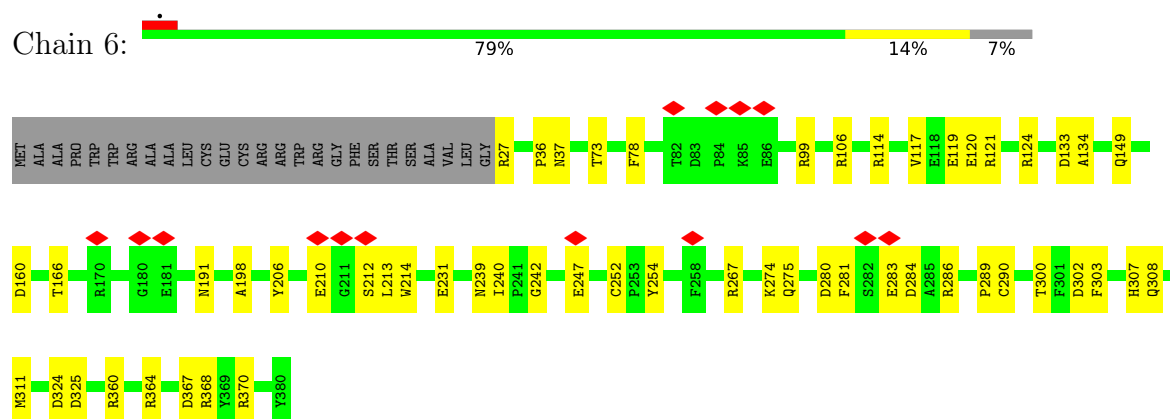
- Molecule 5: 39S ribosomal protein L36, mitochondrial



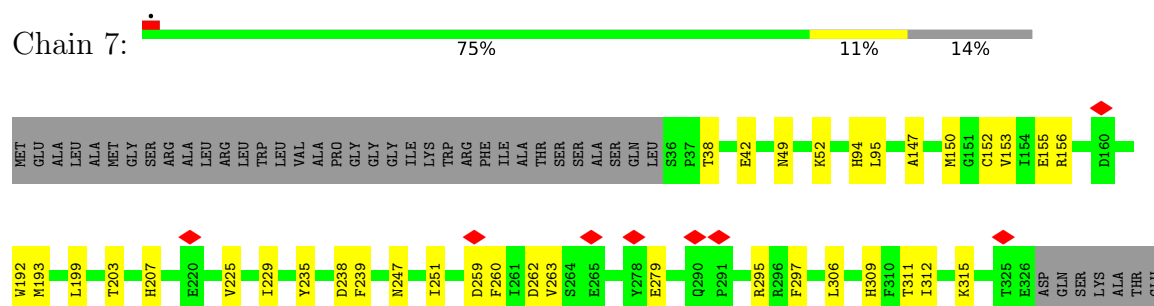
- Molecule 6: 39S ribosomal protein L37, mitochondrial



- Molecule 7: 39S ribosomal protein L38, mitochondrial



- Molecule 8: 39S ribosomal protein L39, mitochondrial



GLU
CYS
THR
SER
THR


- Molecule 9: 39S ribosomal protein L40, mitochondrial

Chain 8: 

MET THR ALA SER VAL LEU ARG SER ILE LEU LEU ALA ARG PRO THR SER GLY LEU LEU GLY THR TRP GLN THR GLN LEU ARG ARG GLU THR HIS GLN ARG ALA SER LEU LEU SER PHE TRP LEU LEU ILE PRO MET ARG SER GLU PRO LEU ARG LYS LYS VAL ASP PRO LYS H60

E63 E67 K74 E76 E77 E78 T79 E86 K97 A98 R99 E100 E110 F111 R113 R114 A115 L116 K119 R137 E141 D165 F169 P170 E172 Q186 V198 TYR THR GLN VAL PHE LYS ARG

- Molecule 10: 39S ribosomal protein L41, mitochondrial

Chain 9: 

MET GLY VAL LEU ALA ALA ALA CYS ARG LEU VAL ARG G14 A15 D16 R17 M18 T22 S23 K24 R25 R28 R36 Q52 Q53 K54 T66 G67 E82 E83 D106 G107 T108 E115 L127 N134 F135 L136 R137

- Molecule 11: 16S mitochondrial rRNA

Chain XA: 

G1671 C1672 C1678 U1679 A1680 A1681 G1682 C1683 C1684 C1685 G1689 C1690 C1691 C1692 C1693 C1694 C1695 C1696 U1700 U1704 G1707 G1708 G1709 Q52 Q53 K54 T66 G67 E82 E83 D106 G107 T108 E115 L127 N134 F135 L136 R137

C1764 C1765 C1769 G1770 C1771 A1777 U1780 G1787 A1790 G1791 G1792 U1799 G1800 A1803 A1804 A1805 A1808 U1809 A1810 A1811 G1816 C1817 A1818 A1821 U1822 A1823 U1824 A1825 G1826 G1827 A1828 A1829 A1832 A1836 C1837 C1838 C1839 C1840 A1844 C1845 G1748 G1749 G1750 A1751 G1760 A1761 A1762 A1763 A1855 A1856

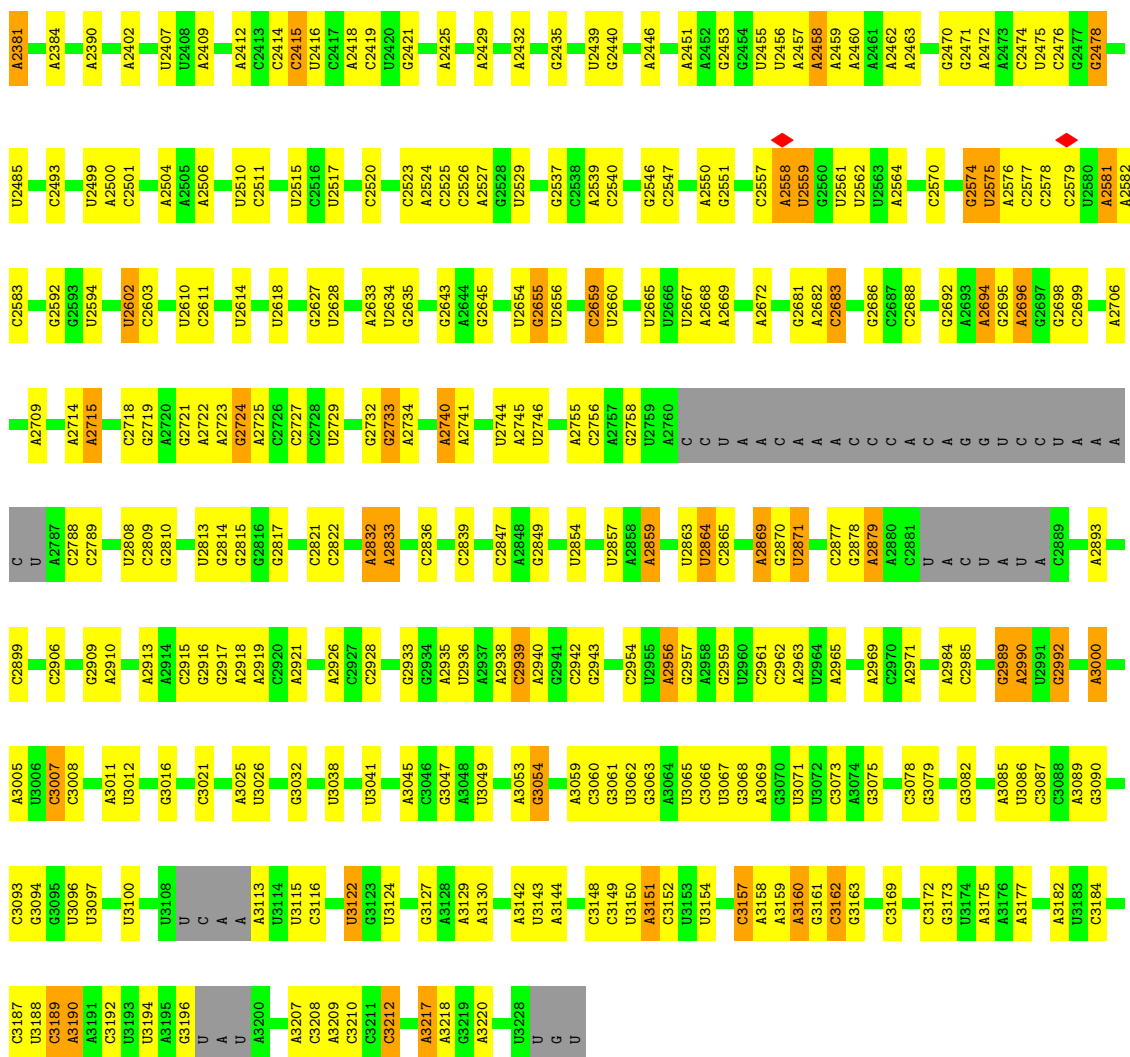
A1859 A1860 A1861 A1862 A1863 A1864 G1868 A1869 U1872 A1873 A1874 U1877 U1878 A1882 A1883 G1884 G1885 G1886 A1887 A1891 A1892 A1893 G1894 G1895 U1896 A1897 A1898 C1902 C1903 A1909 A1917 G1918 C1919 A1936 A1937 A1938 G1939 A1940 A1944 U1950 A1953 U1954 G1955 U1956 G1957 G1958

A1962 G1973 A1974 U1975 U1976 U1977 A1978 U1979 A1980 A1984 A1985 A1986 G1990 A1991 C1992 A1993 A1994 C2000 C2001 G2002 A2003 G2004 C2005 C2006 U2010 G2015 C2016 U2017 U2021 G2022 U2030 C2036 U2037 U2038 A2039 C2043 A2044 A2045 U2055 G2056 C2057 C2058 A2060 A2067 C2068 U C

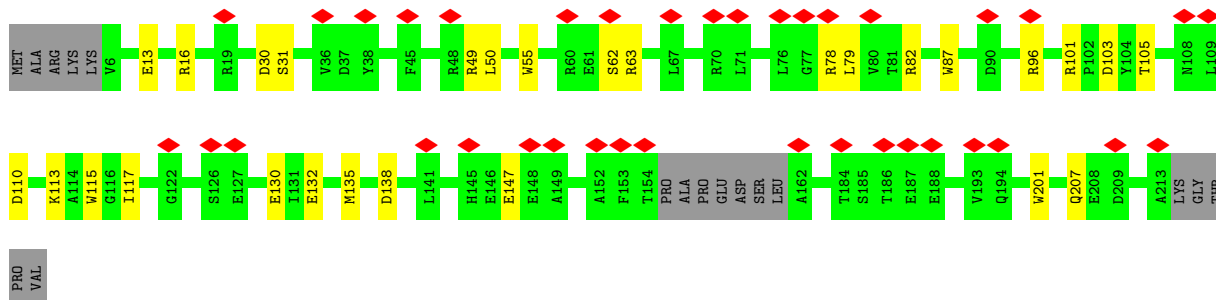
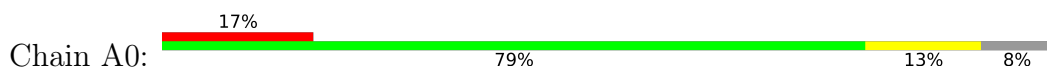
U A2072 A2073 C2079 A2080 A2091 C2092 U2093 G2094 U2095 U2096 U2099 C2100 A2103 C2111 G2112 G2113 U2118 U2119 C2123 A2124 C2125 U2126 A2135 U2138 U2139 G2145 A2146 G2147 A2148 U2149 U2150 A2151 A2152 U2159 A2160 C2166 A2167 U2168 A2169 C2176 U2177 A2178 A2179 A2180 A2181 G2182

C2183 C2187 A2188 A2191 A2192 A2195 A2196 G2197 A2198 A2199 A2200 C2212 A2213 A2214 C2218 C2219 C2220 C2221 C2222 C2223 C2224 C2225 C2226 C2227 C2228 C2229 C2230 C2231 C2232 C2233 C2234 C2235 C2236 C2237 C2238 C2239 C2240 C2241 C2242 C2243 C2244 C2245 C2246 C2247 C2248 C2249 A2250 A2251 C2261 C2262 C2263 U2266 C2283

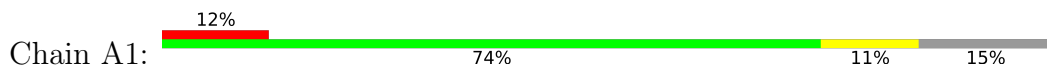
C2284 U2285 A2286 U2287 A2288 G2289 A2290 A2291 A2294 A2295 G2296 U2297 A2298 A2299 A2300 U2305 A2306 U2307 A2308 A2309 G2310 U2316 A2320 A2321 C2322 C2326 C2332 C2333 C2334 C2335 C2336 C2337 U2338 A2339 A2340 A2341 G2342 A2343 A2344 A2345 A2346 A2347 A2348 A2349 A2350 A2351 A2352 A2353 A2354 A2355 A2356 A2357 A2358 A2359 A2360 A2361 A2362 A2363 A2364 A2365 A2366 A2367 A2368 A2369 A2370 A2371 A2372 A2373 A2374 A2375 A2376 A2377 A2378 A2379 A2380

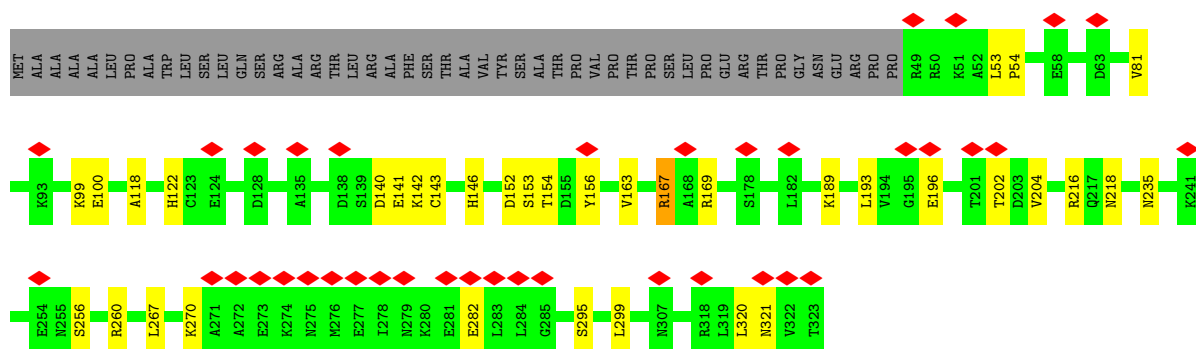


• Molecule 12: 28S ribosomal protein S34, mitochondrial

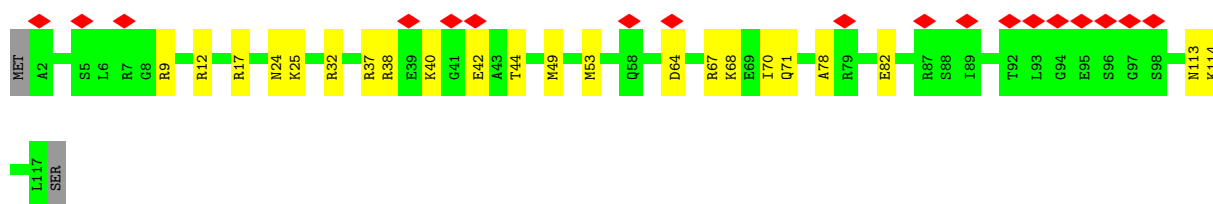
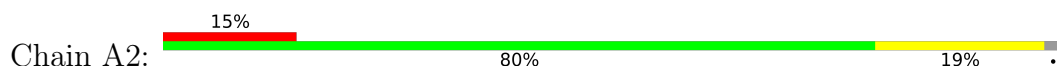


• Molecule 13: 28S ribosomal protein S35, mitochondrial

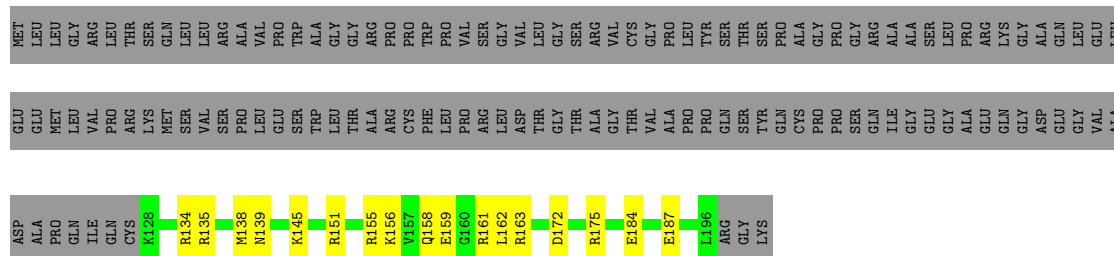




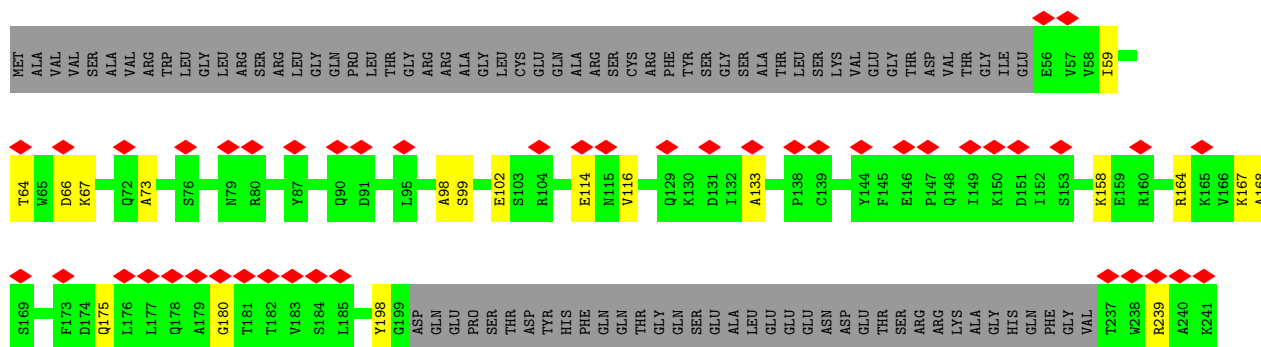
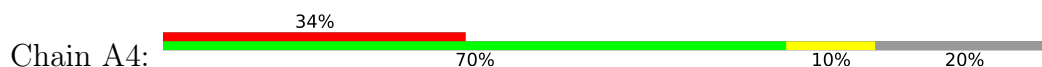
- Molecule 14: Coiled-coil-helix-coiled-coil-helix domain-containing protein 1

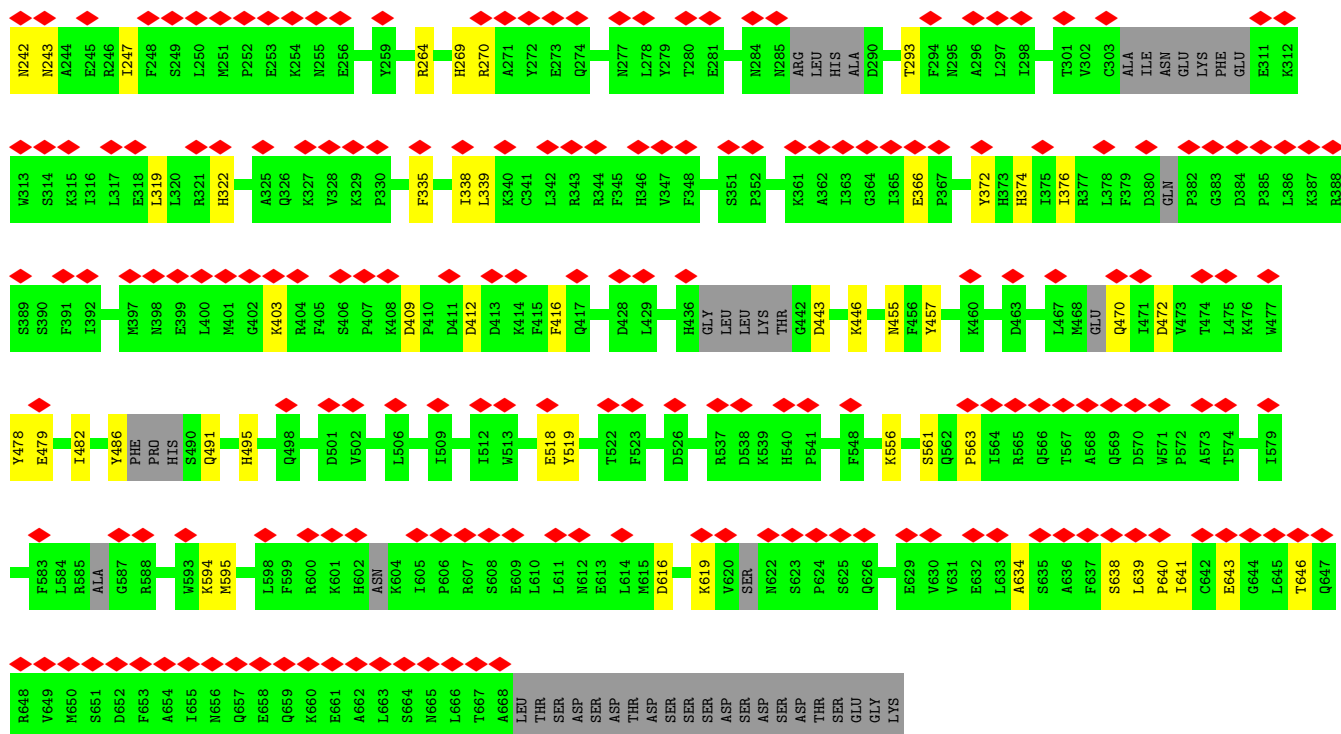


- Molecule 15: Aurora kinase A-interacting protein



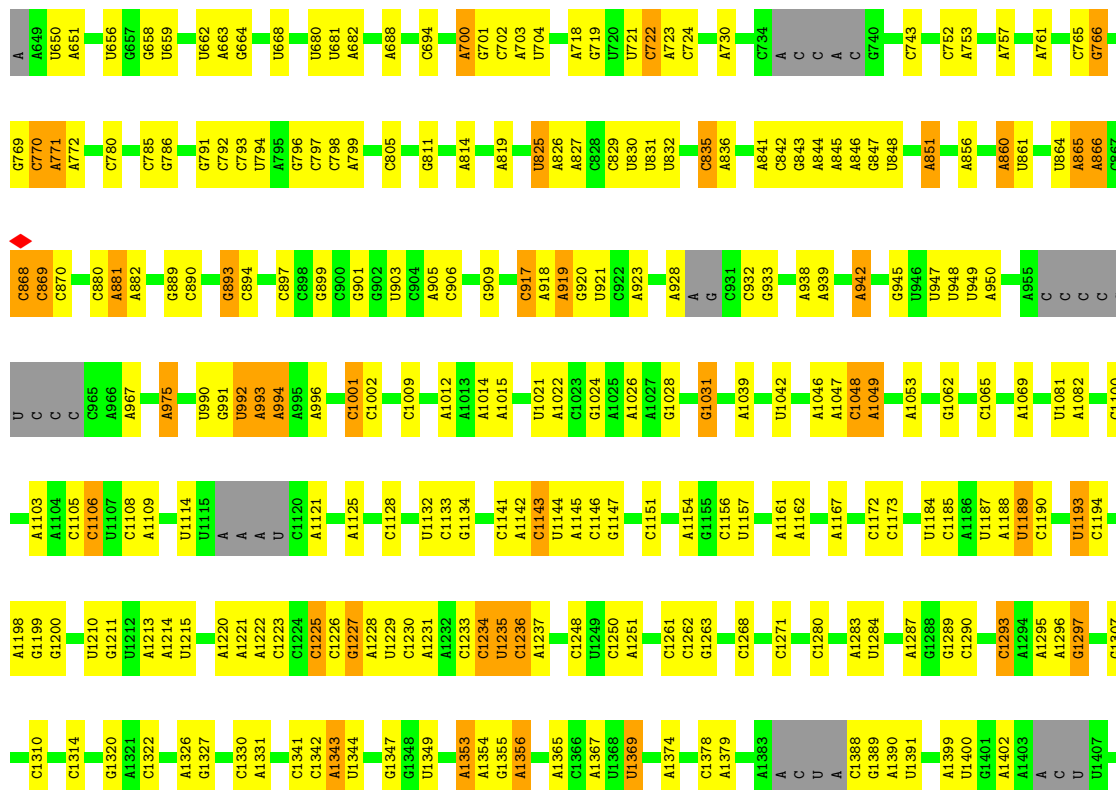
- Molecule 16: Pentatricopeptide repeat domain-containing protein 3, mitochondrial

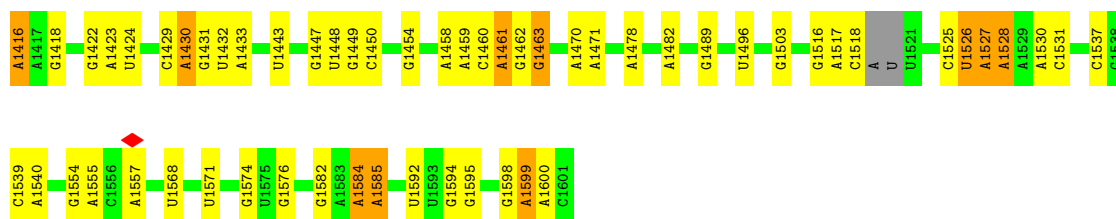




• Molecule 17: 12S mitochondrial rRNA

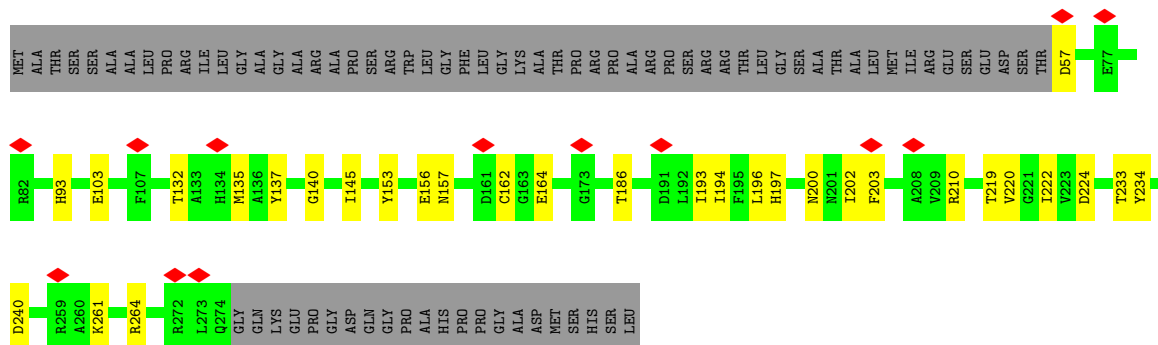
Chain AA: 64% 27% 5% •





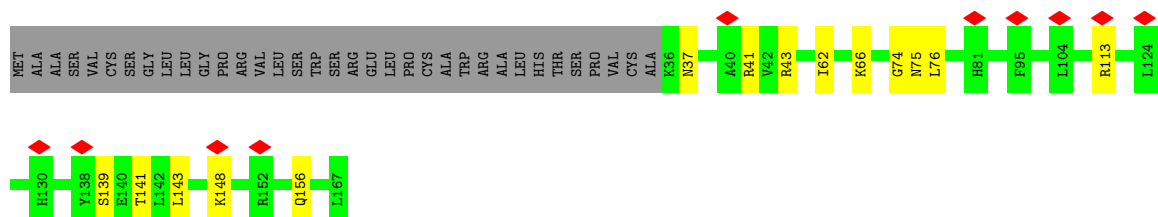
- Molecule 18: 28S ribosomal protein S2, mitochondrial

Chain AB: 63% 10% 26%



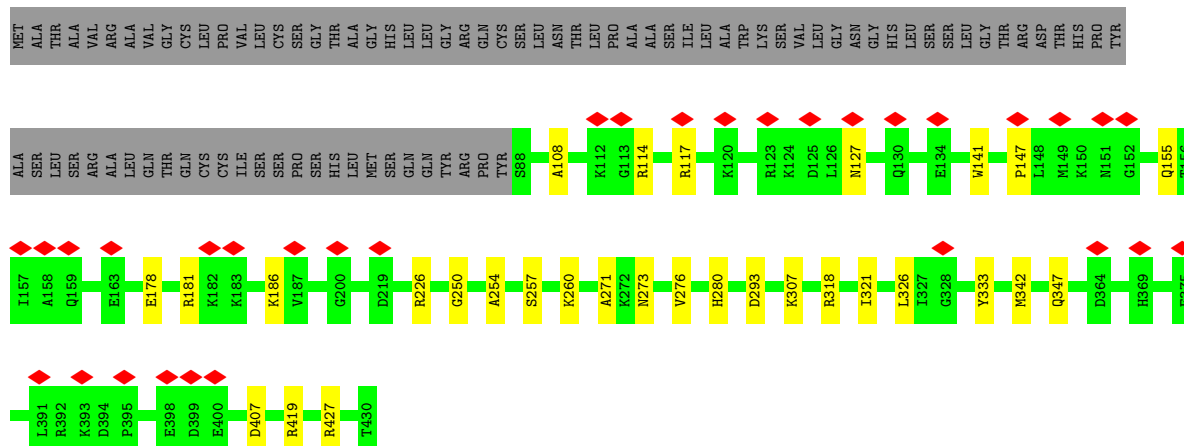
- Molecule 19: 28S ribosomal protein S24, mitochondrial

Chain AC: 6% 71% 8% 21%

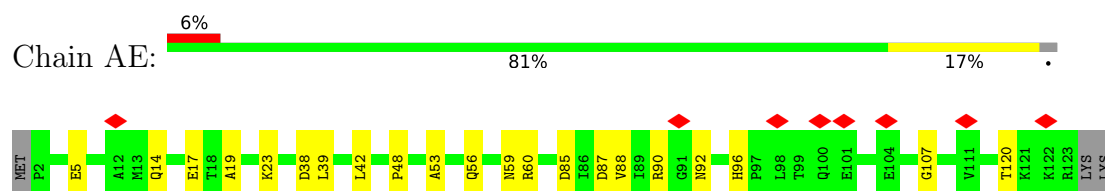


- Molecule 20: 28S ribosomal protein S5, mitochondrial

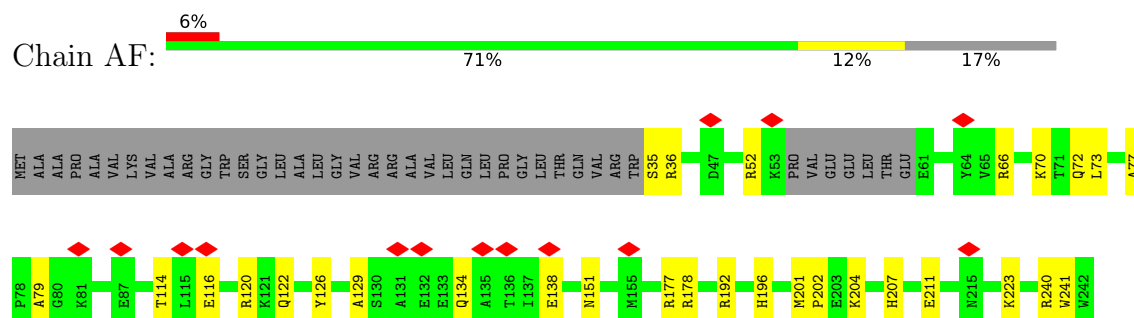
Chain AD: 7% 73% 7% 20%



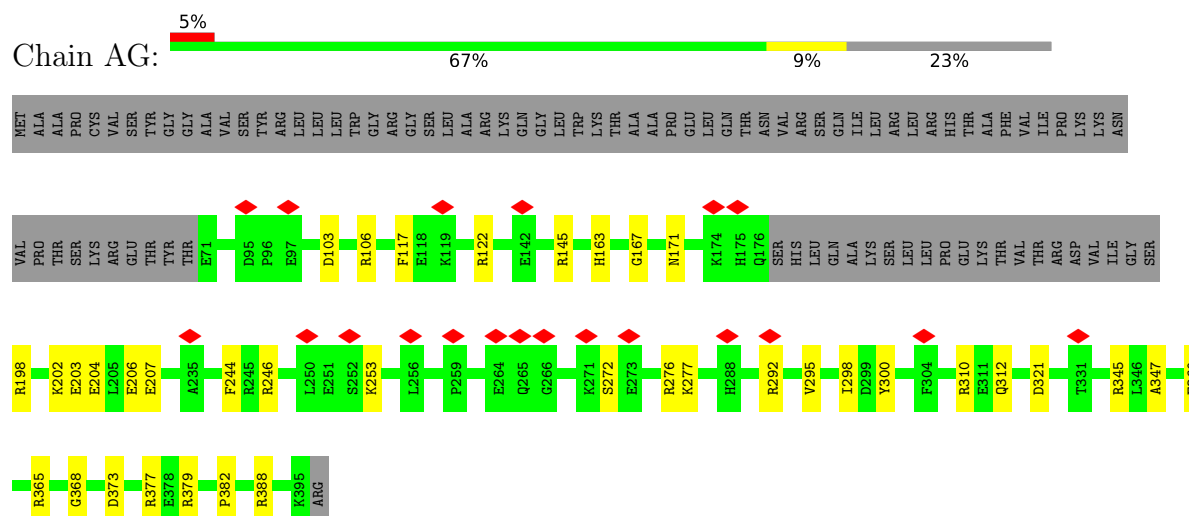
- Molecule 21: 28S ribosomal protein S6, mitochondrial



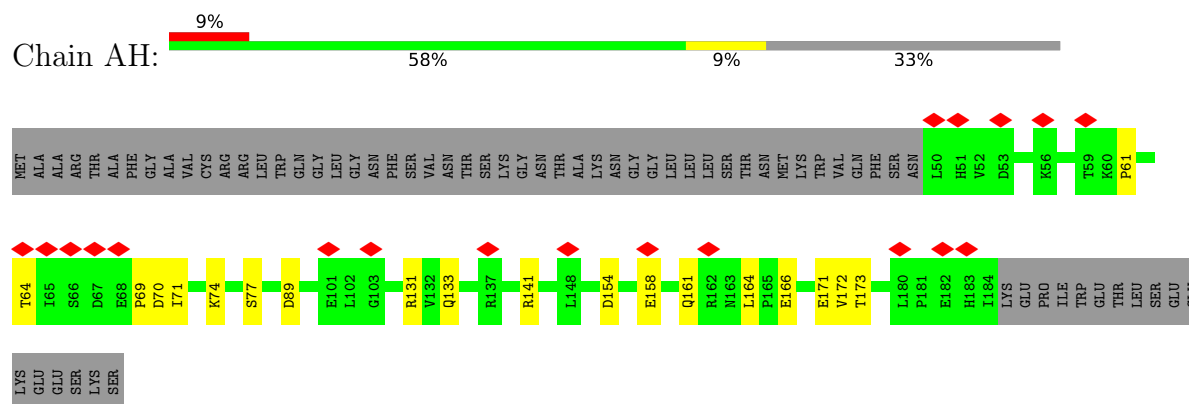
- Molecule 22: 28S ribosomal protein S7, mitochondrial



- Molecule 23: 28S ribosomal protein S9, mitochondrial

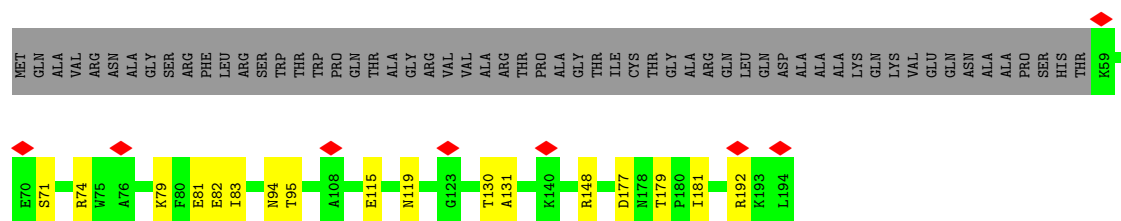


- Molecule 24: 28S ribosomal protein S10, mitochondrial



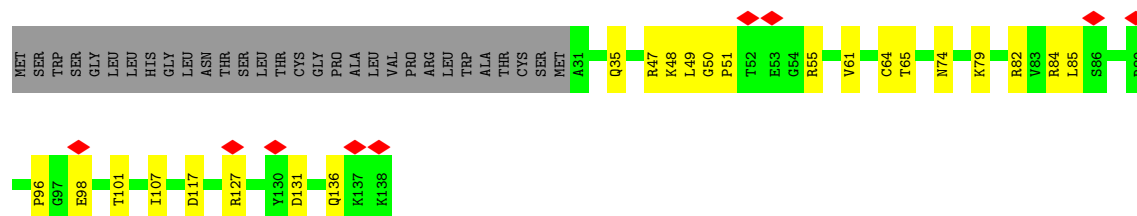
- Molecule 25: 28S ribosomal protein S11, mitochondrial

Chain AI: 



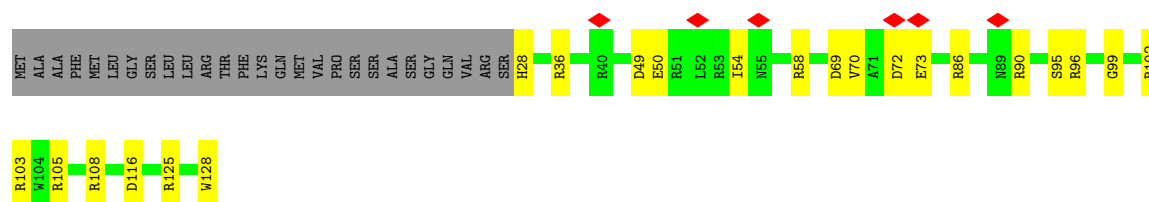
- Molecule 26: 28S ribosomal protein S12, mitochondrial

Chain AJ: 



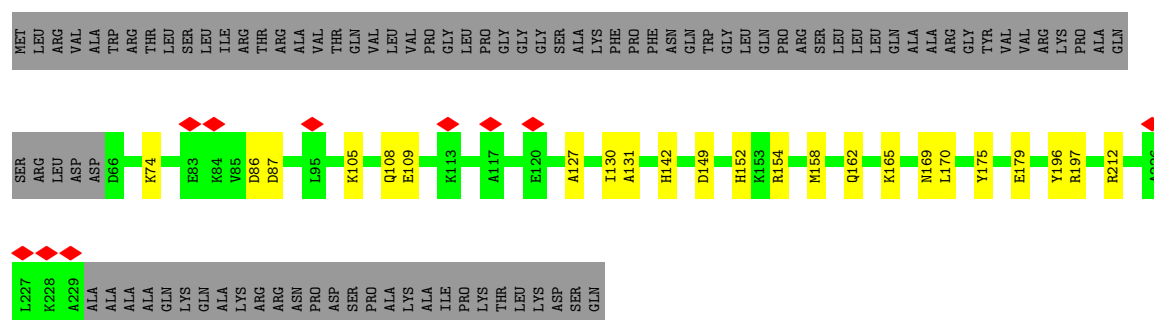
- Molecule 27: 28S ribosomal protein S14, mitochondrial

Chain AK: 




- Molecule 28: 28S ribosomal protein S15, mitochondrial

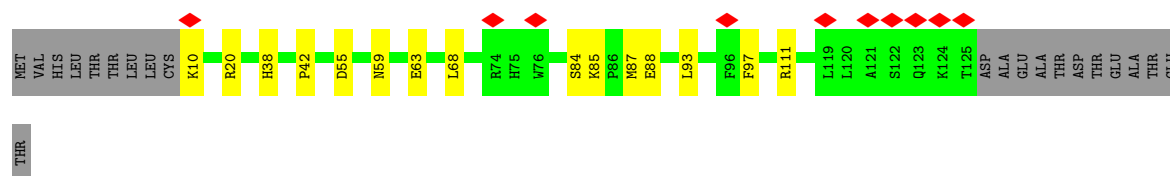
Chain AL: 



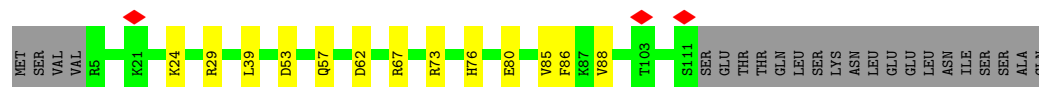
- Molecule 29: 28S ribosomal protein S16, mitochondrial

Chain AM: 

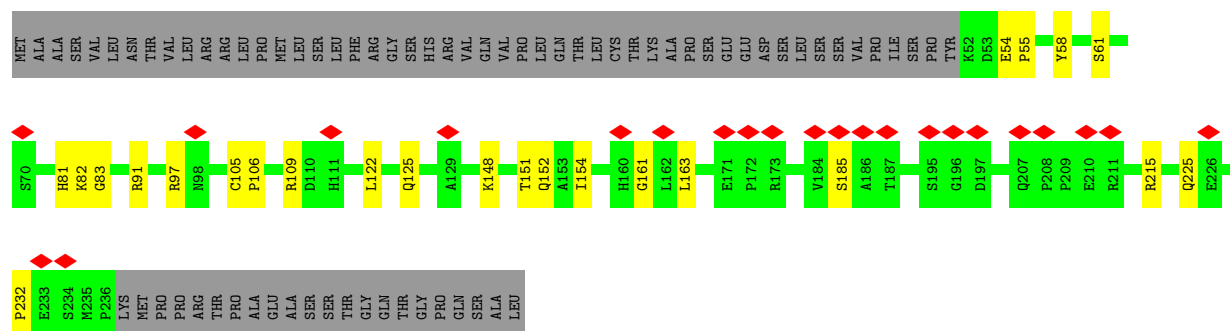




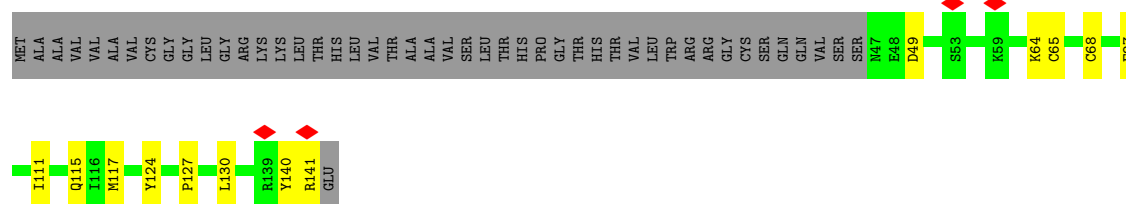
- Molecule 30: 28S ribosomal protein S17, mitochondrial



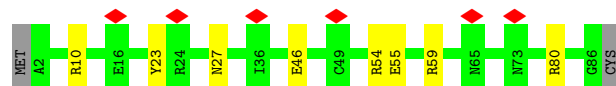
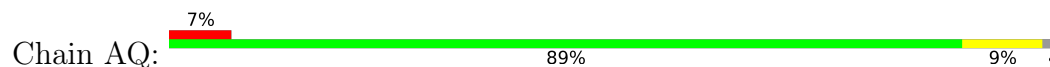
- Molecule 31: 28S ribosomal protein S18b, mitochondrial



- Molecule 32: 28S ribosomal protein S18c, mitochondrial

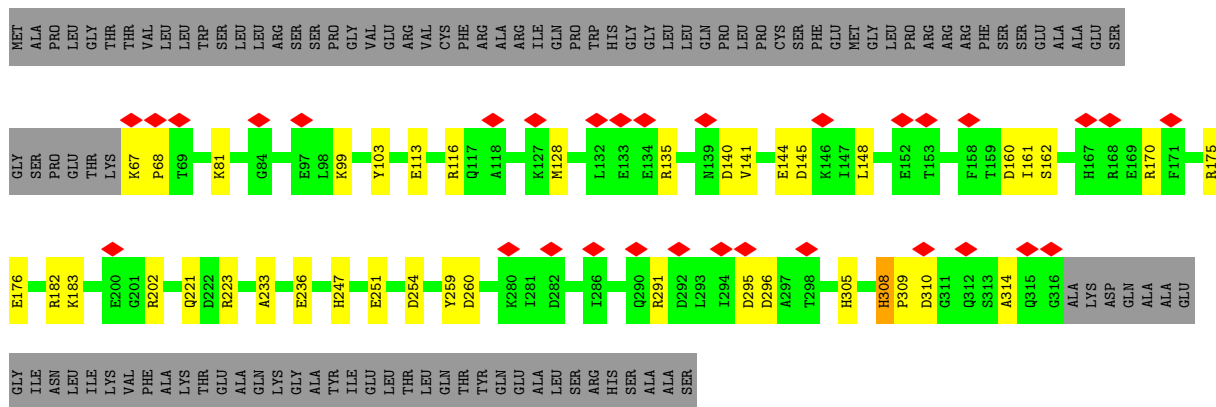


- Molecule 33: 28S ribosomal protein S21, mitochondrial

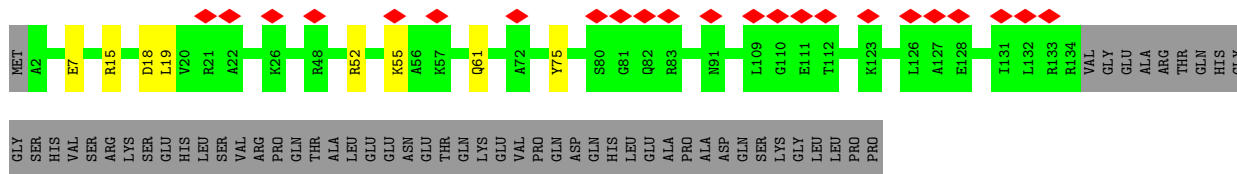


- Molecule 34: 28S ribosomal protein S22, mitochondrial

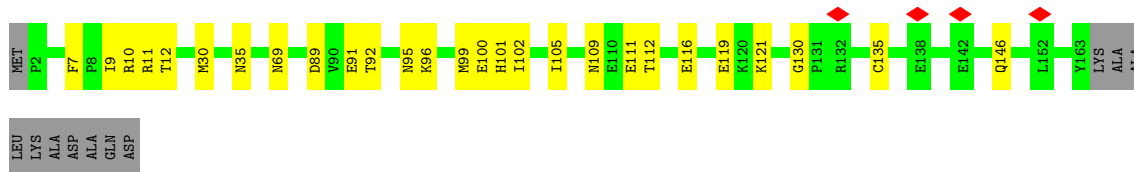
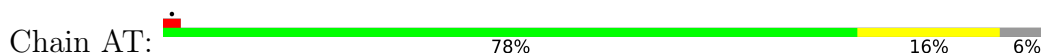




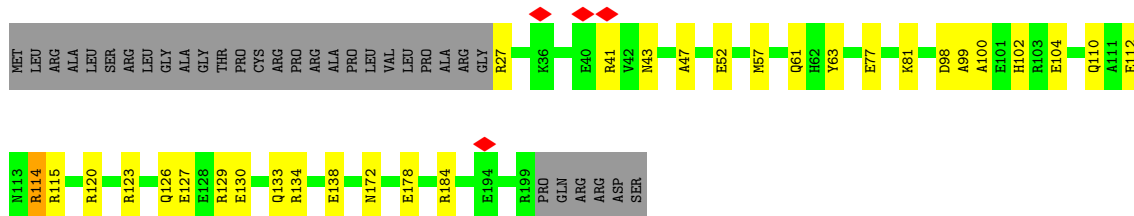
- Molecule 35: 28S ribosomal protein S23, mitochondrial



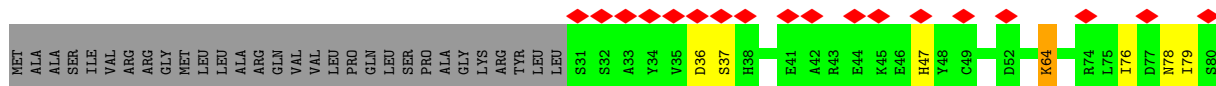
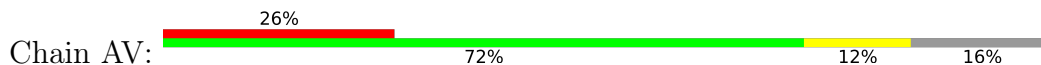
- Molecule 36: 28S ribosomal protein S25, mitochondrial



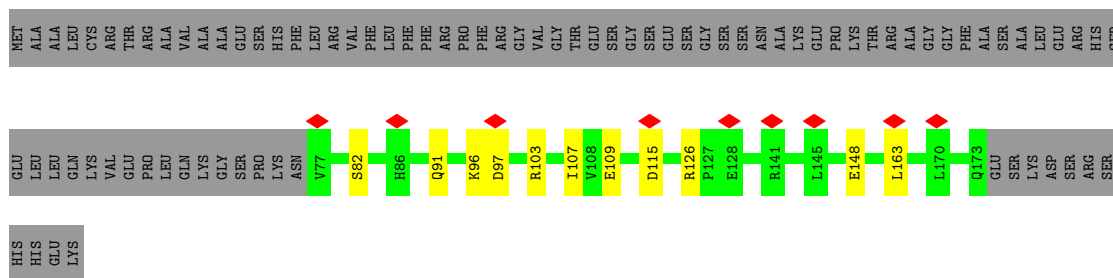
- Molecule 37: 28S ribosomal protein S26, mitochondrial



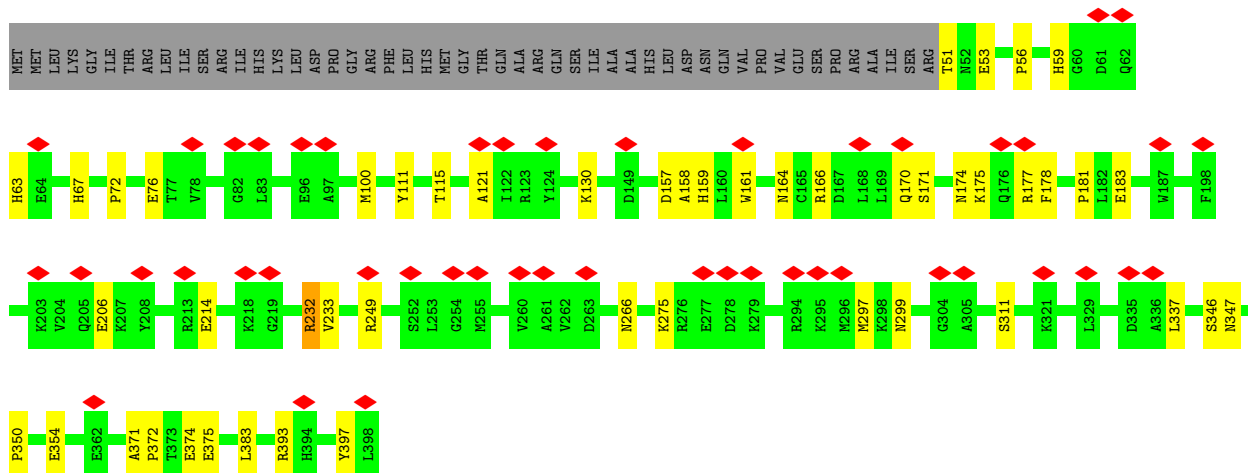
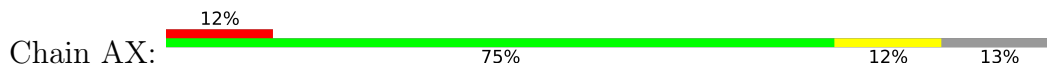
- Molecule 38: 28S ribosomal protein S27, mitochondrial



- Molecule 39: 28S ribosomal protein S28, mitochondrial



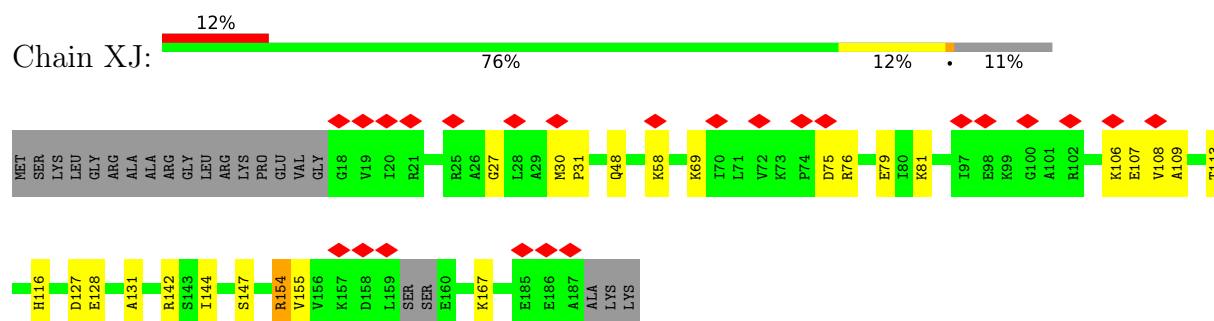
- Molecule 40: 28S ribosomal protein S29, mitochondrial



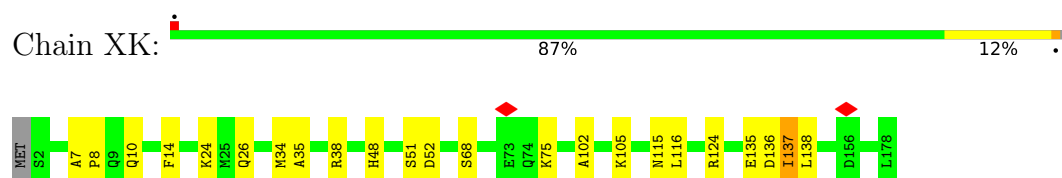
- Molecule 41: 28S ribosomal protein S31, mitochondrial



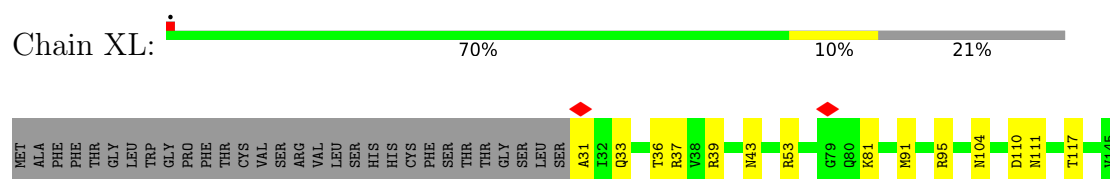
- Molecule 49: 39S ribosomal protein L11, mitochondrial



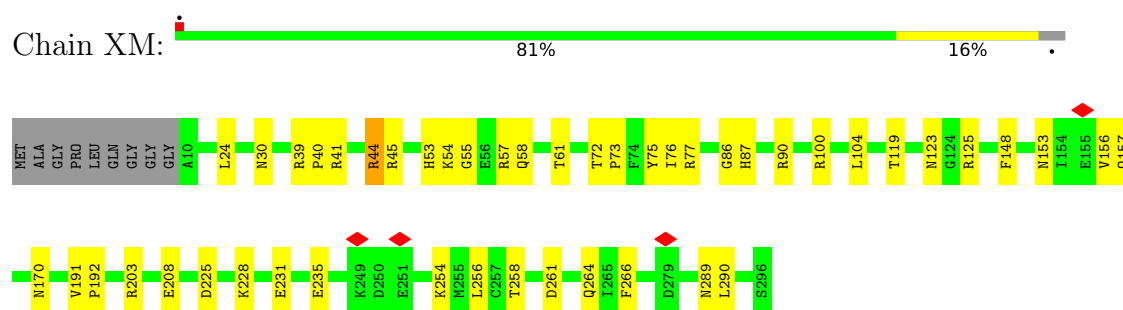
- Molecule 50: 39S ribosomal protein L13, mitochondrial



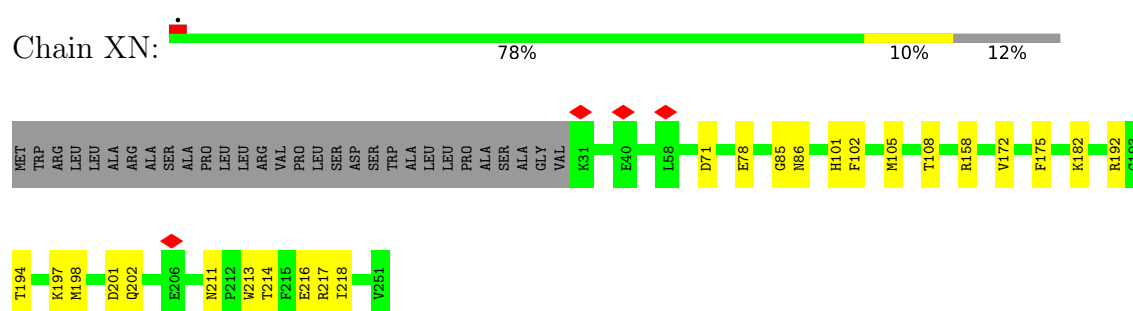
- Molecule 51: 39S ribosomal protein L14, mitochondrial



- Molecule 52: 39S ribosomal protein L15, mitochondrial

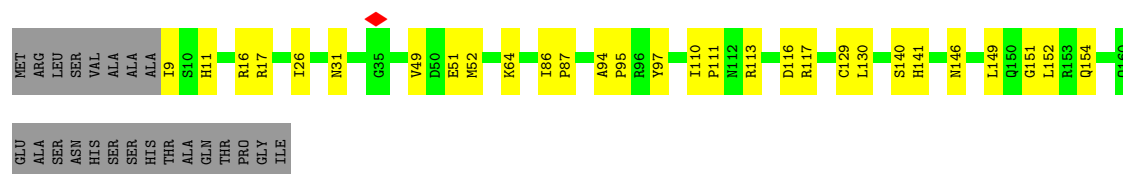


- Molecule 53: 39S ribosomal protein L16, mitochondrial




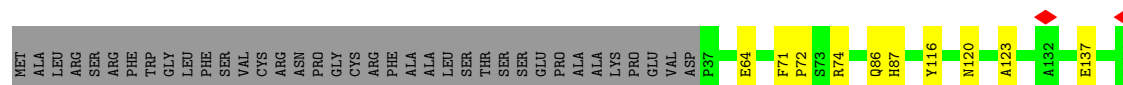
- Molecule 54: 39S ribosomal protein L17, mitochondrial

Chain XO: 




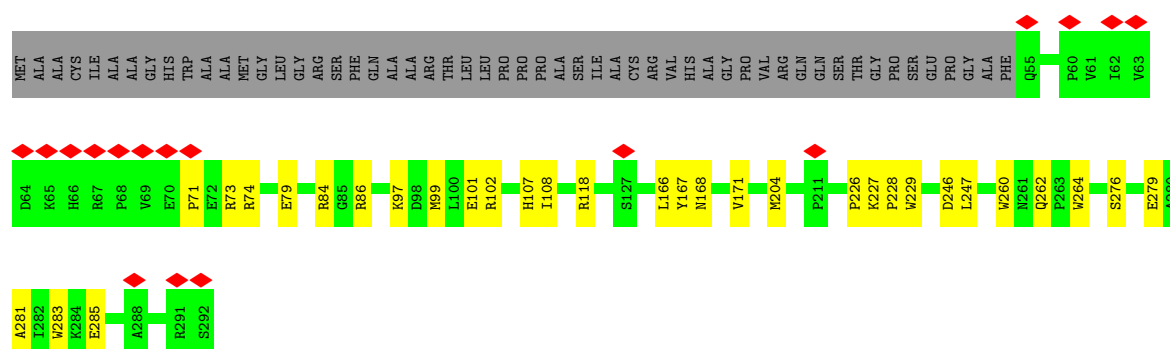
- Molecule 55: 39S ribosomal protein L18, mitochondrial

Chain XP: 




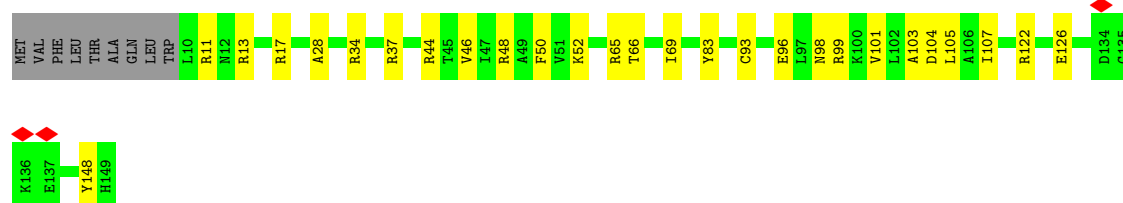
- Molecule 56: 39S ribosomal protein L19, mitochondrial

Chain XQ: 



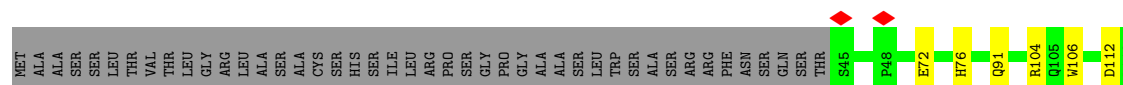
- Molecule 57: 39S ribosomal protein L20, mitochondrial

Chain XR: 



- Molecule 58: 39S ribosomal protein L21, mitochondrial

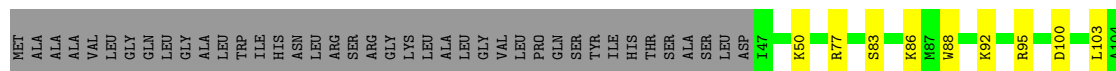
Chain XS: 





- Molecule 59: 39S ribosomal protein L22, mitochondrial

Chain XT: 68% 12% 19%



- Molecule 60: 39S ribosomal protein L23, mitochondrial

Chain XU: 78% 14% 8%



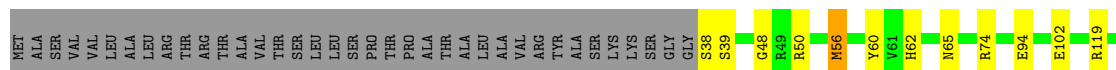
- Molecule 61: 39S ribosomal protein L24, mitochondrial

Chain XV: 79% 13% 6%



- Molecule 62: 39S ribosomal protein L27, mitochondrial

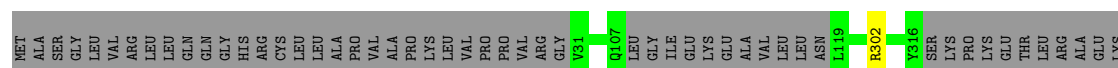
Chain XW: 66% 8% 25%



- Molecule 63: 39S ribosomal protein L28, mitochondrial

Chain XX: 84% 11% 5%





SER
ILE
THR
ALA
SER

- Molecule 69: 39S ribosomal protein L45, mitochondrial


Chain d: 

MET ALA ALA PRO ILE GLN PHE CYS LEU SER ARG PHE LEU GLY TRP PHE ARG GLN VAL LEU VAL THR GLN SER ALA ILE VAL PRO VAL MET ARG LYS THR LYS ARG PHE THR PRO ILE TYR PRO LYS PHE LYS THR LYS GLU LYS F63 H64 Q65 H66 A67

A70 G71 L72 V73 I74 P75 P76 E77 K78 Y95 G100 ASP ALA ARG ILE SER LEU LYS GLY LEU ILE ARG THR ARG MET LYS T115 R123 M202 M203 L277 L287 K288 P289 E290 E291 E292 TYR GLU GLU ALA GLN GLY GLU ALA LYS

PRO
GLN
LEU
ALA

- Molecule 70: 39S ribosomal protein L46, mitochondrial

Chain e: 

MET ALA ALA VAL ARG ARG THR LEU LEU VAL ALA GLY TRP ARG ARG PHE GLU ARG LEU TRP ALA GLY SER LEU SER SER ARG SER LEU ALA ALA PRO SER ASN GLY S43 R46 Y84 R90 D93 E94 R97 K100 K101 K102 A103 D104

LEU HIS ASP GLU GLU VAL ASP GLU GLN ASP LEU ILE LEU L116 Q130 A135 R136 I137 T138 E139 A140 K143 N144 D145 G166 D167 Q168 D169 V170 Q175 A176 E177 N199 A202 L205 G206 F217 PRO GLN ALA MET ARG THR GLU SER ASN L227 F233 G241 D242 F243

A246 G247 N248 K249 G250 H251 D262 K265 R273 R274 S277 D278 L279


- Molecule 71: 39S ribosomal protein L48, mitochondrial

Chain f: 

MET SER GLY THR LEU LYS VAL CYS ARG ASN ASN THR PHE LYS GLN ALA PHE SER LEU LEU ARG PHE ARG THR GLY GLU LYS PRO TYR VAL GLY GLY ILE LEU SER ILE SER ARG ARG PRO Y48 A65 E66 GLU PRO LYS LYS LYS GLY VAL

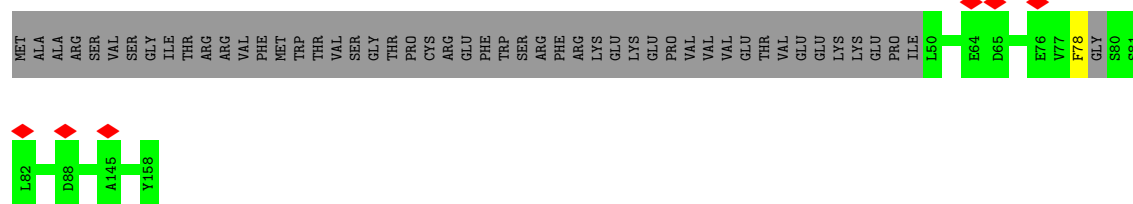
GLU VAL ARG ALA ILE MET PHE ARG ALA THR LEU LEU GLY T84 Q138 ASP GLN GLY SER LYS M144 L145 L146 R183 A200 R201 P202 A209 K210 L211 K212

- Molecule 72: 39S ribosomal protein L49, mitochondrial

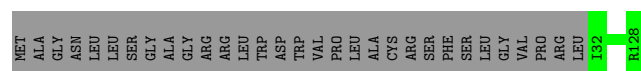
Chain g: 

MET ALA ALA THR MET PHE ARG ALA THR LEU LEU ARG GLY TRP ARG THR PHE VAL GLN ARG GLY CYS GLY LEU LEU ARG LEU LEU SER GLN THR GLN GLY PRO ASP Y35 P36 R37 G71 F166

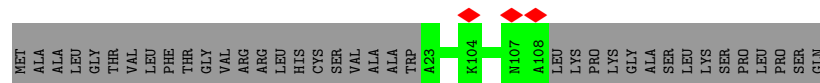
- Molecule 73: 39S ribosomal protein L50, mitochondrial



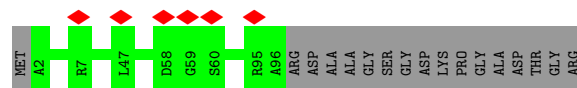
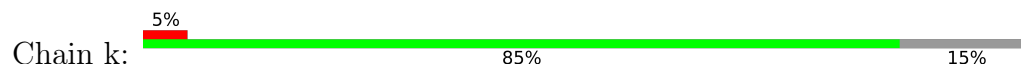
- Molecule 74: 39S ribosomal protein L51, mitochondrial



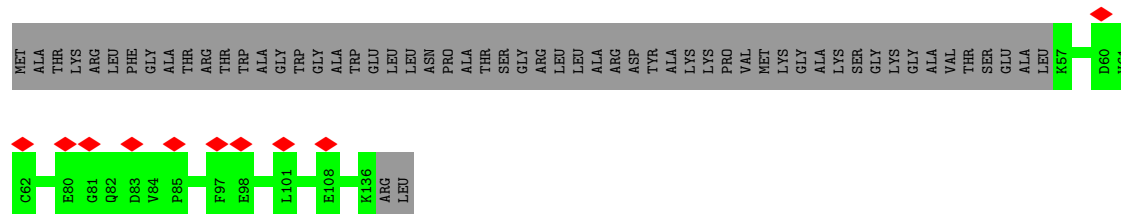
- Molecule 75: 39S ribosomal protein L52, mitochondrial



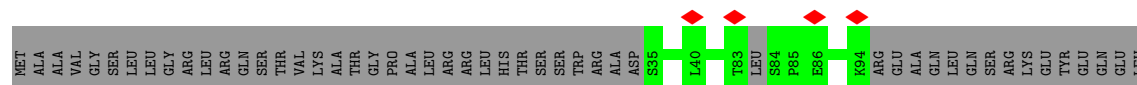
- Molecule 76: 39S ribosomal protein L53, mitochondrial



- Molecule 77: 39S ribosomal protein L54, mitochondrial



- Molecule 78: 39S ribosomal protein L55, mitochondrial



SER ASP
PHE ASP
LEU THR
HIS VAL
LEU VAL
GLU ARG
TYR ARG
GLN ARG
PHE THR
THR THR
ARG THR
LYS THR
LYS

- Molecule 79: Ribosomal protein 63, mitochondrial

Chain o:  92% 8%

MET PHE
LEU THR
ALA LEU
LEU VAL
TRP TRP
R9 S102


- Molecule 80: Peptidyl-tRNA hydrolase ICT1, mitochondrial

Chain p:  62% 38%

MET ALA
ALA THR
THR THR
CYS VAL
LEU VAL
ARG TRP
GLY TRP
SER THR
PRO THR
GLY THR
VAL THR
LEU THR
LEU THR
PRO THR
PRO THR
ALA THR
CYS THR
ARG THR
ARG THR
ALA THR
HIS THR
LYS THR
GLN THR
LYS THR
ASP THR
GLY THR
THR THR
E38 V61
PRO ASN
GLY THR
LYS THR
GLN THR
ALA THR
ASP THR
SER THR
D70 R75
S83
SER THR
GLY THR
PRO THR
GLY THR
GLN THR

ASN VAL
VAL ASN
LYS THR
V95 E109
Q163 THR
PRO THR
LYS THR
GLY THR
GLY THR
VAL THR
ASP THR
VAL THR
K174 Q190
I193
HIS THR
SER THR
ALA THR
VAL THR
LYS THR
SER THR
ARG THR
VAL THR
MET THR
ASP THR


- Molecule 81: Growth arrest and DNA damage-inducible proteins-interacting protein 1

Chain q:  14% 73% 26%

MET ALA
ALA THR
SER THR
VAL THR
ARG THR
GLN THR
ALA THR
ARG THR
SER THR
LEU THR
GLY THR
GLY THR
VAL THR
VAL THR
ALA THR
THR THR
LEU THR
LEU THR
ALA THR
PRO THR
GLY THR
SER THR
SER THR
GLY THR
Y25 R34
Q147
R152
R153
A154
R155
A158
E159
A160
Q161
E162
L163
L164
G165
Y166
D169
P170
R171
S172
A173
R174
F175
Q176
E177
L178
L179
Q180
D181
L182
E183

K184
K185
E186
R187
K188
LEU THR
LEU THR
GLY THR
GLY THR
LYS THR
GLY THR
GLN THR
LYS THR
ARG THR
ALA THR
LYS THR
LYS THR
GLY THR
LEU THR
ALA THR
ALA THR
ALA THR
ALA THR
ALA THR
ALA THR
VAL THR
ALA THR
GLN THR
ASP THR
PRO THR
ARG THR
ALA THR
ALA THR
SER THR
GLY THR
ALA THR
PRO THR
SER THR

- Molecule 82: 39S ribosomal protein S18a, mitochondrial

Chain r:  78% 22%

MET ALA
ALA THR
LEU THR
LYS THR
ALA THR
LEU THR
VAL THR
SER THR
GLY THR
CYS THR
GLY THR
GLY THR
LEU THR
LEU THR
ARG THR
GLY THR
LEU THR
LEU THR
ALA THR
GLY THR
PRO THR
ALA THR
ALA THR
THR THR
SER THR
THR THR
SER THR
ARG THR
LEU THR
PRO THR
ALA THR
ALA THR
ARG THR
GLY THR
F35 T41
GLN THR
E43 G44
P136
GLY THR
VAL THR
VAL THR
PRO THR
LYS THR
SER THR
LYS THR
PRO THR
Q146 H196

- Molecule 83: mRNA

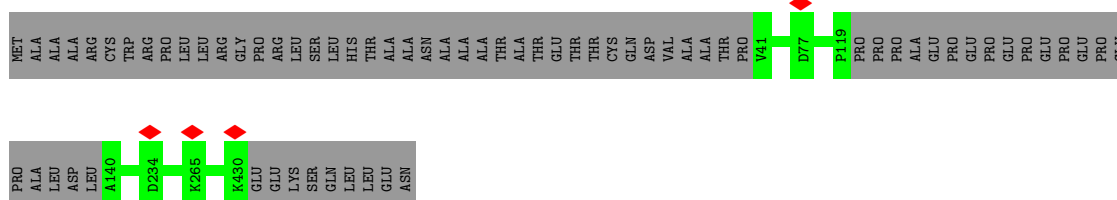
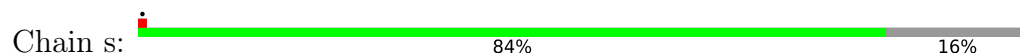
Chain r1:  100%

YSP46
YSP47
YSP48
YSP49

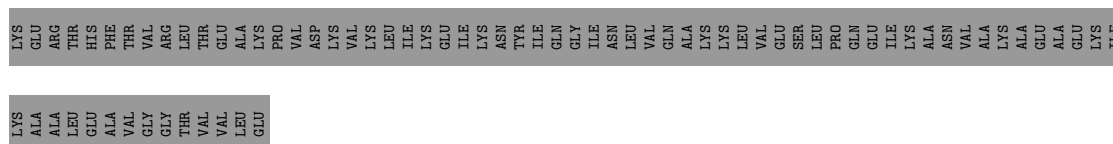
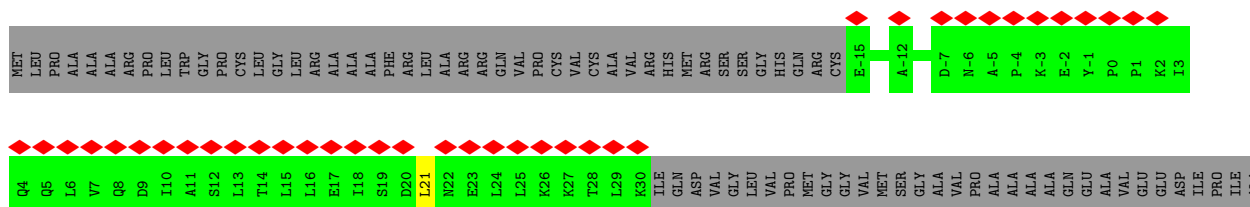
- Molecule 84: P-site tRNA

Chain r3:  5% 100%

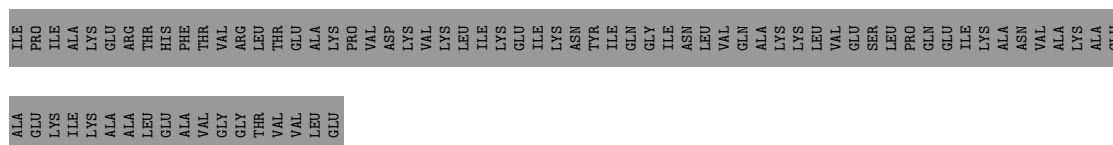
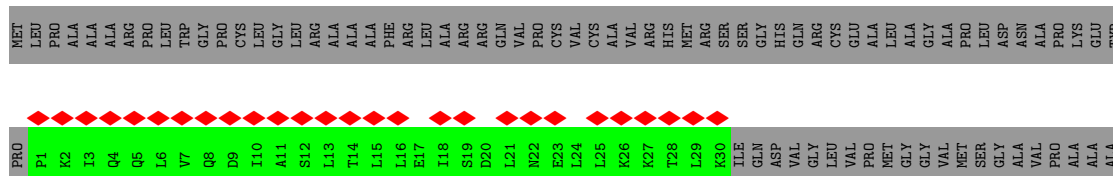
- Molecule 85: 39S ribosomal protein S30, mitochondrial



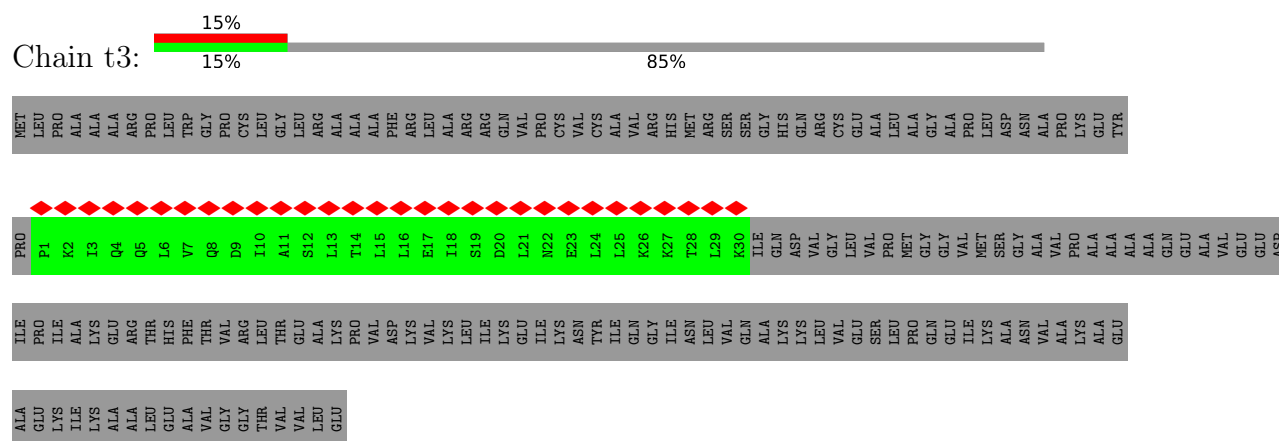
- Molecule 86: 39S ribosomal protein L12, mitochondrial



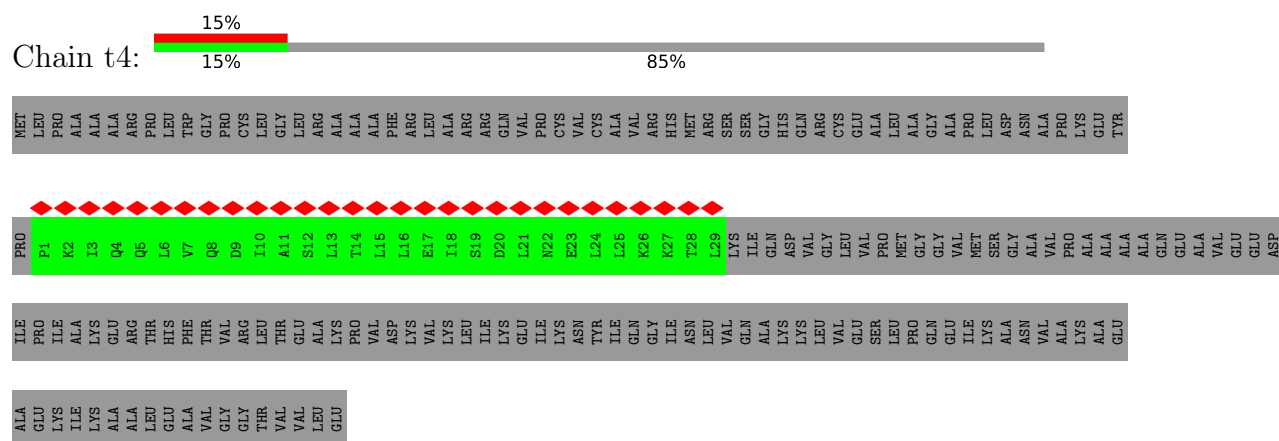
- Molecule 86: 39S ribosomal protein L12, mitochondrial



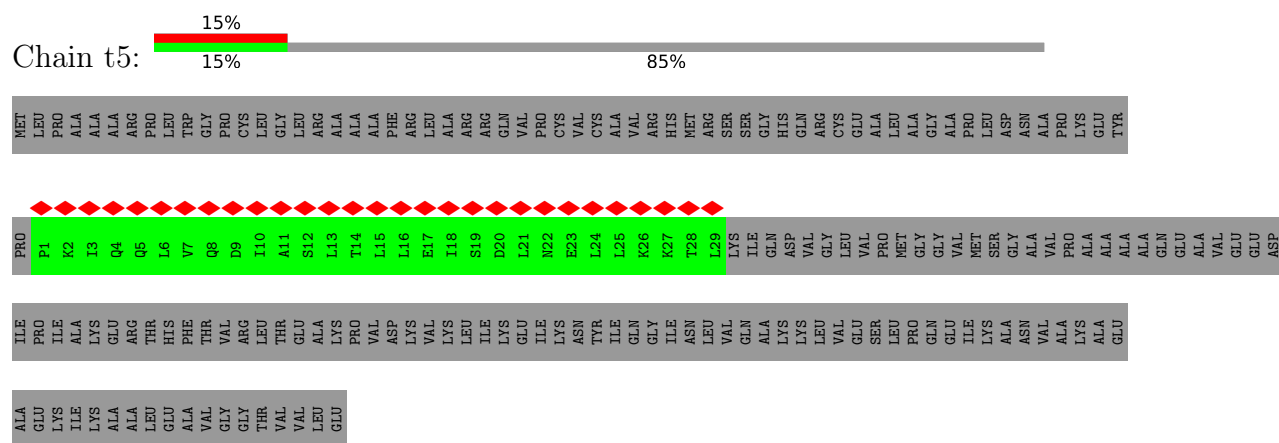
- Molecule 86: 39S ribosomal protein L12, mitochondrial



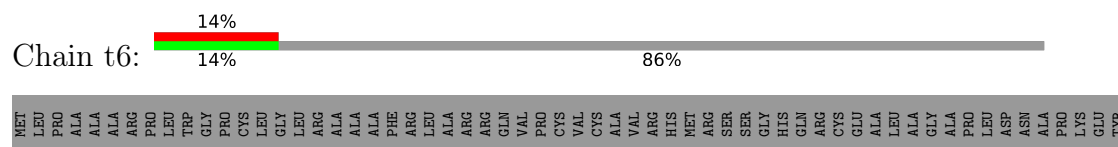
- Molecule 86: 39S ribosomal protein L12, mitochondrial

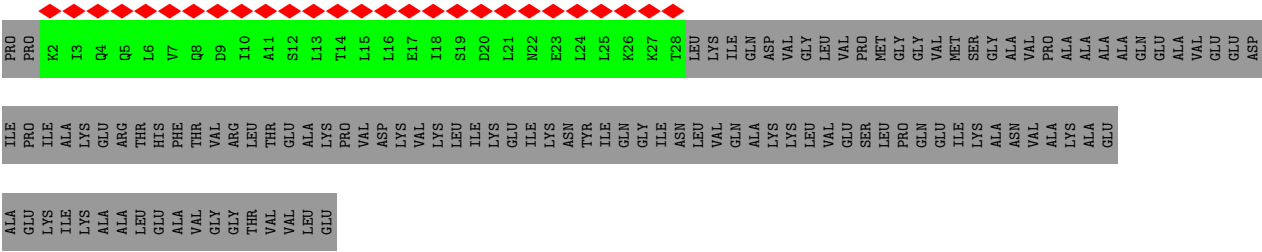


- Molecule 86: 39S ribosomal protein L12, mitochondrial



- Molecule 86: 39S ribosomal protein L12, mitochondrial





● Molecule 87: Quinupristin



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6692	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	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.239	Depositor
Minimum map value	-0.167	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	546.0, 546.0, 546.0	wwPDB
Map dimensions	520, 520, 520	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: DBB, 004, P5P, MHV, MHT, MG, GTP, MHU, ZN, Y5P, MHW, DOL

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	0	0.27	0/895	0.44	0/1201
2	1	0.26	0/444	0.45	0/591
3	2	0.32	0/382	0.42	0/507
4	3	0.32	0/852	0.46	0/1136
5	4	0.27	0/349	0.44	0/461
6	5	0.26	0/3298	0.43	0/4492
7	6	0.27	0/3042	0.42	0/4140
8	7	0.25	0/2420	0.41	0/3270
9	8	1.81	1/1199 (0.1%)	0.46	2/1612 (0.1%)
10	9	0.28	0/1024	0.43	0/1379
11	XA	0.35	0/35615	0.79	0/55429
12	A0	0.23	0/1727	0.42	0/2338
13	A1	0.24	0/2276	0.40	0/3079
14	A2	0.25	0/939	0.43	0/1256
15	A3	0.28	0/621	0.44	0/820
16	A4	0.25	0/4559	0.41	0/6149
17	AA	0.23	0/21952	0.76	1/34164 (0.0%)
18	AB	0.25	0/1819	0.41	0/2462
19	AC	0.25	0/1112	0.41	0/1505
20	AD	0.25	0/2768	0.43	0/3707
21	AE	0.25	0/989	0.44	0/1335
22	AF	0.24	0/1708	0.39	0/2291
23	AG	0.25	0/2559	0.41	0/3429
24	AH	0.25	0/1128	0.43	0/1529
25	AI	0.25	0/1031	0.42	0/1390
26	AJ	0.25	0/854	0.46	0/1148
27	AK	0.23	0/879	0.41	0/1182
28	AL	0.25	0/1406	0.40	0/1878
29	AM	0.25	0/941	0.41	0/1265
30	AN	0.25	0/864	0.44	0/1169
31	AO	0.24	0/1580	0.40	0/2150
32	AP	0.25	0/782	0.38	0/1050

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	AQ	0.24	0/746	0.43	0/993
34	AR	0.30	1/2103 (0.0%)	0.52	3/2842 (0.1%)
35	AS	0.25	0/1127	0.39	0/1518
36	AT	0.25	0/1361	0.42	0/1829
37	AU	0.24	0/1482	0.41	0/1987
38	AV	0.24	0/2925	0.40	0/3948
39	AW	0.25	0/778	0.45	0/1048
40	AX	0.25	0/2886	0.43	0/3909
41	AY	0.25	0/985	0.37	0/1329
42	AZ	0.25	0/748	0.39	0/1000
43	XB	0.20	0/1400	0.73	0/2168
44	XD	0.28	0/1879	0.46	0/2527
45	XE	0.29	0/2465	0.44	0/3344
46	XF	0.32	0/2071	0.49	0/2817
47	XH	0.26	0/798	0.44	0/1073
48	XI	0.26	0/1727	0.44	0/2340
49	XJ	0.24	0/1309	0.40	0/1764
50	XK	0.29	0/1495	0.42	0/2029
51	XL	0.27	0/904	0.44	0/1218
52	XM	0.31	0/2359	0.45	0/3185
53	XN	0.28	0/1825	0.45	0/2458
54	XO	0.26	0/1269	0.44	0/1708
55	XP	0.26	0/1190	0.42	0/1611
56	XQ	0.26	0/2026	0.44	0/2734
57	XR	0.33	0/1174	0.45	0/1572
58	XS	0.29	0/1311	0.47	0/1778
59	XT	0.31	0/1402	0.44	0/1886
60	XU	0.28	0/1200	0.43	0/1623
61	XV	0.26	0/1693	0.45	0/2297
62	XW	0.29	0/893	0.45	0/1204
63	XX	0.29	1/2090 (0.0%)	0.43	0/2825
64	XY	0.27	0/1571	0.43	0/2106
65	XZ	0.29	0/1003	0.44	0/1354
66	a	0.27	0/838	0.45	0/1138
67	b	0.29	0/1202	0.47	0/1626
68	c	0.26	0/2264	0.41	0/3059
69	d	0.25	0/1807	0.42	0/2450
70	e	1.42	6/1797 (0.3%)	0.43	0/2422
71	f	0.26	0/1169	0.42	0/1576
72	g	0.44	2/1134 (0.2%)	0.45	0/1547
73	h	0.25	0/905	0.43	0/1233
74	i	0.32	0/849	0.48	0/1135
75	j	0.27	0/703	0.41	0/947

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	k	0.24	0/743	0.45	0/1003
77	l	0.24	0/692	0.38	0/939
78	m	0.23	0/508	0.44	0/682
79	o	0.28	0/818	0.46	0/1097
80	p	0.23	0/1071	0.42	0/1433
81	q	0.26	0/1413	0.42	0/1906
82	r	0.26	0/1282	0.41	0/1734
85	s	0.26	0/3114	0.44	0/4225
86	t1	0.26	0/366	0.39	0/497
86	t2	0.22	0/238	0.38	0/319
86	t3	0.22	0/238	0.37	0/319
86	t4	0.22	0/229	0.37	0/308
86	t5	0.23	0/229	0.37	0/308
86	t6	0.24	0/213	0.40	0/286
87	A	0.55	0/13	0.66	0/15
All	All	0.35	11/176044 (0.0%)	0.58	6/249742 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
44	XD	0	1
48	XI	0	1
50	XK	0	1
70	e	0	1
71	f	0	1
72	g	0	1
73	h	0	1
87	A	2	3
All	All	2	10

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	8	99	ARG	CG-CD	61.84	3.06	1.51
70	e	84	TYR	CD2-CE2	31.66	1.86	1.39
70	e	84	TYR	CD1-CE1	31.19	1.86	1.39
70	e	84	TYR	CE2-CZ	21.63	1.66	1.38
70	e	84	TYR	CE1-CZ	21.08	1.66	1.38
70	e	84	TYR	CG-CD1	18.93	1.63	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
70	e	84	TYR	CG-CD2	17.09	1.61	1.39
72	g	37	ARG	C-N	-9.83	1.11	1.34
34	AR	308	HIS	C-N	6.96	1.47	1.34
72	g	36	PRO	N-CD	5.84	1.56	1.47
63	XX	149	PRO	N-CD	5.16	1.55	1.47

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	AR	309	PRO	O-C-N	11.63	141.32	122.70
34	AR	309	PRO	CA-C-N	-8.78	97.89	117.20
9	8	99	ARG	CG-CD-NE	5.94	124.27	111.80
34	AR	309	PRO	C-N-CA	-5.91	106.92	121.70
9	8	99	ARG	CB-CG-CD	5.59	126.12	111.60
17	AA	765	C	C2-N1-C1'	5.32	124.66	118.80

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
87	A	2	THR	CB
87	A	4	PRO	CA

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
87	A	3	DBB	Peptide
87	A	4	PRO	Peptide
87	A	5	MHU	Peptide
44	XD	206	TYR	Peptide
48	XI	197	LEU	Peptide
50	XK	137	ILE	Peptide
70	e	265	LYS	Peptide
71	f	138	GLN	Peptide
72	g	37	ARG	Mainchain
73	h	78	PHE	Peptide

5.2 Too-close contacts

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

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	880	903	903	13	0
2	1	439	480	480	7	0
3	2	376	406	406	7	0
4	3	831	883	883	16	0
5	4	341	362	361	3	0
6	5	3204	3200	3200	35	0
7	6	2947	2839	2841	37	0
8	7	2365	2373	2372	23	0
9	8	1175	1202	1202	8	0
10	9	996	987	987	12	0
11	XA	31833	16160	16167	297	0
12	A0	1684	1685	1685	17	0
13	A1	2230	2261	2261	26	0
14	A2	925	964	964	14	0
15	A3	610	682	682	16	0
16	A4	4470	4485	4486	43	0
17	AA	19628	9964	9971	163	0
18	AB	1776	1769	1769	21	0
19	AC	1082	1088	1088	12	0
20	AD	2716	2785	2785	21	0
21	AE	972	1001	1001	14	0
22	AF	1668	1715	1716	24	0
23	AG	2505	2491	2490	29	0
24	AH	1105	1136	1136	15	0
25	AI	1011	1052	1052	11	0
26	AJ	838	887	887	20	0
27	AK	861	885	885	17	0
28	AL	1382	1472	1472	16	0
29	AM	920	951	951	13	0
30	AN	846	908	908	10	0
31	AO	1528	1490	1490	18	0
32	AP	765	796	796	9	0
33	AQ	734	749	749	6	0
34	AR	2060	2074	2074	30	0
35	AS	1100	1103	1103	7	0
36	AT	1330	1343	1343	16	0
37	AU	1461	1471	1471	23	0
38	AV	2867	2862	2862	29	0
39	AW	766	785	785	7	0
40	AX	2814	2805	2804	28	0
41	AY	956	912	911	13	0
42	AZ	731	734	734	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	XB	1255	635	640	12	0
44	XD	1842	1896	1896	25	0
45	XE	2396	2402	2402	21	0
46	XF	2013	2045	2044	32	0
47	XH	784	832	832	5	0
48	XI	1691	1783	1783	12	0
49	XJ	1291	1367	1364	16	0
50	XK	1451	1448	1448	16	0
51	XL	889	941	941	10	0
52	XM	2305	2378	2378	32	0
53	XN	1778	1808	1808	15	0
54	XO	1245	1283	1283	20	0
55	XP	1164	1162	1162	9	0
56	XQ	1978	2022	2022	21	0
57	XR	1153	1214	1214	23	0
58	XS	1284	1354	1354	14	0
59	XT	1368	1410	1410	18	0
60	XU	1171	1164	1164	15	0
61	XV	1648	1656	1654	26	0
62	XW	871	898	898	9	0
63	XX	2035	2054	2054	19	0
64	XY	1534	1575	1575	29	0
65	XZ	978	1030	1030	9	0
66	a	813	777	777	0	0
67	b	1178	1180	1180	0	0
68	c	2217	2220	2220	0	0
69	d	1758	1743	1742	0	0
70	e	1762	1767	1767	0	0
71	f	1149	1165	1165	0	0
72	g	1097	1086	1084	0	0
73	h	882	866	867	0	0
74	i	827	857	857	0	0
75	j	689	678	678	0	0
76	k	732	745	745	0	0
77	l	673	654	653	0	0
78	m	500	525	525	0	0
79	o	797	804	804	0	0
80	p	1058	1083	1083	0	0
81	q	1379	1358	1359	0	0
82	r	1247	1267	1267	0	0
83	r1	72	0	49	0	0
84	r3	1459	0	829	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
85	s	3036	3022	3022	0	0
86	t1	354	379	374	0	0
86	t2	238	268	270	0	0
86	t3	238	268	270	0	0
86	t4	229	255	257	0	0
86	t5	229	255	257	0	0
86	t6	214	236	236	0	0
87	A	73	67	64	4	0
88	0	1	0	0	0	0
88	4	1	0	0	0	0
88	AB	1	0	0	0	0
88	AO	1	0	0	0	0
88	AP	1	0	0	0	0
88	AT	1	0	0	0	0
88	r	1	0	0	0	0
89	9	1	0	0	0	0
89	A2	1	0	0	0	0
89	AA	45	0	0	0	0
89	XA	142	0	0	0	0
89	XD	1	0	0	0	0
89	XE	1	0	0	0	0
89	XM	2	0	0	0	0
89	XW	1	0	0	0	0
89	g	1	0	0	0	0
90	XA	48	50	50	4	0
91	AX	32	10	12	1	0
All	All	169034	143042	143932	1266	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (1266) 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)
63:XX:144:TYR:O	63:XX:148:THR:HG23	1.56	1.05
4:3:104:ARG:NH1	4:3:160:LYS:O	2.03	0.90
11:XA:2517:U:OP1	44:XD:287:ARG:NH2	2.04	0.90
23:AG:276:ARG:NH1	23:AG:373:ASP:OD2	2.04	0.90
45:XE:216:GLN:NE2	45:XE:261:MET:SD	2.45	0.90
51:XL:31:ALA:N	51:XL:91:MET:SD	2.46	0.89
29:AM:93:LEU:O	34:AR:175:ARG:NH2	2.06	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:XA:2954:C:O2	53:XN:182:LYS:NZ	2.05	0.88
14:A2:38:ARG:NH2	17:AA:1184:U:OP1	2.06	0.88
11:XA:3063:G:O2'	11:XA:3066:C:OP2	1.92	0.87
11:XA:2458:A:OP2	54:XO:9:ILE:N	2.06	0.87
11:XA:2145:G:OP1	58:XS:169:ARG:NH2	2.07	0.87
11:XA:1777:A:N6	11:XA:1780:U:OP2	2.09	0.86
1:O:95:ARG:NH1	11:XA:1821:A:OP2	2.08	0.86
11:XA:1723:A:N6	11:XA:1726:C:OP2	2.08	0.86
34:AR:305:HIS:HD2	34:AR:314:ALA:HB2	1.40	0.85
14:A2:44:THR:O	22:AF:240:ARG:NH2	2.08	0.85
25:AI:71:SER:O	25:AI:74:ARG:NH1	2.10	0.85
13:A1:154:THR:OG1	24:AH:172:VAL:O	1.93	0.85
23:AG:198:ARG:N	23:AG:246:ARG:O	2.10	0.85
60:XU:16:GLN:NE2	60:XU:17:LEU:O	2.09	0.85
17:AA:701:G:N2	17:AA:841:A:O2'	2.10	0.84
22:AF:72:GLN:NE2	22:AF:73:LEU:O	2.11	0.84
11:XA:2822:C:O2'	11:XA:2915:C:OP2	1.95	0.83
11:XA:1689:C:O2	64:XY:213:ARG:NH2	2.11	0.83
12:A0:49:ARG:NH2	37:AU:41:ARG:O	2.12	0.83
17:AA:826:A:OP1	26:AJ:55:ARG:NH1	2.11	0.83
17:AA:1530:A:OP1	38:AV:64:LYS:NZ	2.12	0.82
11:XA:1828:A:N6	11:XA:2683:C:O2	2.12	0.82
36:AT:89:ASP:OD2	37:AU:120:ARG:NH2	2.12	0.82
29:AM:55:ASP:OD2	36:AT:146:GLN:NE2	2.13	0.82
44:XD:64:VAL:O	44:XD:80:ARG:NH2	2.12	0.82
63:XX:163:ARG:NH2	63:XX:205:GLY:O	2.13	0.82
7:6:27:ARG:N	11:XA:2832:A:N1	2.27	0.81
11:XA:2191:A:N6	11:XA:2198:A:OP2	2.12	0.81
37:AU:126:GLN:OE1	37:AU:129:ARG:NH2	2.13	0.81
11:XA:2167:A:N6	11:XA:2212:C:OP2	2.13	0.81
14:A2:17:ARG:NH2	17:AA:1022:A:OP2	2.13	0.81
22:AF:79:ALA:O	23:AG:312:GLN:NE2	2.12	0.81
11:XA:1696:C:OP2	64:XY:180:LYS:NZ	2.12	0.81
33:AQ:55:GLU:OE2	33:AQ:59:ARG:NE	2.13	0.81
11:XA:2537:G:O2'	11:XA:2634:U:OP2	1.98	0.81
11:XA:1689:C:OP2	63:XX:5:LYS:NZ	2.14	0.81
17:AA:752:C:O2'	17:AA:793:C:N4	2.14	0.80
20:AD:307:LYS:NZ	34:AR:103:TYR:OH	2.14	0.80
46:XF:167:MET:SD	46:XF:279:ARG:NH1	2.54	0.80
34:AR:176:GLU:OE2	34:AR:182:ARG:NE	2.15	0.80
11:XA:1962:A:OP2	11:XA:2501:C:N4	2.13	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:AB:103:GLU:OE2	35:AS:52:ARG:NH2	2.14	0.80
44:XD:128:GLN:NE2	44:XD:129:VAL:O	2.15	0.80
26:AJ:84:ARG:NH1	26:AJ:85:LEU:O	2.14	0.80
5:4:84:ARG:NE	11:XA:3188:U:OP2	2.15	0.79
40:AX:53:GLU:N	40:AX:67:HIS:O	2.16	0.79
11:XA:2724:G:OP1	46:XF:131:LYS:NZ	2.16	0.79
17:AA:825:U:N3	17:AA:827:A:OP1	2.14	0.79
1:0:93:ARG:NH2	11:XA:2310:G:OP2	2.16	0.79
11:XA:2166:C:O2	11:XA:2214:A:N6	2.15	0.79
17:AA:860:A:N7	17:AA:919:A:O2'	2.16	0.78
17:AA:868:C:OP2	17:AA:870:C:N4	2.17	0.78
34:AR:305:HIS:HD2	34:AR:314:ALA:CB	1.97	0.78
56:XQ:71:PRO:O	56:XQ:73:ARG:NH1	2.16	0.78
22:AF:151:ASN:O	22:AF:223:LYS:NZ	2.17	0.77
4:3:169:ARG:NH2	11:XA:1892:A:OP1	2.17	0.77
63:XX:36:ARG:NH1	63:XX:37:THR:O	2.17	0.77
60:XU:11:ARG:NH2	61:XV:212:LYS:O	2.17	0.77
23:AG:103:ASP:OD1	23:AG:106:ARG:NH2	2.16	0.77
17:AA:906:C:OP1	20:AD:117:ARG:NE	2.18	0.77
57:XR:122:ARG:NH2	57:XR:126:GLU:OE2	2.18	0.77
11:XA:2093:U:O2	11:XA:2266:U:O2'	2.02	0.76
22:AF:126:TYR:O	22:AF:134:GLN:NE2	2.17	0.76
3:2:85:LYS:NZ	11:XA:1792:G:OP2	2.17	0.76
31:AO:185:SER:O	34:AR:183:LYS:NZ	2.18	0.76
11:XA:2351:U:O2	11:XA:2362:A:N6	2.19	0.76
12:A0:78:ARG:NH1	38:AV:171:GLU:OE1	2.19	0.76
64:XY:151:ASP:OD1	64:XY:154:ARG:NH2	2.17	0.76
53:XN:201:ASP:OD1	53:XN:202:GLN:N	2.18	0.76
22:AF:52:ARG:NH2	23:AG:360:GLU:OE1	2.18	0.76
38:AV:156:ASN:ND2	38:AV:159:ASP:OD2	2.18	0.76
11:XA:3220:A:OP1	45:XE:260:LYS:NZ	2.19	0.76
11:XA:2369:A:OP1	64:XY:117:GLN:NE2	2.19	0.75
11:XA:2863:U:O2	11:XA:2869:A:N6	2.19	0.75
14:A2:12:ARG:NH2	17:AA:1125:A:O4'	2.18	0.75
45:XE:230:THR:O	45:XE:233:GLN:NE2	2.19	0.75
59:XT:126:ASP:OD1	59:XT:127:MET:N	2.20	0.75
10:9:28:ARG:NE	11:XA:2376:A:O2'	2.20	0.75
10:9:83:GLU:OE2	64:XY:91:ARG:NH2	2.20	0.74
15:A3:161:ARG:NH1	17:AA:1147:G:OP2	2.20	0.74
11:XA:2643:G:O2'	11:XA:2645:G:OP2	2.05	0.74
14:A2:42:GLU:N	22:AF:241:TRP:O	2.19	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:XA:2515:U:O2'	44:XD:282:ALA:O	2.05	0.74
61:XV:150:SER:O	61:XV:152:ARG:NH1	2.20	0.74
13:A1:143:CYS:SG	24:AH:74:LYS:NZ	2.61	0.74
7:6:367:ASP:OD1	7:6:370:ARG:NH1	2.21	0.74
11:XA:2096:U:O4	52:XM:57:ARG:NH1	2.20	0.74
17:AA:826:A:N7	26:AJ:55:ARG:NE	2.36	0.74
40:AX:174:ASN:OD1	40:AX:177:ARG:NH1	2.20	0.74
11:XA:2682:A:OP1	57:XR:34:ARG:NH2	2.20	0.74
19:AC:113:ARG:NH2	24:AH:166:GLU:OE2	2.21	0.74
11:XA:1958:G:OP2	59:XT:160:GLY:N	2.20	0.74
13:A1:100:GLU:O	19:AC:156:GLN:NE2	2.21	0.74
16:A4:269:HIS:O	16:A4:270:ARG:NE	2.20	0.74
15:A3:187:GLU:O	28:AL:212:ARG:NH2	2.21	0.74
40:AX:111:TYR:O	40:AX:115:THR:OG1	2.05	0.74
38:AV:132:LYS:NZ	38:AV:166:GLU:OE1	2.20	0.73
11:XA:2524:A:OP1	44:XD:67:LYS:NZ	2.21	0.73
61:XV:49:ILE:O	61:XV:81:ARG:NH1	2.21	0.73
17:AA:659:U:OP1	20:AD:226:ARG:NH2	2.19	0.73
54:XO:113:ARG:O	54:XO:117:ARG:NH1	2.21	0.73
41:AY:340:SER:OG	41:AY:377:ARG:NH2	2.20	0.73
17:AA:1014:A:O2'	17:AA:1031:G:O4'	2.06	0.73
50:XK:52:ASP:OD2	50:XK:124:ARG:NH2	2.21	0.73
11:XA:3175:A:OP2	11:XA:3187:C:N4	2.21	0.73
17:AA:1496:U:OP1	26:AJ:82:ARG:NH1	2.21	0.73
63:XX:144:TYR:O	63:XX:148:THR:CG2	2.35	0.73
20:AD:127:ASN:O	42:AZ:72:ARG:NH1	2.22	0.73
20:AD:178:GLU:OE2	20:AD:181:ARG:NH2	2.23	0.72
17:AA:1314:C:N3	22:AF:36:ARG:NH2	2.36	0.72
11:XA:2139:U:O4	65:XZ:77:ARG:NH1	2.22	0.72
20:AD:147:PRO:O	20:AD:155:GLN:NE2	2.23	0.72
63:XX:61:ARG:NH2	63:XX:63:GLU:OE2	2.22	0.72
4:3:132:LYS:NZ	11:XA:2909:G:OP1	2.16	0.72
17:AA:1280:C:O3'	18:AB:210:ARG:NH2	2.23	0.72
11:XA:2511:C:O2'	44:XD:257:ILE:O	2.06	0.72
41:AY:303:GLN:NE2	41:AY:307:GLU:OE1	2.22	0.72
11:XA:1874:A:O2'	11:XA:2090:A:O2'	2.08	0.72
9:8:110:GLU:OE2	9:8:114:ARG:NE	2.22	0.72
26:AJ:96:PRO:O	26:AJ:127:ARG:NH2	2.22	0.71
16:A4:479:GLU:HA	16:A4:482:ILE:HD12	1.71	0.71
40:AX:121:ALA:N	40:AX:299:ASN:OD1	2.22	0.71
7:6:117:VAL:O	7:6:121:ARG:NH2	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:AV:362:GLU:N	38:AV:362:GLU:OE1	2.23	0.71
11:XA:3068:G:OP2	11:XA:3068:G:N2	2.22	0.71
38:AV:132:LYS:O	38:AV:136:GLY:N	2.23	0.71
11:XA:2665:U:OP2	54:XO:17:ARG:NH1	2.23	0.71
52:XM:203:ARG:NH2	52:XM:261:ASP:O	2.23	0.71
13:A1:163:VAL:O	41:AY:317:ASN:ND2	2.23	0.71
49:XJ:154:ARG:NH1	49:XJ:155:VAL:O	2.24	0.71
11:XA:2294:A:OP2	52:XM:39:ARG:NH2	2.24	0.71
11:XA:2145:G:O2'	11:XA:2147:G:OP1	2.08	0.71
17:AA:1310:C:HO2'	27:AK:128:TRP:HE1	1.39	0.71
17:AA:1231:A:O2'	17:AA:1236:C:N4	2.24	0.70
19:AC:74:GLY:O	27:AK:103:ARG:NH2	2.24	0.70
37:AU:77:GLU:OE1	37:AU:81:LYS:NZ	2.23	0.70
58:XS:72:GLU:O	58:XS:76:HIS:ND1	2.23	0.70
11:XA:2692:G:N1	11:XA:2696:A:OP2	2.23	0.70
15:A3:155:ARG:NH2	17:AA:1154:A:OP2	2.24	0.70
23:AG:382:PRO:O	24:AH:131:ARG:NH1	2.24	0.70
11:XA:2864:U:O5'	62:XW:50:ARG:NH1	2.24	0.70
13:A1:81:VAL:O	13:A1:99:LYS:NZ	2.25	0.70
25:AI:79:LYS:N	25:AI:82:GLU:OE2	2.24	0.70
35:AS:75:TYR:OH	39:AW:91:GLN:O	2.10	0.70
1:0:98:GLN:NE2	11:XA:2709:A:N3	2.39	0.70
7:6:368:ARG:NH2	11:XA:2859:A:OP2	2.24	0.70
11:XA:1864:A:OP1	57:XR:17:ARG:NH1	2.25	0.70
40:AX:56:PRO:O	40:AX:59:HIS:NE2	2.24	0.70
16:A4:470:GLN:OE1	16:A4:472:ASP:N	2.25	0.70
64:XY:76:GLN:NE2	64:XY:78:LYS:O	2.25	0.70
7:6:284:ASP:OD1	7:6:286:ARG:NH2	2.25	0.70
40:AX:266:ASN:ND2	40:AX:311:SER:O	2.26	0.69
54:XO:113:ARG:NH1	54:XO:116:ASP:OD2	2.25	0.69
4:3:131:LYS:NZ	11:XA:2909:G:N7	2.40	0.69
7:6:364:ARG:NE	11:XA:2859:A:OP2	2.22	0.69
58:XS:91:GLN:N	58:XS:91:GLN:OE1	2.25	0.69
11:XA:2248:U:OP1	57:XR:99:ARG:NH2	2.25	0.69
4:3:172:TYR:O	4:3:178:GLN:NE2	2.26	0.69
10:9:24:LYS:NZ	11:XA:2421:G:OP1	2.26	0.68
11:XA:2111:C:OP1	48:XI:35:ARG:NH1	2.26	0.68
56:XQ:226:PRO:O	56:XQ:229:TRP:NE1	2.27	0.68
11:XA:2938:A:OP1	11:XA:2984:A:N6	2.26	0.68
25:AI:81:GLU:O	25:AI:148:ARG:NH1	2.26	0.68
32:AP:140:TYR:O	32:AP:141:ARG:NE	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:AX:206:GLU:OE1	40:AX:249:ARG:NH1	2.26	0.68
45:XE:54:SER:OG	45:XE:57:ASN:OD1	2.11	0.68
52:XM:148:PHE:O	52:XM:170:ASN:ND2	2.26	0.68
64:XY:91:ARG:O	64:XY:149:ARG:NH2	2.25	0.68
53:XN:86:ASN:OD1	53:XN:192:ARG:NH2	2.26	0.68
50:XK:34:MET:SD	50:XK:35:ALA:N	2.66	0.68
6:5:334:LYS:N	6:5:362:THR:OG1	2.27	0.68
50:XK:14:PHE:O	59:XT:206:ARG:NH2	2.27	0.68
57:XR:93:CYS:O	58:XS:146:LYS:NZ	2.27	0.68
17:AA:1287:A:OP2	20:AD:260:LYS:NZ	2.25	0.67
8:7:192:TRP:O	8:7:295:ARG:NH1	2.27	0.67
17:AA:928:A:O3'	20:AD:419:ARG:NH1	2.27	0.67
23:AG:117:PHE:O	23:AG:122:ARG:NH1	2.27	0.67
38:AV:82:ARG:NH2	38:AV:119:TYR:O	2.28	0.67
56:XQ:102:ARG:NH1	56:XQ:167:TYR:O	2.27	0.67
64:XY:143:ASP:OD1	64:XY:144:LYS:N	2.27	0.67
21:AE:92:ASN:ND2	32:AP:117:MET:SD	2.67	0.67
90:XA:5143:DOL:H311	90:XA:5143:DOL:H343	1.77	0.67
17:AA:668:U:O2'	31:AO:83:GLY:O	2.12	0.67
17:AA:1021:U:O4	33:AQ:59:ARG:NH1	2.28	0.67
17:AA:1053:A:N1	17:AA:1100:C:O2'	2.28	0.67
37:AU:98:ASP:O	37:AU:102:HIS:ND1	2.27	0.67
56:XQ:79:GLU:OE2	56:XQ:167:TYR:OH	2.13	0.67
11:XA:1787:G:N2	11:XA:1790:A:OP2	2.28	0.67
13:A1:169:ARG:O	13:A1:218:ASN:ND2	2.28	0.67
54:XO:140:SER:O	54:XO:146:ASN:ND2	2.28	0.67
7:6:308:GLN:NE2	7:6:311:MET:SD	2.68	0.67
27:AK:90:ARG:NH2	27:AK:95:SER:O	2.28	0.67
11:XA:2288:A:O2'	46:XF:101:MET:SD	2.54	0.66
17:AA:917:C:OP2	31:AO:91:ARG:NH2	2.27	0.66
2:1:53:ARG:NH2	11:XA:2879:A:O2'	2.28	0.66
55:XP:72:PRO:O	55:XP:74:ARG:NH2	2.28	0.66
11:XA:1805:A:OP2	61:XV:94:HIS:NE2	2.29	0.66
60:XU:75:GLY:O	60:XU:88:LYS:NZ	2.28	0.66
4:3:118:HIS:NE2	11:XA:1891:A:OP1	2.28	0.66
16:A4:478:TYR:CE2	16:A4:482:ILE:HD11	2.31	0.66
12:A0:101:ARG:NH1	17:AA:1528:A:OP1	2.29	0.65
21:AE:5:GLU:OE2	21:AE:96:HIS:ND1	2.29	0.65
10:9:16:ASP:OD1	10:9:25:ARG:NH1	2.30	0.65
34:AR:305:HIS:CD2	34:AR:314:ALA:HB2	2.26	0.65
11:XA:1672:C:OP1	59:XT:50:LYS:N	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:XI:101:ASN:OD1	48:XI:151:ASN:N	2.29	0.65
2:1:47:ASP:O	2:1:51:LYS:N	2.29	0.65
3:2:82:ARG:NH2	11:XA:1791:G:OP2	2.30	0.65
13:A1:256:SER:O	13:A1:260:ARG:NH1	2.29	0.65
14:A2:32:ARG:NH1	17:AA:1599:A:OP2	2.28	0.65
17:AA:949:U:O3'	30:AN:29:ARG:NH1	2.29	0.65
11:XA:2727:C:O2'	11:XA:2815:G:N2	2.30	0.65
11:XA:2602:U:O2	11:XA:3078:C:O2'	2.13	0.65
16:A4:198:TYR:O	16:A4:239:ARG:NH1	2.28	0.65
17:AA:893:G:OP2	26:AJ:79:LYS:NZ	2.30	0.65
4:3:113:ARG:NH1	52:XM:75:TYR:O	2.30	0.65
7:6:149:GLN:OE1	7:6:166:THR:OG1	2.15	0.65
11:XA:1770:G:OP2	57:XR:11:ARG:NH1	2.28	0.65
23:AG:272:SER:OG	23:AG:347:ALA:O	2.15	0.65
32:AP:65:CYS:SG	32:AP:68:CYS:N	2.69	0.65
11:XA:2833:A:OP1	62:XW:74:ARG:NH1	2.31	0.64
48:XI:224:HIS:O	48:XI:228:GLN:N	2.26	0.64
61:XV:54:TRP:NE1	61:XV:56:LEU:O	2.30	0.64
11:XA:1777:A:OP1	46:XF:115:LYS:NZ	2.30	0.64
11:XA:1985:G:OP1	44:XD:90:ARG:NH2	2.30	0.64
17:AA:722:C:N3	17:AA:798:C:O2'	2.31	0.64
17:AA:1429:C:OP1	23:AG:388:ARG:NH2	2.30	0.64
19:AC:76:LEU:O	27:AK:103:ARG:NH2	2.30	0.64
11:XA:1883:G:N7	46:XF:281:ARG:NH1	2.44	0.64
17:AA:1454:G:OP2	23:AG:377:ARG:NH2	2.30	0.64
62:XW:62:HIS:N	62:XW:65:ASN:OD1	2.30	0.64
11:XA:2149:G:OP2	57:XR:65:ARG:NH2	2.31	0.64
11:XA:2714:A:OP2	45:XE:239:ARG:NH1	2.30	0.64
1:0:139:ARG:NH2	11:XA:2322:C:OP1	2.28	0.64
56:XQ:227:LYS:O	56:XQ:229:TRP:N	2.31	0.64
6:5:112:ARG:NH1	6:5:301:PRO:O	2.30	0.64
11:XA:1957:A:OP2	87:A:8:MHT:H7A	1.98	0.64
17:AA:1225:C:O2'	17:AA:1449:G:O2'	2.16	0.64
16:A4:478:TYR:CD2	16:A4:482:ILE:HD11	2.32	0.64
44:XD:111:ARG:NH1	44:XD:243:THR:OG1	2.31	0.64
7:6:239:ASN:OD1	7:6:275:GLN:NE2	2.31	0.64
11:XA:2581:A:O2'	11:XA:2583:C:N4	2.29	0.64
11:XA:3078:C:N4	11:XA:3079:G:O6	2.31	0.63
11:XA:3127:G:O2'	11:XA:3130:A:N6	2.31	0.63
54:XO:64:LYS:NZ	54:XO:97:TYR:O	2.31	0.63
64:XY:133:ASP:OD1	64:XY:134:LYS:N	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:AB:219:THR:O	18:AB:233:THR:OG1	2.15	0.63
39:AW:148:GLU:OE2	39:AW:163:LEU:N	2.30	0.63
17:AA:901:G:O6	26:AJ:74:ASN:ND2	2.31	0.63
23:AG:310:ARG:NH1	40:AX:383:LEU:O	2.31	0.63
34:AR:144:GLU:N	34:AR:144:GLU:OE1	2.32	0.63
46:XF:220:ASP:O	46:XF:245:ALA:N	2.31	0.63
11:XA:2192:A:OP1	49:XJ:142:ARG:NE	2.32	0.63
36:AT:109:ASN:ND2	36:AT:111:GLU:OE2	2.31	0.63
34:AR:113:GLU:OE1	34:AR:116:ARG:NH1	2.32	0.63
38:AV:173:PHE:O	38:AV:178:THR:OG1	2.16	0.63
7:6:160:ASP:OD2	7:6:267:ARG:NH1	2.31	0.63
34:AR:305:HIS:CD2	34:AR:314:ALA:HA	2.34	0.62
11:XA:2510:U:OP2	11:XA:2539:A:N6	2.31	0.62
58:XS:164:THR:OG1	58:XS:190:GLN:NE2	2.32	0.62
16:A4:455:ASN:O	16:A4:486:TYR:OH	2.17	0.62
28:AL:169:ASN:OD1	28:AL:170:LEU:N	2.32	0.62
17:AA:869:C:OP2	31:AO:97:ARG:NH2	2.31	0.62
21:AE:85:ASP:OD1	44:XD:171:ARG:NH1	2.31	0.62
37:AU:110:GLN:O	37:AU:114:ARG:NE	2.31	0.62
6:5:112:ARG:N	6:5:264:ASP:OD2	2.33	0.62
17:AA:780:C:N3	28:AL:197:ARG:NH2	2.46	0.62
17:AA:949:U:O2'	30:AN:29:ARG:NH1	2.33	0.62
49:XJ:27:GLY:O	49:XJ:58:LYS:NZ	2.32	0.62
11:XA:1953:A:O2'	11:XA:2463:A:OP1	2.18	0.62
11:XA:2926:A:O2'	11:XA:3087:C:OP1	2.17	0.62
29:AM:87:MET:SD	29:AM:88:GLU:N	2.73	0.62
27:AK:28:HIS:NE2	42:AZ:60:GLU:OE2	2.32	0.62
17:AA:766:G:OP2	30:AN:76:HIS:NE2	2.31	0.62
10:9:22:THR:OG1	10:9:36:ARG:NH1	2.33	0.61
15:A3:134:ARG:NH2	17:AA:1585:A:OP1	2.33	0.61
8:7:238:ASP:OD1	8:7:239:PHE:N	2.33	0.61
11:XA:2326:C:O2	54:XO:31:ASN:ND2	2.34	0.61
11:XA:2195:A:O2'	11:XA:2196:A:O5'	2.18	0.61
5:4:88:TRP:NE1	11:XA:2160:A:OP2	2.29	0.61
12:A0:13:GLU:OE1	12:A0:16:ARG:NH1	2.33	0.61
10:9:18:MET:SD	10:9:18:MET:N	2.74	0.61
11:XA:3082:G:N2	11:XA:3085:A:OP2	2.32	0.61
11:XA:1800:G:N1	11:XA:1803:A:OP2	2.33	0.61
11:XA:1864:A:O3'	57:XR:13:ARG:NH1	2.30	0.61
28:AL:149:ASP:OD2	28:AL:152:HIS:ND1	2.33	0.61
1:0:181:ARG:NH1	1:0:186:THR:O	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:XA:1816:G:OP2	57:XR:37:ARG:NE	2.34	0.61
17:AA:1293:C:N4	33:AQ:80:ARG:O	2.33	0.61
32:AP:111:ILE:O	32:AP:115:GLN:NE2	2.34	0.61
34:AR:202:ARG:NE	34:AR:233:ALA:O	2.33	0.61
11:XA:2756:C:OP1	47:XH:121:ASN:ND2	2.34	0.60
5:4:87:ARG:NH2	5:4:102:GLN:O	2.33	0.60
38:AV:47:HIS:N	38:AV:78:ASN:OD1	2.33	0.60
44:XD:280:GLY:O	44:XD:285:LYS:NZ	2.33	0.60
6:5:182:ASP:OD1	6:5:183:ASN:N	2.33	0.60
36:AT:91:GLU:OE2	37:AU:123:ARG:NH1	2.34	0.60
12:A0:82:ARG:NH2	12:A0:138:ASP:O	2.34	0.60
11:XA:2187:C:O3'	49:XJ:106:LYS:NZ	2.34	0.60
1:0:138:ARG:NH1	11:XA:2320:A:O3'	2.34	0.60
6:5:306:PRO:O	6:5:310:ARG:NE	2.34	0.60
11:XA:2475:U:N3	11:XA:2478:G:OP2	2.35	0.60
46:XF:97:HIS:NE2	46:XF:101:MET:SD	2.74	0.60
50:XK:10:GLN:NE2	59:XT:203:LEU:O	2.34	0.60
13:A1:282:GLU:N	13:A1:282:GLU:OE2	2.34	0.60
11:XA:2015:G:N2	11:XA:2038:U:OP1	2.35	0.59
41:AY:292:GLN:OE1	41:AY:292:GLN:N	2.35	0.59
11:XA:2715:A:O2'	45:XE:245:THR:O	2.20	0.59
64:XY:97:ASP:OD1	64:XY:98:LEU:N	2.35	0.59
6:5:122:TRP:O	6:5:215:ARG:NE	2.26	0.59
6:5:141:ASP:O	6:5:142:ASP:N	2.35	0.59
7:6:124:ARG:NH2	9:8:112:GLU:OE1	2.35	0.59
11:XA:1844:A:OP2	57:XR:48:ARG:NH2	2.34	0.59
16:A4:99:SER:N	16:A4:102:GLU:OE2	2.33	0.59
58:XS:166:SER:N	58:XS:190:GLN:OE1	2.35	0.59
11:XA:1678:C:O4'	61:XV:42:ARG:NH2	2.33	0.59
11:XA:2145:G:N3	58:XS:104:ARG:NH2	2.50	0.59
63:XX:80:TRP:O	63:XX:131:THR:OG1	2.20	0.59
11:XA:2462:A:OP1	45:XE:237:HIS:NE2	2.36	0.59
8:7:279:GLU:N	8:7:279:GLU:OE1	2.35	0.59
16:A4:339:LEU:O	16:A4:374:HIS:NE2	2.36	0.59
16:A4:443:ASP:O	16:A4:446:LYS:NZ	2.35	0.59
11:XA:1936:A:O5'	11:XA:1937:A:N6	2.35	0.59
49:XJ:69:LYS:NZ	49:XJ:128:GLU:OE1	2.36	0.59
17:AA:700:A:OP2	37:AU:27:ARG:NH1	2.36	0.58
29:AM:68:LEU:O	34:AR:161:ILE:N	2.35	0.58
64:XY:206:ASP:OD1	64:XY:207:HIS:N	2.35	0.58
43:XB:1625:A:N7	55:XP:86:GLN:NE2	2.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:AJ:107:ILE:N	26:AJ:131:ASP:OD2	2.34	0.58
6:5:33:TRP:O	6:5:39:ARG:NH2	2.36	0.58
15:A3:145:LYS:NZ	17:AA:1584:A:OP1	2.36	0.58
17:AA:1574:G:N1	17:AA:1592:U:O4	2.37	0.58
3:2:57:ASN:ND2	11:XA:2340:C:OP2	2.34	0.58
34:AR:260:ASP:OD2	34:AR:291:ARG:NH2	2.35	0.58
17:AA:819:A:O2'	17:AA:831:U:O2'	2.16	0.58
61:XV:197:GLU:OE1	64:XY:95:ASN:ND2	2.37	0.58
7:6:252:CYS:SG	7:6:286:ARG:NH2	2.76	0.58
11:XA:2529:U:OP2	44:XD:208:ARG:NH1	2.37	0.58
22:AF:122:GLN:NE2	22:AF:138:GLU:O	2.36	0.58
7:6:198:ALA:O	7:6:254:TYR:OH	2.22	0.58
11:XA:1749:C:OP2	11:XA:2899:C:O2'	2.20	0.58
17:AA:947:U:OP1	28:AL:162:GLN:NE2	2.36	0.58
46:XF:75:GLU:OE2	46:XF:210:ARG:NE	2.32	0.58
11:XA:1878:U:O2'	46:XF:92:ARG:NH2	2.37	0.58
47:XH:136:ASN:OD1	47:XH:137:LYS:N	2.36	0.58
2:1:23:GLU:OE2	2:1:57:VAL:N	2.37	0.58
17:AA:1320:G:OP1	19:AC:41:ARG:NH1	2.36	0.57
4:3:156:LYS:NZ	11:XA:2091:A:OP2	2.31	0.57
17:AA:945:G:O2'	28:AL:154:ARG:NH2	2.37	0.57
43:XB:1639:U:O4	43:XB:1640:A:N6	2.36	0.57
44:XD:132:ASP:OD2	44:XD:135:ARG:NH1	2.37	0.57
51:XL:31:ALA:O	51:XL:33:GLN:NE2	2.37	0.57
11:XA:2139:U:OP2	65:XZ:74:SER:N	2.34	0.57
21:AE:53:ALA:N	21:AE:56:GLN:O	2.33	0.57
11:XA:2296:U:O4	58:XS:181:LYS:NZ	2.36	0.57
34:AR:305:HIS:CD2	34:AR:314:ALA:CA	2.88	0.57
45:XE:56:GLU:OE2	54:XO:141:HIS:ND1	2.36	0.57
31:AO:122:LEU:O	31:AO:125:GLN:NE2	2.38	0.57
17:AA:975:A:OP1	21:AE:90:ARG:NH1	2.37	0.57
17:AA:1199:G:O6	17:AA:1424:U:O4	2.23	0.57
11:XA:2381:A:N6	11:XA:2412:A:N1	2.52	0.57
17:AA:996:A:OP2	25:AI:119:ASN:ND2	2.38	0.57
11:XA:2813:U:N3	11:XA:2817:G:OP2	2.38	0.56
17:AA:1108:C:N4	17:AA:1125:A:N7	2.52	0.56
52:XM:264:GLN:NE2	52:XM:266:PHE:O	2.38	0.56
55:XP:64:GLU:OE1	55:XP:64:GLU:N	2.38	0.56
60:XU:16:GLN:N	61:XV:206:GLU:OE2	2.35	0.56
7:6:231:GLU:N	7:6:231:GLU:OE1	2.37	0.56
11:XA:3217:A:O4'	56:XQ:86:ARG:NH2	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:AA:1048:C:O2'	28:AL:196:TYR:O	2.24	0.56
18:AB:197:HIS:NE2	18:AB:240:ASP:O	2.39	0.56
10:9:28:ARG:NH1	11:XA:2376:A:O3'	2.32	0.56
27:AK:116:ASP:OD1	27:AK:125:ARG:NH2	2.39	0.56
21:AE:42:LEU:O	37:AU:184:ARG:NE	2.39	0.56
11:XA:1694:U:O4'	64:XY:162:ARG:NH2	2.38	0.56
13:A1:156:TYR:O	13:A1:167:ARG:NH1	2.39	0.56
17:AA:1048:C:O2'	17:AA:1049:A:OP1	2.20	0.56
46:XF:121:ARG:O	46:XF:142:ARG:NE	2.37	0.56
1:0:166:SER:N	1:0:169:ASP:OD1	2.38	0.56
18:AB:137:TYR:O	18:AB:264:ARG:NH2	2.38	0.56
52:XM:289:ASN:OD1	52:XM:290:LEU:N	2.39	0.56
11:XA:1840:C:OP1	50:XK:115:ASN:ND2	2.34	0.56
17:AA:1233:C:O2'	27:AK:86:ARG:NH2	2.37	0.56
36:AT:95:ASN:OD1	36:AT:96:LYS:N	2.39	0.56
7:6:106:ARG:NH1	43:XB:1621:A:OP2	2.38	0.56
11:XA:1761:A:O2'	11:XA:1762:A:O5'	2.24	0.56
11:XA:2039:A:N6	11:XA:2729:U:O2	2.38	0.56
27:AK:105:ARG:NH1	42:AZ:50:ASP:O	2.39	0.56
34:AR:305:HIS:HD2	34:AR:314:ALA:CA	2.18	0.56
2:1:34:ARG:NH2	2:1:35:ASN:O	2.38	0.56
6:5:142:ASP:O	6:5:146:HIS:ND1	2.37	0.56
16:A4:73:ALA:HB2	24:AH:61:PRO:HG2	1.88	0.56
17:AA:1198:A:N6	17:AA:1199:G:O6	2.39	0.56
21:AE:14:GLN:N	21:AE:17:GLU:OE2	2.34	0.56
23:AG:379:ARG:NH2	24:AH:133:GLN:OE1	2.39	0.56
38:AV:222:SER:OG	38:AV:277:ARG:NH1	2.39	0.56
64:XY:91:ARG:NE	64:XY:148:GLU:OE2	2.39	0.56
6:5:350:ARG:NH1	6:5:384:GLN:O	2.39	0.55
14:A2:113:ASN:OD1	14:A2:114:LYS:N	2.39	0.55
17:AA:1230:C:N4	17:AA:1447:G:O4'	2.39	0.55
38:AV:159:ASP:OD1	38:AV:160:ALA:N	2.39	0.55
4:3:182:ASP:OD1	4:3:183:ARG:N	2.37	0.55
17:AA:1322:C:OP1	19:AC:43:ARG:NH1	2.38	0.55
24:AH:89:ASP:OD1	24:AH:141:ARG:NH1	2.39	0.55
32:AP:49:ASP:OD2	39:AW:82:SER:N	2.39	0.55
11:XA:2755:A:O2'	63:XX:112:ARG:NH2	2.39	0.55
15:A3:135:ARG:NH2	15:A3:139:ASN:OD1	2.39	0.55
15:A3:172:ASP:OD1	15:A3:175:ARG:NH1	2.39	0.55
22:AF:207:HIS:NE2	22:AF:211:GLU:OE2	2.40	0.55
9:8:100:GLU:N	9:8:100:GLU:OE1	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:XA:1939:G:O5'	44:XD:259:LYS:NZ	2.33	0.55
12:A0:103:ASP:OD2	12:A0:105:THR:OG1	2.23	0.55
33:AQ:23:TYR:O	33:AQ:27:ASN:ND2	2.39	0.55
11:XA:2239:A:OP2	50:XK:75:LYS:NZ	2.40	0.55
16:A4:175:GLN:O	16:A4:180:GLY:N	2.40	0.55
16:A4:264:ARG:HE	16:A4:293:THR:HG22	1.72	0.55
6:5:160:HIS:HA	6:5:164:TRP:HB2	1.88	0.55
11:XA:2058:C:O2	65:XZ:109:LYS:NZ	2.35	0.55
47:XH:95:GLU:OE2	47:XH:112:VAL:N	2.40	0.55
11:XA:1845:C:OP2	58:XS:176:LYS:NZ	2.39	0.55
12:A0:87:TRP:O	31:A0:215:ARG:NH2	2.39	0.55
17:AA:1461:A:OP2	22:AF:177:ARG:NH2	2.40	0.55
22:AF:70:LYS:O	23:AG:365:ARG:NH1	2.39	0.55
42:AZ:66:ARG:NH1	42:AZ:76:GLN:OE1	2.40	0.55
43:XB:1644:G:O6	55:XP:87:HIS:NE2	2.34	0.55
11:XA:2103:A:HO2'	65:XZ:35:LYS:N	2.04	0.54
29:AM:59:ASN:ND2	29:AM:63:GLU:OE2	2.40	0.54
31:A0:58:TYR:O	31:A0:61:SER:OG	2.25	0.54
13:A1:154:THR:OG1	24:AH:171:GLU:OE2	2.25	0.54
17:AA:1233:C:OP1	17:AA:1353:A:N6	2.40	0.54
29:AM:97:PHE:HE2	37:AU:63:TYR:HH	1.55	0.54
11:XA:2095:U:OP2	52:XM:57:ARG:NE	2.41	0.54
17:AA:1433:A:N3	17:AA:1458:A:N6	2.56	0.54
20:AD:342:MET:SD	20:AD:342:MET:N	2.78	0.54
17:AA:894:C:N4	26:AJ:117:ASP:OD2	2.40	0.54
38:AV:108:THR:O	38:AV:111:THR:OG1	2.22	0.54
14:A2:24:ASN:OD1	14:A2:25:LYS:N	2.41	0.54
27:AK:99:GLY:O	27:AK:108:ARG:N	2.40	0.54
35:AS:7:GLU:N	35:AS:7:GLU:OE1	2.40	0.54
40:AX:214:GLU:OE2	40:AX:232:ARG:NH2	2.40	0.54
57:XR:104:ASP:OD1	57:XR:105:LEU:N	2.41	0.54
11:XA:2499:U:OP2	11:XA:2504:A:N6	2.33	0.54
17:AA:947:U:OP1	28:AL:165:LYS:NZ	2.37	0.54
20:AD:407:ASP:OD1	20:AD:407:ASP:N	2.41	0.54
50:XK:34:MET:HE2	50:XK:38:ARG:HD3	1.90	0.54
4:3:122:TRP:HD1	4:3:155:SER:HG	1.55	0.54
11:XA:1974:A:OP2	44:XD:265:TRP:NE1	2.34	0.54
17:AA:942:A:N6	17:AA:1047:A:OP1	2.40	0.54
27:AK:58:ARG:NE	27:AK:72:ASP:OD1	2.38	0.54
63:XX:83:GLU:N	63:XX:83:GLU:OE1	2.41	0.54
12:A0:96:ARG:N	12:A0:117:ILE:O	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:AA:703:A:OP2	37:AU:43:ASN:ND2	2.39	0.53
63:XX:207:THR:N	63:XX:210:GLU:OE2	2.38	0.53
13:A1:54:PRO:HD2	16:A4:518:GLU:OE2	2.08	0.53
17:AA:769:G:OP1	30:AN:24:LYS:NZ	2.41	0.53
52:XM:153:ASN:ND2	52:XM:256:LEU:O	2.42	0.53
55:XP:120:ASN:OD1	55:XP:123:ALA:N	2.35	0.53
64:XY:140:ASP:OD1	64:XY:141:ALA:N	2.41	0.53
11:XA:1737:A:N6	11:XA:1760:G:O2'	2.39	0.53
17:AA:1114:U:OP1	35:AS:55:LYS:NZ	2.35	0.53
17:AA:1429:C:O2	17:AA:1460:C:N4	2.41	0.53
50:XK:24:LYS:O	50:XK:26:GLN:NE2	2.41	0.53
8:7:49:ASN:OD1	8:7:52:LYS:NZ	2.42	0.53
22:AF:77:ALA:N	23:AG:368:GLY:O	2.41	0.53
49:XJ:79:GLU:OE2	49:XJ:81:LYS:NZ	2.34	0.53
13:A1:118:ALA:O	13:A1:122:HIS:ND1	2.40	0.53
28:AL:142:HIS:NE2	28:AL:149:ASP:OD2	2.34	0.53
11:XA:2472:A:N3	11:XA:2474:C:N4	2.57	0.53
11:XA:3151:A:N6	11:XA:3163:G:O2'	2.41	0.53
17:AA:819:A:HO2'	17:AA:831:U:HO2'	1.50	0.53
7:6:119:GLU:OE1	7:6:119:GLU:N	2.42	0.53
17:AA:650:U:OP1	20:AD:427:ARG:NH1	2.42	0.53
17:AA:1143:C:N4	17:AA:1576:G:OP1	2.42	0.53
23:AG:244:PHE:O	23:AG:246:ARG:NH1	2.41	0.53
63:XX:36:ARG:NH1	63:XX:37:THR:OG1	2.42	0.52
8:7:247:ASN:ND2	8:7:251:ILE:O	2.43	0.52
11:XA:1769:C:O2'	57:XR:11:ARG:NH2	2.42	0.52
57:XR:83:TYR:OH	57:XR:99:ARG:NH2	2.42	0.52
38:AV:192:LYS:NZ	38:AV:194:THR:O	2.43	0.52
8:7:94:HIS:NE2	59:XT:135:GLU:OE2	2.41	0.52
17:AA:881:A:O2'	17:AA:882:A:O4'	2.22	0.52
3:2:70:LEU:O	64:XY:198:ARG:NH2	2.43	0.52
11:XA:1747:G:OP2	11:XA:1749:C:N4	2.42	0.52
13:A1:142:LYS:O	13:A1:146:HIS:ND1	2.43	0.52
45:XE:334:ASP:OD1	45:XE:335:GLU:N	2.40	0.52
52:XM:39:ARG:NH2	52:XM:41:ARG:HE	2.07	0.52
60:XU:71:ARG:NE	60:XU:96:TYR:OH	2.43	0.52
10:9:134:ASN:OD1	10:9:135:PHE:N	2.42	0.52
18:AB:156:GLU:OE1	23:AG:163:HIS:ND1	2.42	0.52
62:XW:38:SER:OG	62:XW:39:SER:N	2.43	0.52
62:XW:60:TYR:OH	62:XW:94:GLU:OE2	2.27	0.52
17:AA:835:C:N4	17:AA:851:A:OP2	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:XA:2043:C:C2	11:XA:2044:A:C8	2.98	0.52
32:AP:87:PHE:O	33:AQ:10:ARG:N	2.42	0.52
34:AR:140:ASP:OD1	34:AR:141:VAL:N	2.43	0.52
40:AX:157:ASP:OD1	40:AX:158:ALA:N	2.43	0.52
11:XA:1680:A:O3'	61:XV:18:HIS:NE2	2.40	0.52
12:A0:30:ASP:OD1	12:A0:31:SER:N	2.41	0.52
11:XA:2402:A:OP1	44:XD:102:GLN:NE2	2.39	0.51
17:AA:845:A:O2'	17:AA:846:A:O4'	2.25	0.51
36:AT:35:ASN:ND2	36:AT:69:ASN:OD1	2.43	0.51
8:7:262:ASP:OD1	8:7:263:VAL:N	2.44	0.51
12:A0:50:LEU:O	12:A0:55:TRP:NE1	2.41	0.51
13:A1:267:LEU:O	13:A1:270:LYS:NZ	2.40	0.51
17:AA:1234:C:O2'	17:AA:1235:U:OP1	2.24	0.51
24:AH:161:GLN:HA	24:AH:164:LEU:CD1	2.40	0.51
49:XJ:107:GLU:OE1	49:XJ:109:ALA:N	2.43	0.51
11:XA:2990:A:O2'	11:XA:2992:G:OP2	2.27	0.51
46:XF:228:GLN:O	46:XF:232:GLU:OE1	2.29	0.51
17:AA:1347:G:OP1	27:AK:36:ARG:NH1	2.40	0.51
7:6:133:ASP:OD1	7:6:134:ALA:N	2.43	0.51
11:XA:2148:A:OP2	57:XR:65:ARG:NH1	2.43	0.51
16:A4:478:TYR:O	16:A4:482:ILE:HG13	2.11	0.51
7:6:206:TYR:OH	7:6:242:GLY:O	2.23	0.51
36:AT:9:ILE:O	36:AT:12:THR:OG1	2.29	0.51
37:AU:178:GLU:N	37:AU:178:GLU:OE1	2.43	0.51
63:XX:118:ILE:O	63:XX:168:ARG:NH1	2.43	0.51
11:XA:2123:C:OP2	65:XZ:76:ARG:NH2	2.44	0.51
13:A1:196:GLU:N	13:A1:196:GLU:OE1	2.43	0.51
16:A4:98:ALA:N	16:A4:102:GLU:OE2	2.44	0.51
17:AA:798:C:H2'	17:AA:799:A:C8	2.46	0.51
46:XF:94:ASP:N	46:XF:94:ASP:OD1	2.43	0.51
46:XF:191:ASP:OD1	46:XF:192:SER:N	2.43	0.51
61:XV:148:THR:HG22	61:XV:149:ARG:HD3	1.91	0.51
7:6:114:ARG:NH1	43:XB:1643:A:OP1	2.43	0.51
38:AV:235:GLU:O	38:AV:239:GLY:N	2.44	0.51
11:XA:2836:C:OP1	62:XW:48:GLY:N	2.42	0.51
28:AL:105:LYS:O	28:AL:108:GLN:HG3	2.11	0.51
38:AV:131:ASN:ND2	38:AV:134:GLN:OE1	2.44	0.51
17:AA:1227:G:O3'	27:AK:96:ARG:NH2	2.44	0.51
34:AR:247:HIS:O	34:AR:251:GLU:OE1	2.28	0.51
45:XE:316:PHE:HB3	45:XE:317:PRO:HD3	1.92	0.50
63:XX:53:ASN:ND2	63:XX:56:ASN:OD1	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:XX:169:LEU:O	63:XX:172:GLN:NE2	2.42	0.50
6:5:51:GLU:OE1	6:5:51:GLU:N	2.44	0.50
11:XA:1955:G:O2'	11:XA:1958:G:O2'	2.26	0.50
13:A1:152:ASP:N	13:A1:152:ASP:OD1	2.44	0.50
17:AA:1517:A:O2'	17:AA:1518:C:O4'	2.29	0.50
3:2:82:ARG:NH2	11:XA:1790:A:OP1	2.44	0.50
6:5:337:GLU:N	6:5:337:GLU:OE1	2.45	0.50
23:AG:292:ARG:NH1	23:AG:300:TYR:OH	2.44	0.50
38:AV:271:GLU:N	38:AV:271:GLU:OE1	2.45	0.50
17:AA:1039:A:C6	28:AL:158:MET:HE1	2.47	0.50
17:AA:1369:U:O4	22:AF:192:ARG:NH2	2.44	0.50
36:AT:130:GLY:N	36:AT:135:CYS:SG	2.85	0.50
61:XV:184:GLU:O	64:XY:93:LYS:NZ	2.43	0.50
7:6:191:ASN:ND2	55:XP:137:GLU:O	2.45	0.50
8:7:203:THR:O	8:7:207:HIS:ND1	2.44	0.50
11:XA:3012:U:O4'	11:XA:3173:G:N2	2.42	0.50
11:XA:2614:U:O3'	51:XL:53:ARG:NH1	2.43	0.50
18:AB:153:TYR:O	18:AB:157:ASN:ND2	2.45	0.50
17:AA:663:A:H2'	17:AA:664:G:H8	1.77	0.50
11:XA:2307:U:H2'	11:XA:2308:A:O4'	2.12	0.49
40:AX:161:TRP:NE1	40:AX:183:GLU:OE2	2.45	0.49
40:AX:170:GLN:OE1	40:AX:175:LYS:NZ	2.38	0.49
53:XN:102:PHE:HA	53:XN:105:MET:SD	2.52	0.49
55:XP:71:PHE:HB3	55:XP:72:PRO:HD3	1.93	0.49
61:XV:132:GLU:O	61:XV:148:THR:OG1	2.26	0.49
9:8:186:GLN:N	9:8:186:GLN:OE1	2.45	0.49
11:XA:2506:A:N6	11:XA:3093:C:O4'	2.45	0.49
11:XA:3011:A:O2'	11:XA:3173:G:N2	2.46	0.49
18:AB:200:ASN:OD1	18:AB:203:PHE:N	2.45	0.49
51:XL:110:ASP:OD1	51:XL:111:ASN:N	2.45	0.49
11:XA:1877:U:O3'	52:XM:30:ASN:ND2	2.45	0.49
45:XE:159:THR:O	45:XE:163:GLU:OE1	2.30	0.49
17:AA:918:A:O2'	17:AA:919:A:O4'	2.30	0.49
28:AL:74:LYS:NZ	28:AL:109:GLU:OE2	2.35	0.49
29:AM:20:ARG:NH1	29:AM:42:PRO:O	2.35	0.49
11:XA:1917:A:O5'	11:XA:1984:A:N6	2.46	0.49
11:XA:2681:G:O6	11:XA:2682:A:N6	2.45	0.49
25:AI:115:GLU:OE2	25:AI:131:ALA:N	2.46	0.49
38:AV:83:GLU:O	38:AV:87:HIS:ND1	2.41	0.49
43:XB:1615:A:O2'	43:XB:1616:A:O4'	2.25	0.49
48:XI:40:MET:SD	48:XI:44:ARG:NH1	2.85	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:242:ARG:HA	6:5:245:ILE:HG12	1.95	0.49
11:XA:1868:G:H2'	52:XM:40:PRO:HG3	1.95	0.49
17:AA:1320:G:OP2	19:AC:37:ASN:ND2	2.45	0.49
34:AR:145:ASP:OD2	34:AR:148:LEU:N	2.39	0.49
7:6:27:ARG:N	11:XA:2073:A:OP2	2.46	0.49
11:XA:2575:U:O2	11:XA:2582:A:N6	2.46	0.49
37:AU:99:ALA:HA	37:AU:102:HIS:CE1	2.48	0.49
6:5:270:ILE:HG22	6:5:270:ILE:O	2.13	0.49
11:XA:2004:G:H2'	11:XA:2005:C:C6	2.48	0.49
11:XA:2166:C:N4	11:XA:2212:C:OP2	2.46	0.49
46:XF:86:VAL:O	46:XF:179:THR:OG1	2.30	0.49
61:XV:66:GLU:N	61:XV:66:GLU:OE1	2.46	0.49
37:AU:52:GLU:OE1	37:AU:52:GLU:N	2.43	0.49
38:AV:123:ASP:OD1	38:AV:124:LYS:N	2.44	0.49
39:AW:103:ARG:O	39:AW:115:ASP:N	2.46	0.49
56:XQ:260:TRP:O	56:XQ:262:GLN:NE2	2.46	0.49
11:XA:2287:U:O4	11:XA:2288:A:N6	2.46	0.48
11:XA:3075:G:C6	11:XA:3094:G:N1	2.81	0.48
17:AA:843:G:N1	17:AA:847:G:O6	2.46	0.48
21:AE:19:ALA:O	21:AE:23:LYS:HG2	2.13	0.48
57:XR:96:GLU:OE1	57:XR:96:GLU:N	2.46	0.48
38:AV:215:GLN:OE1	38:AV:224:GLN:NE2	2.45	0.48
11:XA:3159:A:O3'	45:XE:213:LYS:NZ	2.44	0.48
13:A1:216:ARG:NH2	41:AY:326:SER:O	2.43	0.48
52:XM:72:THR:OG1	52:XM:77:ARG:NH2	2.46	0.48
60:XU:109:ASP:OD1	60:XU:110:LEU:N	2.45	0.48
1:0:91:ARG:HG3	1:0:95:ARG:HE	1.79	0.48
11:XA:2345:G:OP2	11:XA:2425:A:N6	2.45	0.48
18:AB:132:THR:HA	18:AB:135:MET:SD	2.52	0.48
38:AV:76:ILE:O	38:AV:115:GLN:NE2	2.45	0.48
48:XI:181:ILE:O	48:XI:184:THR:N	2.45	0.48
4:3:116:ARG:NH2	4:3:159:ASP:OD1	2.46	0.48
6:5:188:CYS:HG	6:5:418:TYR:HD2	1.57	0.48
7:6:283:GLU:OE2	7:6:307:HIS:NE2	2.41	0.48
10:9:127:LEU:O	10:9:134:ASN:ND2	2.38	0.48
11:XA:3097:U:C6	87:A:7:004:HD2	2.49	0.48
17:AA:723:A:OP1	17:AA:724:C:N4	2.38	0.48
21:AE:38:ASP:OD1	21:AE:39:LEU:N	2.45	0.48
27:AK:69:ASP:O	27:AK:73:GLU:OE1	2.31	0.48
6:5:173:ARG:HA	6:5:176:TYR:CE2	2.48	0.48
48:XI:163:GLU:O	48:XI:166:ARG:HG3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:173:ARG:NE	6:5:297:ALA:O	2.46	0.48
11:XA:1748:G:C5	11:XA:1750:G:N2	2.81	0.48
11:XA:2151:A:OP2	11:XA:2249:G:N1	2.37	0.48
17:AA:1526:U:O2'	17:AA:1527:A:O4'	2.31	0.48
18:AB:202:ILE:O	18:AB:202:ILE:HG22	2.14	0.48
11:XA:1859:A:OP1	11:XA:2299:U:O2'	2.31	0.48
18:AB:135:MET:O	18:AB:140:GLY:N	2.37	0.48
34:AR:176:GLU:N	34:AR:176:GLU:OE1	2.46	0.48
40:AX:171:SER:OG	40:AX:178:PHE:O	2.32	0.48
43:XB:1618:A:OP2	43:XB:1620:A:N6	2.47	0.48
9:8:137:ARG:O	9:8:141:GLU:OE1	2.32	0.48
11:XA:2814:G:OP1	11:XA:2839:C:O2'	2.28	0.48
11:XA:2939:C:H2'	11:XA:2940:A:O4'	2.14	0.48
17:AA:1431:G:N2	17:AA:1458:A:OP2	2.38	0.48
6:5:183:ASN:OD1	6:5:184:LEU:N	2.47	0.48
11:XA:3047:G:O3'	51:XL:81:LYS:NZ	2.47	0.48
17:AA:1430:A:OP1	23:AG:388:ARG:NH2	2.40	0.48
56:XQ:246:ASP:OD1	56:XQ:247:LEU:N	2.47	0.48
11:XA:3059:A:OP1	11:XA:3061:G:O2'	2.24	0.47
11:XA:3160:A:OP1	45:XE:213:LYS:NZ	2.47	0.47
13:A1:216:ARG:NH1	41:AY:326:SER:O	2.45	0.47
17:AA:743:C:HO2'	29:AM:38:HIS:HE2	1.62	0.47
40:AX:51:THR:O	40:AX:67:HIS:N	2.45	0.47
17:AA:662:U:H2'	17:AA:663:A:O4'	2.15	0.47
22:AF:129:ALA:O	22:AF:134:GLN:NE2	2.47	0.47
30:AN:39:LEU:O	36:AT:11:ARG:NH1	2.47	0.47
30:AN:62:ASP:OD1	30:AN:88:VAL:N	2.41	0.47
12:A0:132:GLU:OE2	12:A0:207:GLN:N	2.46	0.47
59:XT:77:ARG:HE	59:XT:120:VAL:CG2	2.27	0.47
7:6:73:THR:OG1	62:XW:102:GLU:OE2	2.26	0.47
11:XA:1680:A:OP1	64:XY:230:LYS:NZ	2.41	0.47
11:XA:2234:C:O2'	11:XA:2235:C:OP2	2.32	0.47
11:XA:2550:A:C2	11:XA:2551:G:C8	3.02	0.47
17:AA:1187:U:OP2	17:AA:1189:U:N3	2.41	0.47
26:AJ:64:CYS:SG	26:AJ:65:THR:N	2.87	0.47
28:AL:86:ASP:OD1	28:AL:87:ASP:N	2.47	0.47
42:AZ:76:GLN:NE2	42:AZ:77:ASP:OD1	2.46	0.47
64:XY:133:ASP:HA	64:XY:136:VAL:HG12	1.96	0.47
11:XA:3008:C:C2	11:XA:3032:G:N2	2.83	0.47
14:A2:67:ARG:HA	14:A2:70:ILE:HG22	1.95	0.47
17:AA:1433:A:C4	17:AA:1458:A:N6	2.83	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:AM:84:SER:O	29:AM:87:MET:HG3	2.14	0.47
43:XB:1630:A:N1	43:XB:1637:C:N4	2.63	0.47
56:XQ:108:ILE:O	56:XQ:108:ILE:HG13	2.14	0.47
57:XR:148:TYR:OH	58:XS:146:LYS:O	2.32	0.47
6:5:343:GLN:NE2	6:5:417:LEU:O	2.48	0.47
10:9:52:GLN:NE2	11:XA:2416:U:O3'	2.43	0.47
16:A4:366:GLU:OE1	16:A4:366:GLU:N	2.42	0.47
18:AB:57:ASP:OD1	18:AB:57:ASP:N	2.47	0.47
47:XH:120:ARG:NH2	63:XX:136:ASP:OD2	2.41	0.47
48:XI:111:LEU:O	48:XI:115:GLN:OE1	2.33	0.47
52:XM:44:ARG:HD3	52:XM:45:ARG:HG3	1.96	0.47
6:5:409:GLU:OE1	6:5:409:GLU:N	2.48	0.47
11:XA:1882:A:N6	11:XA:1893:A:O4'	2.48	0.47
11:XA:2694:A:N3	11:XA:2942:C:O2'	2.41	0.47
11:XA:3025:A:C2	11:XA:3026:U:C5	3.02	0.47
17:AA:798:C:OP1	29:AM:10:LYS:N	2.47	0.47
37:AU:100:ALA:O	37:AU:104:GLU:OE1	2.33	0.47
52:XM:119:THR:O	52:XM:123:ASN:ND2	2.47	0.47
56:XQ:118:ARG:NH2	56:XQ:204:MET:O	2.42	0.47
6:5:300:ARG:HA	6:5:303:ARG:HE	1.80	0.47
8:7:306:LEU:O	8:7:306:LEU:HG	2.15	0.47
11:XA:2457:A:N3	54:XO:17:ARG:NH2	2.63	0.47
6:5:200:ARG:NH1	6:5:234:ASP:OD2	2.48	0.47
11:XA:1764:C:H3'	11:XA:1765:C:C5'	2.44	0.47
11:XA:1838:C:O3'	50:XK:116:LEU:HD21	2.15	0.47
11:XA:2956:A:C4	11:XA:2969:A:N1	2.83	0.47
11:XA:2959:G:O2'	11:XA:2965:A:N6	2.48	0.47
14:A2:9:ARG:NH2	17:AA:1021:U:OP2	2.48	0.47
17:AA:847:G:C2	17:AA:848:U:C5	3.03	0.47
17:AA:889:G:N1	17:AA:905:A:OP2	2.40	0.47
25:AI:83:ILE:O	25:AI:148:ARG:NH1	2.45	0.47
43:XB:1620:A:N3	43:XB:1620:A:H2'	2.30	0.47
53:XN:85:GLY:O	53:XN:192:ARG:NH2	2.46	0.47
11:XA:2005:C:N3	11:XA:2006:C:C5	2.84	0.46
11:XA:2459:A:H4'	45:XE:216:GLN:HA	1.97	0.46
11:XA:2744:U:O2'	11:XA:2746:U:O4	2.31	0.46
11:XA:3000:A:C6	11:XA:3061:G:C6	3.03	0.46
17:AA:1193:U:O2'	22:AF:178:ARG:NH1	2.48	0.46
40:AX:346:SER:OG	40:AX:347:ASN:N	2.47	0.46
54:XO:110:ILE:HG13	54:XO:111:PRO:HD2	1.97	0.46
54:XO:129:CYS:SG	54:XO:130:LEU:N	2.88	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:XY:220:LYS:O	64:XY:224:GLU:OE1	2.33	0.46
11:XA:1750:G:O2'	11:XA:1751:A:O4'	2.33	0.46
15:A3:159:GLU:OE1	15:A3:163:ARG:NH2	2.47	0.46
21:AE:87:ASP:OD1	21:AE:88:VAL:N	2.47	0.46
34:AR:295:ASP:OD1	34:AR:296:ASP:N	2.48	0.46
52:XM:231:GLU:O	52:XM:235:GLU:OE1	2.33	0.46
58:XS:106:TRP:CD2	58:XS:114:ILE:HD11	2.50	0.46
64:XY:169:ARG:NH1	64:XY:194:TYR:OH	2.44	0.46
2:1:23:GLU:OE1	2:1:23:GLU:N	2.44	0.46
6:5:215:ARG:O	6:5:216:GLU:HG3	2.15	0.46
11:XA:1744:A:OP1	52:XM:87:HIS:NE2	2.42	0.46
17:AA:1221:A:OP2	17:AA:1222:A:O2'	2.21	0.46
20:AD:254:ALA:O	20:AD:280:HIS:N	2.44	0.46
23:AG:253:LYS:HD2	23:AG:253:LYS:O	2.14	0.46
61:XV:196:GLU:O	61:XV:200:GLU:OE1	2.33	0.46
11:XA:2683:C:OP1	57:XR:34:ARG:NH1	2.49	0.46
38:AV:144:PHE:CZ	38:AV:167:VAL:HG21	2.51	0.46
11:XA:1829:A:N3	57:XR:52:LYS:NZ	2.54	0.46
11:XA:2696:A:H1'	11:XA:2698:G:OP2	2.16	0.46
11:XA:3071:U:H2'	90:XA:5143:DOL:H483	1.97	0.46
23:AG:203:GLU:O	23:AG:207:GLU:OE1	2.34	0.46
41:AY:327:GLU:O	41:AY:331:HIS:ND1	2.44	0.46
11:XA:2261:C:O2'	58:XS:184:ARG:NH1	2.49	0.46
11:XA:2471:G:OP1	51:XL:37:ARG:N	2.42	0.46
54:XO:86:ILE:HB	54:XO:87:PRO:HD3	1.98	0.46
65:XZ:81:TRP:O	65:XZ:84:ASP:OD1	2.34	0.46
10:9:54:LYS:NZ	11:XA:2415:C:O3'	2.49	0.46
11:XA:2017:U:OP1	52:XM:54:LYS:NZ	2.39	0.46
11:XA:2453:G:O6	11:XA:2672:A:N6	2.49	0.46
12:A0:115:TRP:CG	12:A0:130:GLU:HA	2.51	0.46
25:AI:181:ILE:O	25:AI:181:ILE:HG13	2.16	0.46
40:AX:130:LYS:O	40:AX:130:LYS:HG3	2.16	0.46
41:AY:367:LYS:O	41:AY:371:GLU:OE1	2.33	0.46
42:AZ:77:ASP:O	42:AZ:80:ASP:OD1	2.34	0.46
49:XJ:113:THR:OG1	49:XJ:116:HIS:ND1	2.38	0.46
52:XM:225:ASP:OD2	52:XM:228:LYS:NZ	2.49	0.46
57:XR:28:ALA:HB2	57:XR:46:VAL:CG2	2.46	0.46
37:AU:126:GLN:O	37:AU:130:GLU:OE1	2.34	0.46
64:XY:130:GLU:O	64:XY:133:ASP:OD1	2.33	0.46
64:XY:137:ASP:O	64:XY:140:ASP:OD1	2.34	0.46
8:7:155:GLU:OE2	8:7:156:ARG:NH1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:XA:1826:G:H4'	11:XA:1828:A:C2	2.51	0.46
21:AE:48:PRO:O	32:AP:124:TYR:OH	2.30	0.46
11:XA:2470:G:O2'	51:XL:36:THR:HG22	2.16	0.46
11:XA:2698:G:OP1	11:XA:2699:C:N4	2.43	0.46
17:AA:1431:G:HO2'	17:AA:1432:U:P	2.39	0.46
20:AD:257:SER:OG	20:AD:271:ALA:O	2.33	0.46
37:AU:134:ARG:O	37:AU:138:GLU:OE1	2.34	0.46
39:AW:109:GLU:O	39:AW:126:ARG:NH1	2.43	0.46
41:AY:277:LEU:O	41:AY:281:GLU:OE1	2.34	0.46
63:XX:189:ASP:O	63:XX:192:LYS:NZ	2.43	0.46
7:6:210:GLU:OE1	7:6:274:LYS:NZ	2.46	0.45
13:A1:140:ASP:OD1	13:A1:141:GLU:N	2.49	0.45
34:AR:221:GLN:OE1	34:AR:223:ARG:NH2	2.49	0.45
35:AS:61:GLN:OE1	35:AS:61:GLN:N	2.49	0.45
16:A4:66:ASP:OD1	16:A4:67:LYS:N	2.49	0.45
16:A4:556:LYS:HD3	16:A4:595:MET:HE1	1.98	0.45
26:AJ:98:GLU:OE2	26:AJ:136:GLN:NE2	2.49	0.45
51:XL:39:ARG:NH1	51:XL:104:ASN:OD1	2.48	0.45
52:XM:86:GLY:O	52:XM:90:ARG:N	2.41	0.45
8:7:38:THR:O	8:7:42:GLU:OE1	2.33	0.45
8:7:193:MET:SD	8:7:193:MET:N	2.87	0.45
11:XA:1909:A:O2'	11:XA:2733:G:O2'	2.26	0.45
11:XA:2376:A:C6	11:XA:2421:G:O6	2.70	0.45
11:XA:2379:C:O2	11:XA:2379:C:O4'	2.35	0.45
11:XA:2419:C:OP2	60:XU:50:ARG:NE	2.49	0.45
11:XA:2459:A:C4	11:XA:2460:A:C8	3.04	0.45
11:XA:2877:C:H2'	11:XA:2878:G:O4'	2.16	0.45
12:A0:135:MET:SD	12:A0:135:MET:N	2.89	0.45
15:A3:156:LYS:O	15:A3:159:GLU:HG3	2.16	0.45
16:A4:164:ARG:H	16:A4:167:LYS:HE3	1.82	0.45
22:AF:201:MET:N	22:AF:202:PRO:HD2	2.31	0.45
23:AG:312:GLN:OE1	23:AG:345:ARG:NH2	2.50	0.45
54:XO:151:GLY:O	54:XO:154:GLN:NE2	2.48	0.45
59:XT:77:ARG:HE	59:XT:120:VAL:HG22	1.82	0.45
11:XA:1799:U:H2'	11:XA:1800:G:O4'	2.16	0.45
11:XA:2003:A:OP2	11:XA:2734:A:O2'	2.33	0.45
11:XA:3007:C:N4	11:XA:3054:G:N7	2.64	0.45
26:AJ:49:LEU:HD23	26:AJ:50:GLY:H	1.81	0.45
46:XF:228:GLN:O	46:XF:231:VAL:HG12	2.16	0.45
56:XQ:166:LEU:HD12	56:XQ:167:TYR:CE1	2.52	0.45
56:XQ:276:SER:O	56:XQ:279:GLU:HG3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:XA:2942:C:C2	11:XA:2943:G:N7	2.84	0.45
38:AV:106:ASN:OD1	38:AV:107:TRP:N	2.50	0.45
6:5:393:LYS:O	6:5:396:VAL:HG12	2.16	0.45
8:7:259:ASP:OD1	8:7:260:PHE:N	2.50	0.45
11:XA:2245:A:H1'	11:XA:2246:A:C8	2.52	0.45
11:XA:3113:A:N6	11:XA:3144:A:N1	2.65	0.45
15:A3:139:ASN:ND2	17:AA:1141:C:OP1	2.50	0.45
16:A4:133:ALA:HB2	19:AC:148:LYS:HB2	1.98	0.45
38:AV:208:LEU:CD2	38:AV:223:SER:O	2.64	0.45
56:XQ:97:LYS:O	56:XQ:101:GLU:OE1	2.34	0.45
58:XS:112:ASP:OD1	58:XS:195:ILE:HB	2.16	0.45
59:XT:95:ARG:NH2	59:XT:145:SER:O	2.50	0.45
11:XA:2574:G:O2'	11:XA:2575:U:P	2.75	0.45
12:A0:62:SER:OG	12:A0:63:ARG:N	2.50	0.45
17:AA:682:A:N6	17:AA:865:A:H61	2.15	0.45
37:AU:123:ARG:O	37:AU:127:GLU:OE1	2.35	0.45
56:XQ:281:ALA:O	56:XQ:285:GLU:OE1	2.34	0.45
59:XT:149:ARG:NH1	59:XT:168:GLU:OE2	2.40	0.45
64:XY:94:SER:OG	64:XY:95:ASN:N	2.50	0.45
87:A:1:MHW:OG1	87:A:1:MHW:O	2.33	0.45
4:3:177:TYR:O	4:3:181:HIS:ND1	2.41	0.45
8:7:147:ALA:O	8:7:150:MET:HG2	2.17	0.45
11:XA:1861:U:H2'	11:XA:1862:U:C6	2.52	0.45
11:XA:2044:A:C4	11:XA:2045:A:C8	3.05	0.45
11:XA:3127:G:N2	11:XA:3130:A:OP2	2.46	0.45
11:XA:3161:G:O2'	11:XA:3162:C:H2'	2.17	0.45
17:AA:1389:G:N1	17:AA:1416:A:OP2	2.45	0.45
46:XF:254:LEU:CD2	52:XM:24:LEU:HD22	2.46	0.45
54:XO:16:ARG:NE	54:XO:51:GLU:OE2	2.50	0.45
6:5:201:ARG:NH1	6:5:418:TYR:O	2.47	0.45
8:7:95:LEU:O	59:XT:137:ARG:NH2	2.41	0.45
11:XA:1769:C:C5	46:XF:108:ARG:HD2	2.52	0.45
14:A2:64:ASP:N	14:A2:64:ASP:OD1	2.50	0.45
22:AF:116:GLU:O	22:AF:120:ARG:HG2	2.16	0.45
31:AO:106:PRO:HA	31:AO:109:ARG:HG2	1.99	0.45
31:AO:225:GLN:NE2	37:AU:47:ALA:O	2.50	0.45
40:AX:337:LEU:HG	40:AX:337:LEU:O	2.16	0.45
46:XF:103:GLN:HA	46:XF:106:PHE:CE2	2.52	0.45
60:XU:50:ARG:HB2	60:XU:68:VAL:HG13	1.98	0.45
11:XA:1837:C:O4'	11:XA:1837:C:O2	2.34	0.45
11:XA:2305:U:OP1	59:XT:149:ARG:NH1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:XA:3038:U:O4	11:XA:3045:A:N6	2.49	0.45
54:XO:49:VAL:HA	54:XO:52:MET:HG2	1.99	0.45
56:XQ:107:HIS:O	56:XQ:108:ILE:HG13	2.17	0.45
61:XV:136:ARG:O	61:XV:143:ARG:NH2	2.49	0.45
1:O:104:LYS:O	59:XT:105:GLN:NE2	2.48	0.44
11:XA:2099:U:H2'	11:XA:2100:C:C6	2.52	0.44
26:AJ:61:VAL:O	26:AJ:84:ARG:N	2.46	0.44
45:XE:69:ASP:OD1	45:XE:154:ARG:NH1	2.41	0.44
11:XA:1827:C:C5	11:XA:2698:G:C2	3.05	0.44
11:XA:1897:A:H2'	11:XA:1898:A:H8	1.82	0.44
13:A1:153:SER:OG	13:A1:154:THR:N	2.50	0.44
15:A3:184:GLU:OE1	15:A3:184:GLU:N	2.50	0.44
16:A4:482:ILE:CG2	16:A4:519:TYR:HE2	2.30	0.44
11:XA:2990:A:O2'	90:XA:5143:DOL:O18	2.22	0.44
17:AA:769:G:N2	17:AA:772:A:OP2	2.42	0.44
17:AA:770:C:O2'	17:AA:771:A:OP1	2.32	0.44
17:AA:1106:C:O2'	17:AA:1108:C:OP2	2.27	0.44
17:AA:1234:C:H2'	17:AA:1234:C:O2	2.16	0.44
19:AC:62:ILE:HA	19:AC:66:LYS:HB2	2.00	0.44
23:AG:295:VAL:N	23:AG:298:ILE:O	2.50	0.44
39:AW:107:ILE:O	39:AW:107:ILE:HG23	2.18	0.44
44:XD:207:ILE:O	44:XD:212:THR:OG1	2.32	0.44
60:XU:14:GLY:O	61:XV:208:ARG:NE	2.47	0.44
60:XU:49:THR:O	60:XU:52:ASP:OD1	2.35	0.44
11:XA:1808:A:O2'	11:XA:1810:A:OP1	2.27	0.44
90:XA:5143:DOL:H311	90:XA:5143:DOL:C34	2.46	0.44
17:AA:1132:U:H2'	17:AA:1133:C:C6	2.53	0.44
23:AG:202:LYS:O	23:AG:206:GLU:OE1	2.35	0.44
50:XK:102:ALA:HA	50:XK:105:LYS:HG2	1.98	0.44
53:XN:211:ASN:ND2	53:XN:213:TRP:O	2.51	0.44
60:XU:127:TYR:O	60:XU:131:GLU:OE1	2.36	0.44
11:XA:3212:C:O2	11:XA:3212:C:O4'	2.35	0.44
17:AA:1289:G:O2'	17:AA:1297:G:OP2	2.31	0.44
46:XF:141:ILE:O	46:XF:142:ARG:HB2	2.18	0.44
46:XF:228:GLN:HA	46:XF:231:VAL:HG12	2.00	0.44
53:XN:71:ASP:N	53:XN:71:ASP:OD1	2.50	0.44
4:3:143:ARG:NH2	11:XA:2871:U:OP2	2.50	0.44
6:5:311:ALA:O	6:5:315:LEU:HD23	2.18	0.44
11:XA:1671:G:C6	11:XA:1818:A:N1	2.86	0.44
11:XA:1990:G:OP1	44:XD:269:ARG:NH2	2.49	0.44
17:AA:702:C:O2'	17:AA:842:C:O2	2.29	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:AA:864:U:O4	17:AA:865:A:N6	2.51	0.44
34:AR:135:ARG:NH1	34:AR:236:GLU:OE2	2.51	0.44
36:AT:112:THR:O	36:AT:116:GLU:OE1	2.35	0.44
37:AU:172:ASN:O	37:AU:172:ASN:ND2	2.51	0.44
42:AZ:65:LEU:HD22	42:AZ:71:TYR:HB2	2.00	0.44
7:6:149:GLN:O	7:6:149:GLN:NE2	2.50	0.44
7:6:231:GLU:OE2	7:6:300:THR:N	2.51	0.44
11:XA:2989:G:H5''	11:XA:2990:A:P	2.58	0.44
19:AC:75:ASN:OD1	19:AC:76:LEU:N	2.50	0.44
20:AD:108:ALA:O	20:AD:114:ARG:NH1	2.48	0.44
23:AG:167:GLY:O	23:AG:171:ASN:ND2	2.51	0.44
26:AJ:49:LEU:HD23	26:AJ:50:GLY:N	2.33	0.44
31:AO:81:HIS:ND1	31:AO:82:LYS:O	2.51	0.44
31:AO:148:LYS:O	31:AO:152:GLN:OE1	2.35	0.44
46:XF:280:TYR:CE2	52:XM:125:ARG:HD3	2.53	0.44
8:7:311:THR:OG1	8:7:315:LYS:NZ	2.51	0.44
11:XA:2195:A:HO2'	11:XA:2196:A:P	2.39	0.44
11:XA:3157:C:N3	56:XQ:84:ARG:NH2	2.66	0.44
12:A0:63:ARG:NH1	12:A0:110:ASP:OD2	2.47	0.44
35:AS:18:ASP:OD1	35:AS:19:LEU:N	2.51	0.44
41:AY:339:GLU:OE1	41:AY:339:GLU:N	2.51	0.44
59:XT:100:ASP:HA	59:XT:103:LEU:CD2	2.48	0.44
7:6:36:PRO:O	7:6:37:ASN:OD1	2.36	0.44
23:AG:321:ASP:C	23:AG:321:ASP:OD1	2.55	0.44
34:AR:308:HIS:C	34:AR:310:ASP:H	2.15	0.44
40:AX:350:PRO:O	40:AX:354:GLU:OE1	2.36	0.44
40:AX:393:ARG:O	40:AX:397:TYR:CD2	2.71	0.44
45:XE:275:ARG:HB3	45:XE:284:TYR:CD2	2.53	0.44
22:AF:35:SER:OG	22:AF:36:ARG:N	2.46	0.43
31:AO:163:LEU:HD23	31:AO:163:LEU:H	1.81	0.43
38:AV:168:MET:SD	38:AV:207:SER:N	2.91	0.43
13:A1:320:LEU:O	13:A1:321:ASN:OD1	2.36	0.43
15:A3:161:ARG:NH2	17:AA:1146:C:OP1	2.45	0.43
17:AA:1449:G:C2	17:AA:1450:C:C6	3.07	0.43
17:AA:1554:G:H2'	17:AA:1555:A:O4'	2.18	0.43
40:AX:100:MET:HB3	91:AX:500:GTP:HN1	1.83	0.43
52:XM:254:LYS:O	52:XM:258:THR:HG23	2.18	0.43
54:XO:149:LEU:HA	54:XO:152:LEU:CD2	2.48	0.43
11:XA:2021:U:O4	52:XM:41:ARG:NH2	2.51	0.43
11:XA:2667:U:C2	11:XA:2668:A:C8	3.07	0.43
25:AI:115:GLU:OE2	25:AI:130:THR:OG1	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AI:177:ASP:O	25:AI:179:THR:N	2.51	0.43
48:XI:181:ILE:O	48:XI:182:ASP:OD1	2.37	0.43
65:XZ:84:ASP:OD1	65:XZ:85:ILE:N	2.51	0.43
6:5:174:GLU:OE1	6:5:298:ASN:ND2	2.51	0.43
11:XA:3148:C:H2'	11:XA:3149:C:C6	2.54	0.43
29:AM:111:ARG:NH2	31:AO:232:PRO:O	2.51	0.43
37:AU:112:GLU:OE2	37:AU:115:ARG:NH1	2.52	0.43
60:XU:40:VAL:HG12	60:XU:41:GLN:N	2.33	0.43
61:XV:148:THR:HG22	61:XV:149:ARG:H	1.82	0.43
6:5:391:VAL:O	6:5:391:VAL:HG13	2.17	0.43
11:XA:3143:U:O4	11:XA:3144:A:N6	2.51	0.43
31:AO:151:THR:O	31:AO:154:ILE:HG22	2.17	0.43
32:AP:127:PRO:HA	32:AP:130:LEU:HD23	2.00	0.43
40:AX:297:MET:O	40:AX:297:MET:HG2	2.19	0.43
41:AY:295:GLN:N	41:AY:295:GLN:OE1	2.51	0.43
52:XM:156:VAL:HG22	52:XM:157:GLN:H	1.83	0.43
56:XQ:227:LYS:N	56:XQ:228:PRO:CD	2.81	0.43
57:XR:50:PHE:CD1	58:XS:170:ILE:HD13	2.54	0.43
59:XT:88:TRP:CH2	59:XT:92:LYS:HD2	2.53	0.43
7:6:212:SER:OG	7:6:213:LEU:N	2.51	0.43
17:AA:865:A:H2'	17:AA:866:A:N9	2.34	0.43
24:AH:154:ASP:O	24:AH:158:GLU:HG2	2.17	0.43
44:XD:216:LEU:HD23	44:XD:216:LEU:H	1.84	0.43
45:XE:292:HIS:ND1	45:XE:293:LYS:O	2.51	0.43
11:XA:2956:A:C6	11:XA:2957:G:C4	3.06	0.43
11:XA:3122:U:O2	11:XA:3122:U:O4'	2.36	0.43
16:A4:634:ALA:HB3	16:A4:641:ILE:HG21	2.01	0.43
17:AA:1399:A:H2'	17:AA:1400:U:C6	2.54	0.43
17:AA:1470:A:H2'	17:AA:1471:A:H8	1.84	0.43
29:AM:84:SER:O	29:AM:88:GLU:OE1	2.36	0.43
29:AM:85:LYS:HA	29:AM:88:GLU:OE2	2.19	0.43
30:AN:67:ARG:NH2	30:AN:80:GLU:OE2	2.51	0.43
34:AR:308:HIS:C	34:AR:310:ASP:N	2.71	0.43
49:XJ:127:ASP:OD1	49:XJ:128:GLU:N	2.51	0.43
53:XN:214:THR:O	53:XN:218:ILE:HD12	2.18	0.43
63:XX:82:GLY:N	63:XX:83:GLU:OE1	2.52	0.43
11:XA:1939:G:O2'	11:XA:1973:G:H4'	2.19	0.43
13:A1:295:SER:O	13:A1:299:LEU:HD23	2.19	0.43
15:A3:138:MET:SD	17:AA:1489:G:H5''	2.58	0.43
17:AA:1235:U:H5''	17:AA:1236:C:OP2	2.18	0.43
22:AF:192:ARG:HG3	22:AF:192:ARG:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AT:99:MET:SD	36:AT:100:GLU:N	2.91	0.43
39:AW:96:LYS:O	39:AW:97:ASP:OD1	2.36	0.43
46:XF:185:ASP:OD1	46:XF:185:ASP:C	2.56	0.43
48:XI:112:MET:O	48:XI:116:LEU:HD23	2.19	0.43
4:3:122:TRP:HB2	4:3:150:CYS:SG	2.59	0.43
11:XA:2308:A:OP2	11:XA:2309:A:O2'	2.27	0.43
40:AX:63:HIS:O	40:AX:63:HIS:ND1	2.51	0.43
52:XM:73:PRO:HD2	52:XM:76:ILE:HG21	2.01	0.43
52:XM:208:GLU:O	52:XM:208:GLU:HG2	2.19	0.43
6:5:30:ALA:N	44:XD:201:GLY:O	2.52	0.43
11:XA:2236:C:N4	11:XA:2688:C:O2	2.52	0.43
11:XA:2384:A:N1	11:XA:2409:A:N6	2.66	0.43
11:XA:2558:A:O5'	17:AA:1001:C:N4	2.52	0.43
11:XA:3142:A:H2'	11:XA:3143:U:O4'	2.18	0.43
17:AA:990:U:H2'	17:AA:991:G:O4'	2.19	0.43
31:AO:161:GLY:O	34:AR:223:ARG:NH2	2.51	0.43
33:AQ:46:GLU:OE1	33:AQ:54:ARG:NH2	2.52	0.43
44:XD:113:ARG:O	44:XD:147:ARG:NH1	2.52	0.43
44:XD:258:GLY:H	44:XD:262:ARG:HE	1.67	0.43
2:1:20:MET:SD	2:1:20:MET:N	2.92	0.42
8:7:199:LEU:O	8:7:203:THR:HG23	2.19	0.42
9:8:116:LEU:O	9:8:119:LYS:HG3	2.19	0.42
11:XA:2118:U:C2	11:XA:2119:U:C5	3.07	0.42
11:XA:3188:U:O2'	11:XA:3192:C:N4	2.44	0.42
16:A4:64:THR:HG22	24:AH:64:THR:CG2	2.48	0.42
18:AB:194:ILE:HA	18:AB:220:VAL:O	2.19	0.42
27:AK:70:VAL:HA	27:AK:73:GLU:OE2	2.19	0.42
28:AL:127:ALA:HA	28:AL:130:ILE:HG12	2.01	0.42
41:AY:377:ARG:HA	41:AY:380:PHE:CE2	2.54	0.42
64:XY:143:ASP:OD1	64:XY:143:ASP:C	2.57	0.42
16:A4:243:ASN:O	16:A4:247:ILE:HG12	2.19	0.42
16:A4:372:TYR:O	16:A4:376:ILE:HG12	2.19	0.42
17:AA:681:U:H2'	17:AA:682:A:C8	2.54	0.42
17:AA:826:A:N7	26:AJ:55:ARG:CZ	2.81	0.42
17:AA:948:U:H2'	17:AA:949:U:O4'	2.19	0.42
17:AA:1134:G:N7	26:AJ:35:GLN:NE2	2.59	0.42
17:AA:1355:G:N2	17:AA:1356:A:N1	2.54	0.42
17:AA:1367:A:N6	17:AA:1388:C:O4'	2.52	0.42
24:AH:77:SER:HB2	24:AH:173:THR:OG1	2.18	0.42
25:AI:94:ASN:OD1	25:AI:95:THR:N	2.52	0.42
11:XA:1884:G:O2'	11:XA:1895:C:O2	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:AA:805:C:O2	17:AA:805:C:O4'	2.36	0.42
23:AG:276:ARG:HG3	23:AG:277:LYS:H	1.84	0.42
43:XB:1623:G:OP2	55:XP:87:HIS:HB2	2.18	0.42
61:XV:176:ASP:OD1	61:XV:177:THR:N	2.52	0.42
6:5:177:CYS:O	6:5:180:ILE:HG22	2.18	0.42
7:6:280:ASP:OD1	7:6:281:PHE:N	2.52	0.42
8:7:150:MET:HE1	8:7:297:PHE:HB2	2.02	0.42
11:XA:2233:U:C2	45:XE:248:ILE:CD1	3.03	0.42
11:XA:2933:G:N2	11:XA:2936:U:O2	2.51	0.42
12:A0:79:LEU:HD11	12:A0:147:GLU:HG3	2.00	0.42
22:AF:196:HIS:HB3	22:AF:204:LYS:HD3	2.01	0.42
28:AL:175:TYR:O	28:AL:179:GLU:OE1	2.37	0.42
53:XN:78:GLU:OE2	53:XN:158:ARG:NE	2.49	0.42
56:XQ:168:ASN:O	56:XQ:171:VAL:HG22	2.19	0.42
63:XX:134:LEU:HD13	63:XX:144:TYR:CE1	2.55	0.42
17:AA:656:U:N3	17:AA:659:U:OP2	2.43	0.42
22:AF:114:THR:HG22	22:AF:202:PRO:HA	2.00	0.42
46:XF:171:ALA:O	46:XF:174:LEU:HD23	2.19	0.42
49:XJ:75:ASP:O	49:XJ:76:ARG:HB3	2.20	0.42
57:XR:98:ASN:OD1	57:XR:101:VAL:HG22	2.18	0.42
16:A4:638:SER:OG	16:A4:640:PRO:HD2	2.20	0.42
17:AA:769:G:OP2	30:AN:73:ARG:NH2	2.53	0.42
36:AT:116:GLU:O	36:AT:119:GLU:HG3	2.19	0.42
38:AV:225:LEU:HD11	38:AV:263:MET:CG	2.50	0.42
50:XK:7:ALA:HB3	50:XK:8:PRO:HD3	2.02	0.42
52:XM:191:VAL:HB	52:XM:192:PRO:HD3	2.01	0.42
8:7:235:TYR:O	8:7:238:ASP:OD1	2.37	0.42
11:XA:3007:C:N4	11:XA:3054:G:C5	2.87	0.42
13:A1:189:LYS:O	13:A1:193:LEU:HD23	2.20	0.42
15:A3:145:LYS:NZ	17:AA:1584:A:P	2.92	0.42
16:A4:319:LEU:HA	16:A4:322:HIS:CD2	2.55	0.42
16:A4:643:GLU:O	16:A4:646:THR:OG1	2.34	0.42
17:AA:991:G:N1	17:AA:992:U:O4	2.52	0.42
17:AA:993:A:OP1	25:AI:192:ARG:NH2	2.50	0.42
20:AD:293:ASP:OD1	20:AD:307:LYS:N	2.43	0.42
26:AJ:49:LEU:HD23	26:AJ:51:PRO:HD2	2.02	0.42
46:XF:225:GLU:OE1	46:XF:225:GLU:N	2.40	0.42
6:5:413:LYS:O	6:5:417:LEU:HD23	2.20	0.42
11:XA:2015:G:H4'	52:XM:55:GLY:HA2	2.02	0.42
11:XA:2453:G:C6	11:XA:2672:A:C6	3.07	0.42
11:XA:2529:U:O2'	44:XD:206:TYR:O	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:A1:53:LEU:HB2	16:A4:518:GLU:OE2	2.20	0.42
17:AA:1156:C:C2	17:AA:1157:U:C5	3.08	0.42
17:AA:1200:G:N2	17:AA:1418:G:O2'	2.52	0.42
44:XD:163:ILE:HG22	44:XD:164:LEU:N	2.34	0.42
45:XE:119:VAL:HG21	45:XE:284:TYR:HB3	2.01	0.42
46:XF:77:VAL:O	46:XF:77:VAL:HG13	2.19	0.42
59:XT:123:GLU:O	59:XT:126:ASP:OD1	2.37	0.42
61:XV:188:VAL:O	61:XV:188:VAL:HG13	2.20	0.42
65:XZ:84:ASP:O	65:XZ:88:MET:HG2	2.19	0.42
7:6:214:TRP:O	7:6:240:ILE:HD12	2.19	0.42
7:6:302:ASP:OD1	7:6:303:PHE:N	2.53	0.42
7:6:360:ARG:NH1	11:XA:2870:G:O6	2.51	0.42
11:XA:2665:U:OP2	54:XO:17:ARG:HD2	2.19	0.42
16:A4:335:PHE:HA	16:A4:338:ILE:HG22	2.01	0.42
17:AA:992:U:O2'	17:AA:994:A:OP2	2.30	0.42
34:AR:254:ASP:OD1	34:AR:259:TYR:OH	2.38	0.42
11:XA:2455:U:C2	11:XA:2456:U:C5	3.08	0.42
16:A4:640:PRO:O	16:A4:643:GLU:HG2	2.20	0.42
17:AA:1343:A:N3	17:AA:1343:A:H2'	2.35	0.42
18:AB:145:ILE:CD1	18:AB:193:ILE:HG23	2.50	0.42
34:AR:67:LYS:N	34:AR:68:PRO:CD	2.82	0.42
38:AV:82:ARG:CZ	38:AV:121:ALA:HB2	2.50	0.42
46:XF:141:ILE:HG22	46:XF:142:ARG:N	2.35	0.42
49:XJ:144:ILE:O	49:XJ:147:SER:OG	2.31	0.42
11:XA:1689:C:N3	11:XA:1690:C:N4	2.68	0.41
11:XA:2135:A:H2'	11:XA:2135:A:N3	2.35	0.41
14:A2:49:MET:O	14:A2:53:MET:HG2	2.20	0.41
18:AB:186:THR:HG23	18:AB:186:THR:O	2.20	0.41
18:AB:220:VAL:HG22	18:AB:234:TYR:HB2	2.02	0.41
28:AL:130:ILE:HG13	28:AL:131:ALA:N	2.35	0.41
30:AN:53:ASP:OD2	30:AN:57:GLN:N	2.52	0.41
38:AV:36:ASP:OD1	38:AV:37:SER:N	2.53	0.41
38:AV:79:ILE:CD1	38:AV:88:ALA:HB2	2.50	0.41
40:AX:72:PRO:O	40:AX:76:GLU:OE1	2.38	0.41
47:XH:58:ARG:NH1	47:XH:77:HIS:O	2.53	0.41
54:XO:26:ILE:CD1	56:XQ:264:TRP:CB	2.98	0.41
56:XQ:99:MET:SD	56:XQ:167:TYR:CE1	3.12	0.41
60:XU:9:LEU:N	64:XY:183:GLN:OE1	2.53	0.41
61:XV:60:ASP:OD1	61:XV:61:THR:N	2.52	0.41
61:XV:190:CYS:O	61:XV:191:LEU:HB3	2.20	0.41
9:8:165:ASP:OD1	9:8:165:ASP:N	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:XA:1770:G:C2	11:XA:1771:C:C5	3.08	0.41
11:XA:2525:C:OP2	11:XA:2526:C:O2'	2.34	0.41
11:XA:2667:U:N3	11:XA:2668:A:C8	2.88	0.41
14:A2:78:ALA:O	14:A2:82:GLU:OE1	2.39	0.41
37:AU:57:MET:O	37:AU:61:GLN:OE1	2.38	0.41
43:XB:1632:U:N3	43:XB:1635:C:OP2	2.49	0.41
44:XD:274:ARG:O	44:XD:276:HIS:ND1	2.51	0.41
50:XK:48:HIS:CD2	50:XK:51:SER:HG	2.38	0.41
50:XK:135:GLU:HA	50:XK:138:LEU:CD2	2.49	0.41
53:XN:105:MET:HA	53:XN:108:THR:HG22	2.02	0.41
65:XZ:71:ARG:NH1	65:XZ:73:LYS:O	2.53	0.41
11:XA:2558:A:C4'	11:XA:2559:U:OP2	2.68	0.41
11:XA:3115:U:H2'	11:XA:3116:C:C6	2.55	0.41
16:A4:455:ASN:HA	16:A4:486:TYR:CE1	2.55	0.41
17:AA:658:G:C2	17:AA:659:U:C5	3.09	0.41
35:AS:15:ARG:O	35:AS:18:ASP:OD1	2.37	0.41
40:AX:159:HIS:NE2	40:AX:266:ASN:OD1	2.54	0.41
46:XF:141:ILE:HG22	46:XF:142:ARG:H	1.86	0.41
53:XN:198:MET:O	53:XN:201:ASP:OD1	2.38	0.41
53:XN:216:GLU:HG2	53:XN:217:ARG:N	2.35	0.41
63:XX:149:PRO:O	63:XX:152:ASP:N	2.53	0.41
7:6:289:PRO:O	7:6:290:CYS:HB2	2.20	0.41
7:6:324:ASP:OD1	7:6:325:ASP:N	2.50	0.41
9:8:169:PHE:HB2	9:8:170:PRO:HD3	2.02	0.41
11:XA:3217:A:H4'	54:XO:11:HIS:ND1	2.35	0.41
15:A3:151:ARG:CD	17:AA:1154:A:O4'	2.68	0.41
16:A4:59:ILE:HG21	24:AH:69:PRO:HB2	2.01	0.41
17:AA:718:A:H2'	17:AA:719:G:O4'	2.20	0.41
17:AA:1374:A:N6	17:AA:1379:A:C6	2.88	0.41
21:AE:59:ASN:OD1	21:AE:60:ARG:N	2.51	0.41
23:AG:204:GLU:HA	23:AG:207:GLU:OE2	2.20	0.41
50:XK:136:ASP:OD1	50:XK:137:ILE:N	2.54	0.41
59:XT:159:HIS:HB2	59:XT:163:ARG:O	2.21	0.41
1:0:138:ARG:HA	1:0:141:ILE:HG12	2.01	0.41
8:7:152:CYS:SG	8:7:153:VAL:N	2.94	0.41
17:AA:1161:A:C2	17:AA:1162:A:C8	3.08	0.41
17:AA:1210:U:H2'	17:AA:1211:G:C8	2.56	0.41
17:AA:1262:C:C4	17:AA:1263:G:C5	3.09	0.41
23:AG:276:ARG:HG3	23:AG:277:LYS:N	2.34	0.41
26:AJ:49:LEU:CD2	26:AJ:51:PRO:HD2	2.51	0.41
44:XD:251:ASP:OD1	44:XD:251:ASP:C	2.58	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:XJ:48:GLN:OE1	49:XJ:76:ARG:NH2	2.48	0.41
57:XR:66:THR:HA	57:XR:69:ILE:HG22	2.03	0.41
3:2:49:ARG:NH2	11:XA:2500:A:C6	2.89	0.41
4:3:169:ARG:H	11:XA:1891:A:P	2.44	0.41
15:A3:158:GLN:O	15:A3:162:LEU:HD23	2.20	0.41
16:A4:561:SER:O	16:A4:563:PRO:HD3	2.21	0.41
16:A4:616:ASP:HA	16:A4:619:LYS:HG2	2.01	0.41
16:A4:639:LEU:N	16:A4:640:PRO:CD	2.83	0.41
21:AE:107:GLY:HA2	32:AP:64:LYS:HG2	2.01	0.41
40:AX:371:ALA:N	40:AX:372:PRO:CD	2.84	0.41
46:XF:109:ILE:O	46:XF:109:ILE:HG13	2.21	0.41
48:XI:166:ARG:HA	48:XI:169:ARG:HG2	2.02	0.41
2:1:14:LYS:NZ	11:XA:2849:G:OP1	2.48	0.41
4:3:154:GLN:O	4:3:158:LEU:HD23	2.21	0.41
6:5:179:VAL:O	6:5:182:ASP:OD1	2.39	0.41
11:XA:2546:G:C2	11:XA:2547:C:C5	3.09	0.41
11:XA:3061:G:H2'	11:XA:3062:U:O4'	2.20	0.41
17:AA:785:C:C2	17:AA:786:G:C8	3.09	0.41
17:AA:920:G:C2	17:AA:921:U:C4	3.08	0.41
17:AA:1283:A:O2'	20:AD:347:GLN:NE2	2.41	0.41
18:AB:162:CYS:O	18:AB:261:LYS:NZ	2.47	0.41
21:AE:120:THR:HG23	21:AE:120:THR:O	2.21	0.41
22:AF:66:ARG:O	22:AF:70:LYS:HG2	2.21	0.41
49:XJ:127:ASP:O	49:XJ:131:ALA:N	2.49	0.41
60:XU:47:GLU:OE1	60:XU:47:GLU:N	2.54	0.41
64:XY:140:ASP:O	64:XY:143:ASP:OD1	2.38	0.41
8:7:225:VAL:O	8:7:229:ILE:HG12	2.21	0.41
11:XA:2290:A:H2'	11:XA:2291:A:O4'	2.20	0.41
11:XA:2439:U:H2'	11:XA:2440:G:C8	2.56	0.41
11:XA:2668:A:C2	11:XA:2669:A:C5	3.09	0.41
11:XA:2721:G:H21	87:A:5:MHU:CE2	2.34	0.41
27:AK:49:ASP:OD1	27:AK:49:ASP:N	2.54	0.41
31:AO:148:LYS:O	31:AO:151:THR:OG1	2.30	0.41
36:AT:7:PHE:HB2	36:AT:10:ARG:HE	1.86	0.41
40:AX:164:ASN:OD1	40:AX:166:ARG:NH1	2.53	0.41
43:XB:1607:U:O2'	43:XB:1608:G:H5'	2.21	0.41
46:XF:116:THR:O	46:XF:120:VAL:HG23	2.21	0.41
52:XM:61:THR:O	52:XM:61:THR:HG22	2.20	0.41
54:XO:94:ALA:HB3	54:XO:95:PRO:HD3	2.03	0.41
61:XV:148:THR:HG22	61:XV:149:ARG:N	2.36	0.41
11:XA:1681:G:OP2	64:XY:230:LYS:NZ	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:XA:1977:U:H2'	11:XA:1978:A:H8	1.86	0.41
11:XA:2056:G:C4	11:XA:2057:C:C5	3.09	0.41
11:XA:2550:A:C6	11:XA:2551:G:N7	2.89	0.41
11:XA:2655:G:N2	11:XA:2659:C:O2'	2.54	0.41
11:XA:3152:C:O4'	51:XL:95:ARG:CZ	2.68	0.41
11:XA:3189:C:C2'	11:XA:3190:A:OP2	2.69	0.41
16:A4:114:GLU:OE2	19:AC:141:THR:CG2	2.68	0.41
16:A4:416:PHE:CE2	16:A4:457:TYR:CG	3.09	0.41
16:A4:491:GLN:O	16:A4:495:HIS:ND1	2.45	0.41
17:AA:1024:G:C4	17:AA:1026:A:OP2	2.74	0.41
17:AA:1516:G:C6	17:AA:1517:A:N6	2.89	0.41
18:AB:93:HIS:NE2	18:AB:224:ASP:OD2	2.54	0.41
20:AD:250:GLY:N	20:AD:326:LEU:O	2.53	0.41
20:AD:273:ASN:HA	20:AD:276:VAL:HG12	2.03	0.41
31:AO:54:GLU:N	31:AO:55:PRO:CD	2.84	0.41
31:AO:105:CYS:HB2	31:AO:106:PRO:HD2	2.02	0.41
36:AT:92:THR:HG22	36:AT:92:THR:O	2.21	0.41
38:AV:347:ILE:O	38:AV:347:ILE:HG22	2.21	0.41
46:XF:184:GLN:O	46:XF:185:ASP:OD1	2.39	0.41
48:XI:181:ILE:O	48:XI:184:THR:OG1	2.34	0.41
51:XL:43:ASN:ND2	51:XL:117:THR:OG1	2.53	0.41
53:XN:101:HIS:O	53:XN:105:MET:SD	2.79	0.41
1:0:155:GLU:HG3	1:0:172:LYS:HE3	2.03	0.41
6:5:120:ALA:HB3	6:5:314:ILE:HD11	2.03	0.41
7:6:78:PHE:HZ	62:XW:134:VAL:HA	1.86	0.41
7:6:120:GLU:OE2	55:XP:116:TYR:OH	2.33	0.41
11:XA:1805:A:O4'	61:XV:94:HIS:NE2	2.53	0.41
11:XA:2808:U:H2'	11:XA:2809:C:O4'	2.21	0.41
46:XF:91:PRO:O	46:XF:176:VAL:HG11	2.20	0.41
48:XI:198:PRO:O	48:XI:199:SER:C	2.60	0.41
50:XK:116:LEU:HD23	50:XK:116:LEU:H	1.85	0.41
52:XM:100:ARG:O	52:XM:104:LEU:HG	2.20	0.41
61:XV:101:THR:HG22	61:XV:101:THR:O	2.21	0.41
61:XV:197:GLU:HA	61:XV:200:GLU:OE2	2.21	0.41
64:XY:231:ALA:HA	64:XY:234:LEU:CD2	2.51	0.41
7:6:247:GLU:OE1	7:6:247:GLU:N	2.51	0.40
11:XA:1805:A:OP2	61:XV:111:SER:OG	2.34	0.40
11:XA:2044:A:C6	11:XA:2045:A:C5	3.08	0.40
11:XA:2187:C:O2'	49:XJ:106:LYS:NZ	2.51	0.40
11:XA:2821:C:O2'	11:XA:2822:C:H5'	2.21	0.40
17:AA:650:U:OP2	20:AD:333:TYR:OH	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:AA:1193:U:O3'	22:AF:178:ARG:NH2	2.50	0.40
19:AC:139:SER:O	19:AC:143:LEU:HG	2.21	0.40
27:AK:50:GLU:O	27:AK:54:ILE:HD12	2.20	0.40
34:AR:128:MET:SD	34:AR:128:MET:N	2.92	0.40
36:AT:99:MET:HA	36:AT:102:ILE:HG12	2.03	0.40
42:AZ:64:THR:O	42:AZ:68:LEU:HD23	2.21	0.40
46:XF:128:TRP:HB2	46:XF:129:PRO:CD	2.51	0.40
56:XQ:74:ARG:HG3	56:XQ:283:TRP:CZ2	2.57	0.40
57:XR:103:ALA:O	57:XR:107:ILE:HG12	2.21	0.40
1:0:84:ARG:HB2	11:XA:2307:U:H1'	2.03	0.40
8:7:309:HIS:H	8:7:312:ILE:HD11	1.86	0.40
11:XA:2138:U:O2'	11:XA:2151:A:N3	2.43	0.40
11:XA:2429:A:C2	11:XA:2435:G:C5	3.09	0.40
11:XA:2459:A:N6	11:XA:2668:A:O2'	2.54	0.40
11:XA:3007:C:O2'	11:XA:3008:C:H5'	2.22	0.40
12:A0:201:TRP:CG	17:AA:844:A:C2	3.09	0.40
13:A1:202:THR:HG23	13:A1:204:VAL:HG22	2.02	0.40
17:AA:1024:G:N2	17:AA:1028:G:C4	2.90	0.40
17:AA:1172:C:C2	17:AA:1173:C:C5	3.09	0.40
17:AA:1443:U:OP2	27:AK:102:ARG:NH1	2.51	0.40
18:AB:222:ILE:O	18:AB:222:ILE:HG13	2.20	0.40
20:AD:318:ARG:HA	20:AD:321:ILE:HG12	2.02	0.40
24:AH:70:ASP:OD1	24:AH:71:ILE:N	2.55	0.40
26:AJ:47:ARG:HE	26:AJ:48:LYS:H	1.68	0.40
34:AR:160:ASP:OD1	34:AR:161:ILE:N	2.53	0.40
34:AR:162:SER:O	34:AR:170:ARG:NH1	2.50	0.40
37:AU:130:GLU:O	37:AU:133:GLN:HG2	2.22	0.40
40:AX:181:PRO:HB2	40:AX:233:VAL:HG22	2.03	0.40
49:XJ:30:MET:HB2	49:XJ:31:PRO:HD3	2.03	0.40
49:XJ:108:VAL:O	49:XJ:108:VAL:HG12	2.21	0.40
59:XT:83:SER:HB3	59:XT:86:LYS:HG2	2.03	0.40
60:XU:58:GLU:OE2	60:XU:65:VAL:N	2.54	0.40
62:XW:56:MET:SD	62:XW:56:MET:N	2.89	0.40
3:2:56:SER:OG	11:XA:1980:A:OP1	2.34	0.40
6:5:295:ASP:OD2	6:5:304:LEU:N	2.54	0.40
11:XA:1683:C:N3	11:XA:1770:G:C6	2.89	0.40
11:XA:2241:A:OP2	50:XK:68:SER:OG	2.28	0.40
11:XA:2561:U:H2'	11:XA:2562:U:O4'	2.21	0.40
13:A1:189:LYS:NZ	13:A1:235:ASN:O	2.43	0.40
16:A4:116:VAL:HG21	20:AD:141:TRP:HZ3	1.87	0.40
17:AA:1012:A:O2'	17:AA:1065:C:N4	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:AA:1526:U:O2'	17:AA:1526:U:O2	2.27	0.40
26:AJ:101:THR:HG23	26:AJ:101:THR:O	2.21	0.40
45:XE:104:LEU:HB2	45:XE:121:LEU:HB2	2.03	0.40
1:O:91:ARG:HG2	1:O:95:ARG:HD2	2.03	0.40
10:9:24:LYS:O	11:XA:2341:C:N4	2.54	0.40
11:XA:1846:C:C4	11:XA:1847:U:C4	3.09	0.40
11:XA:2151:A:H2'	11:XA:2152:A:C8	2.56	0.40
11:XA:2182:G:H2'	11:XA:2183:C:C6	2.55	0.40
11:XA:2610:U:C2	11:XA:2611:C:C5	3.09	0.40
14:A2:68:LYS:O	14:A2:71:GLN:HG3	2.21	0.40
16:A4:167:LYS:HG3	16:A4:168:ALA:N	2.37	0.40
16:A4:409:ASP:O	16:A4:412:ASP:OD2	2.40	0.40
17:AA:1462:G:C2	17:AA:1463:G:C5	3.10	0.40
40:AX:374:GLU:HG2	40:AX:375:GLU:N	2.35	0.40
53:XN:172:VAL:HG13	53:XN:175:PHE:CZ	2.57	0.40
53:XN:194:THR:O	53:XN:197:LYS:HG2	2.21	0.40
8:7:238:ASP:OD1	8:7:238:ASP:C	2.60	0.40
11:XA:2740:A:H2'	11:XA:2741:A:H8	1.86	0.40
11:XA:3207:A:C5	45:XE:176:VAL:HG21	2.56	0.40
17:AA:797:C:C2	17:AA:798:C:C5	3.10	0.40
17:AA:846:A:OP2	17:AA:847:G:N7	2.54	0.40
17:AA:1144:U:O2	17:AA:1145:A:C8	2.75	0.40
17:AA:1389:G:N2	17:AA:1416:A:N7	2.70	0.40
18:AB:164:GLU:OE1	23:AG:145:ARG:NH2	2.54	0.40
18:AB:196:LEU:O	18:AB:222:ILE:HD11	2.21	0.40
24:AH:158:GLU:OE2	41:AY:313:PHE:O	2.39	0.40
30:AN:85:VAL:HG13	30:AN:86:PHE:N	2.37	0.40
36:AT:101:HIS:O	36:AT:105:ILE:HD12	2.21	0.40
52:XM:53:HIS:O	52:XM:58:GLN:NE2	2.55	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	106/188 (56%)	103 (97%)	3 (3%)	0	100	100
2	1	51/65 (78%)	50 (98%)	1 (2%)	0	100	100
3	2	44/92 (48%)	43 (98%)	1 (2%)	0	100	100
4	3	93/188 (50%)	93 (100%)	0	0	100	100
5	4	36/103 (35%)	35 (97%)	1 (3%)	0	100	100
6	5	389/423 (92%)	365 (94%)	24 (6%)	0	100	100
7	6	352/380 (93%)	325 (92%)	27 (8%)	0	100	100
8	7	285/338 (84%)	265 (93%)	20 (7%)	0	100	100
9	8	137/206 (66%)	131 (96%)	6 (4%)	0	100	100
10	9	122/137 (89%)	115 (94%)	7 (6%)	0	100	100
12	A0	197/218 (90%)	189 (96%)	8 (4%)	0	100	100
13	A1	273/323 (84%)	258 (94%)	15 (6%)	0	100	100
14	A2	114/118 (97%)	110 (96%)	4 (4%)	0	100	100
15	A3	67/199 (34%)	66 (98%)	1 (2%)	0	100	100
16	A4	526/689 (76%)	493 (94%)	33 (6%)	0	100	100
18	AB	216/296 (73%)	211 (98%)	5 (2%)	0	100	100
19	AC	130/167 (78%)	128 (98%)	2 (2%)	0	100	100
20	AD	341/430 (79%)	325 (95%)	16 (5%)	0	100	100
21	AE	120/125 (96%)	116 (97%)	4 (3%)	0	100	100
22	AF	197/242 (81%)	195 (99%)	2 (1%)	0	100	100
23	AG	300/396 (76%)	288 (96%)	12 (4%)	0	100	100
24	AH	133/201 (66%)	124 (93%)	9 (7%)	0	100	100
25	AI	134/194 (69%)	126 (94%)	8 (6%)	0	100	100
26	AJ	106/138 (77%)	98 (92%)	8 (8%)	0	100	100
27	AK	99/128 (77%)	97 (98%)	2 (2%)	0	100	100
28	AL	162/257 (63%)	156 (96%)	6 (4%)	0	100	100
29	AM	114/137 (83%)	113 (99%)	1 (1%)	0	100	100
30	AN	105/130 (81%)	103 (98%)	2 (2%)	0	100	100
31	AO	183/258 (71%)	179 (98%)	4 (2%)	0	100	100
32	AP	93/142 (66%)	86 (92%)	7 (8%)	0	100	100
33	AQ	83/87 (95%)	78 (94%)	5 (6%)	0	100	100
34	AR	248/360 (69%)	239 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	AS	131/190 (69%)	123 (94%)	8 (6%)	0	100	100
36	AT	160/173 (92%)	150 (94%)	10 (6%)	0	100	100
37	AU	171/205 (83%)	168 (98%)	3 (2%)	0	100	100
38	AV	341/414 (82%)	318 (93%)	23 (7%)	0	100	100
39	AW	95/187 (51%)	90 (95%)	5 (5%)	0	100	100
40	AX	346/398 (87%)	328 (95%)	18 (5%)	0	100	100
41	AY	111/395 (28%)	106 (96%)	5 (4%)	0	100	100
42	AZ	84/106 (79%)	81 (96%)	3 (4%)	0	100	100
44	XD	234/305 (77%)	217 (93%)	15 (6%)	2 (1%)	17	56
45	XE	302/348 (87%)	291 (96%)	11 (4%)	0	100	100
46	XF	248/311 (80%)	237 (96%)	11 (4%)	0	100	100
47	XH	93/267 (35%)	89 (96%)	4 (4%)	0	100	100
48	XI	209/261 (80%)	193 (92%)	16 (8%)	0	100	100
49	XJ	168/192 (88%)	156 (93%)	12 (7%)	0	100	100
50	XK	175/178 (98%)	167 (95%)	8 (5%)	0	100	100
51	XL	113/145 (78%)	108 (96%)	5 (4%)	0	100	100
52	XM	285/296 (96%)	273 (96%)	12 (4%)	0	100	100
53	XN	219/251 (87%)	208 (95%)	11 (5%)	0	100	100
54	XO	150/175 (86%)	142 (95%)	8 (5%)	0	100	100
55	XP	141/180 (78%)	131 (93%)	10 (7%)	0	100	100
56	XQ	236/292 (81%)	222 (94%)	14 (6%)	0	100	100
57	XR	138/149 (93%)	131 (95%)	7 (5%)	0	100	100
58	XS	158/205 (77%)	151 (96%)	7 (4%)	0	100	100
59	XT	164/206 (80%)	159 (97%)	5 (3%)	0	100	100
60	XU	137/153 (90%)	130 (95%)	7 (5%)	0	100	100
61	XV	200/216 (93%)	191 (96%)	9 (4%)	0	100	100
62	XW	109/148 (74%)	105 (96%)	4 (4%)	0	100	100
63	XX	241/256 (94%)	230 (95%)	10 (4%)	1 (0%)	34	72
64	XY	176/250 (70%)	168 (96%)	8 (4%)	0	100	100
65	XZ	118/161 (73%)	112 (95%)	6 (5%)	0	100	100
66	a	93/142 (66%)	86 (92%)	7 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	b	146/215 (68%)	132 (90%)	14 (10%)	0	100	100
68	c	271/332 (82%)	257 (95%)	14 (5%)	0	100	100
69	d	212/306 (69%)	200 (94%)	11 (5%)	1 (0%)	29	68
70	e	211/279 (76%)	203 (96%)	8 (4%)	0	100	100
71	f	139/212 (66%)	133 (96%)	6 (4%)	0	100	100
72	g	130/166 (78%)	124 (95%)	6 (5%)	0	100	100
73	h	106/158 (67%)	99 (93%)	7 (7%)	0	100	100
74	i	95/128 (74%)	93 (98%)	2 (2%)	0	100	100
75	j	84/123 (68%)	83 (99%)	1 (1%)	0	100	100
76	k	93/112 (83%)	88 (95%)	5 (5%)	0	100	100
77	l	78/138 (56%)	73 (94%)	5 (6%)	0	100	100
78	m	58/128 (45%)	52 (90%)	6 (10%)	0	100	100
79	o	92/102 (90%)	89 (97%)	3 (3%)	0	100	100
80	p	119/206 (58%)	113 (95%)	6 (5%)	0	100	100
81	q	162/222 (73%)	155 (96%)	7 (4%)	0	100	100
82	r	144/196 (74%)	139 (96%)	5 (4%)	0	100	100
85	s	366/439 (83%)	346 (94%)	20 (6%)	0	100	100
86	t1	45/198 (23%)	39 (87%)	6 (13%)	0	100	100
86	t2	28/198 (14%)	28 (100%)	0	0	100	100
86	t3	28/198 (14%)	27 (96%)	1 (4%)	0	100	100
86	t4	27/198 (14%)	26 (96%)	1 (4%)	0	100	100
86	t5	27/198 (14%)	26 (96%)	1 (4%)	0	100	100
86	t6	25/198 (13%)	25 (100%)	0	0	100	100
87	A	2/8 (25%)	0	1 (50%)	1 (50%)	0	0
All	All	13790/19168 (72%)	13114 (95%)	671 (5%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
63	XX	150	LYS
87	A	4	PRO
44	XD	208	ARG
44	XD	207	ILE
69	d	289	PRO

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	0	97/164 (59%)	97 (100%)	0	100	100
2	1	50/60 (83%)	50 (100%)	0	100	100
3	2	40/72 (56%)	40 (100%)	0	100	100
4	3	88/166 (53%)	88 (100%)	0	100	100
5	4	37/89 (42%)	37 (100%)	0	100	100
6	5	353/368 (96%)	352 (100%)	1 (0%)	92	95
7	6	313/332 (94%)	312 (100%)	1 (0%)	92	95
8	7	267/303 (88%)	267 (100%)	0	100	100
9	8	128/190 (67%)	127 (99%)	1 (1%)	81	89
10	9	104/112 (93%)	104 (100%)	0	100	100
12	A0	176/190 (93%)	175 (99%)	1 (1%)	86	92
13	A1	253/291 (87%)	252 (100%)	1 (0%)	91	94
14	A2	99/101 (98%)	97 (98%)	2 (2%)	55	73
15	A3	63/166 (38%)	63 (100%)	0	100	100
16	A4	494/609 (81%)	490 (99%)	4 (1%)	81	89
18	AB	192/249 (77%)	192 (100%)	0	100	100
19	AC	115/143 (80%)	115 (100%)	0	100	100
20	AD	283/357 (79%)	282 (100%)	1 (0%)	91	94
21	AE	104/107 (97%)	104 (100%)	0	100	100
22	AF	178/209 (85%)	178 (100%)	0	100	100
23	AG	264/342 (77%)	264 (100%)	0	100	100
24	AH	125/180 (69%)	125 (100%)	0	100	100
25	AI	104/147 (71%)	104 (100%)	0	100	100
26	AJ	93/118 (79%)	93 (100%)	0	100	100
27	AK	91/113 (80%)	91 (100%)	0	100	100
28	AL	152/226 (67%)	152 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	AM	95/113 (84%)	95 (100%)	0	100	100
30	AN	93/115 (81%)	93 (100%)	0	100	100
31	AO	166/230 (72%)	166 (100%)	0	100	100
32	AP	86/123 (70%)	86 (100%)	0	100	100
33	AQ	77/79 (98%)	77 (100%)	0	100	100
34	AR	229/318 (72%)	227 (99%)	2 (1%)	78	87
35	AS	115/164 (70%)	115 (100%)	0	100	100
36	AT	150/157 (96%)	148 (99%)	2 (1%)	69	82
37	AU	149/174 (86%)	148 (99%)	1 (1%)	84	90
38	AV	315/364 (86%)	314 (100%)	1 (0%)	92	95
39	AW	84/158 (53%)	84 (100%)	0	100	100
40	AX	307/351 (88%)	305 (99%)	2 (1%)	84	90
41	AY	104/357 (29%)	104 (100%)	0	100	100
42	AZ	79/95 (83%)	79 (100%)	0	100	100
44	XD	190/245 (78%)	189 (100%)	1 (0%)	88	93
45	XE	259/290 (89%)	259 (100%)	0	100	100
46	XF	217/262 (83%)	217 (100%)	0	100	100
47	XH	86/228 (38%)	86 (100%)	0	100	100
48	XI	194/232 (84%)	194 (100%)	0	100	100
49	XJ	133/150 (89%)	131 (98%)	2 (2%)	65	80
50	XK	155/156 (99%)	155 (100%)	0	100	100
51	XL	98/124 (79%)	98 (100%)	0	100	100
52	XM	245/249 (98%)	244 (100%)	1 (0%)	91	94
53	XN	188/211 (89%)	188 (100%)	0	100	100
54	XO	133/150 (89%)	133 (100%)	0	100	100
55	XP	125/155 (81%)	125 (100%)	0	100	100
56	XQ	220/256 (86%)	220 (100%)	0	100	100
57	XR	118/126 (94%)	117 (99%)	1 (1%)	81	89
58	XS	145/180 (81%)	145 (100%)	0	100	100
59	XT	146/176 (83%)	144 (99%)	2 (1%)	67	81
60	XU	126/135 (93%)	126 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
61	XV	179/191 (94%)	177 (99%)	2 (1%)	73	85
62	XW	91/119 (76%)	89 (98%)	2 (2%)	52	71
63	XX	219/229 (96%)	218 (100%)	1 (0%)	88	93
64	XY	161/223 (72%)	161 (100%)	0	100	100
65	XZ	111/147 (76%)	110 (99%)	1 (1%)	78	87
66	a	93/133 (70%)	93 (100%)	0	100	100
67	b	130/186 (70%)	130 (100%)	0	100	100
68	c	241/288 (84%)	240 (100%)	1 (0%)	91	94
69	d	196/274 (72%)	196 (100%)	0	100	100
70	e	188/236 (80%)	186 (99%)	2 (1%)	73	85
71	f	128/188 (68%)	128 (100%)	0	100	100
72	g	122/148 (82%)	122 (100%)	0	100	100
73	h	103/148 (70%)	103 (100%)	0	100	100
74	i	86/110 (78%)	86 (100%)	0	100	100
75	j	68/97 (70%)	68 (100%)	0	100	100
76	k	80/90 (89%)	80 (100%)	0	100	100
77	l	74/116 (64%)	74 (100%)	0	100	100
78	m	54/113 (48%)	54 (100%)	0	100	100
79	o	80/87 (92%)	80 (100%)	0	100	100
80	p	117/181 (65%)	117 (100%)	0	100	100
81	q	141/178 (79%)	140 (99%)	1 (1%)	84	90
82	r	138/169 (82%)	138 (100%)	0	100	100
85	s	326/381 (86%)	326 (100%)	0	100	100
86	t1	41/158 (26%)	40 (98%)	1 (2%)	49	69
86	t2	29/158 (18%)	29 (100%)	0	100	100
86	t3	29/158 (18%)	29 (100%)	0	100	100
86	t4	28/158 (18%)	28 (100%)	0	100	100
86	t5	28/158 (18%)	28 (100%)	0	100	100
86	t6	26/158 (16%)	26 (100%)	0	100	100
87	A	2/2 (100%)	2 (100%)	0	100	100
All	All	12399/16509 (75%)	12361 (100%)	38 (0%)	92	95

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	5	310	ARG
7	6	99	ARG
9	8	119	LYS
12	A0	113	LYS
13	A1	167	ARG
14	A2	37	ARG
14	A2	40	LYS
16	A4	158	LYS
16	A4	242	ASN
16	A4	403	LYS
16	A4	594	LYS
20	AD	186	LYS
34	AR	81	LYS
34	AR	99	LYS
36	AT	30	MET
36	AT	121	LYS
37	AU	114	ARG
38	AV	64	LYS
40	AX	232	ARG
40	AX	275	LYS
44	XD	208	ARG
49	XJ	154	ARG
49	XJ	167	LYS
52	XM	44	ARG
57	XR	44	ARG
59	XT	154	LYS
59	XT	163	ARG
61	XV	149	ARG
61	XV	152	ARG
62	XW	56	MET
62	XW	119	ARG
63	XX	36	ARG
65	XZ	152	LYS
68	c	302	ARG
70	e	249	LYS
70	e	273	ARG
81	q	155	ARG
86	t1	21[A]	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
6	5	420	HIS
7	6	234	HIS
7	6	249	GLN
13	A1	279	ASN
13	A1	307	ASN
14	A2	59	ASN
16	A4	242	ASN
16	A4	566	GLN
16	A4	590	GLN
16	A4	656	ASN
22	AF	122	GLN
25	AI	129	GLN
28	AL	146	HIS
31	AO	80	ASN
33	AQ	27	ASN
38	AV	145	ASN
40	AX	54	ASN
40	AX	347	ASN
42	AZ	82	GLN
46	XF	153	HIS
50	XK	9	GLN
52	XM	26	ASN
55	XP	78	HIS
61	XV	92	ASN
67	b	129	GLN
76	k	15	GLN
77	l	135	ASN
85	s	207	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	XA	1490/1561 (95%)	266 (17%)	6 (0%)
17	AA	916/954 (96%)	158 (17%)	3 (0%)
43	XB	54/72 (75%)	10 (18%)	0
83	r1	0/4	-	-
84	r3	0/75	-	-
All	All	2460/2666 (92%)	434 (17%)	9 (0%)

All (434) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	XA	1672	C
11	XA	1681	G
11	XA	1685	C
11	XA	1689	C
11	XA	1692	A
11	XA	1693	C
11	XA	1695	C
11	XA	1700	U
11	XA	1704	U
11	XA	1707	C
11	XA	1708	A
11	XA	1709	G
11	XA	1710	A
11	XA	1711	C
11	XA	1712	A
11	XA	1715	C
11	XA	1724	A
11	XA	1727	A
11	XA	1733	C
11	XA	1734	C
11	XA	1736	A
11	XA	1737	A
11	XA	1741	A
11	XA	1748	G
11	XA	1762	A
11	XA	1763	A
11	XA	1764	C
11	XA	1765	C
11	XA	1770	G
11	XA	1777	A
11	XA	1804	A
11	XA	1805	A
11	XA	1809	U
11	XA	1810	A
11	XA	1811	A
11	XA	1821	A
11	XA	1823	A
11	XA	1824	U
11	XA	1827	C
11	XA	1828	A
11	XA	1832	A
11	XA	1836	A
11	XA	1844	A

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Mol	Chain	Res	Type
11	XA	1853	A
11	XA	1854	U
11	XA	1856	A
11	XA	1869	A
11	XA	1872	U
11	XA	1878	U
11	XA	1882	A
11	XA	1886	G
11	XA	1887	A
11	XA	1893	A
11	XA	1902	C
11	XA	1903	C
11	XA	1909	A
11	XA	1918	G
11	XA	1919	C
11	XA	1940	A
11	XA	1944	C
11	XA	1950	U
11	XA	1958	G
11	XA	1974	A
11	XA	1975	U
11	XA	1985	G
11	XA	1986	A
11	XA	1992	C
11	XA	1993	A
11	XA	1994	A
11	XA	2000	C
11	XA	2001	C
11	XA	2002	G
11	XA	2003	A
11	XA	2010	U
11	XA	2015	G
11	XA	2022	G
11	XA	2030	U
11	XA	2036	C
11	XA	2037	U
11	XA	2039	A
11	XA	2055	U
11	XA	2060	A
11	XA	2067	C
11	XA	2079	C
11	XA	2099	U

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Mol	Chain	Res	Type
11	XA	2111	C
11	XA	2113	G
11	XA	2125	C
11	XA	2126	U
11	XA	2135	A
11	XA	2138	U
11	XA	2147	G
11	XA	2159	U
11	XA	2169	A
11	XA	2176	C
11	XA	2178	A
11	XA	2179	A
11	XA	2180	A
11	XA	2181	A
11	XA	2182	G
11	XA	2188	A
11	XA	2195	A
11	XA	2196	A
11	XA	2198	A
11	XA	2200	A
11	XA	2230	A
11	XA	2237	A
11	XA	2241	A
11	XA	2243	A
11	XA	2244	U
11	XA	2245	A
11	XA	2251	A
11	XA	2262	C
11	XA	2263	C
11	XA	2283	C
11	XA	2284	C
11	XA	2285	U
11	XA	2297	A
11	XA	2299	U
11	XA	2300	G
11	XA	2316	U
11	XA	2322	C
11	XA	2332	C
11	XA	2345	G
11	XA	2357	C
11	XA	2374	A
11	XA	2375	C

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Mol	Chain	Res	Type
11	XA	2381	A
11	XA	2390	A
11	XA	2407	U
11	XA	2414	C
11	XA	2415	C
11	XA	2418	A
11	XA	2432	A
11	XA	2446	A
11	XA	2451	A
11	XA	2458	A
11	XA	2476	C
11	XA	2478	G
11	XA	2485	U
11	XA	2493	C
11	XA	2520	C
11	XA	2523	C
11	XA	2527	A
11	XA	2540	C
11	XA	2557	C
11	XA	2558	A
11	XA	2559	U
11	XA	2564	A
11	XA	2570	C
11	XA	2575	U
11	XA	2576	A
11	XA	2577	C
11	XA	2578	C
11	XA	2579	C
11	XA	2581	A
11	XA	2592	G
11	XA	2594	U
11	XA	2602	U
11	XA	2603	C
11	XA	2618	U
11	XA	2627	G
11	XA	2628	U
11	XA	2633	A
11	XA	2635	G
11	XA	2654	U
11	XA	2655	G
11	XA	2656	U
11	XA	2659	C

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Mol	Chain	Res	Type
11	XA	2660	U
11	XA	2683	C
11	XA	2686	G
11	XA	2694	A
11	XA	2695	G
11	XA	2696	A
11	XA	2706	A
11	XA	2715	A
11	XA	2718	C
11	XA	2719	G
11	XA	2722	A
11	XA	2723	A
11	XA	2724	G
11	XA	2725	A
11	XA	2732	G
11	XA	2733	G
11	XA	2740	A
11	XA	2745	A
11	XA	2758	G
11	XA	2788	C
11	XA	2789	C
11	XA	2810	G
11	XA	2832	A
11	XA	2833	A
11	XA	2847	C
11	XA	2854	U
11	XA	2857	U
11	XA	2859	A
11	XA	2864	U
11	XA	2865	C
11	XA	2869	A
11	XA	2871	U
11	XA	2879	A
11	XA	2893	A
11	XA	2906	C
11	XA	2910	A
11	XA	2913	A
11	XA	2916	G
11	XA	2917	G
11	XA	2918	A
11	XA	2919	A
11	XA	2921	A

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Mol	Chain	Res	Type
11	XA	2928	C
11	XA	2935	A
11	XA	2939	C
11	XA	2956	A
11	XA	2962	C
11	XA	2963	A
11	XA	2971	A
11	XA	2985	C
11	XA	2989	G
11	XA	2990	A
11	XA	2992	G
11	XA	3000	A
11	XA	3005	A
11	XA	3007	C
11	XA	3016	G
11	XA	3021	C
11	XA	3041	U
11	XA	3049	U
11	XA	3053	A
11	XA	3054	G
11	XA	3060	C
11	XA	3065	U
11	XA	3067	U
11	XA	3069	A
11	XA	3073	C
11	XA	3086	U
11	XA	3089	A
11	XA	3090	G
11	XA	3096	U
11	XA	3100	U
11	XA	3122	U
11	XA	3124	U
11	XA	3129	A
11	XA	3150	U
11	XA	3151	A
11	XA	3154	U
11	XA	3157	C
11	XA	3158	A
11	XA	3160	A
11	XA	3162	C
11	XA	3169	C
11	XA	3172	C

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Mol	Chain	Res	Type
11	XA	3177	A
11	XA	3182	A
11	XA	3184	C
11	XA	3189	C
11	XA	3190	A
11	XA	3194	U
11	XA	3196	G
11	XA	3208	C
11	XA	3209	A
11	XA	3210	C
11	XA	3212	C
11	XA	3217	A
11	XA	3218	A
17	AA	651	A
17	AA	680	U
17	AA	688	A
17	AA	694	C
17	AA	700	A
17	AA	704	U
17	AA	721	U
17	AA	722	C
17	AA	730	A
17	AA	753	A
17	AA	757	A
17	AA	761	A
17	AA	766	G
17	AA	771	A
17	AA	791	G
17	AA	792	C
17	AA	794	U
17	AA	796	G
17	AA	811	G
17	AA	814	A
17	AA	825	U
17	AA	829	C
17	AA	830	U
17	AA	832	U
17	AA	835	C
17	AA	836	A
17	AA	851	A
17	AA	856	A
17	AA	860	A

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Mol	Chain	Res	Type
17	AA	861	U
17	AA	865	A
17	AA	866	A
17	AA	868	C
17	AA	869	C
17	AA	880	C
17	AA	881	A
17	AA	890	C
17	AA	893	G
17	AA	897	C
17	AA	899	G
17	AA	903	U
17	AA	909	G
17	AA	917	C
17	AA	919	A
17	AA	923	A
17	AA	932	C
17	AA	933	G
17	AA	938	A
17	AA	939	A
17	AA	942	A
17	AA	950	A
17	AA	967	A
17	AA	975	A
17	AA	992	U
17	AA	993	A
17	AA	994	A
17	AA	1001	C
17	AA	1002	C
17	AA	1009	C
17	AA	1015	A
17	AA	1031	G
17	AA	1042	U
17	AA	1046	A
17	AA	1049	A
17	AA	1062	G
17	AA	1069	A
17	AA	1081	U
17	AA	1082	A
17	AA	1103	A
17	AA	1105	C
17	AA	1106	C

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Mol	Chain	Res	Type
17	AA	1109	A
17	AA	1121	A
17	AA	1128	C
17	AA	1142	A
17	AA	1143	C
17	AA	1151	C
17	AA	1167	A
17	AA	1185	C
17	AA	1188	A
17	AA	1189	U
17	AA	1190	C
17	AA	1193	U
17	AA	1194	C
17	AA	1213	A
17	AA	1214	A
17	AA	1215	U
17	AA	1220	A
17	AA	1223	C
17	AA	1225	C
17	AA	1226	C
17	AA	1227	G
17	AA	1228	A
17	AA	1229	U
17	AA	1235	U
17	AA	1236	C
17	AA	1237	A
17	AA	1248	C
17	AA	1250	C
17	AA	1251	A
17	AA	1261	C
17	AA	1268	C
17	AA	1271	C
17	AA	1284	U
17	AA	1290	C
17	AA	1293	C
17	AA	1295	A
17	AA	1296	A
17	AA	1297	G
17	AA	1307	G
17	AA	1326	A
17	AA	1327	G
17	AA	1330	C

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Mol	Chain	Res	Type
17	AA	1331	A
17	AA	1341	C
17	AA	1342	C
17	AA	1343	A
17	AA	1344	U
17	AA	1349	U
17	AA	1353	A
17	AA	1354	A
17	AA	1356	A
17	AA	1365	A
17	AA	1369	U
17	AA	1378	C
17	AA	1390	A
17	AA	1391	U
17	AA	1402	A
17	AA	1416	A
17	AA	1422	G
17	AA	1423	A
17	AA	1430	A
17	AA	1448	U
17	AA	1459	A
17	AA	1461	A
17	AA	1463	G
17	AA	1478	A
17	AA	1482	A
17	AA	1503	G
17	AA	1525	C
17	AA	1526	U
17	AA	1527	A
17	AA	1528	A
17	AA	1531	C
17	AA	1537	C
17	AA	1539	C
17	AA	1540	A
17	AA	1557	A
17	AA	1568	U
17	AA	1571	U
17	AA	1582	G
17	AA	1584	A
17	AA	1585	A
17	AA	1594	G
17	AA	1595	G

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Mol	Chain	Res	Type
17	AA	1598	G
17	AA	1599	A
17	AA	1600	A
43	XB	1608	G
43	XB	1609	U
43	XB	1611	G
43	XB	1615	A
43	XB	1619	C
43	XB	1620	A
43	XB	1621	A
43	XB	1646	U
43	XB	1649	C
43	XB	1659	U

All (9) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	XA	2195	A
11	XA	2558	A
11	XA	2574	G
11	XA	2602	U
11	XA	2961	C
11	XA	2962	C
17	AA	770	C
17	AA	1048	C
17	AA	1234	C

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
84	P5P	r3	10	84	16,23,24	0.95	1 (6%)	14,33,36	1.98	3 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	DBB	A	3	87	4,5,6	0.56	0	1,5,7	0.66	0
84	Y5P	r3	32	84	14,19,20	3.14	3 (21%)	18,26,29	0.56	0
84	Y5P	r3	61	84	14,19,20	3.13	3 (21%)	18,26,29	0.56	0
84	P5P	r3	37	84	16,23,24	0.96	1 (6%)	14,33,36	1.98	3 (21%)
84	Y5P	r3	53	84	14,19,20	3.15	3 (21%)	18,26,29	0.58	0
84	Y5P	r3	60	84	14,19,20	3.13	3 (21%)	18,26,29	0.59	0
84	P5P	r3	23	84	16,23,24	0.95	1 (6%)	14,33,36	2.00	3 (21%)
84	P5P	r3	42	84	16,23,24	0.96	1 (6%)	14,33,36	1.99	3 (21%)
83	Y5P	r1	46	83	14,19,20	3.13	3 (21%)	18,26,29	0.62	0
84	Y5P	r3	67	84	14,19,20	3.13	3 (21%)	18,26,29	0.58	0
87	MHV	A	6	87	7,9,10	0.35	0	7,11,13	1.73	2 (28%)
84	P5P	r3	15	84	16,23,24	0.97	1 (6%)	14,33,36	1.96	3 (21%)
84	Y5P	r3	59	84	14,19,20	3.14	3 (21%)	18,26,29	0.57	0
84	P5P	r3	3	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)
84	Y5P	r3	54	84	14,19,20	3.14	3 (21%)	18,26,29	0.59	0
84	P5P	r3	11	84	16,23,24	0.95	1 (6%)	14,33,36	1.98	3 (21%)
84	P5P	r3	14	84	16,23,24	0.95	1 (6%)	14,33,36	2.02	3 (21%)
84	Y5P	r3	16	84	14,19,20	3.13	3 (21%)	18,26,29	0.60	0
84	Y5P	r3	36	84	14,19,20	3.11	3 (21%)	18,26,29	0.59	0
84	P5P	r3	55	84	16,23,24	0.95	1 (6%)	14,33,36	1.96	3 (21%)
84	P5P	r3	29	84	16,23,24	0.95	1 (6%)	14,33,36	2.00	3 (21%)
87	004	A	7	87	9,10,11	1.08	1 (11%)	9,12,14	1.80	3 (33%)
84	P5P	r3	8	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)
87	MHU	A	5	87	14,15,16	0.44	0	18,19,21	1.23	3 (16%)
84	P5P	r3	52	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)
84	P5P	r3	68	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)
84	P5P	r3	31	84	16,23,24	0.94	1 (6%)	14,33,36	1.97	3 (21%)
84	Y5P	r3	38	84	14,19,20	3.13	3 (21%)	18,26,29	0.57	0
84	Y5P	r3	39	84	14,19,20	3.13	3 (21%)	18,26,29	0.59	0
84	Y5P	r3	28	84	14,19,20	3.13	3 (21%)	18,26,29	0.59	0
84	P5P	r3	21	84	16,23,24	0.95	1 (6%)	14,33,36	1.96	3 (21%)
84	P5P	r3	57	84	16,23,24	0.94	1 (6%)	14,33,36	1.93	3 (21%)
84	Y5P	r3	7	84	14,19,20	3.11	3 (21%)	18,26,29	0.62	0
84	Y5P	r3	47	84	14,19,20	3.14	3 (21%)	18,26,29	0.60	0
84	Y5P	r3	62	84	14,19,20	3.14	3 (21%)	18,26,29	0.59	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
84	P5P	r3	74	84	16,23,24	0.97	1 (6%)	14,33,36	2.03	3 (21%)
84	Y5P	r3	12	84	14,19,20	3.12	3 (21%)	18,26,29	0.56	0
84	P5P	r3	46	84	16,23,24	0.96	1 (6%)	14,33,36	1.99	3 (21%)
84	Y5P	r3	58	84	14,19,20	3.13	4 (28%)	18,26,29	0.66	0
84	Y5P	r3	25	84	14,19,20	3.14	3 (21%)	18,26,29	0.60	0
84	Y5P	r3	40	84	14,19,20	3.13	3 (21%)	18,26,29	0.59	0
84	Y5P	r3	41	84	14,19,20	3.13	3 (21%)	18,26,29	0.56	0
87	MHW	A	1	87	9,9,10	0.82	0	10,11,13	3.06	3 (30%)
84	Y5P	r3	34	84	14,19,20	3.13	3 (21%)	18,26,29	0.58	0
84	P5P	r3	6	84	16,23,24	0.95	1 (6%)	14,33,36	2.01	3 (21%)
84	P5P	r3	45	84	16,23,24	0.95	1 (6%)	14,33,36	1.95	3 (21%)
84	Y5P	r3	1	84	18,20,20	2.78	3 (16%)	25,29,29	0.67	0
84	Y5P	r3	65	84	14,19,20	3.13	3 (21%)	18,26,29	0.63	0
84	P5P	r3	17(A)	84	16,23,24	0.93	1 (6%)	14,33,36	2.01	3 (21%)
83	Y5P	r1	47	83	14,19,20	3.12	3 (21%)	18,26,29	0.56	0
84	Y5P	r3	73	84	14,19,20	3.11	3 (21%)	18,26,29	0.54	0
84	Y5P	r3	64	84	14,19,20	3.13	3 (21%)	18,26,29	0.58	0
84	Y5P	r3	56	84	14,19,20	3.13	3 (21%)	18,26,29	0.64	0
84	P5P	r3	71	84	16,23,24	0.95	1 (6%)	14,33,36	1.98	3 (21%)
84	P5P	r3	43	84	16,23,24	0.94	1 (6%)	14,33,36	1.97	3 (21%)
84	P5P	r3	66	84	16,23,24	0.94	1 (6%)	14,33,36	2.01	3 (21%)
84	P5P	r3	30	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)
84	Y5P	r3	72	84	14,19,20	3.10	3 (21%)	18,26,29	0.65	0
84	Y5P	r3	33	84	14,19,20	3.13	3 (21%)	18,26,29	0.58	0
84	Y5P	r3	69	84	14,19,20	3.13	3 (21%)	18,26,29	0.53	0
84	P5P	r3	5	84	16,23,24	0.95	1 (6%)	14,33,36	2.01	3 (21%)
84	P5P	r3	26	84	16,23,24	0.95	1 (6%)	14,33,36	2.00	3 (21%)
84	Y5P	r3	63	84	14,19,20	3.14	3 (21%)	18,26,29	0.57	0
83	Y5P	r1	48	83	14,19,20	3.13	3 (21%)	18,26,29	0.57	0
84	P5P	r3	4	84	16,23,24	0.96	1 (6%)	14,33,36	2.00	3 (21%)
84	Y5P	r3	17	84	14,19,20	3.16	3 (21%)	18,26,29	0.56	0
84	Y5P	r3	50	84	14,19,20	3.15	3 (21%)	18,26,29	0.58	0
84	Y5P	r3	24	84	14,19,20	3.13	3 (21%)	18,26,29	0.61	0
84	P5P	r3	18	84	16,23,24	0.95	1 (6%)	14,33,36	2.01	3 (21%)
84	P5P	r3	9	84	16,23,24	0.98	1 (6%)	14,33,36	1.98	3 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
84	P5P	r3	51	84	16,23,24	0.96	1 (6%)	14,33,36	1.99	3 (21%)
84	P5P	r3	19	84	16,23,24	0.96	1 (6%)	14,33,36	2.01	3 (21%)
84	Y5P	r3	27	84	14,19,20	3.14	3 (21%)	18,26,29	0.55	0
84	Y5P	r3	70	84	14,19,20	3.13	3 (21%)	18,26,29	0.59	0
84	Y5P	r3	2	84	14,19,20	3.13	3 (21%)	18,26,29	0.57	0
84	Y5P	r3	13	84	14,19,20	3.13	4 (28%)	18,26,29	0.64	0
84	Y5P	r3	20	84	14,19,20	3.13	3 (21%)	18,26,29	0.58	0
84	Y5P	r3	49	84	14,19,20	3.14	3 (21%)	18,26,29	0.56	0
84	P5P	r3	44	84	16,23,24	0.96	1 (6%)	14,33,36	1.97	3 (21%)
84	P5P	r3	35	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)
84	P5P	r3	22	84	16,23,24	0.95	1 (6%)	14,33,36	1.98	3 (21%)
83	Y5P	r1	49	83	14,19,20	3.14	3 (21%)	18,26,29	0.57	0
84	P5P	r3	48	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
84	P5P	r3	10	84	-	0/3/25/26	0/3/3/3
87	DBB	A	3	87	-	0/3/4/6	-
84	Y5P	r3	32	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	61	84	-	3/7/33/34	0/2/2/2
84	P5P	r3	37	84	-	0/3/25/26	0/3/3/3
84	Y5P	r3	53	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	60	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	23	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	42	84	-	0/3/25/26	0/3/3/3
83	Y5P	r1	46	83	-	5/7/33/34	0/2/2/2
84	Y5P	r3	67	84	-	1/7/33/34	0/2/2/2
87	MHV	A	6	87	-	0/1/12/14	0/1/1/1
84	P5P	r3	15	84	-	0/3/25/26	0/3/3/3
84	Y5P	r3	59	84	-	4/7/33/34	0/2/2/2
84	P5P	r3	3	84	-	3/3/25/26	0/3/3/3
84	Y5P	r3	54	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	11	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	14	84	-	1/3/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
84	Y5P	r3	16	84	-	2/7/33/34	0/2/2/2
84	Y5P	r3	36	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	55	84	-	2/3/25/26	0/3/3/3
84	P5P	r3	29	84	-	0/3/25/26	0/3/3/3
87	004	A	7	87	-	1/4/6/8	0/1/1/1
84	P5P	r3	8	84	-	0/3/25/26	0/3/3/3
87	MHU	A	5	87	-	5/9/12/14	0/1/1/1
84	P5P	r3	52	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	68	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	31	84	-	2/3/25/26	0/3/3/3
84	Y5P	r3	38	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	39	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	28	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	21	84	-	3/3/25/26	0/3/3/3
84	P5P	r3	57	84	-	1/3/25/26	0/3/3/3
84	Y5P	r3	7	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	47	84	-	2/7/33/34	0/2/2/2
84	Y5P	r3	62	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	74	84	-	0/3/25/26	0/3/3/3
84	Y5P	r3	12	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	46	84	-	1/3/25/26	0/3/3/3
84	Y5P	r3	58	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	25	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	40	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	41	84	-	1/7/33/34	0/2/2/2
87	MHW	A	1	87	-	0/2/2/4	0/1/1/1
84	Y5P	r3	34	84	-	3/7/33/34	0/2/2/2
84	P5P	r3	6	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	45	84	-	0/3/25/26	0/3/3/3
84	Y5P	r3	1	84	-	1/10/34/34	0/2/2/2
84	Y5P	r3	65	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	17(A)	84	-	3/3/25/26	0/3/3/3
83	Y5P	r1	47	83	-	5/7/33/34	0/2/2/2
84	Y5P	r3	73	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	64	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	56	84	-	4/7/33/34	0/2/2/2
84	P5P	r3	71	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	43	84	-	1/3/25/26	0/3/3/3
84	P5P	r3	66	84	-	2/3/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
84	P5P	r3	30	84	-	0/3/25/26	0/3/3/3
84	Y5P	r3	72	84	-	2/7/33/34	0/2/2/2
84	Y5P	r3	33	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	69	84	-	3/7/33/34	0/2/2/2
84	P5P	r3	5	84	-	2/3/25/26	0/3/3/3
84	P5P	r3	26	84	-	2/3/25/26	0/3/3/3
84	Y5P	r3	63	84	-	3/7/33/34	0/2/2/2
83	Y5P	r1	48	83	-	1/7/33/34	0/2/2/2
84	P5P	r3	4	84	-	3/3/25/26	0/3/3/3
84	Y5P	r3	17	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	50	84	-	4/7/33/34	0/2/2/2
84	Y5P	r3	24	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	18	84	-	2/3/25/26	0/3/3/3
84	P5P	r3	9	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	51	84	-	2/3/25/26	0/3/3/3
84	P5P	r3	19	84	-	2/3/25/26	0/3/3/3
84	Y5P	r3	27	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	70	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	2	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	13	84	-	5/7/33/34	0/2/2/2
84	Y5P	r3	20	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	49	84	-	3/7/33/34	0/2/2/2
84	P5P	r3	44	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	35	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	22	84	-	0/3/25/26	0/3/3/3
83	Y5P	r1	49	83	-	3/7/33/34	0/2/2/2
84	P5P	r3	48	84	-	1/3/25/26	0/3/3/3

All (168) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	r3	17	Y5P	C6-C5	10.59	1.52	1.33
84	r3	27	Y5P	C6-C5	10.59	1.52	1.33
84	r3	32	Y5P	C6-C5	10.56	1.52	1.33
84	r3	59	Y5P	C6-C5	10.55	1.52	1.33
84	r3	1	Y5P	C6-C5	10.54	1.52	1.33
84	r3	47	Y5P	C6-C5	10.54	1.52	1.33
84	r3	63	Y5P	C6-C5	10.54	1.52	1.33
84	r3	61	Y5P	C6-C5	10.53	1.52	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	r3	67	Y5P	C6-C5	10.53	1.52	1.33
83	r1	48	Y5P	C6-C5	10.53	1.52	1.33
84	r3	50	Y5P	C6-C5	10.53	1.52	1.33
83	r1	49	Y5P	C6-C5	10.53	1.52	1.33
84	r3	24	Y5P	C6-C5	10.53	1.52	1.33
84	r3	53	Y5P	C6-C5	10.53	1.52	1.33
84	r3	33	Y5P	C6-C5	10.53	1.52	1.33
84	r3	64	Y5P	C6-C5	10.53	1.52	1.33
84	r3	38	Y5P	C6-C5	10.52	1.52	1.33
84	r3	25	Y5P	C6-C5	10.52	1.52	1.33
84	r3	60	Y5P	C6-C5	10.52	1.52	1.33
84	r3	39	Y5P	C6-C5	10.52	1.52	1.33
84	r3	69	Y5P	C6-C5	10.52	1.52	1.33
84	r3	20	Y5P	C6-C5	10.52	1.52	1.33
84	r3	41	Y5P	C6-C5	10.52	1.52	1.33
84	r3	70	Y5P	C6-C5	10.51	1.52	1.33
84	r3	65	Y5P	C6-C5	10.51	1.52	1.33
84	r3	56	Y5P	C6-C5	10.51	1.52	1.33
84	r3	62	Y5P	C6-C5	10.51	1.52	1.33
84	r3	16	Y5P	C6-C5	10.51	1.52	1.33
84	r3	49	Y5P	C6-C5	10.51	1.52	1.33
84	r3	58	Y5P	C6-C5	10.51	1.52	1.33
84	r3	54	Y5P	C6-C5	10.50	1.52	1.33
84	r3	13	Y5P	C6-C5	10.50	1.52	1.33
83	r1	47	Y5P	C6-C5	10.50	1.52	1.33
84	r3	34	Y5P	C6-C5	10.50	1.52	1.33
84	r3	28	Y5P	C6-C5	10.48	1.52	1.33
83	r1	46	Y5P	C6-C5	10.48	1.52	1.33
84	r3	73	Y5P	C6-C5	10.48	1.52	1.33
84	r3	2	Y5P	C6-C5	10.48	1.52	1.33
84	r3	40	Y5P	C6-C5	10.47	1.52	1.33
84	r3	36	Y5P	C6-C5	10.46	1.52	1.33
84	r3	12	Y5P	C6-C5	10.46	1.52	1.33
84	r3	7	Y5P	C6-C5	10.45	1.52	1.33
84	r3	72	Y5P	C6-C5	10.43	1.51	1.33
84	r3	62	Y5P	C2-N1	3.90	1.45	1.36
84	r3	53	Y5P	C2-N1	3.89	1.45	1.36
84	r3	50	Y5P	C2-N1	3.88	1.45	1.36
84	r3	28	Y5P	C2-N1	3.87	1.45	1.36
84	r3	25	Y5P	C2-N1	3.86	1.45	1.36
84	r3	56	Y5P	C2-N1	3.86	1.45	1.36
84	r3	2	Y5P	C2-N1	3.85	1.45	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	r3	49	Y5P	C2-N1	3.85	1.45	1.36
84	r3	63	Y5P	C2-N1	3.85	1.45	1.36
84	r3	65	Y5P	C2-N1	3.84	1.45	1.36
84	r3	13	Y5P	C2-N1	3.84	1.45	1.36
83	r1	46	Y5P	C2-N1	3.84	1.45	1.36
84	r3	59	Y5P	C2-N1	3.84	1.45	1.36
83	r1	49	Y5P	C2-N1	3.83	1.45	1.36
84	r3	20	Y5P	C2-N1	3.83	1.45	1.36
84	r3	54	Y5P	C2-N1	3.83	1.45	1.36
84	r3	40	Y5P	C2-N1	3.83	1.45	1.36
84	r3	12	Y5P	C2-N1	3.83	1.45	1.36
84	r3	1	Y5P	C2-N1	3.82	1.45	1.36
84	r3	33	Y5P	C2-N1	3.82	1.45	1.36
84	r3	67	Y5P	C2-N1	3.82	1.45	1.36
84	r3	17	Y5P	C2-N1	3.81	1.45	1.36
84	r3	16	Y5P	C2-N1	3.81	1.45	1.36
84	r3	7	Y5P	C2-N1	3.81	1.45	1.36
84	r3	41	Y5P	C2-N1	3.80	1.45	1.36
84	r3	47	Y5P	C2-N1	3.80	1.45	1.36
84	r3	58	Y5P	C2-N1	3.80	1.45	1.36
84	r3	70	Y5P	C2-N1	3.80	1.45	1.36
83	r1	48	Y5P	C2-N1	3.80	1.45	1.36
84	r3	24	Y5P	C2-N1	3.79	1.45	1.36
83	r1	47	Y5P	C2-N1	3.79	1.45	1.36
84	r3	61	Y5P	C2-N1	3.79	1.45	1.36
84	r3	27	Y5P	C2-N1	3.79	1.45	1.36
84	r3	36	Y5P	C2-N1	3.79	1.45	1.36
84	r3	32	Y5P	C2-N1	3.78	1.45	1.36
84	r3	34	Y5P	C2-N1	3.78	1.45	1.36
84	r3	60	Y5P	C2-N1	3.77	1.45	1.36
84	r3	38	Y5P	C2-N1	3.77	1.45	1.36
84	r3	72	Y5P	C2-N1	3.77	1.45	1.36
84	r3	39	Y5P	C2-N1	3.77	1.45	1.36
84	r3	64	Y5P	C2-N1	3.75	1.45	1.36
84	r3	69	Y5P	C2-N1	3.75	1.45	1.36
84	r3	73	Y5P	C2-N1	3.74	1.45	1.36
87	A	7	004	CB-CA	-2.99	1.49	1.52
84	r3	54	Y5P	C6-N1	2.69	1.44	1.37
84	r3	20	Y5P	C6-N1	2.68	1.44	1.37
84	r3	24	Y5P	C6-N1	2.68	1.44	1.37
84	r3	49	Y5P	C6-N1	2.68	1.44	1.37
84	r3	58	Y5P	C6-N1	2.68	1.44	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	r3	53	Y5P	C6-N1	2.67	1.44	1.37
84	r3	17	Y5P	C6-N1	2.67	1.44	1.37
84	r3	60	Y5P	C6-N1	2.67	1.43	1.37
84	r3	27	Y5P	C6-N1	2.67	1.43	1.37
84	r3	47	Y5P	C6-N1	2.66	1.43	1.37
84	r3	1	Y5P	C6-N1	2.66	1.43	1.37
84	r3	25	Y5P	C6-N1	2.66	1.43	1.37
84	r3	33	Y5P	C6-N1	2.66	1.43	1.37
84	r3	64	Y5P	C6-N1	2.65	1.43	1.37
83	r1	47	Y5P	C6-N1	2.65	1.43	1.37
84	r3	16	Y5P	C6-N1	2.65	1.43	1.37
84	r3	61	Y5P	C6-N1	2.65	1.43	1.37
83	r1	46	Y5P	C6-N1	2.65	1.43	1.37
84	r3	2	Y5P	C6-N1	2.65	1.43	1.37
84	r3	34	Y5P	C6-N1	2.65	1.43	1.37
84	r3	63	Y5P	C6-N1	2.64	1.43	1.37
84	r3	40	Y5P	C6-N1	2.64	1.43	1.37
83	r1	49	Y5P	C6-N1	2.64	1.43	1.37
84	r3	50	Y5P	C6-N1	2.64	1.43	1.37
84	r3	13	Y5P	C6-N1	2.64	1.43	1.37
84	r3	7	Y5P	C6-N1	2.64	1.43	1.37
84	r3	41	Y5P	C6-N1	2.63	1.43	1.37
84	r3	28	Y5P	C6-N1	2.63	1.43	1.37
84	r3	56	Y5P	C6-N1	2.63	1.43	1.37
84	r3	65	Y5P	C6-N1	2.63	1.43	1.37
84	r3	59	Y5P	C6-N1	2.62	1.43	1.37
84	r3	32	Y5P	C6-N1	2.62	1.43	1.37
84	r3	62	Y5P	C6-N1	2.62	1.43	1.37
83	r1	48	Y5P	C6-N1	2.62	1.43	1.37
84	r3	12	Y5P	C6-N1	2.62	1.43	1.37
84	r3	38	Y5P	C6-N1	2.62	1.43	1.37
84	r3	67	Y5P	C6-N1	2.62	1.43	1.37
84	r3	70	Y5P	C6-N1	2.61	1.43	1.37
84	r3	69	Y5P	C6-N1	2.61	1.43	1.37
84	r3	39	Y5P	C6-N1	2.60	1.43	1.37
84	r3	72	Y5P	C6-N1	2.59	1.43	1.37
84	r3	36	Y5P	C6-N1	2.59	1.43	1.37
84	r3	73	Y5P	C6-N1	2.57	1.43	1.37
84	r3	71	P5P	C5-C4	-2.24	1.35	1.40
84	r3	74	P5P	C5-C4	-2.24	1.35	1.40
84	r3	37	P5P	C5-C4	-2.23	1.35	1.40
84	r3	35	P5P	C5-C4	-2.22	1.35	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	r3	51	P5P	C5-C4	-2.22	1.35	1.40
84	r3	43	P5P	C5-C4	-2.22	1.35	1.40
84	r3	3	P5P	C5-C4	-2.22	1.35	1.40
84	r3	30	P5P	C5-C4	-2.22	1.35	1.40
84	r3	42	P5P	C5-C4	-2.22	1.35	1.40
84	r3	21	P5P	C5-C4	-2.22	1.35	1.40
84	r3	11	P5P	C5-C4	-2.21	1.35	1.40
84	r3	22	P5P	C5-C4	-2.20	1.35	1.40
84	r3	44	P5P	C5-C4	-2.20	1.35	1.40
84	r3	31	P5P	C5-C4	-2.20	1.35	1.40
84	r3	68	P5P	C5-C4	-2.20	1.35	1.40
84	r3	52	P5P	C5-C4	-2.20	1.35	1.40
84	r3	18	P5P	C5-C4	-2.20	1.35	1.40
84	r3	48	P5P	C5-C4	-2.19	1.35	1.40
84	r3	29	P5P	C5-C4	-2.19	1.35	1.40
84	r3	4	P5P	C5-C4	-2.19	1.35	1.40
84	r3	6	P5P	C5-C4	-2.19	1.35	1.40
84	r3	19	P5P	C5-C4	-2.19	1.35	1.40
84	r3	66	P5P	C5-C4	-2.19	1.35	1.40
84	r3	9	P5P	C5-C4	-2.19	1.35	1.40
84	r3	26	P5P	C5-C4	-2.18	1.35	1.40
84	r3	46	P5P	C5-C4	-2.18	1.35	1.40
84	r3	5	P5P	C5-C4	-2.18	1.35	1.40
84	r3	8	P5P	C5-C4	-2.18	1.35	1.40
84	r3	15	P5P	C5-C4	-2.17	1.35	1.40
84	r3	14	P5P	C5-C4	-2.17	1.35	1.40
84	r3	57	P5P	C5-C4	-2.17	1.35	1.40
84	r3	10	P5P	C5-C4	-2.17	1.35	1.40
84	r3	45	P5P	C5-C4	-2.16	1.35	1.40
84	r3	23	P5P	C5-C4	-2.16	1.35	1.40
84	r3	55	P5P	C5-C4	-2.13	1.35	1.40
84	r3	17(A)	P5P	C5-C4	-2.13	1.35	1.40
84	r3	58	Y5P	C4-N3	2.02	1.48	1.46
84	r3	13	Y5P	C4-N3	2.00	1.48	1.46

All (119) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
87	A	1	MHW	O-C-CA	-8.04	116.60	124.22
84	r3	42	P5P	N1-C2-N3	-6.00	119.97	127.65
84	r3	11	P5P	N1-C2-N3	-5.97	120.01	127.65
84	r3	48	P5P	N1-C2-N3	-5.97	120.01	127.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	r3	66	P5P	N1-C2-N3	-5.97	120.01	127.65
84	r3	51	P5P	N1-C2-N3	-5.97	120.02	127.65
84	r3	19	P5P	N1-C2-N3	-5.95	120.04	127.65
84	r3	52	P5P	N1-C2-N3	-5.95	120.04	127.65
84	r3	26	P5P	N1-C2-N3	-5.94	120.05	127.65
84	r3	74	P5P	N1-C2-N3	-5.94	120.05	127.65
84	r3	8	P5P	N1-C2-N3	-5.93	120.06	127.65
84	r3	68	P5P	N1-C2-N3	-5.93	120.06	127.65
84	r3	30	P5P	N1-C2-N3	-5.93	120.06	127.65
84	r3	29	P5P	N1-C2-N3	-5.93	120.06	127.65
84	r3	46	P5P	N1-C2-N3	-5.93	120.06	127.65
84	r3	4	P5P	N1-C2-N3	-5.92	120.07	127.65
84	r3	5	P5P	N1-C2-N3	-5.92	120.08	127.65
84	r3	10	P5P	N1-C2-N3	-5.91	120.08	127.65
84	r3	43	P5P	N1-C2-N3	-5.91	120.09	127.65
84	r3	22	P5P	N1-C2-N3	-5.91	120.09	127.65
84	r3	37	P5P	N1-C2-N3	-5.90	120.09	127.65
84	r3	71	P5P	N1-C2-N3	-5.90	120.10	127.65
84	r3	35	P5P	N1-C2-N3	-5.90	120.10	127.65
84	r3	6	P5P	N1-C2-N3	-5.89	120.11	127.65
84	r3	23	P5P	N1-C2-N3	-5.89	120.12	127.65
84	r3	3	P5P	N1-C2-N3	-5.89	120.12	127.65
84	r3	44	P5P	N1-C2-N3	-5.86	120.16	127.65
84	r3	21	P5P	N1-C2-N3	-5.85	120.16	127.65
84	r3	18	P5P	N1-C2-N3	-5.85	120.17	127.65
84	r3	9	P5P	N1-C2-N3	-5.84	120.18	127.65
84	r3	14	P5P	N1-C2-N3	-5.84	120.18	127.65
84	r3	31	P5P	N1-C2-N3	-5.84	120.18	127.65
84	r3	55	P5P	N1-C2-N3	-5.82	120.20	127.65
84	r3	17(A)	P5P	N1-C2-N3	-5.80	120.22	127.65
84	r3	45	P5P	N1-C2-N3	-5.80	120.23	127.65
84	r3	15	P5P	N1-C2-N3	-5.72	120.33	127.65
84	r3	57	P5P	N1-C2-N3	-5.62	120.45	127.65
87	A	1	MHW	C-CA-N	4.01	121.92	115.41
84	r3	14	P5P	C1'-N9-C4	3.29	132.42	126.64
84	r3	15	P5P	C1'-N9-C4	3.25	132.35	126.64
84	r3	17(A)	P5P	C1'-N9-C4	3.23	132.31	126.64
87	A	7	004	CG2-CB-CA	-3.21	115.48	120.65
84	r3	57	P5P	C1'-N9-C4	3.19	132.24	126.64
84	r3	66	P5P	C6-N1-C2	3.18	120.39	115.84
84	r3	5	P5P	C6-N1-C2	3.16	120.36	115.84
84	r3	18	P5P	C1'-N9-C4	3.15	132.18	126.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	r3	30	P5P	C6-N1-C2	3.12	120.31	115.84
84	r3	48	P5P	C6-N1-C2	3.12	120.31	115.84
84	r3	43	P5P	C6-N1-C2	3.12	120.31	115.84
84	r3	74	P5P	C1'-N9-C4	3.12	132.12	126.64
84	r3	51	P5P	C6-N1-C2	3.12	120.30	115.84
84	r3	11	P5P	C6-N1-C2	3.11	120.30	115.84
84	r3	29	P5P	C6-N1-C2	3.09	120.27	115.84
84	r3	52	P5P	C6-N1-C2	3.09	120.27	115.84
84	r3	74	P5P	C6-N1-C2	3.08	120.25	115.84
87	A	7	004	CG1-CB-CA	3.08	125.62	120.65
84	r3	19	P5P	C6-N1-C2	3.08	120.25	115.84
84	r3	42	P5P	C6-N1-C2	3.07	120.24	115.84
84	r3	23	P5P	C1'-N9-C4	3.07	132.03	126.64
84	r3	26	P5P	C6-N1-C2	3.06	120.23	115.84
84	r3	6	P5P	C1'-N9-C4	3.06	132.02	126.64
84	r3	4	P5P	C6-N1-C2	3.06	120.22	115.84
84	r3	10	P5P	C6-N1-C2	3.06	120.22	115.84
84	r3	6	P5P	C6-N1-C2	3.06	120.22	115.84
84	r3	45	P5P	C6-N1-C2	3.05	120.20	115.84
84	r3	31	P5P	C6-N1-C2	3.04	120.20	115.84
84	r3	37	P5P	C6-N1-C2	3.04	120.20	115.84
84	r3	46	P5P	C6-N1-C2	3.04	120.20	115.84
84	r3	22	P5P	C6-N1-C2	3.03	120.19	115.84
84	r3	35	P5P	C6-N1-C2	3.03	120.19	115.84
84	r3	55	P5P	C6-N1-C2	3.03	120.19	115.84
84	r3	3	P5P	C6-N1-C2	3.03	120.18	115.84
84	r3	9	P5P	C1'-N9-C4	3.03	131.96	126.64
84	r3	71	P5P	C6-N1-C2	3.03	120.17	115.84
84	r3	8	P5P	C6-N1-C2	3.02	120.17	115.84
84	r3	44	P5P	C6-N1-C2	3.02	120.17	115.84
84	r3	9	P5P	C6-N1-C2	3.02	120.16	115.84
84	r3	18	P5P	C6-N1-C2	3.01	120.15	115.84
84	r3	23	P5P	C6-N1-C2	3.01	120.15	115.84
84	r3	68	P5P	C6-N1-C2	3.01	120.14	115.84
84	r3	14	P5P	C6-N1-C2	3.00	120.13	115.84
84	r3	17(A)	P5P	C6-N1-C2	2.99	120.12	115.84
84	r3	5	P5P	C1'-N9-C4	2.98	131.88	126.64
84	r3	35	P5P	C1'-N9-C4	2.98	131.88	126.64
84	r3	21	P5P	C6-N1-C2	2.97	120.10	115.84
84	r3	3	P5P	C1'-N9-C4	2.93	131.79	126.64
84	r3	68	P5P	C1'-N9-C4	2.92	131.78	126.64
84	r3	15	P5P	C6-N1-C2	2.92	120.02	115.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	r3	55	P5P	C1'-N9-C4	2.92	131.76	126.64
84	r3	8	P5P	C1'-N9-C4	2.91	131.76	126.64
84	r3	71	P5P	C1'-N9-C4	2.90	131.74	126.64
87	A	7	004	CB-CA-N	-2.89	105.49	112.40
84	r3	21	P5P	C1'-N9-C4	2.88	131.70	126.64
84	r3	37	P5P	C1'-N9-C4	2.88	131.70	126.64
84	r3	45	P5P	C1'-N9-C4	2.87	131.68	126.64
84	r3	57	P5P	C6-N1-C2	2.87	119.95	115.84
84	r3	29	P5P	C1'-N9-C4	2.86	131.66	126.64
84	r3	22	P5P	C1'-N9-C4	2.86	131.66	126.64
84	r3	66	P5P	C1'-N9-C4	2.85	131.64	126.64
84	r3	51	P5P	C1'-N9-C4	2.83	131.61	126.64
84	r3	44	P5P	C1'-N9-C4	2.82	131.60	126.64
84	r3	31	P5P	C1'-N9-C4	2.82	131.59	126.64
84	r3	26	P5P	C1'-N9-C4	2.80	131.56	126.64
84	r3	10	P5P	C1'-N9-C4	2.79	131.55	126.64
84	r3	19	P5P	C1'-N9-C4	2.77	131.51	126.64
84	r3	52	P5P	C1'-N9-C4	2.75	131.47	126.64
87	A	5	MHU	O-C-CA	-2.74	117.60	124.78
84	r3	46	P5P	C1'-N9-C4	2.69	131.37	126.64
87	A	6	MHV	CD2-CG-CB	2.66	119.86	115.89
87	A	1	MHW	CE-N-CA	2.66	121.26	116.69
84	r3	43	P5P	C1'-N9-C4	2.64	131.27	126.64
84	r3	30	P5P	C1'-N9-C4	2.60	131.21	126.64
84	r3	11	P5P	C1'-N9-C4	2.57	131.16	126.64
84	r3	48	P5P	C1'-N9-C4	2.56	131.13	126.64
84	r3	4	P5P	C1'-N9-C4	2.53	131.09	126.64
84	r3	42	P5P	C1'-N9-C4	2.48	131.00	126.64
87	A	6	MHV	CB-CA-N	-2.42	107.50	112.50
87	A	5	MHU	CM-N-CA	2.37	121.00	113.64
87	A	5	MHU	CB-CA-N	-2.11	107.38	110.65

There are no chirality outliers.

All (130) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
83	r1	46	Y5P	C4'-C5'-O5'-P
83	r1	46	Y5P	C3'-C4'-C5'-O5'
83	r1	47	Y5P	C3'-C4'-C5'-O5'
83	r1	48	Y5P	O4'-C1'-N1-C2
84	r3	3	P5P	O4'-C4'-C5'-O5'
84	r3	16	Y5P	C4'-C5'-O5'-P

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Mol	Chain	Res	Type	Atoms
84	r3	18	P5P	O4'-C4'-C5'-O5'
84	r3	19	P5P	C3'-C4'-C5'-O5'
84	r3	21	P5P	C3'-C4'-C5'-O5'
84	r3	21	P5P	C4'-C5'-O5'-P
84	r3	24	Y5P	O4'-C1'-N1-C2
84	r3	27	Y5P	O4'-C1'-N1-C2
84	r3	34	Y5P	O4'-C4'-C5'-O5'
84	r3	34	Y5P	C3'-C4'-C5'-O5'
84	r3	36	Y5P	O4'-C1'-N1-C2
84	r3	41	Y5P	O4'-C1'-N1-C2
84	r3	50	Y5P	O4'-C1'-N1-C2
84	r3	53	Y5P	O4'-C1'-N1-C2
84	r3	54	Y5P	O4'-C1'-N1-C2
84	r3	59	Y5P	O4'-C4'-C5'-O5'
84	r3	63	Y5P	O4'-C4'-C5'-O5'
84	r3	63	Y5P	C3'-C4'-C5'-O5'
84	r3	67	Y5P	O4'-C1'-N1-C2
84	r3	73	Y5P	O4'-C1'-N1-C2
87	A	5	MHU	O-C-CA-CB
83	r1	47	Y5P	O4'-C1'-N1-C2
83	r1	49	Y5P	O4'-C1'-N1-C2
84	r3	12	Y5P	O4'-C1'-N1-C2
84	r3	25	Y5P	O4'-C1'-N1-C2
84	r3	28	Y5P	O4'-C1'-N1-C2
84	r3	32	Y5P	O4'-C1'-N1-C2
84	r3	33	Y5P	O4'-C1'-N1-C2
84	r3	34	Y5P	O4'-C1'-N1-C2
84	r3	38	Y5P	O4'-C1'-N1-C2
84	r3	49	Y5P	O4'-C1'-N1-C2
84	r3	59	Y5P	O4'-C1'-N1-C2
84	r3	60	Y5P	O4'-C1'-N1-C2
84	r3	61	Y5P	O4'-C1'-N1-C2
84	r3	62	Y5P	O4'-C1'-N1-C2
84	r3	63	Y5P	O4'-C1'-N1-C2
84	r3	64	Y5P	O4'-C1'-N1-C2
84	r3	65	Y5P	O4'-C1'-N1-C2
84	r3	69	Y5P	O4'-C1'-N1-C2
84	r3	70	Y5P	O4'-C1'-N1-C2
83	r1	46	Y5P	O4'-C1'-N1-C6
87	A	5	MHU	CE1-CZ-NZ-CZ2
87	A	5	MHU	CE2-CZ-NZ-CZ1
87	A	5	MHU	CE1-CZ-NZ-CZ1

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Mol	Chain	Res	Type	Atoms
87	A	5	MHU	CE2-CZ-NZ-CZ2
84	r3	47	Y5P	C4'-C5'-O5'-P
83	r1	47	Y5P	O4'-C4'-C5'-O5'
84	r3	3	P5P	C3'-C4'-C5'-O5'
84	r3	17(A)	P5P	C3'-C4'-C5'-O5'
84	r3	17(A)	P5P	O4'-C4'-C5'-O5'
84	r3	31	P5P	O4'-C4'-C5'-O5'
84	r3	50	Y5P	O4'-C4'-C5'-O5'
84	r3	53	Y5P	C3'-C4'-C5'-O5'
84	r3	61	Y5P	O4'-C4'-C5'-O5'
84	r3	61	Y5P	C3'-C4'-C5'-O5'
84	r3	40	Y5P	O4'-C1'-N1-C6
84	r3	40	Y5P	C2'-C1'-N1-C6
84	r3	13	Y5P	C4'-C5'-O5'-P
84	r3	43	P5P	C4'-C5'-O5'-P
83	r1	46	Y5P	O4'-C4'-C5'-O5'
84	r3	4	P5P	C3'-C4'-C5'-O5'
84	r3	4	P5P	O4'-C4'-C5'-O5'
84	r3	7	Y5P	O4'-C4'-C5'-O5'
84	r3	18	P5P	C3'-C4'-C5'-O5'
84	r3	21	P5P	O4'-C4'-C5'-O5'
84	r3	53	Y5P	O4'-C4'-C5'-O5'
84	r3	55	P5P	C3'-C4'-C5'-O5'
84	r3	55	P5P	O4'-C4'-C5'-O5'
84	r3	59	Y5P	C3'-C4'-C5'-O5'
84	r3	16	Y5P	O4'-C1'-N1-C2
84	r3	39	Y5P	O4'-C1'-N1-C2
84	r3	13	Y5P	C2'-C1'-N1-C2
84	r3	40	Y5P	C2'-C1'-N1-C2
84	r3	13	Y5P	C2'-C1'-N1-C6
84	r3	72	Y5P	O4'-C1'-N1-C2
84	r3	31	P5P	C3'-C4'-C5'-O5'
84	r3	7	Y5P	C3'-C4'-C5'-O5'
84	r3	49	Y5P	C3'-C4'-C5'-O5'
84	r3	5	P5P	C3'-C4'-C5'-O5'
84	r3	19	P5P	O4'-C4'-C5'-O5'
84	r3	25	Y5P	O4'-C4'-C5'-O5'
84	r3	50	Y5P	C3'-C4'-C5'-O5'
84	r3	51	P5P	C3'-C4'-C5'-O5'
84	r3	69	Y5P	C3'-C4'-C5'-O5'
84	r3	46	P5P	C4'-C5'-O5'-P
87	A	7	004	C-CA-CB-CG1

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Mol	Chain	Res	Type	Atoms
83	r1	49	Y5P	O4'-C4'-C5'-O5'
84	r3	26	P5P	O4'-C4'-C5'-O5'
84	r3	49	Y5P	O4'-C4'-C5'-O5'
84	r3	66	P5P	O4'-C4'-C5'-O5'
84	r3	13	Y5P	O4'-C1'-N1-C6
84	r3	7	Y5P	O4'-C1'-N1-C2
84	r3	13	Y5P	O4'-C1'-N1-C2
84	r3	3	P5P	C4'-C5'-O5'-P
84	r3	17(A)	P5P	C4'-C5'-O5'-P
84	r3	20	Y5P	O4'-C1'-N1-C2
84	r3	59	Y5P	C4'-C5'-O5'-P
84	r3	58	Y5P	O4'-C1'-N1-C2
84	r3	4	P5P	C4'-C5'-O5'-P
84	r3	14	P5P	C4'-C5'-O5'-P
84	r3	51	P5P	O4'-C4'-C5'-O5'
84	r3	69	Y5P	O4'-C4'-C5'-O5'
84	r3	2	Y5P	O4'-C1'-N1-C2
84	r3	47	Y5P	O4'-C1'-N1-C2
84	r3	17	Y5P	O4'-C1'-N1-C2
84	r3	50	Y5P	C4'-C5'-O5'-P
84	r3	1	Y5P	O4'-C1'-N1-C2
84	r3	25	Y5P	C3'-C4'-C5'-O5'
84	r3	2	Y5P	C2'-C1'-N1-C2
84	r3	56	Y5P	O4'-C1'-N1-C2
84	r3	17	Y5P	C2'-C1'-N1-C2
84	r3	5	P5P	O4'-C4'-C5'-O5'
84	r3	57	P5P	O4'-C4'-C5'-O5'
83	r1	47	Y5P	C2'-C1'-N1-C6
84	r3	72	Y5P	C4'-C5'-O5'-P
83	r1	46	Y5P	C2'-C1'-N1-C2
84	r3	56	Y5P	C2'-C1'-N1-C2
83	r1	49	Y5P	C3'-C4'-C5'-O5'
84	r3	66	P5P	C3'-C4'-C5'-O5'
84	r3	48	P5P	C4'-C5'-O5'-P
84	r3	56	Y5P	O4'-C4'-C5'-O5'
84	r3	26	P5P	C3'-C4'-C5'-O5'
84	r3	2	Y5P	O4'-C1'-N1-C6
84	r3	17	Y5P	O4'-C1'-N1-C6
83	r1	47	Y5P	C4'-C5'-O5'-P
84	r3	56	Y5P	C4'-C5'-O5'-P

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	A	7	004	1	0
87	A	5	MHU	1	0
87	A	1	MHW	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 204 ligands modelled in this entry, 202 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
91	GTP	AX	500	-	26,34,34	1.13	2 (7%)	32,54,54	1.53	6 (18%)
90	DOL	XA	5143	-	43,50,50	3.48	15 (34%)	51,70,70	2.66	10 (19%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
91	GTP	AX	500	-	-	8/18/38/38	0/3/3/3
90	DOL	XA	5143	-	-	16/58/77/77	0/2/3/3

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
90	XA	5143	DOL	C28-C29	9.91	1.55	1.32
90	XA	5143	DOL	C22-C23	9.51	1.56	1.32
90	XA	5143	DOL	C19-C20	7.30	1.57	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
90	XA	5143	DOL	C6-N5	6.38	1.49	1.34
90	XA	5143	DOL	C26-N25	6.38	1.48	1.34
90	XA	5143	DOL	C22-C20	5.66	1.58	1.45
90	XA	5143	DOL	O36-C37	5.31	1.46	1.34
90	XA	5143	DOL	C42-S39	5.03	1.86	1.78
90	XA	5143	DOL	C13-C10	4.38	1.57	1.50
90	XA	5143	DOL	C16-C14	4.06	1.56	1.51
91	AX	500	GTP	C5-C6	-3.99	1.39	1.47
90	XA	5143	DOL	C28-C26	3.78	1.56	1.48
90	XA	5143	DOL	O18-C17	-2.89	1.38	1.43
90	XA	5143	DOL	C8-C6	2.84	1.55	1.50
90	XA	5143	DOL	O27-C26	-2.75	1.19	1.24
90	XA	5143	DOL	C13-C14	2.32	1.56	1.52
91	AX	500	GTP	C2-N3	2.23	1.38	1.33

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
90	XA	5143	DOL	O40-S39-O41	-14.97	101.12	118.19
90	XA	5143	DOL	C24-N25-C26	-5.00	113.94	122.03
90	XA	5143	DOL	C23-C22-C20	-4.38	119.27	125.89
91	AX	500	GTP	PA-O3A-PB	-3.92	119.36	132.83
90	XA	5143	DOL	C4-N5-C1	-3.44	108.23	112.45
91	AX	500	GTP	C5-C6-N1	3.31	119.79	113.95
91	AX	500	GTP	PB-O3B-PG	-3.12	122.13	132.83
91	AX	500	GTP	C2-N1-C6	-3.07	119.45	125.10
91	AX	500	GTP	C8-N7-C5	3.05	108.79	102.99
90	XA	5143	DOL	C30-C32-C33	-2.98	108.66	115.98
90	XA	5143	DOL	O36-C32-C30	2.97	112.05	107.09
90	XA	5143	DOL	C32-O36-C37	-2.81	112.96	117.78
90	XA	5143	DOL	C3-C4-N5	2.55	105.95	103.33
90	XA	5143	DOL	C30-C29-C28	-2.26	120.26	126.44
91	AX	500	GTP	O6-C6-C5	-2.15	120.18	124.37
90	XA	5143	DOL	C28-C26-N25	-2.04	111.13	114.97

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
90	XA	5143	DOL	C3-C2-S39-C42
90	XA	5143	DOL	C1-C2-S39-O41
90	XA	5143	DOL	C1-C2-S39-O40

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Mol	Chain	Res	Type	Atoms
90	XA	5143	DOL	C43-C42-S39-C2
90	XA	5143	DOL	C43-C42-S39-O41
90	XA	5143	DOL	C29-C30-C32-C33
90	XA	5143	DOL	C31-C30-C32-C33
91	AX	500	GTP	PB-O3B-PG-O3G
91	AX	500	GTP	C5'-O5'-PA-O3A
90	XA	5143	DOL	C3-C2-S39-O41
91	AX	500	GTP	O4'-C4'-C5'-O5'
90	XA	5143	DOL	C31-C30-C32-O36
91	AX	500	GTP	C5'-O5'-PA-O2A
90	XA	5143	DOL	C29-C30-C32-O36
91	AX	500	GTP	C3'-C4'-C5'-O5'
90	XA	5143	DOL	C3-C2-S39-O40
90	XA	5143	DOL	O18-C17-C19-C20
90	XA	5143	DOL	C16-C17-C19-C20
91	AX	500	GTP	PB-O3B-PG-O1G
90	XA	5143	DOL	C28-C29-C30-C31
91	AX	500	GTP	PB-O3B-PG-O2G
90	XA	5143	DOL	C42-C43-N44-C47
91	AX	500	GTP	C5'-O5'-PA-O1A
90	XA	5143	DOL	C42-C43-N44-C45

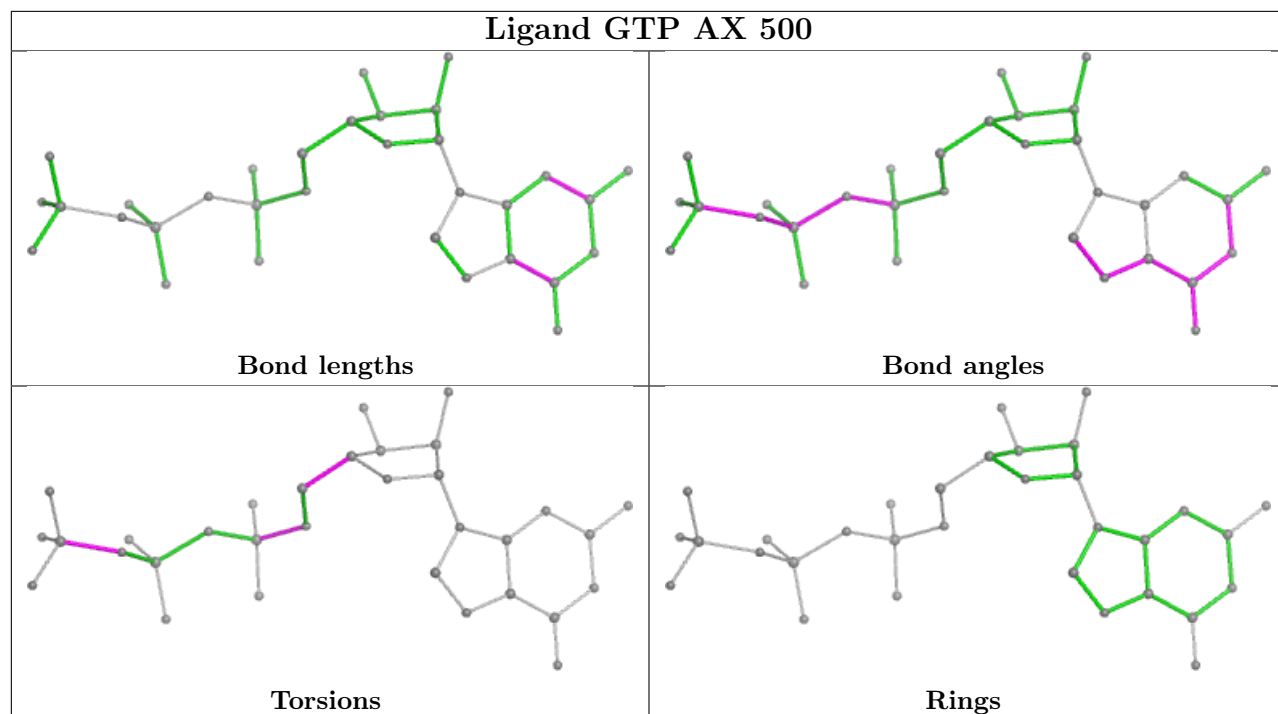
There are no ring outliers.

2 monomers are involved in 5 short contacts:

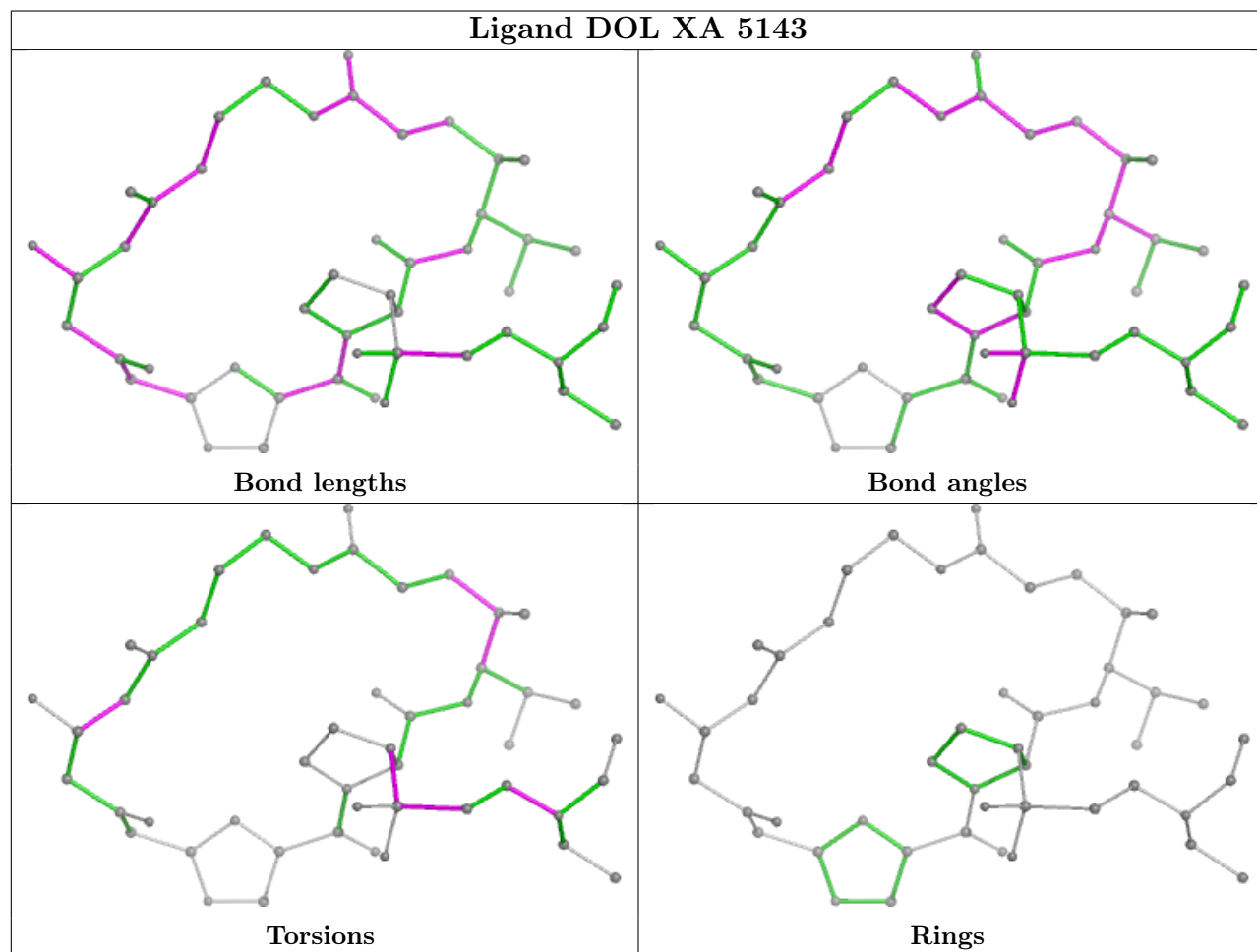
Mol	Chain	Res	Type	Clashes	Symm-Clashes
91	AX	500	GTP	1	0
90	XA	5143	DOL	4	0

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

Ligand GTP AX 500



Ligand DOL XA 5143



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
16	A4	2
8	7	2
82	r	1
38	AV	1
6	5	1
72	g	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A4	537:ARG	C	538:ASP	N	6.17
1	7	285:ASN	C	286:LEU	N	6.12
1	r	134:ARG	C	135:LEU	N	5.70
1	AV	269:SER	C	270:PRO	N	4.50
1	7	185:LEU	C	186:ASP	N	3.18
1	A4	143:GLU	C	144:TYR	N	3.07
1	5	141:ASP	C	142:ASP	N	3.05
1	g	37:ARG	C	38:PHE	N	1.11

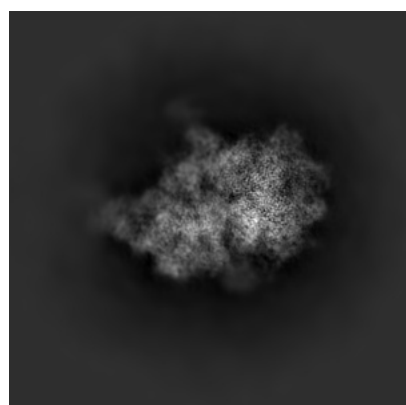
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11392. These allow visual inspection of the internal detail of the map and identification of artifacts.

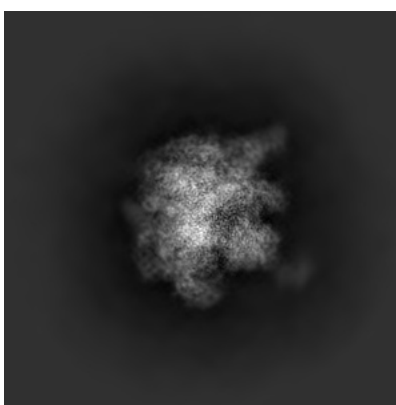
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

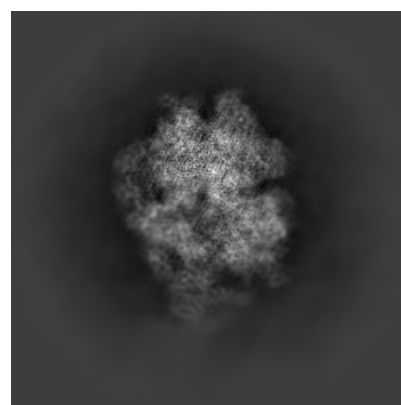
6.1.1 Primary map



X



Y

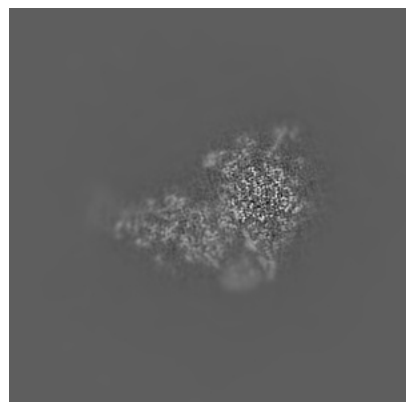


Z

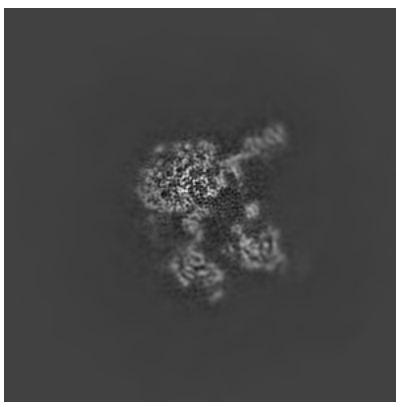
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

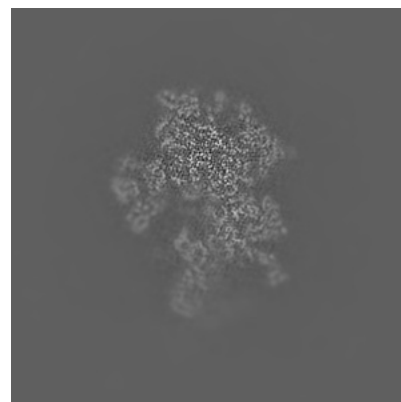
6.2.1 Primary map



X Index: 260



Y Index: 260

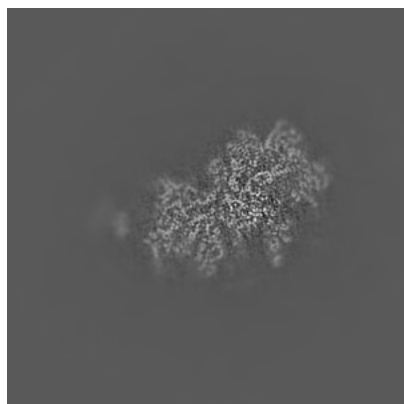


Z Index: 260

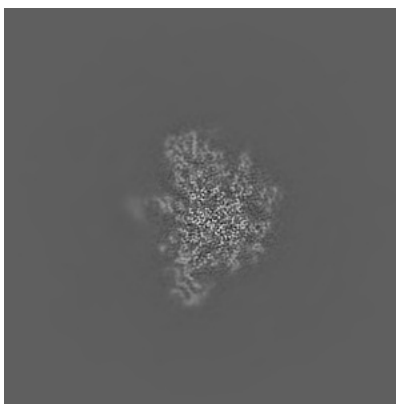
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

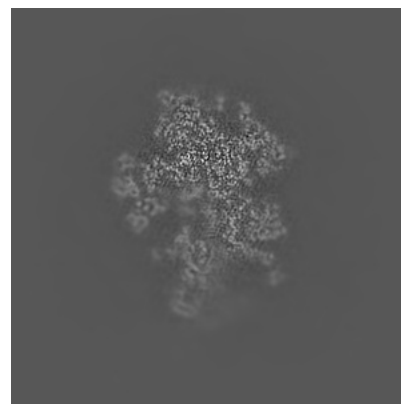
6.3.1 Primary map



X Index: 282



Y Index: 320

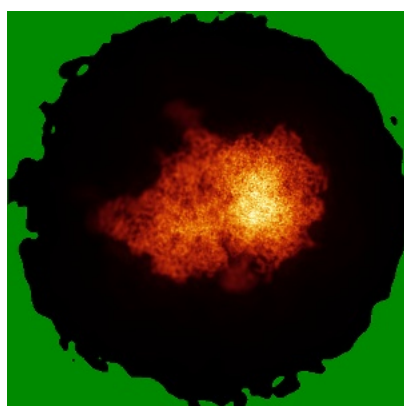


Z Index: 257

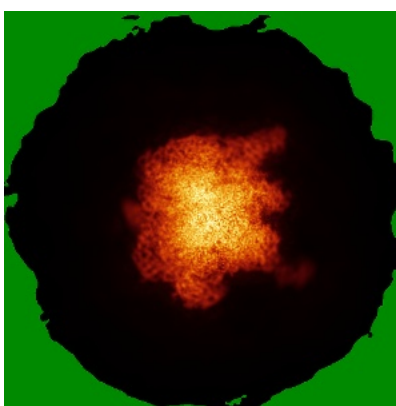
The images above show the largest variance slices of the map in three orthogonal directions.

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

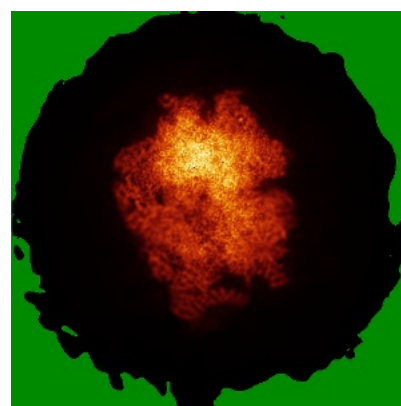
6.4.1 Primary map



X



Y

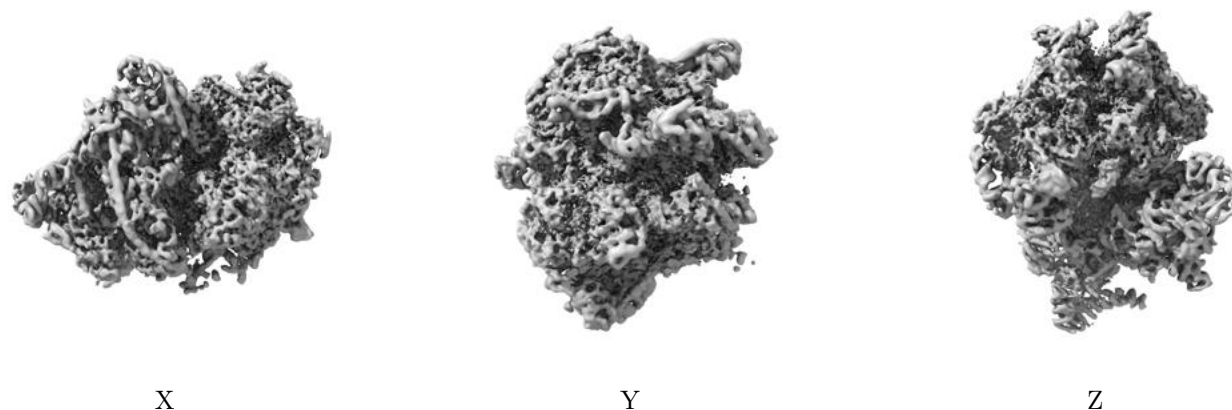


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

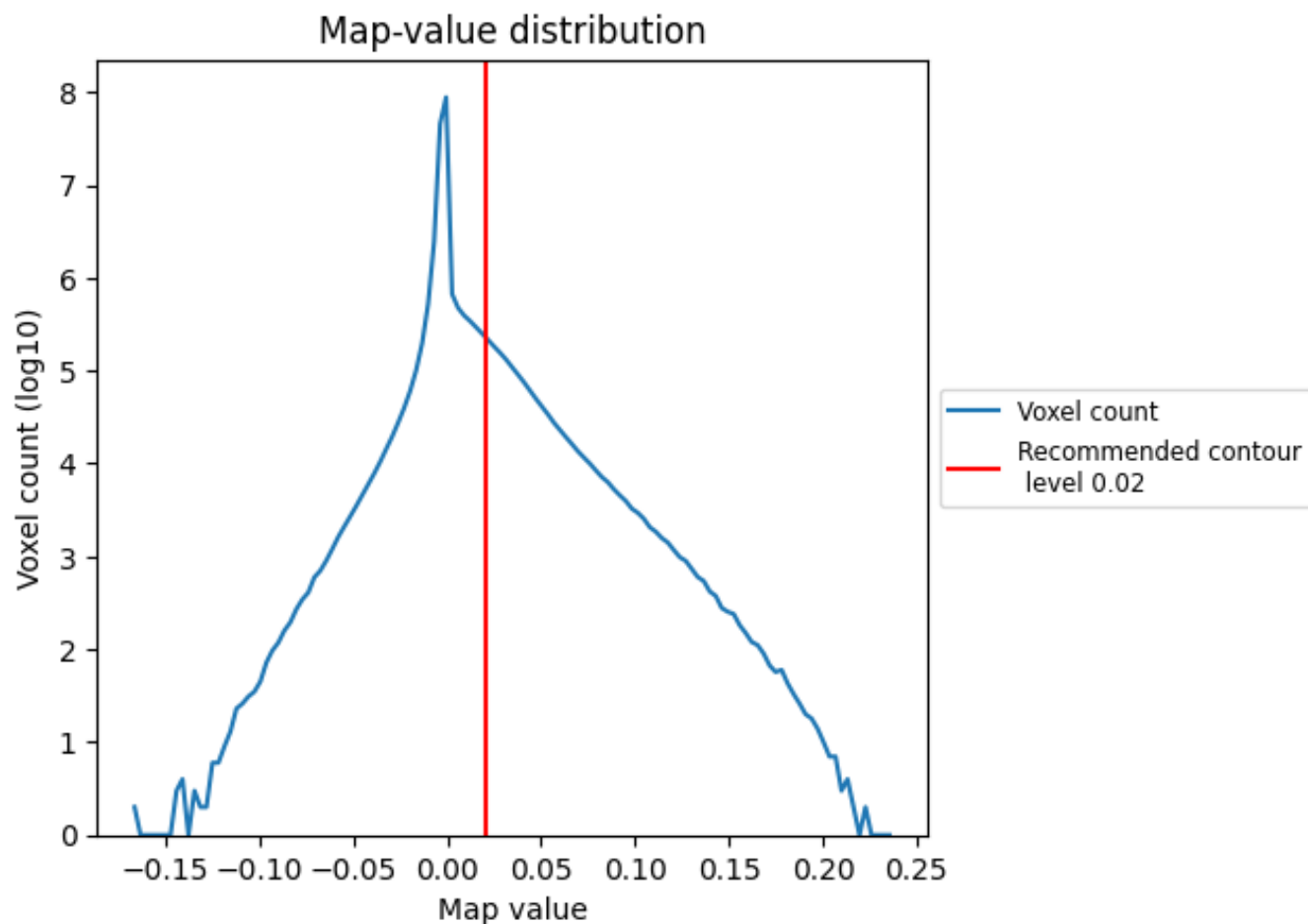
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

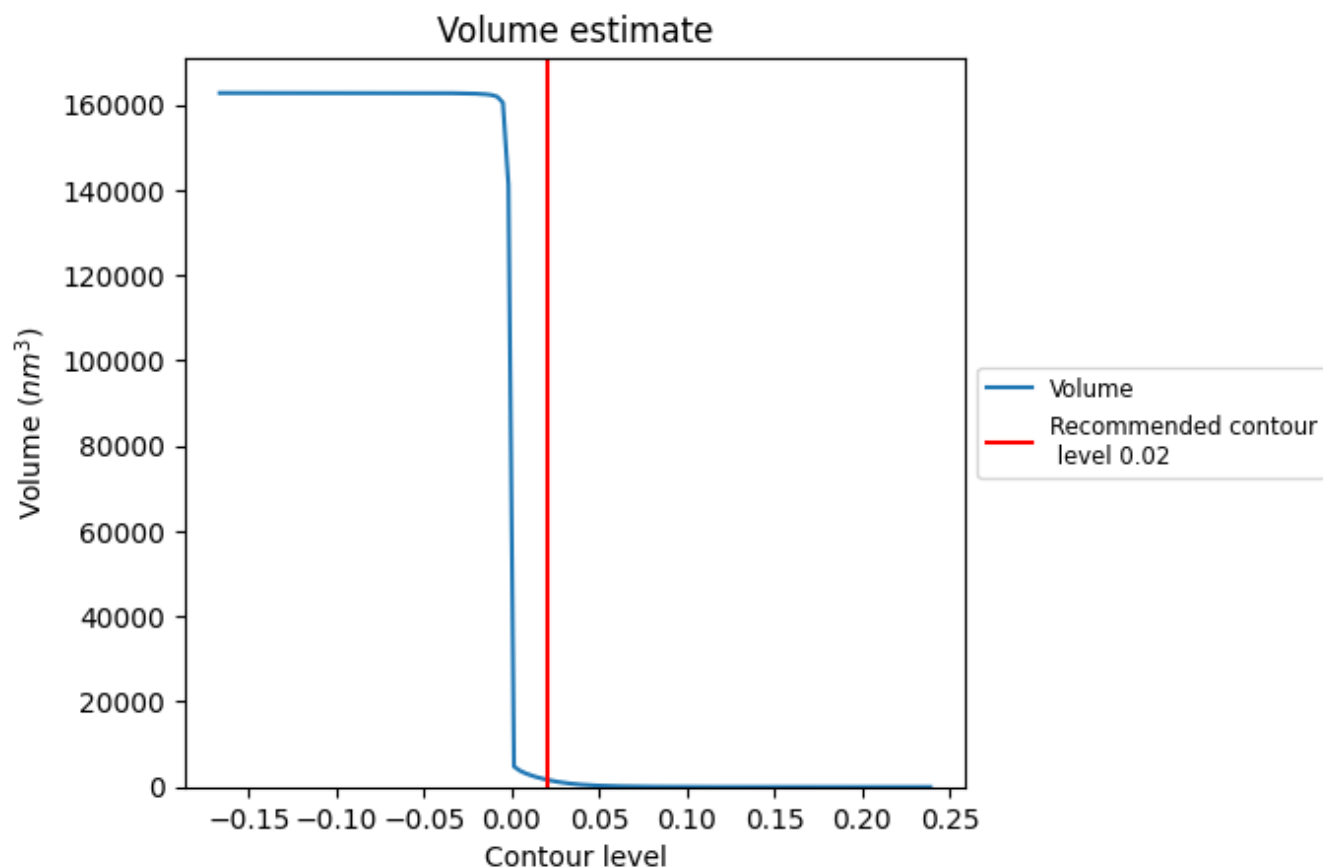
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

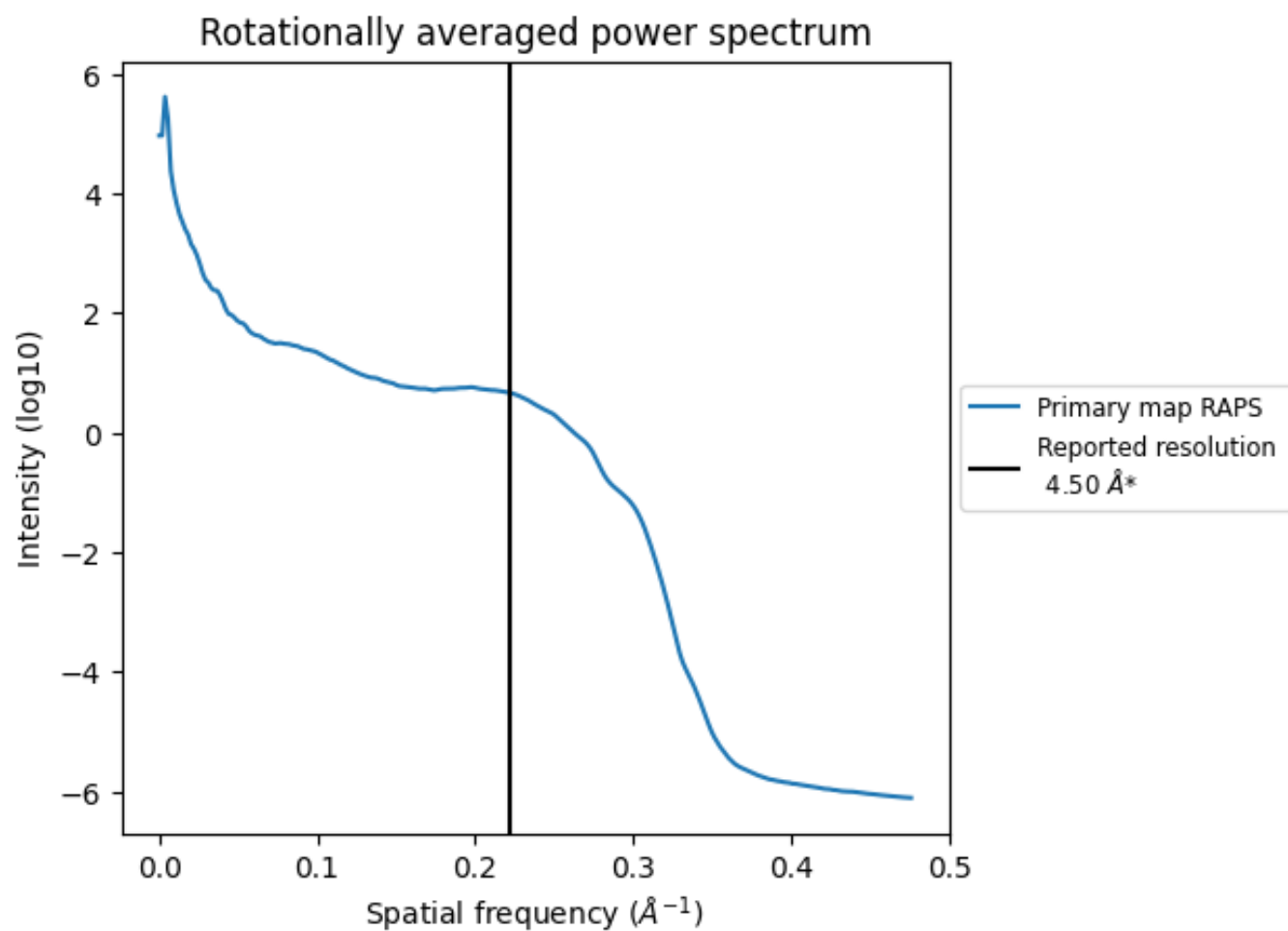
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1693 nm³; this corresponds to an approximate mass of 1529 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.222 Å⁻¹

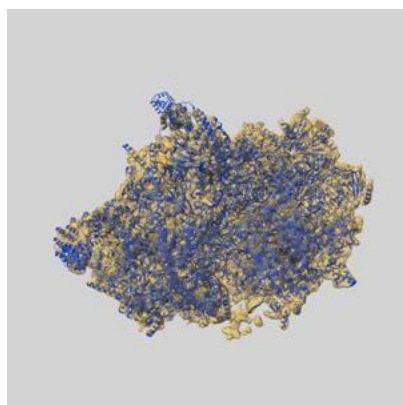
8 Fourier-Shell correlation

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

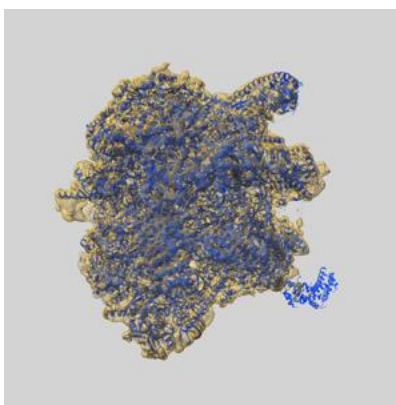
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11392 and PDB model 6ZSB. Per-residue inclusion information can be found in [section 3](#) on [page 22](#).

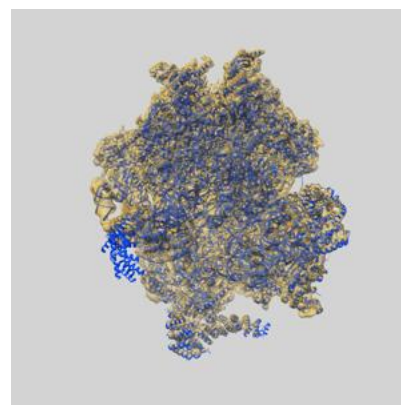
9.1 Map-model overlay [i](#)



X



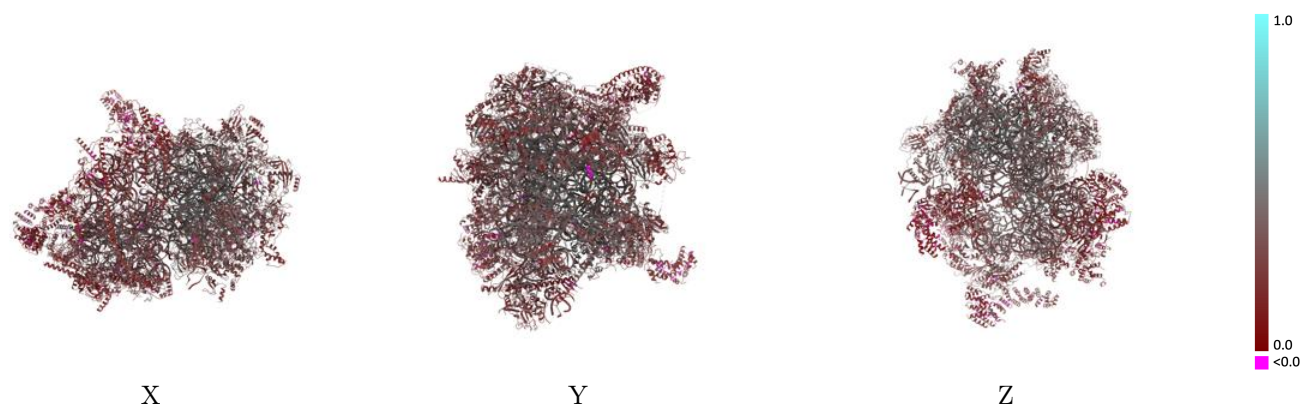
Y



Z

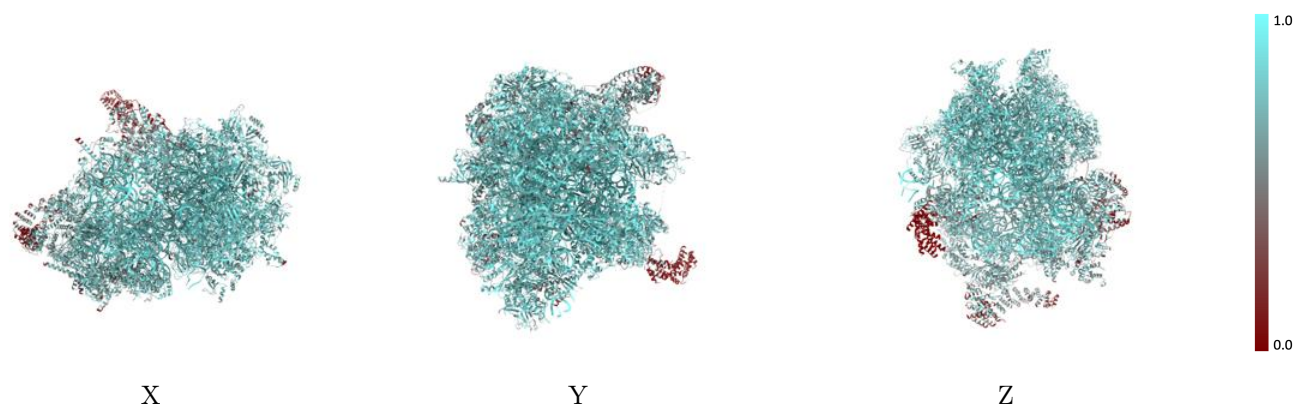
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



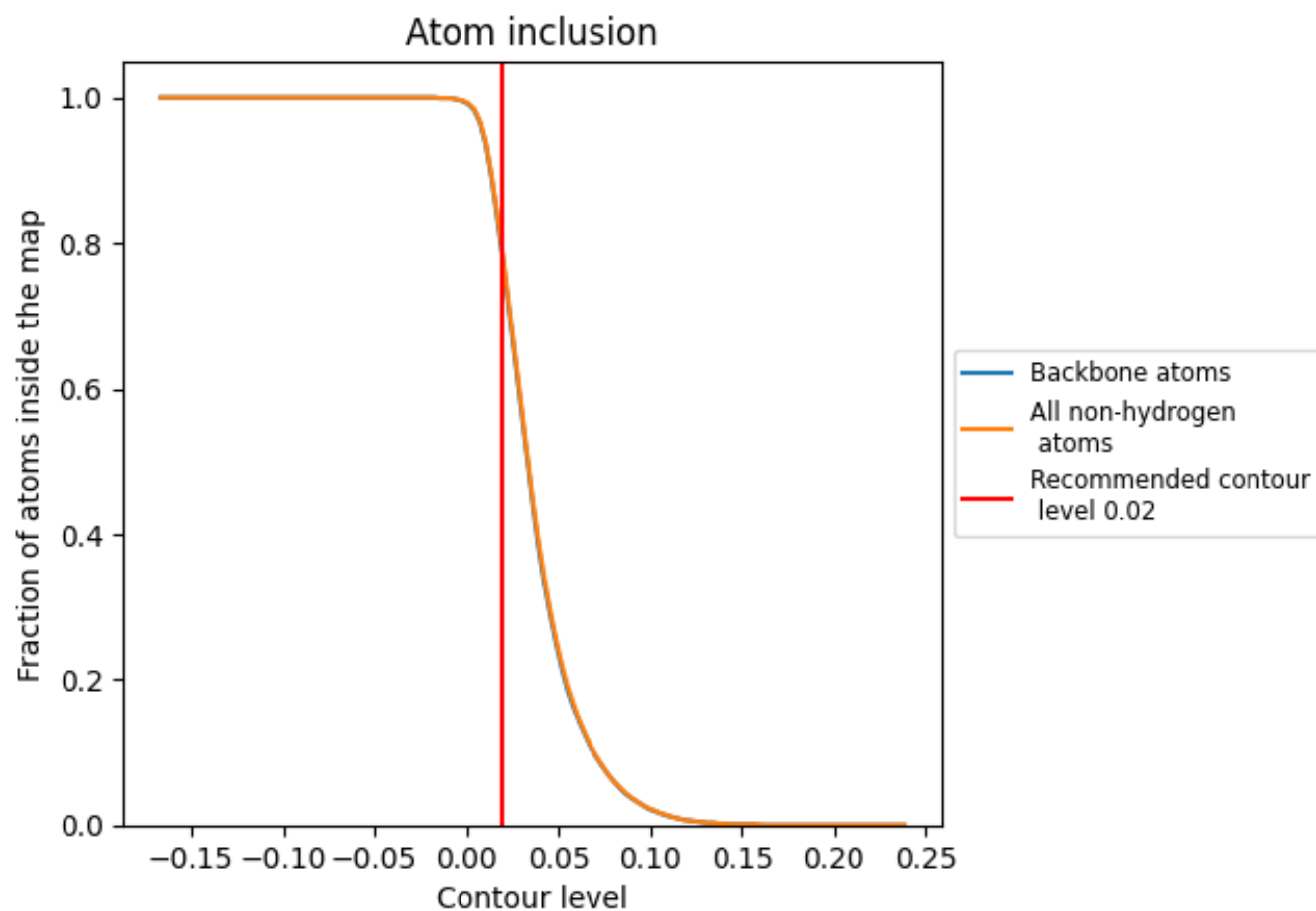
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 78% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7840	 0.3100
0	 0.8200	 0.3430
1	 0.7980	 0.3280
2	 0.8720	 0.4530
3	 0.8530	 0.4210
4	 0.8590	 0.3650
5	 0.7840	 0.3060
6	 0.7620	 0.2900
7	 0.7460	 0.2780
8	 0.6490	 0.1910
9	 0.7870	 0.3350
A	 0.8220	 0.3910
A0	 0.6010	 0.1780
A1	 0.6160	 0.2050
A2	 0.6660	 0.2640
A3	 0.8350	 0.3590
A4	 0.4540	 0.1600
AA	 0.9310	 0.3270
AB	 0.7120	 0.2560
AC	 0.7040	 0.2780
AD	 0.7010	 0.2810
AE	 0.7180	 0.3060
AF	 0.6950	 0.2510
AG	 0.6810	 0.2350
AH	 0.6710	 0.2560
AI	 0.7190	 0.2900
AJ	 0.7510	 0.3030
AK	 0.7160	 0.2460
AL	 0.7440	 0.2700
AM	 0.6620	 0.1890
AN	 0.7650	 0.2980
AO	 0.6760	 0.2350
AP	 0.7410	 0.2930
AQ	 0.7680	 0.3060
AR	 0.6240	 0.1820



































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Chain	Atom inclusion	Q-score
AS	 0.6320	 0.2340
AT	 0.7350	 0.2680
AU	 0.6940	 0.2140
AV	 0.5240	 0.1670
AW	 0.6800	 0.2480
AX	 0.6320	 0.1800
AY	 0.6090	 0.2000
AZ	 0.6560	 0.2050
XA	 0.9360	 0.4010
XB	 0.9520	 0.2910
XD	 0.8430	 0.3800
XE	 0.8240	 0.3740
XF	 0.8520	 0.3880
XH	 0.7380	 0.3080
XI	 0.5470	 0.2060
XJ	 0.6300	 0.1820
XK	 0.8390	 0.3820
XL	 0.8380	 0.3760
XM	 0.8380	 0.3820
XN	 0.8120	 0.3680
XO	 0.8120	 0.3450
XP	 0.7950	 0.3140
XQ	 0.7370	 0.3180
XR	 0.8300	 0.3830
XS	 0.8220	 0.3870
XT	 0.8590	 0.4030
XU	 0.8210	 0.3640
XV	 0.7800	 0.2970
XW	 0.8660	 0.4180
XX	 0.7870	 0.3210
XY	 0.8380	 0.3420
XZ	 0.8510	 0.3950
a	 0.7980	 0.3590
b	 0.8590	 0.3880
c	 0.7920	 0.3170
d	 0.6960	 0.2630
e	 0.6410	 0.1700
f	 0.6630	 0.2160
g	 0.8230	 0.3520
h	 0.7600	 0.2910
i	 0.8590	 0.4120
j	 0.7960	 0.3400

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Chain	Atom inclusion	Q-score
k	 0.6980	 0.2030
l	 0.6700	 0.2020
m	 0.7500	 0.2220
o	 0.8680	 0.3940
p	 0.7740	 0.2760
q	 0.6460	 0.2420
r	 0.8280	 0.3240
r1	 0.7640	 0.3090
r3	 0.8600	 0.2650
s	 0.8050	 0.3260
t1	 0.1590	 0.1780
t2	 0.0920	 0.1670
t3	 0.0000	 0.1750
t4	 0.0000	 0.1220
t5	 0.0000	 0.1440
t6	 0.0000	 0.0900