



Full wwPDB EM Validation Report ⓘ

Feb 28, 2024 – 02:58 pm GMT

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.dev70
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) : 2.36

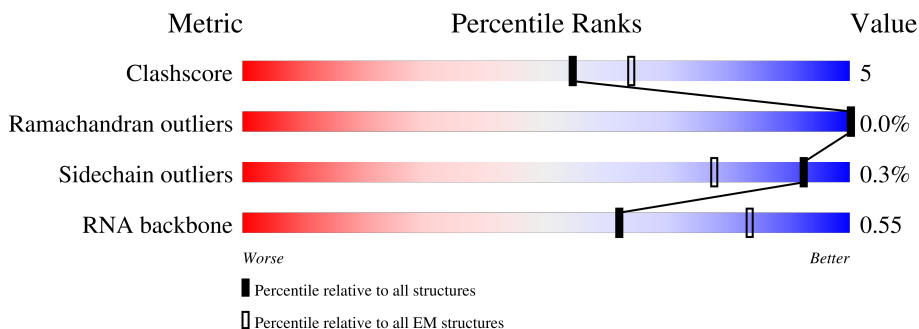
1 Overall quality at a glance

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.





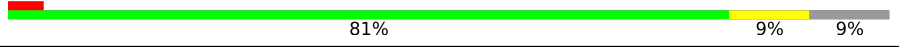
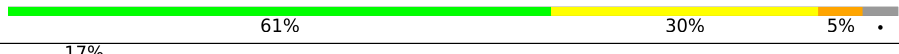




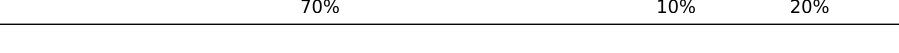
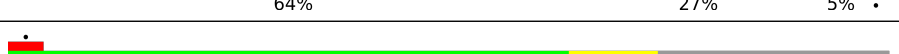
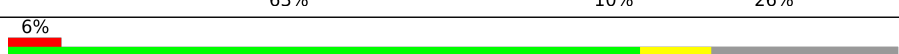

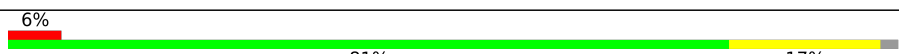
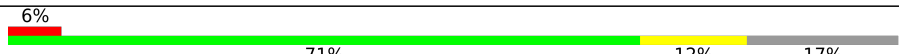
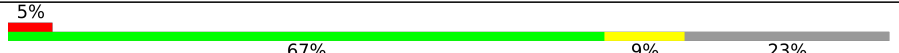




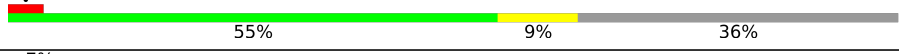





Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	

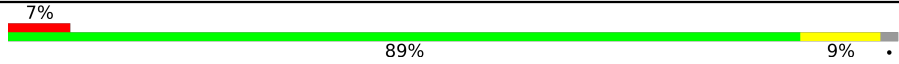
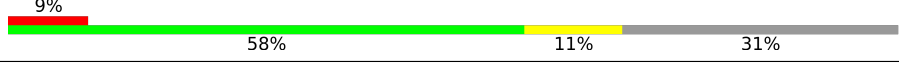
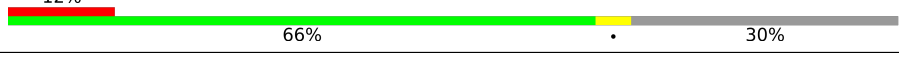



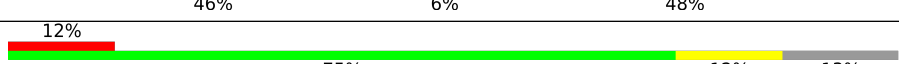
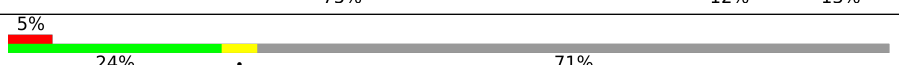
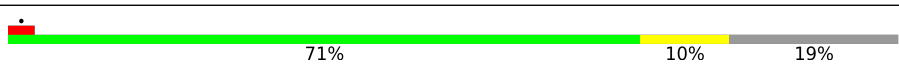


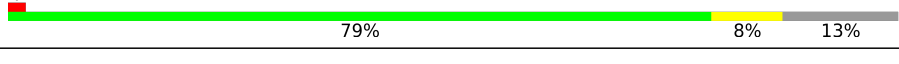
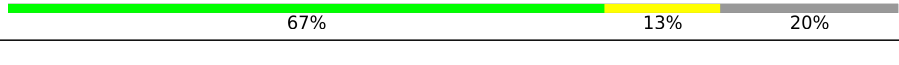

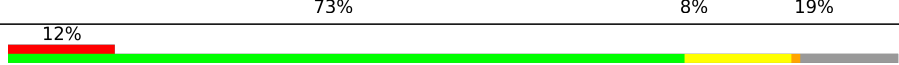










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Mol	Chain	Length	Quality of chain
8	7	338	
9	8	206	
10	9	137	
11	XA	1561	
12	A0	218	
13	A1	323	
14	A2	118	
15	A3	199	
16	A4	689	
17	AA	954	
18	AB	296	
19	AC	167	
20	AD	430	
21	AE	125	
22	AF	242	
23	AG	396	
24	AH	201	
25	AI	194	
26	AJ	138	
27	AK	128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



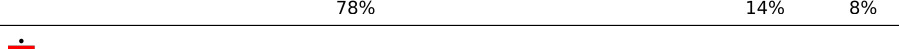
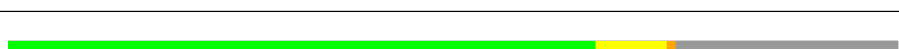



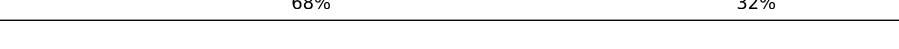



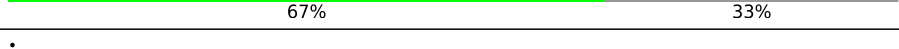

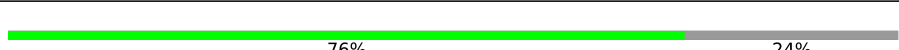


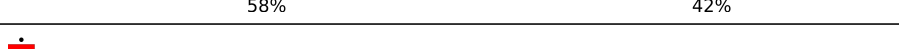







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Mol	Chain	Length	Quality of chain
33	AQ	87	
34	AR	360	
35	AS	190	
36	AT	173	
37	AU	205	
38	AV	414	
39	AW	187	
40	AX	398	
41	AY	395	
42	AZ	106	
43	XB	72	
44	XD	305	
45	XE	348	
46	XF	311	
47	XH	267	
48	XI	261	
49	XJ	192	
50	XK	178	
51	XL	145	
52	XM	296	
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	
			Total	C	H	N	O			S
1	0	108	1783	545	903	172	157	6	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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	
			Total	C	H	N	O			S
34	AR	250	4134	1314	2074	353	385	8	0	0

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

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

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

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

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

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

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

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

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

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

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

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

- 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 tRNAVal.

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	
			Total	C	H	N	O			S
48	XI	211	3474	1086	1783	303	291	11	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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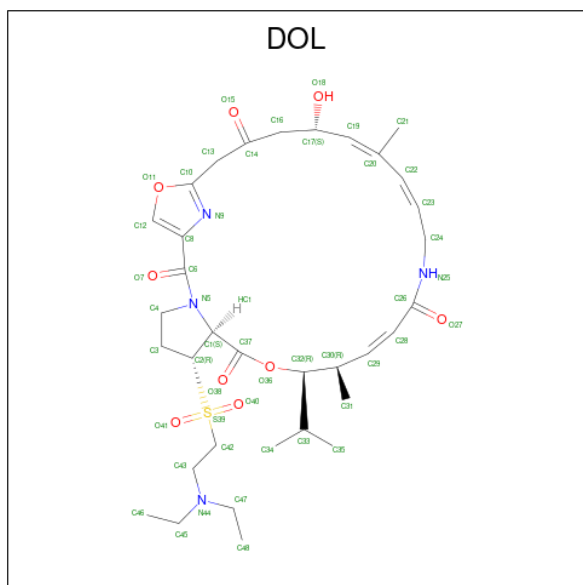
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Mol	Chain	Residues	Atoms		AltConf
88	4	1	Total 1	Zn 1	0
88	AB	1	Total 1	Zn 1	0
88	AO	1	Total 1	Zn 1	0
88	AP	1	Total 1	Zn 1	0
88	AT	1	Total 1	Zn 1	0
88	r	1	Total 1	Zn 1	0

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

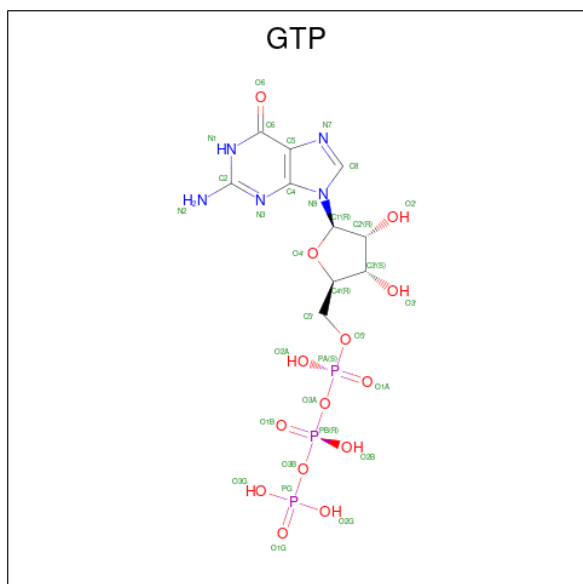
Mol	Chain	Residues	Atoms		AltConf
89	9	1	Total 1	Mg 1	0
89	XA	142	Total 142	Mg 142	0
89	A2	1	Total 1	Mg 1	0
89	AA	45	Total 45	Mg 45	0
89	XD	1	Total 1	Mg 1	0
89	XE	1	Total 1	Mg 1	0
89	XM	2	Total 2	Mg 2	0
89	XW	1	Total 1	Mg 1	0
89	g	1	Total 1	Mg 1	0

- 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	
			Total	C	H	N	O		S
90	XA	1	98	34	50	4	9	1	0

- 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	
			Total	C	H	N	O		P
91	AX	1	42	10	10	5	14	3	0


- Molecule 5: 39S ribosomal protein L36, mitochondrial

Chain 4:  33% 63%

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

LEU PRO ALA LEU LEU GLY F66 R84 R87 W88 Q102 M103

- Molecule 6: 39S ribosomal protein L37, mitochondrial


Chain 5:  80% 13% 7%

MET ALA ALA SER GLY PRO ARG ALA ARG ALA LEU LEU GLY GLN LEU LEU GLY LEU LEU PHE GLY ALA PRO ARG ARG A30 W33 R39 E51 A297 N298 R112 A120 L121 W122 V140 D141 D142 P143 R144 N145 H146 H160 V164 R173 E174 Y175 C177

R178 V179 I180 V181 I182 N183 L184 C188 R200 R201 R215 E216 G226 D234 R242 I245 T255 D264 I270 K274 D295 K296 A297 N298 L299 R300 P301 R302 R303 L304 Q305 P306 R310 A311 I314 L315 K334 E337 Q343 R350 T362

Q384 V391 I392 K393 V396 E409 K413 L417 Y418 A422 ALA

- Molecule 7: 39S ribosomal protein L38, mitochondrial


Chain 6:  79% 14% 7%

MET ALA PRO TRP ARG ALA LEU CYS GLU CYS ARG TRP ARG GLY PHE SER SER VAL LEU R27 P36 N37 T73 F78 T82 D83 P84 K85 E86 R99 R106 R114 V117 E118 E119 R121 R124 D133 A134 Q149

D160 T166 R170 G180 E181 N191 A198 Y206 E210 G211 S212 L213 W214 E231 N239 L240 F241 G242 E247 C252 P253 Y254 F259 R267 K274 Q275 D280 F281 S282 E283 D284 A285 R286 P289 C290 T300 F301 D302 F303 H307 Q308

H311 D324 D325 R360 R364 R367 R368 Y369 R370 Y380

- Molecule 8: 39S ribosomal protein L39, mitochondrial

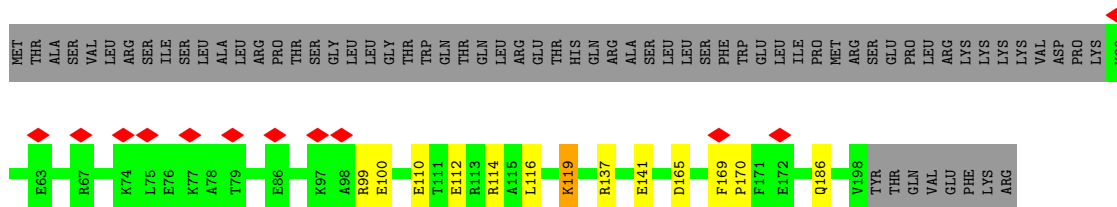
Chain 7:  75% 11% 14%

MET GLU LEU MET GLY SER ARG ALA LEU ARG LEU TRP LEU VAL ALA PRO GLY GLY GLY ILE LYS TRP ARG PHE ILE ALA THR SER SER ALA GLN LEU S36 P37 T38 E42 N49 K52 H94 L95 A147 M150 G151 C152 V153 I154 E155 R156 D160

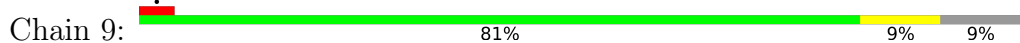
W192 M193 L199 T203 H207 E220 V225 L229 Y235 D238 F239 N247 L251 D259 F260 T261 D262 V263 S264 E265 Y278 E279 Q290 P291 R295 R296 F297 L306 H309 F310 T311 I312 K315 T325 E326 ASP GLN SER LYS ALA THR GLU

GLU
CYS
THR
THR

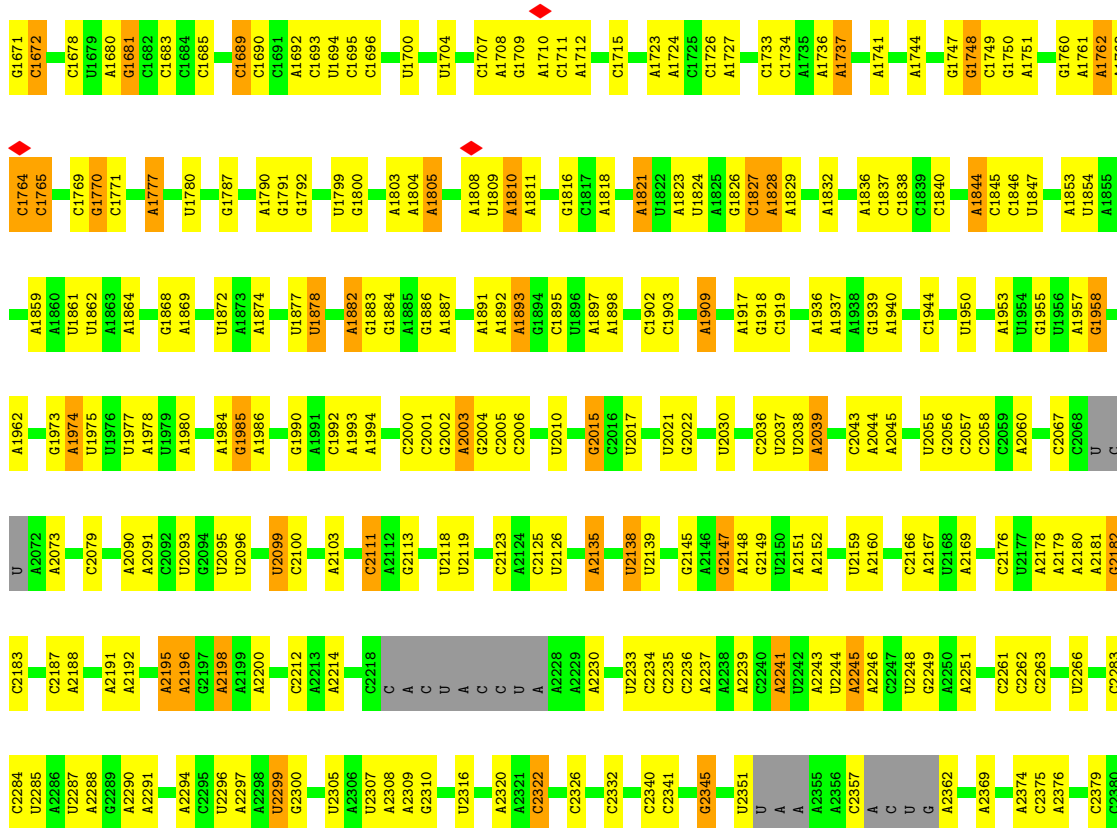
- Molecule 9: 39S ribosomal protein L40, mitochondrial

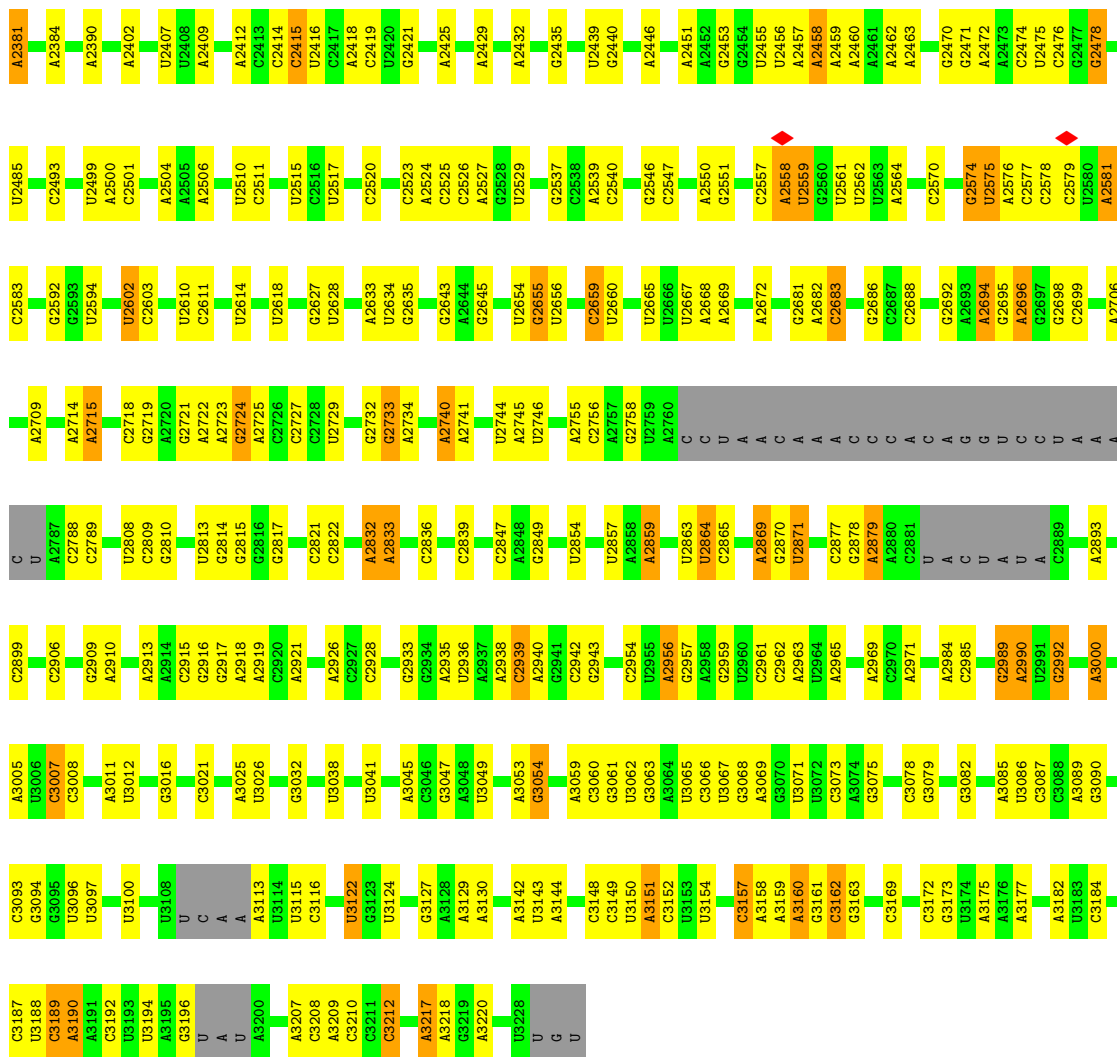


- Molecule 10: 39S ribosomal protein L41, mitochondrial

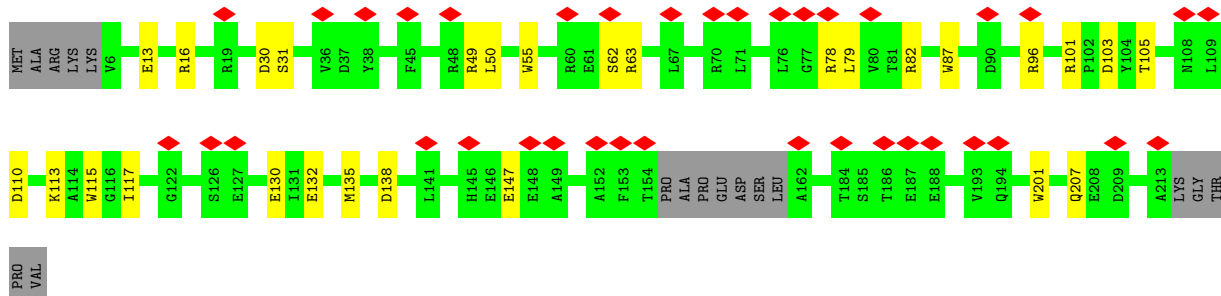
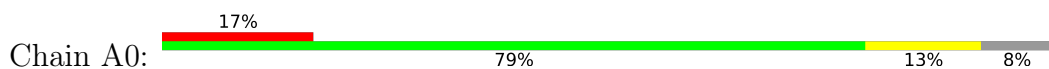


- Molecule 11: 16S mitochondrial rRNA

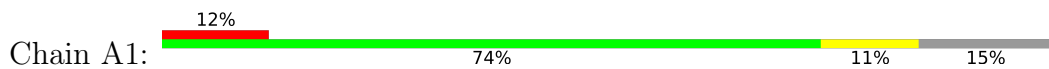


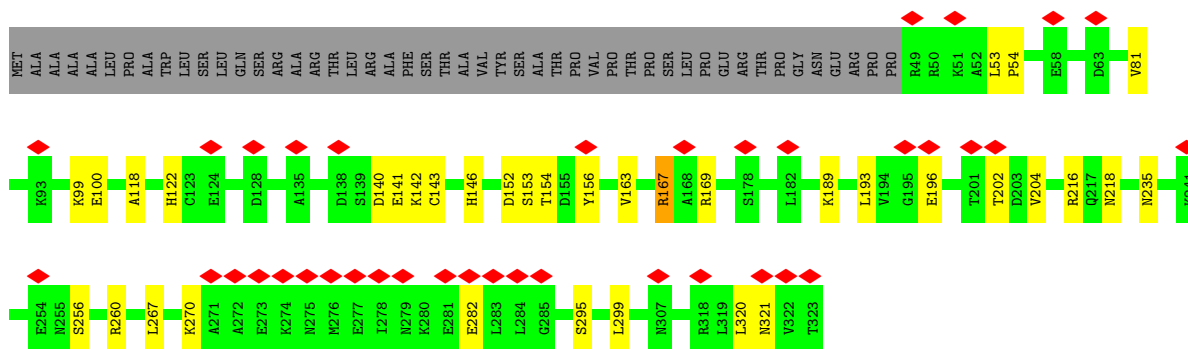


• Molecule 12: 28S ribosomal protein S34, mitochondrial

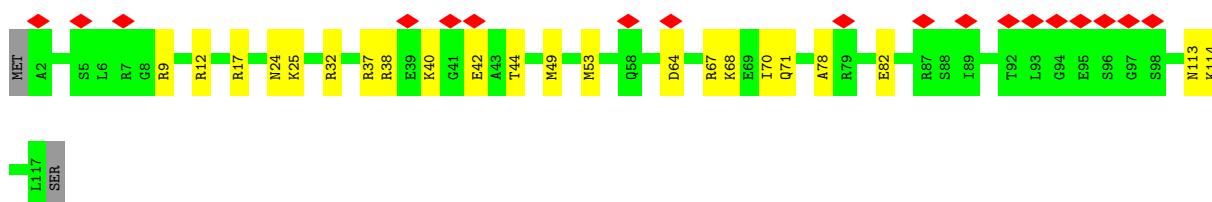
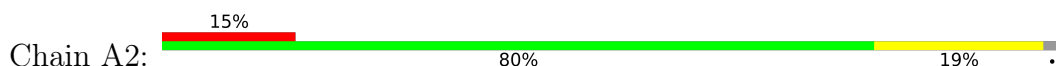


• Molecule 13: 28S ribosomal protein S35, mitochondrial

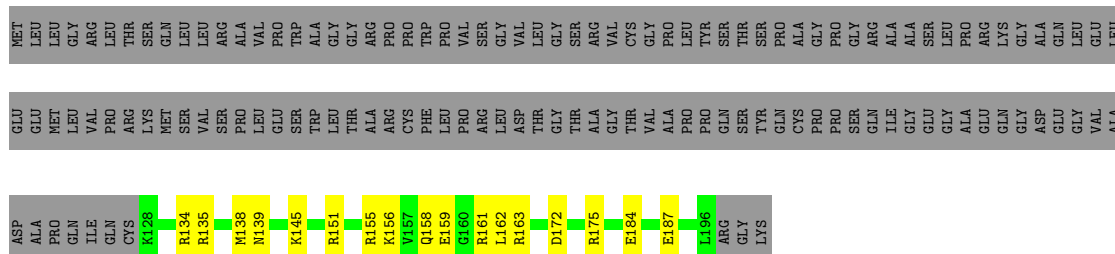




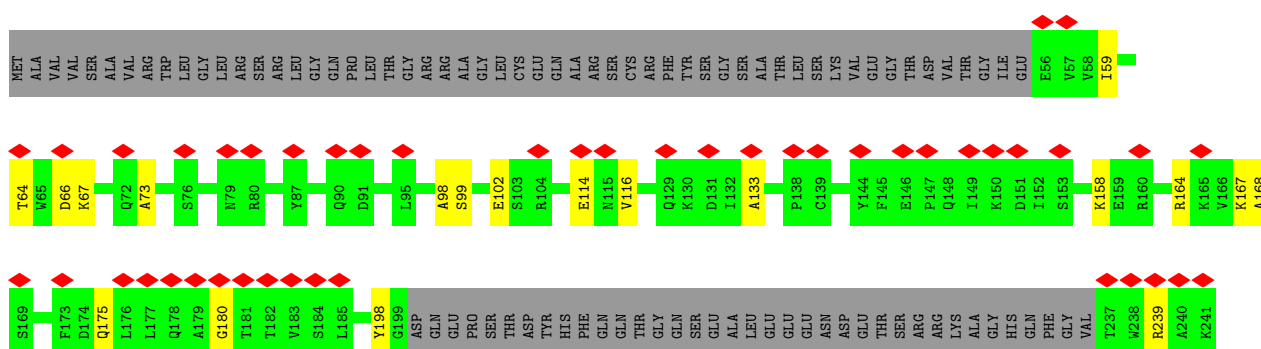
• Molecule 14: Coiled-coil-helix-coiled-coil-helix domain-containing protein 1

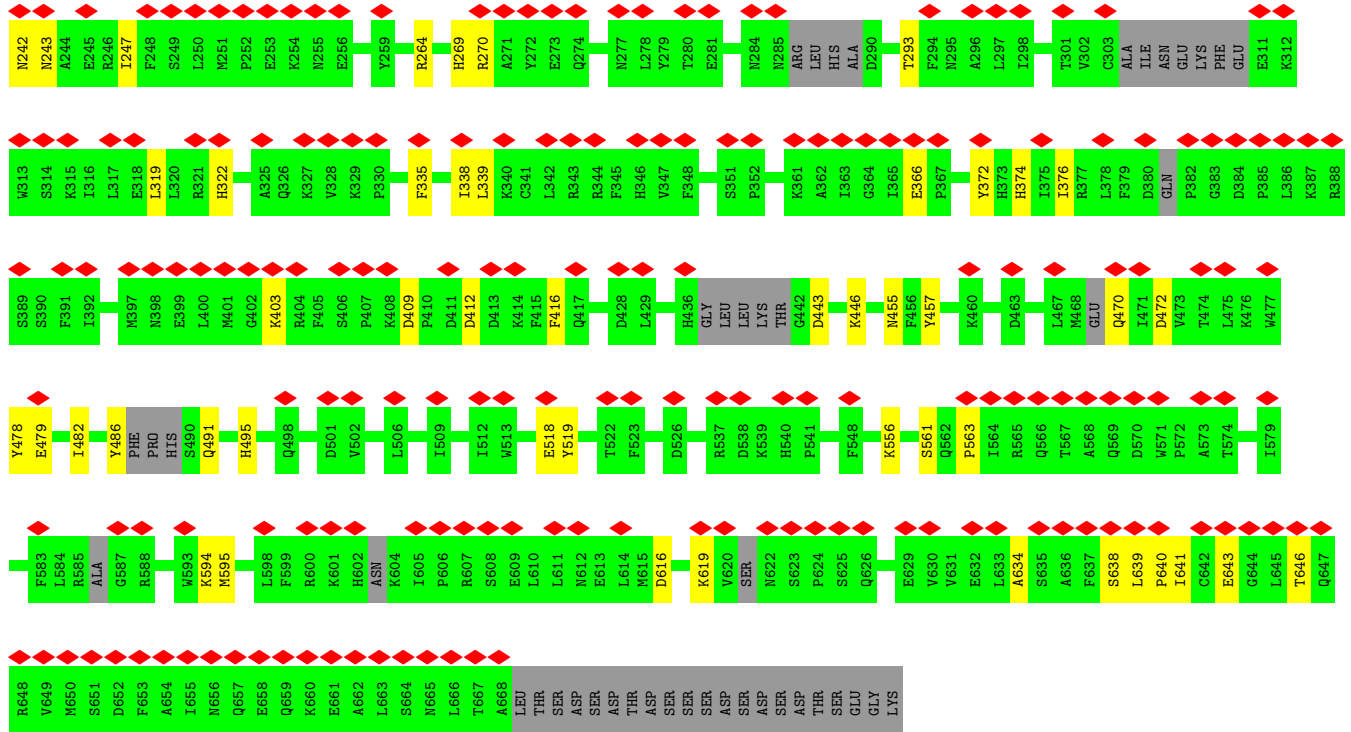


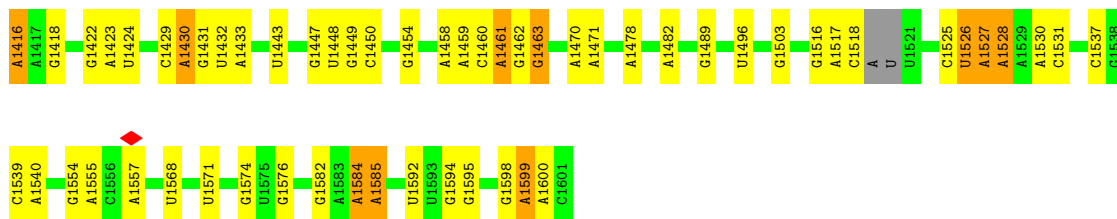
• Molecule 15: Aurora kinase A-interacting protein



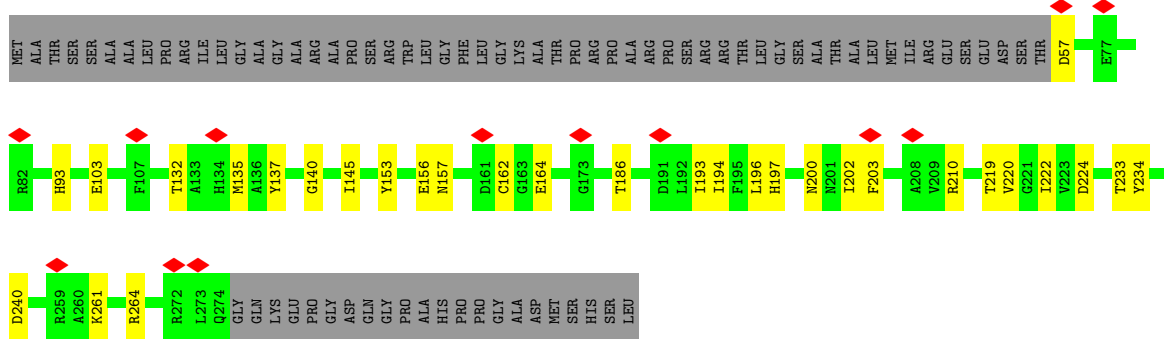
• Molecule 16: Pentatricopeptide repeat domain-containing protein 3, mitochondrial



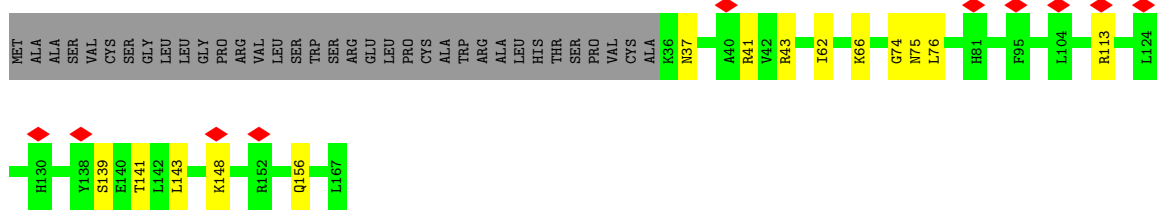




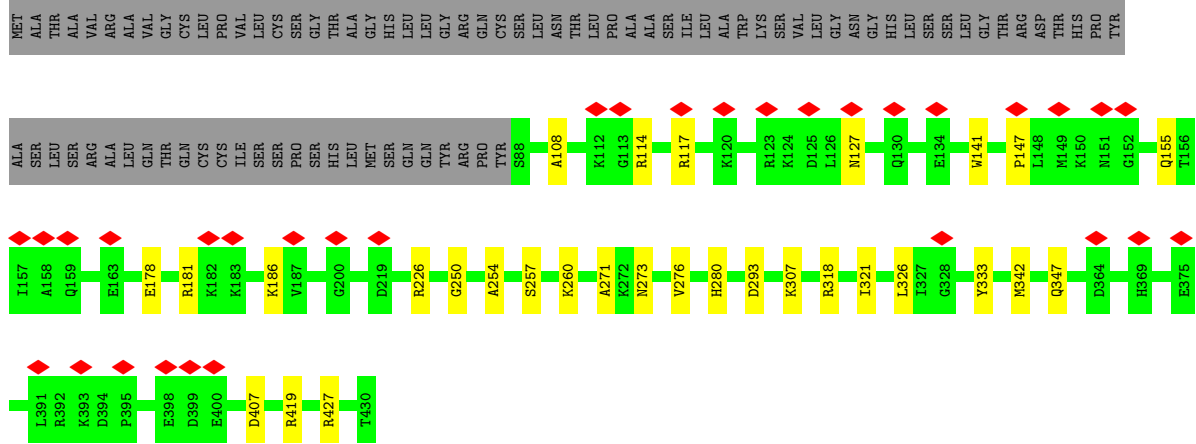
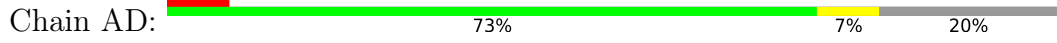
• Molecule 18: 28S ribosomal protein S2, mitochondrial



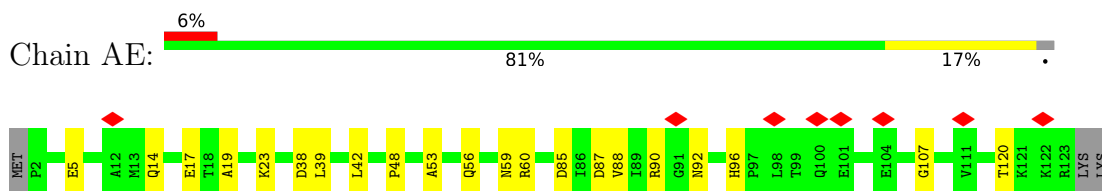
• Molecule 19: 28S ribosomal protein S24, mitochondrial



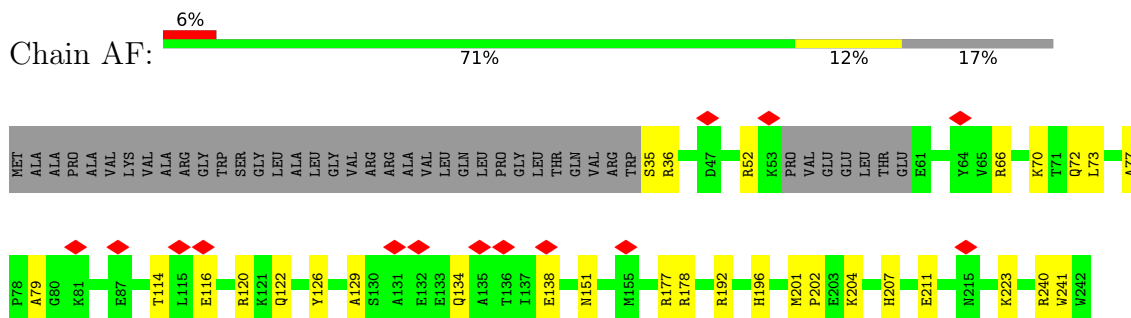
• Molecule 20: 28S ribosomal protein S5, mitochondrial



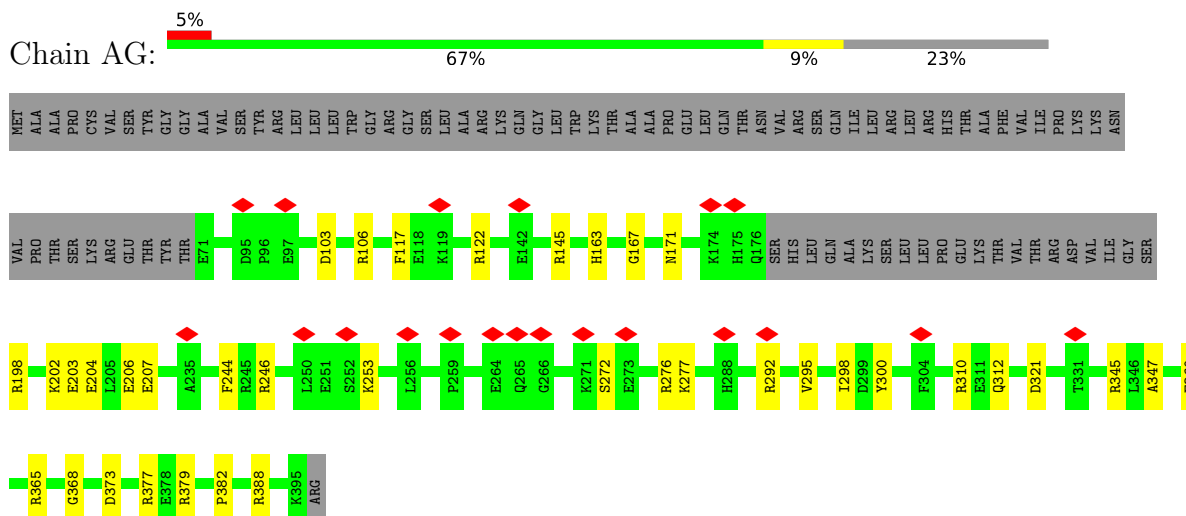
- Molecule 21: 28S ribosomal protein S6, mitochondrial



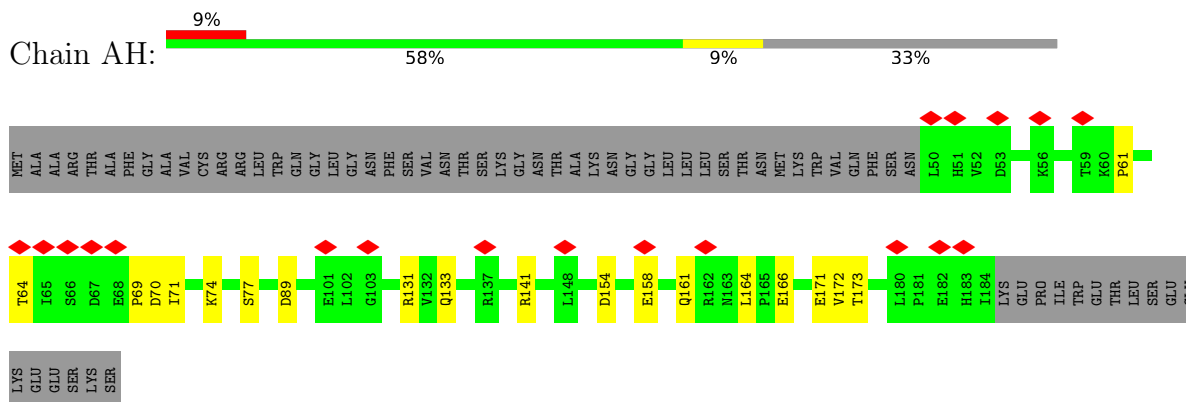
- Molecule 22: 28S ribosomal protein S7, mitochondrial



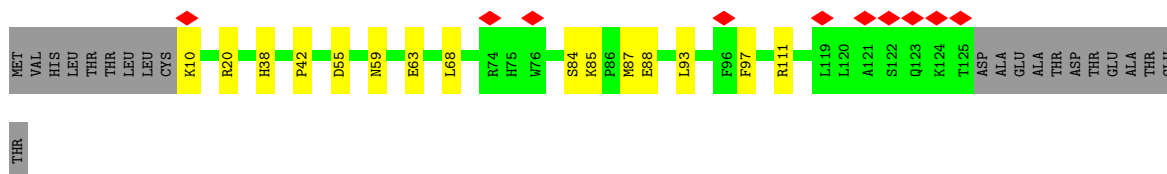
- Molecule 23: 28S ribosomal protein S9, mitochondrial



- Molecule 24: 28S ribosomal protein S10, mitochondrial



- Molecule 25: 28S ribosomal protein S11, mitochondrial



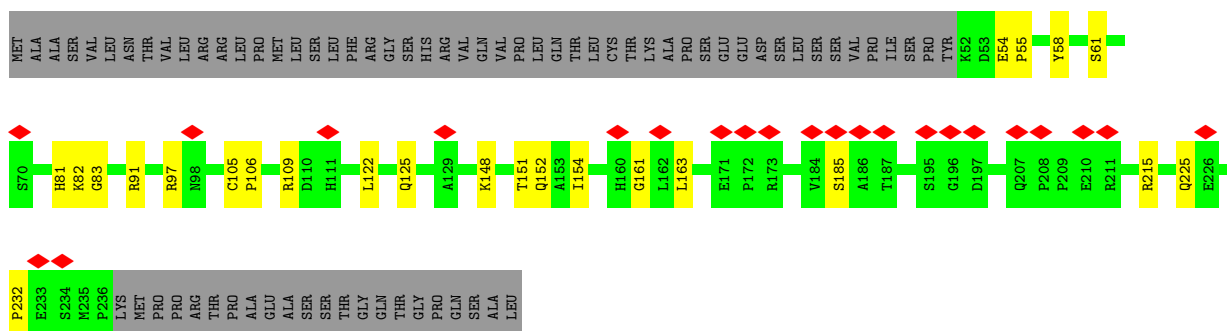
- Molecule 30: 28S ribosomal protein S17, mitochondrial

Chain AN: 72% 10% 18%



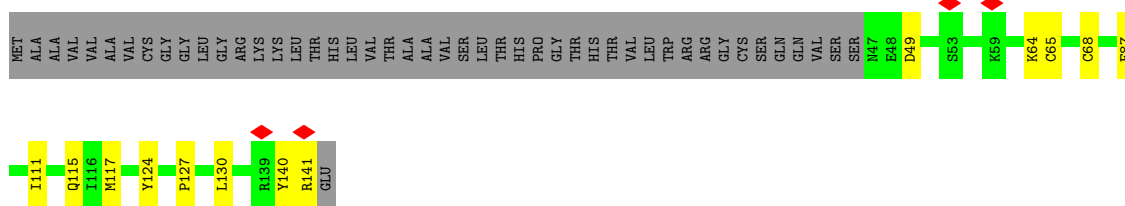
- Molecule 31: 28S ribosomal protein S18b, mitochondrial

Chain AO: 9% 62% 9% 28%



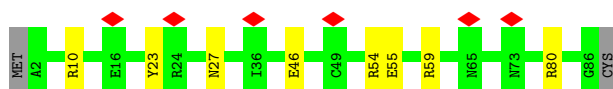
- Molecule 32: 28S ribosomal protein S18c, mitochondrial

Chain AP: 58% 9% 33%



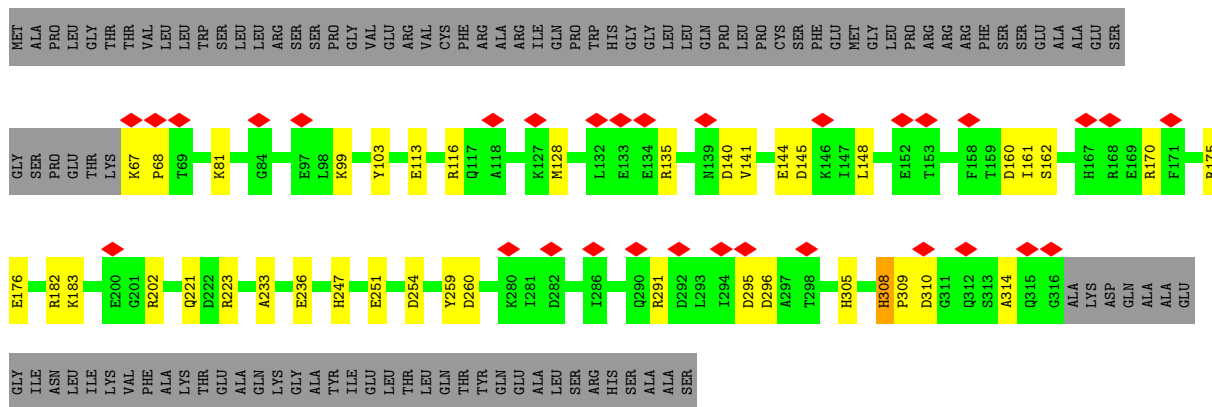
- Molecule 33: 28S ribosomal protein S21, mitochondrial

Chain AQ: 7% 89% 9%

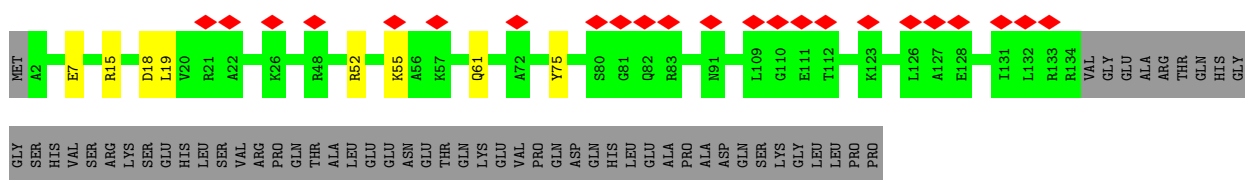


- Molecule 34: 28S ribosomal protein S22, mitochondrial

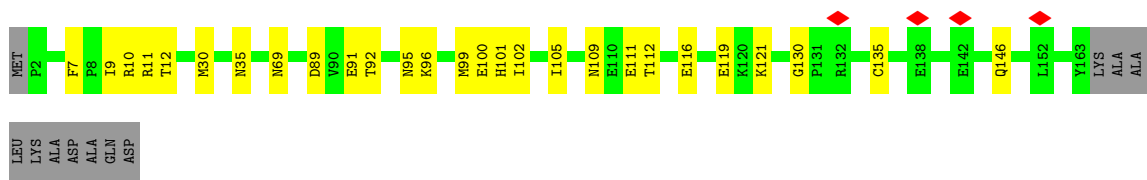
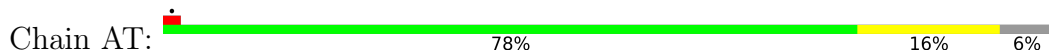
Chain AR: 9% 58% 11% 31%



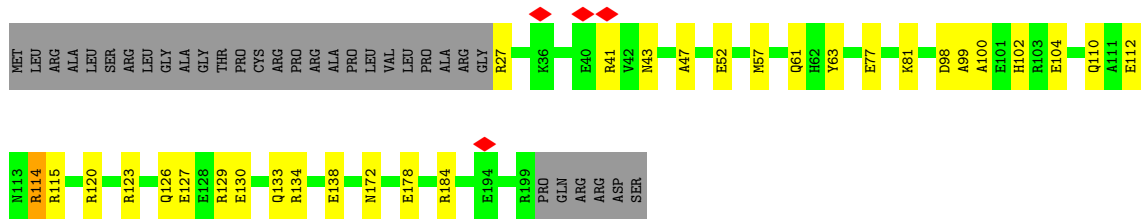
• Molecule 35: 28S ribosomal protein S23, mitochondrial



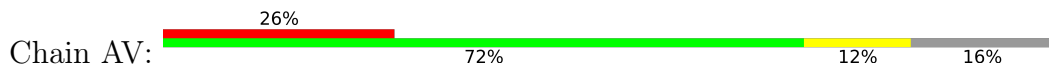
• Molecule 36: 28S ribosomal protein S25, mitochondrial

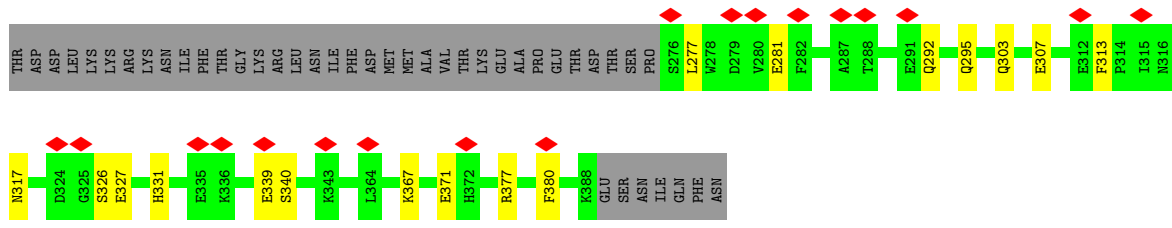
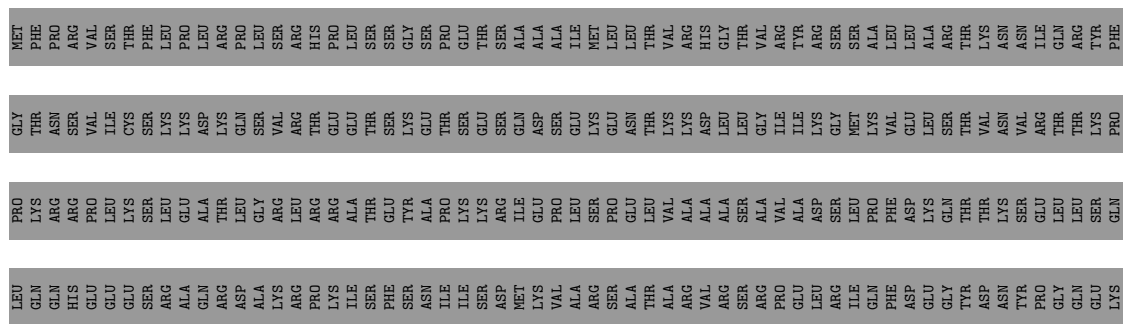


• Molecule 37: 28S ribosomal protein S26, mitochondrial

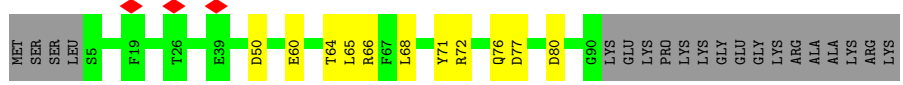


• Molecule 38: 28S ribosomal protein S27, mitochondrial

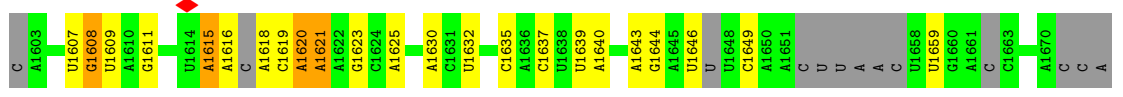




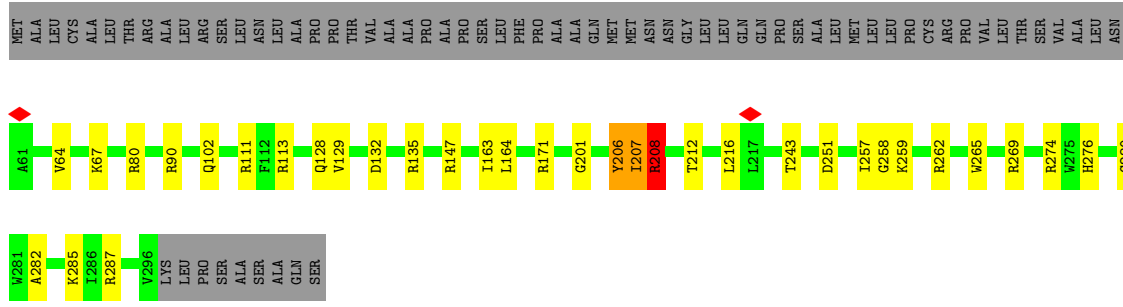
• Molecule 42: 28S ribosomal protein S33, mitochondrial



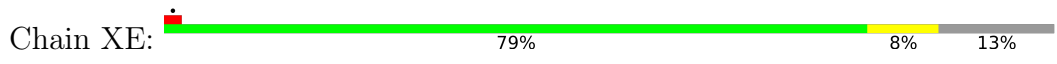
• Molecule 43: mitochondrial tRNA^{Val}

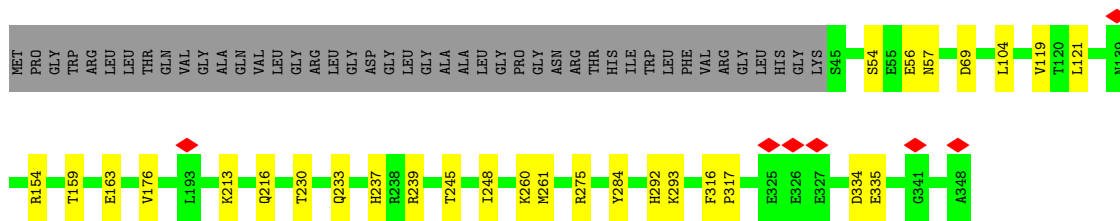


• Molecule 44: 39S ribosomal protein L2, mitochondrial

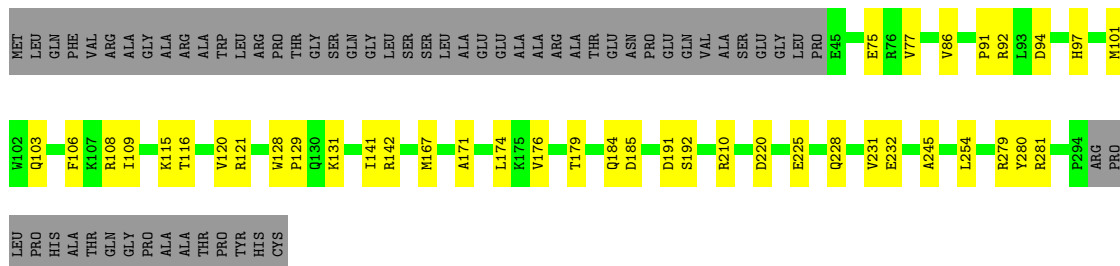


• Molecule 45: 39S ribosomal protein L3, mitochondrial

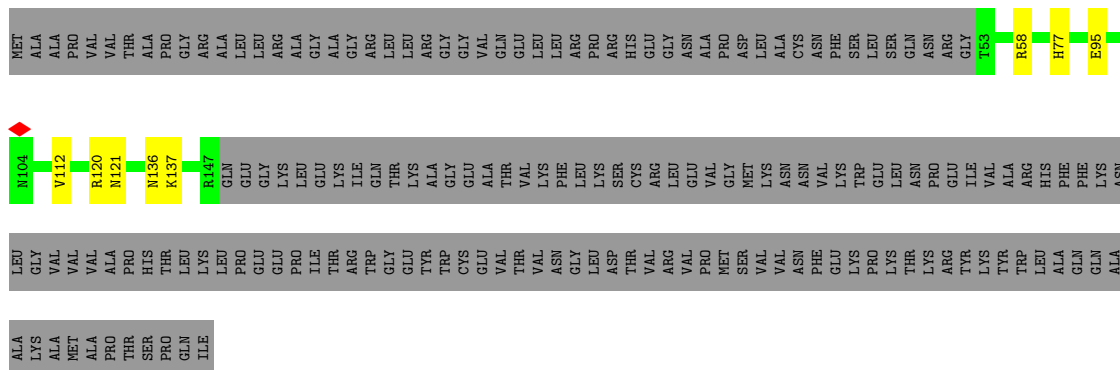




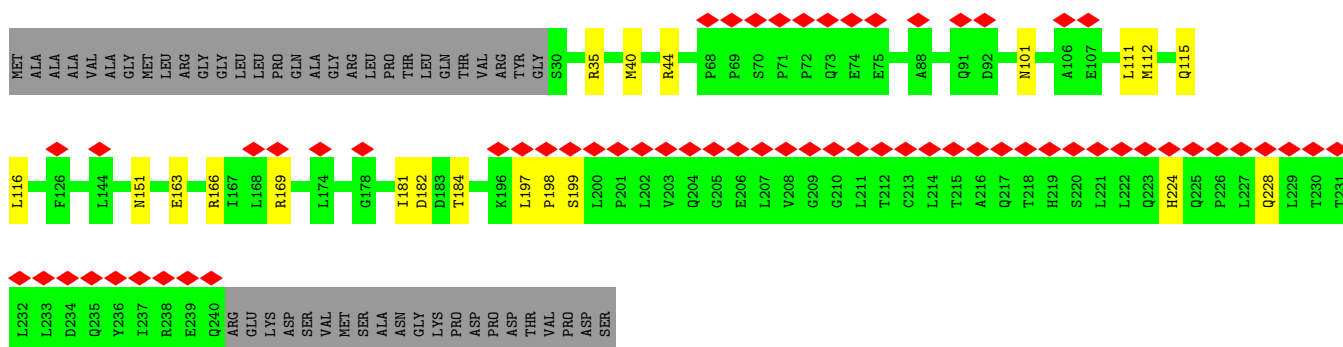
• Molecule 46: 39S ribosomal protein L4, mitochondrial



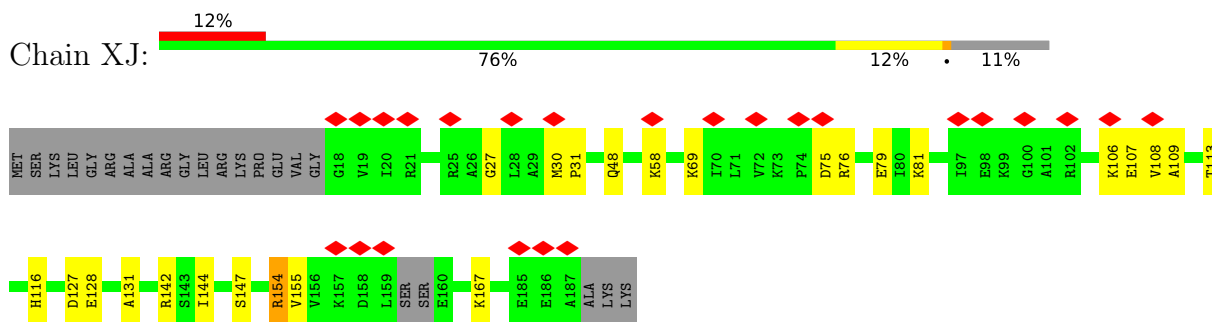
• Molecule 47: 39S ribosomal protein L9, mitochondrial



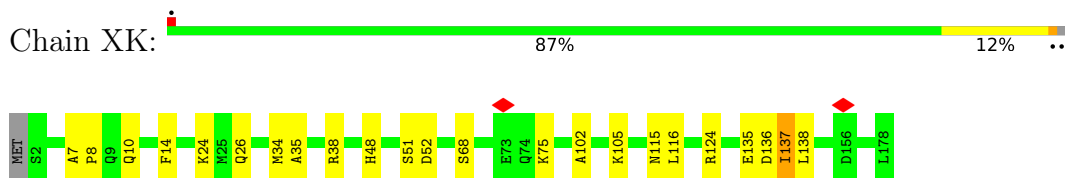
• Molecule 48: 39S ribosomal protein L10, mitochondrial



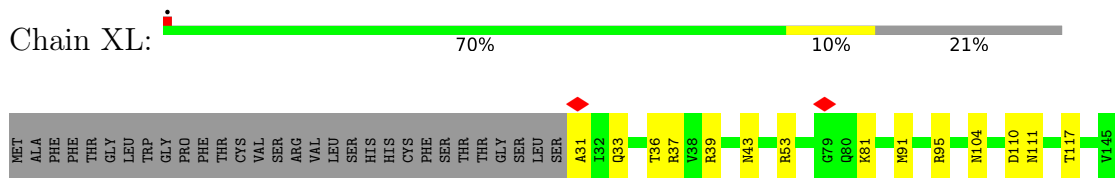
• Molecule 49: 39S ribosomal protein L11, mitochondrial



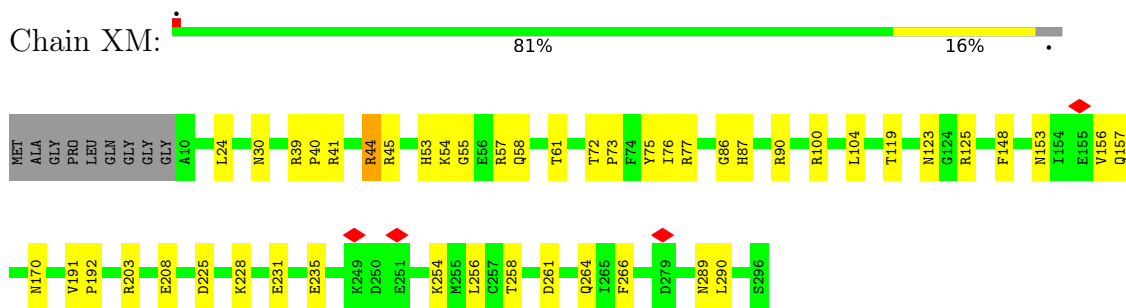
• Molecule 50: 39S ribosomal protein L13, mitochondrial



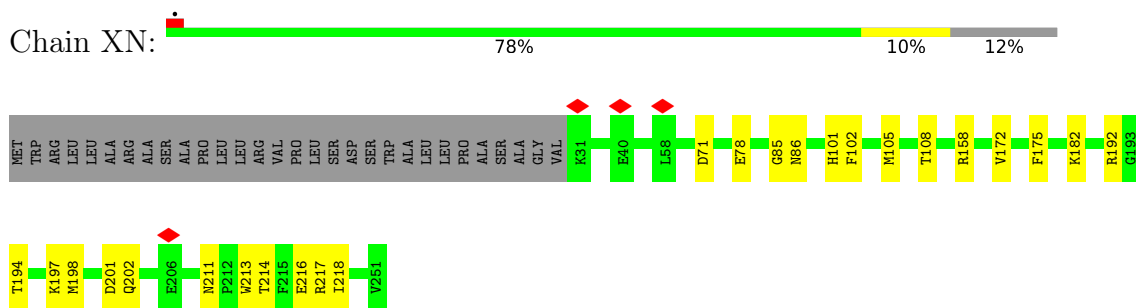
• Molecule 51: 39S ribosomal protein L14, mitochondrial



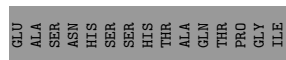
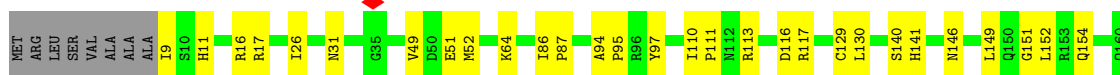
• Molecule 52: 39S ribosomal protein L15, mitochondrial



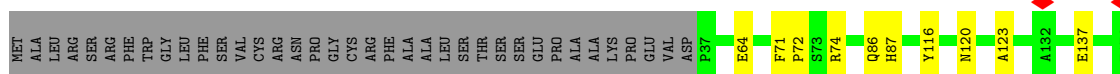
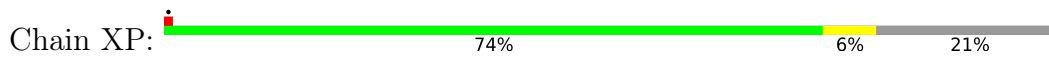
• Molecule 53: 39S ribosomal protein L16, mitochondrial



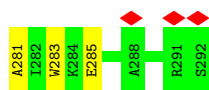
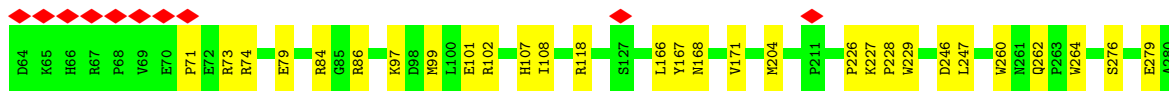
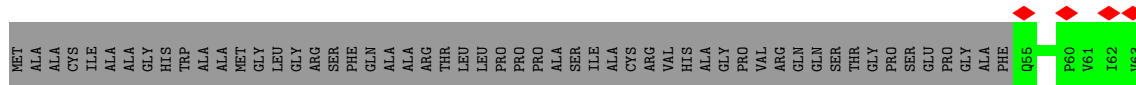
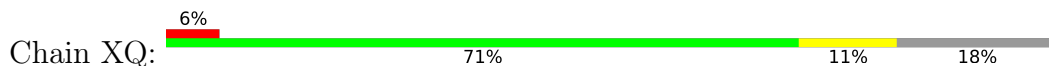
• Molecule 54: 39S ribosomal protein L17, mitochondrial



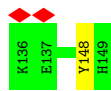
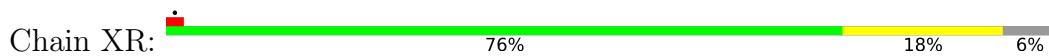
- Molecule 55: 39S ribosomal protein L18, mitochondrial



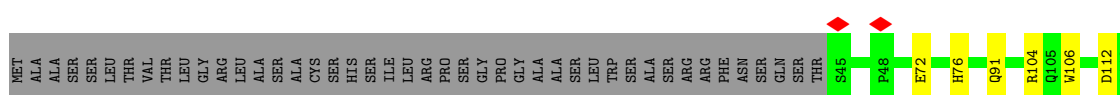
- Molecule 56: 39S ribosomal protein L19, mitochondrial



- Molecule 57: 39S ribosomal protein L20, mitochondrial

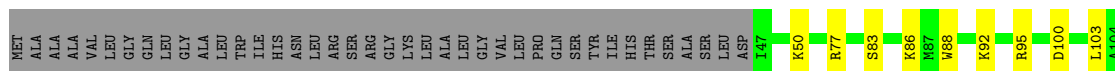


- Molecule 58: 39S ribosomal protein L21, mitochondrial

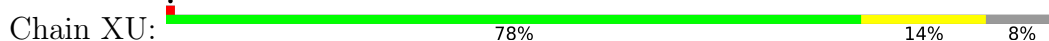




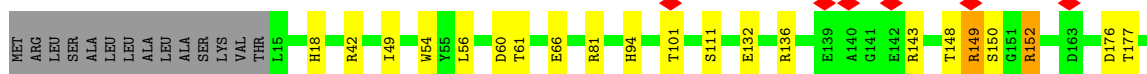
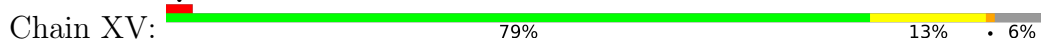
• Molecule 59: 39S ribosomal protein L22, mitochondrial



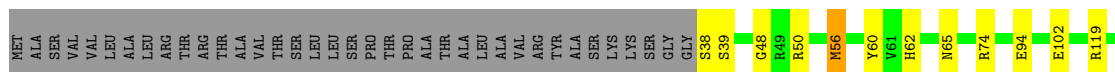
• Molecule 60: 39S ribosomal protein L23, mitochondrial



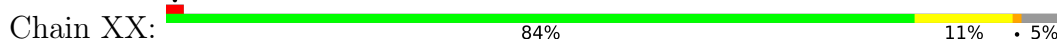
• Molecule 61: 39S ribosomal protein L24, mitochondrial

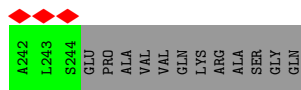


• Molecule 62: 39S ribosomal protein L27, mitochondrial

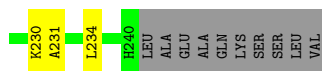


• Molecule 63: 39S ribosomal protein L28, mitochondrial

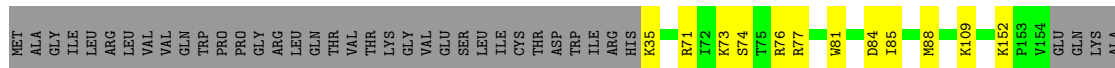




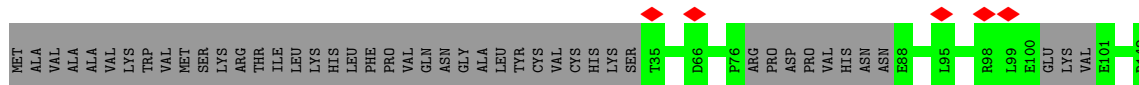
• Molecule 64: 39S ribosomal protein L47, mitochondrial



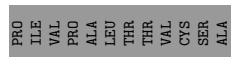
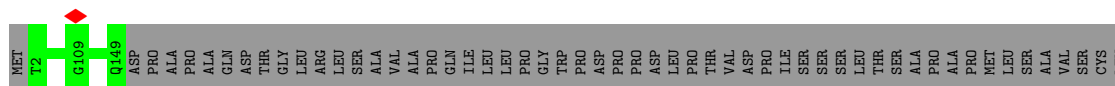
• Molecule 65: 39S ribosomal protein L30, mitochondrial



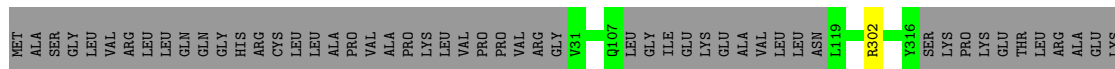
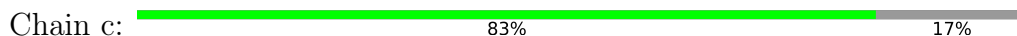
• Molecule 66: 39S ribosomal protein L42, mitochondrial



• Molecule 67: 39S ribosomal protein L43, mitochondrial



• Molecule 68: 39S ribosomal protein L44, mitochondrial



SER
ILE
THR
ALA
SER

• Molecule 69: 39S ribosomal protein L45, mitochondrial

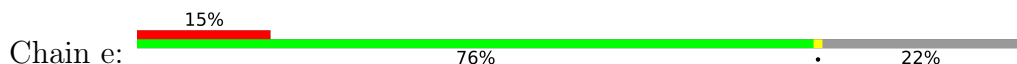


MET
ALA
ALA
PRO
ILE
PRO
GLN
PHE
CYS
SER
LEU
SER
ARG
PHE
LEU
LEU
TRP
TRP
PHE
ARG
GLN
PRO
VAL
LEU
VAL
VAL
GLN
SER
SER
ALA
ALA
ILE
VAL
PRO
VAL
ARG
THR
LYS
LYS
PHE
THR
PRO
PRO
ILE
TYR
GLN
PRO
LYS
PHE
LYS
THR
GLU
LYS
GLU
F63
H64
Q65
H66
A67

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

PRO
GLN
LEU
ALA

• Molecule 70: 39S ribosomal protein L46, mitochondrial



MET
ALA
ALA
PRO
VAL
ARG
ARG
THR
LEU
LEU
GLY
VAL
ALA
GLY
TRP
ARG
ARG
PHE
GLU
LEU
TRP
ALA
GLY
SER
LEU
SER
SER
ARG
SER
LEU
ALA
ALA
PRO
SER
SER
ASN
GLY
S43
R46
Y84
R90
D95
E94
R97
K100
K101
K102
A103
D104

LEU
HIS
ASP
GLU
GLU
ASP
GLN
ASP
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
E243

A246
G247
R248
K249
G250
H251
D262
K265
R273
R274
S277
D278
L279

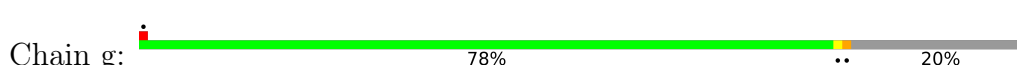
• Molecule 71: 39S ribosomal protein L48, mitochondrial



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

GLU
VAL
ARG
ALA
ILE
MET
ASN
PHE
ARG
ALA
THR
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



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

• Molecule 73: 39S ribosomal protein L50, mitochondrial

Chain h:  68% 32%

MET ALA ALA ARG SER VAL SER ILE THR ARG ARG PHE MET TRP THR VAL SER GLY THR PRO CYS ARG ARG PHE TRP ARG ARG LYS GLU LYS PRO VAL VAL VAL THR GLU LYS LYS PRO PRO ILE LEU E64 D65 E76 V77 F78 GLY S80 S81

L82 D88 A145 Y158

- Molecule 74: 39S ribosomal protein L51, mitochondrial

Chain i:  76% 24%


MET ALA GLY ASN LEU LEU SER GLY ALA ARG ARG TRP ASP TRP VAL CYS SER LEU LEU ALA CYS ARG SER PHE SER LEU VAL VAL ARG LEU I32 R128

- Molecule 75: 39S ribosomal protein L52, mitochondrial

Chain j:  70% 30%

MET ALA ALA LEU THR VAL LEU PHE THR GLY VAL ARG ARG LEU HIS CYS SER VAL VAL ALA CYS ARG TRP A23 K104 N107 A108 LEU LYS PRO LYS GLY ALA SER LEU LYS SER PRO PRO SER GLN

- Molecule 76: 39S ribosomal protein L53, mitochondrial

Chain k:  5% 85% 15%

MET A2 E7 L47 D58 Q59 S60 R95 A96 ARG ASP ALA ALA GLY SER GLY ASP LYS PRO GLY ALA ASP THR GLY ARG

- Molecule 77: 39S ribosomal protein L54, mitochondrial

Chain l:  7% 58% 42%

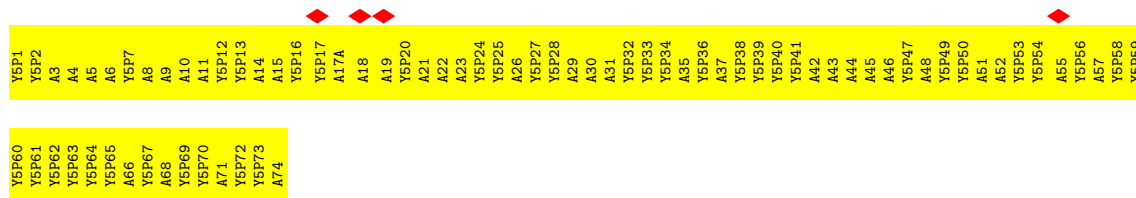
MET THR LYS ARG LEU PHE GLY ALA THR ARG TRP ALA GLY TRP GLY ASN PRO ALA THR SER GLY ARG LEU ALA ARG ASP TYR VAL LYS LYS PRO MET GLY ALA LYS SER GLY LYS GLY ALA VAL THR SER GLU ALA LEU K57 D60 V61

C52 E80 G81 Q82 D83 V84 P85 F97 E98 L101 E108 K136 ARG LEU

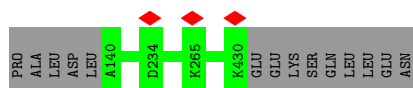
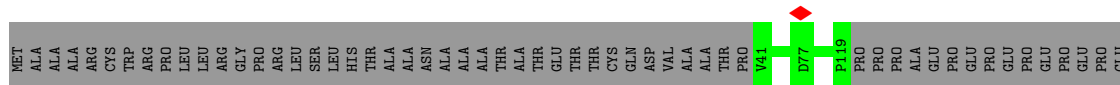
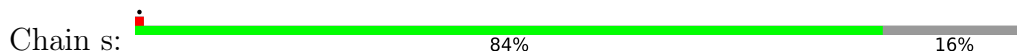
- Molecule 78: 39S ribosomal protein L55, mitochondrial

Chain m:  47% 53%

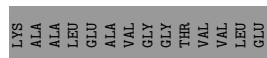
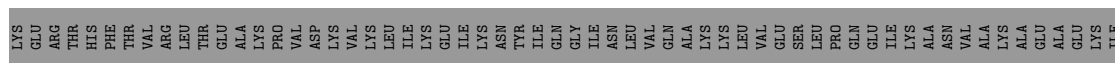
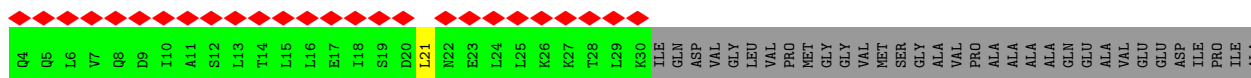
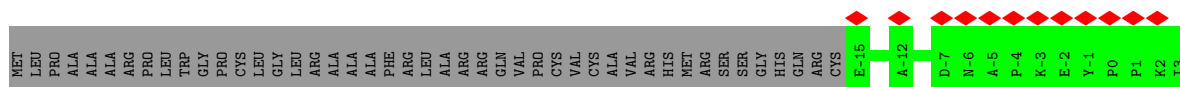
MET ALA VAL GLY SER LEU GLY ARG ARG GLN SER THR VAL LYS ALA THR GLY PRO ALA LEU ARG ARG LEU HIS THR SER TRP ARG ALA ASP S35 L40 T83 LEU S84 P85 E86 K94 ARG GLU ALA GLN GLN GLN ARG LYS TYR GLU GLN GLU LEU



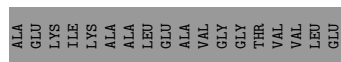
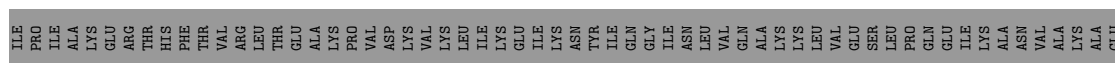
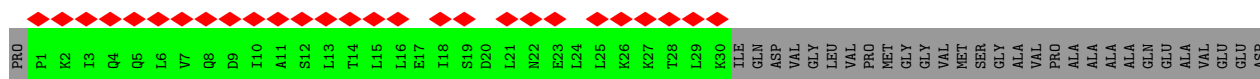
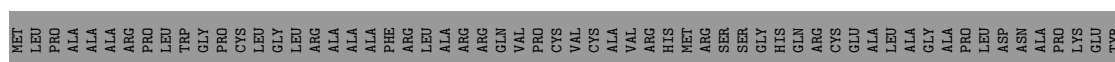
• Molecule 85: 39S ribosomal protein S30, mitochondrial



• Molecule 86: 39S ribosomal protein L12, mitochondrial



• Molecule 86: 39S ribosomal protein L12, mitochondrial



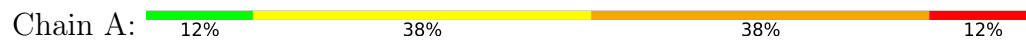
• Molecule 86: 39S ribosomal protein L12, mitochondrial

PRO	K2	T3	Q4	Q5	L6	V7	Q8	D9	I10	A11	S12	L13	T14	L15	L16	E17	I18	S19	D20	L21	N22	E23	L24	L25	K26	K27	T28	LEU	LYS	ILE	GLN	ASP	LYS	GLY	LEU	VAL	PRO	GLY	GLY	VAL	MET	LYS	GLY	ASN	VAL	PRO	ALA	ALA	ALA	ALA	GLN	GLU	ALA	GLU	ASP
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ILE	PRO	ALA	LYS	GLU	THR	HIS	THR	VAL	ARG	LEU	THR	ALA	LYS	PRO	VAL	ASP	LYS	VAL	LYS	LEU	ILE	LYS	ILE	ASN	TYR	ILE	GLN	GLY	ILE	ASN	LEU	VAL	GLN	ALA	LYS	LYS	LEU	VAL	GLU	SER	PRO	PRO	GLY	GLY	VAL	GLN	ILE	LYS	ALA	ASN	VAL	VAL	ALA	LYS	ALA	GLU
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ALA	GLU	LYS	ILE	LYS	ALA	LEU	GLU	ALA	VAL	GLY	GLY	THR	VAL	LEU	GLU
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• Molecule 87: Quinupristin



MHV1	T2	P4	F5	MHV6	0047	MHT8
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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 i

5.1 Standard geometry i

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

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
1:0:91:ARG:HG2	1:0:95: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 [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	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 [i](#)

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 [i](#)

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	Y5P	r3	28	84	14,19,20	3.13	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	11	84	16,23,24	0.95	1 (6%)	14,33,36	1.98	3 (21%)
84	Y5P	r3	12	84	14,19,20	3.12	3 (21%)	18,26,29	0.56	0
83	Y5P	r1	49	83	14,19,20	3.14	3 (21%)	18,26,29	0.57	0
84	Y5P	r3	69	84	14,19,20	3.13	3 (21%)	18,26,29	0.53	0
84	Y5P	r3	58	84	14,19,20	3.13	4 (28%)	18,26,29	0.66	0
84	Y5P	r3	32	84	14,19,20	3.14	3 (21%)	18,26,29	0.56	0
84	P5P	r3	22	84	16,23,24	0.95	1 (6%)	14,33,36	1.98	3 (21%)
84	Y5P	r3	39	84	14,19,20	3.13	3 (21%)	18,26,29	0.59	0
84	P5P	r3	29	84	16,23,24	0.95	1 (6%)	14,33,36	2.00	3 (21%)
84	Y5P	r3	33	84	14,19,20	3.13	3 (21%)	18,26,29	0.58	0
84	P5P	r3	43	84	16,23,24	0.94	1 (6%)	14,33,36	1.97	3 (21%)
84	P5P	r3	9	84	16,23,24	0.98	1 (6%)	14,33,36	1.98	3 (21%)
84	P5P	r3	42	84	16,23,24	0.96	1 (6%)	14,33,36	1.99	3 (21%)
84	P5P	r3	6	84	16,23,24	0.95	1 (6%)	14,33,36	2.01	3 (21%)
84	Y5P	r3	36	84	14,19,20	3.11	3 (21%)	18,26,29	0.59	0
84	P5P	r3	37	84	16,23,24	0.96	1 (6%)	14,33,36	1.98	3 (21%)
84	P5P	r3	57	84	16,23,24	0.94	1 (6%)	14,33,36	1.93	3 (21%)
84	P5P	r3	52	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)
84	P5P	r3	35	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)
84	P5P	r3	15	84	16,23,24	0.97	1 (6%)	14,33,36	1.96	3 (21%)
84	Y5P	r3	53	84	14,19,20	3.15	3 (21%)	18,26,29	0.58	0
84	Y5P	r3	72	84	14,19,20	3.10	3 (21%)	18,26,29	0.65	0
84	Y5P	r3	25	84	14,19,20	3.14	3 (21%)	18,26,29	0.60	0
84	P5P	r3	71	84	16,23,24	0.95	1 (6%)	14,33,36	1.98	3 (21%)
84	Y5P	r3	61	84	14,19,20	3.13	3 (21%)	18,26,29	0.56	0
84	Y5P	r3	47	84	14,19,20	3.14	3 (21%)	18,26,29	0.60	0
84	P5P	r3	5	84	16,23,24	0.95	1 (6%)	14,33,36	2.01	3 (21%)
84	Y5P	r3	70	84	14,19,20	3.13	3 (21%)	18,26,29	0.59	0
84	Y5P	r3	73	84	14,19,20	3.11	3 (21%)	18,26,29	0.54	0
84	P5P	r3	74	84	16,23,24	0.97	1 (6%)	14,33,36	2.03	3 (21%)
84	Y5P	r3	64	84	14,19,20	3.13	3 (21%)	18,26,29	0.58	0
84	Y5P	r3	62	84	14,19,20	3.14	3 (21%)	18,26,29	0.59	0
84	Y5P	r3	7	84	14,19,20	3.11	3 (21%)	18,26,29	0.62	0
84	Y5P	r3	40	84	14,19,20	3.13	3 (21%)	18,26,29	0.59	0
84	P5P	r3	44	84	16,23,24	0.96	1 (6%)	14,33,36	1.97	3 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
84	Y5P	r3	59	84	14,19,20	3.14	3 (21%)	18,26,29	0.57	0
87	MHU	A	5	87	14,15,16	0.44	0	18,19,21	1.23	3 (16%)
84	Y5P	r3	54	84	14,19,20	3.14	3 (21%)	18,26,29	0.59	0
84	P5P	r3	14	84	16,23,24	0.95	1 (6%)	14,33,36	2.02	3 (21%)
84	P5P	r3	10	84	16,23,24	0.95	1 (6%)	14,33,36	1.98	3 (21%)
84	Y5P	r3	1	84	18,20,20	2.78	3 (16%)	25,29,29	0.67	0
84	Y5P	r3	17	84	14,19,20	3.16	3 (21%)	18,26,29	0.56	0
84	Y5P	r3	49	84	14,19,20	3.14	3 (21%)	18,26,29	0.56	0
84	P5P	r3	55	84	16,23,24	0.95	1 (6%)	14,33,36	1.96	3 (21%)
84	P5P	r3	17(A)	84	16,23,24	0.93	1 (6%)	14,33,36	2.01	3 (21%)
87	DBB	A	3	87	4,5,6	0.56	0	1,5,7	0.66	0
84	Y5P	r3	2	84	14,19,20	3.13	3 (21%)	18,26,29	0.57	0
84	Y5P	r3	34	84	14,19,20	3.13	3 (21%)	18,26,29	0.58	0
84	Y5P	r3	50	84	14,19,20	3.15	3 (21%)	18,26,29	0.58	0
84	P5P	r3	23	84	16,23,24	0.95	1 (6%)	14,33,36	2.00	3 (21%)
84	P5P	r3	68	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)
84	P5P	r3	18	84	16,23,24	0.95	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	P5P	r3	46	84	16,23,24	0.96	1 (6%)	14,33,36	1.99	3 (21%)
84	Y5P	r3	41	84	14,19,20	3.13	3 (21%)	18,26,29	0.56	0
84	Y5P	r3	65	84	14,19,20	3.13	3 (21%)	18,26,29	0.63	0
84	P5P	r3	66	84	16,23,24	0.94	1 (6%)	14,33,36	2.01	3 (21%)
84	P5P	r3	3	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)
84	P5P	r3	26	84	16,23,24	0.95	1 (6%)	14,33,36	2.00	3 (21%)
84	P5P	r3	21	84	16,23,24	0.95	1 (6%)	14,33,36	1.96	3 (21%)
84	Y5P	r3	67	84	14,19,20	3.13	3 (21%)	18,26,29	0.58	0
84	Y5P	r3	38	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
83	Y5P	r1	47	83	14,19,20	3.12	3 (21%)	18,26,29	0.56	0
84	P5P	r3	51	84	16,23,24	0.96	1 (6%)	14,33,36	1.99	3 (21%)
87	MHW	A	1	87	9,9,10	0.82	0	10,11,13	3.06	3 (30%)
83	Y5P	r1	48	83	14,19,20	3.13	3 (21%)	18,26,29	0.57	0
84	Y5P	r3	27	84	14,19,20	3.14	3 (21%)	18,26,29	0.55	0
87	MHV	A	6	87	7,9,10	0.35	0	7,11,13	1.73	2 (28%)
83	Y5P	r1	46	83	14,19,20	3.13	3 (21%)	18,26,29	0.62	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	004	A	7	87	9,10,11	1.08	1 (11%)	9,12,14	1.80	3 (33%)
84	Y5P	r3	63	84	14,19,20	3.14	3 (21%)	18,26,29	0.57	0
84	Y5P	r3	56	84	14,19,20	3.13	3 (21%)	18,26,29	0.64	0
84	Y5P	r3	16	84	14,19,20	3.13	3 (21%)	18,26,29	0.60	0
84	P5P	r3	8	84	16,23,24	0.95	1 (6%)	14,33,36	1.99	3 (21%)
84	Y5P	r3	24	84	14,19,20	3.13	3 (21%)	18,26,29	0.61	0
84	Y5P	r3	20	84	14,19,20	3.13	3 (21%)	18,26,29	0.58	0
84	P5P	r3	4	84	16,23,24	0.96	1 (6%)	14,33,36	2.00	3 (21%)
84	Y5P	r3	60	84	14,19,20	3.13	3 (21%)	18,26,29	0.59	0
84	P5P	r3	45	84	16,23,24	0.95	1 (6%)	14,33,36	1.95	3 (21%)
84	P5P	r3	19	84	16,23,24	0.96	1 (6%)	14,33,36	2.01	3 (21%)
84	P5P	r3	31	84	16,23,24	0.94	1 (6%)	14,33,36	1.97	3 (21%)
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	Y5P	r3	28	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	11	84	-	0/3/25/26	0/3/3/3
84	Y5P	r3	12	84	-	1/7/33/34	0/2/2/2
83	Y5P	r1	49	83	-	3/7/33/34	0/2/2/2
84	Y5P	r3	69	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	58	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	32	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	22	84	-	0/3/25/26	0/3/3/3
84	Y5P	r3	39	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	29	84	-	0/3/25/26	0/3/3/3
84	Y5P	r3	33	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	43	84	-	1/3/25/26	0/3/3/3
84	P5P	r3	9	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	42	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	6	84	-	0/3/25/26	0/3/3/3
84	Y5P	r3	36	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	37	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	57	84	-	1/3/25/26	0/3/3/3
84	P5P	r3	52	84	-	0/3/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
84	P5P	r3	35	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	15	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	72	84	-	2/7/33/34	0/2/2/2
84	Y5P	r3	25	84	-	3/7/33/34	0/2/2/2
84	P5P	r3	71	84	-	0/3/25/26	0/3/3/3
84	Y5P	r3	61	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	47	84	-	2/7/33/34	0/2/2/2
84	P5P	r3	5	84	-	2/3/25/26	0/3/3/3
84	Y5P	r3	70	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	73	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	64	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	62	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	7	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	40	84	-	3/7/33/34	0/2/2/2
84	P5P	r3	44	84	-	0/3/25/26	0/3/3/3
84	Y5P	r3	59	84	-	4/7/33/34	0/2/2/2
87	MHU	A	5	87	-	5/9/12/14	0/1/1/1
84	Y5P	r3	54	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	14	84	-	1/3/25/26	0/3/3/3
84	P5P	r3	10	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	17	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	49	84	-	3/7/33/34	0/2/2/2
84	P5P	r3	55	84	-	2/3/25/26	0/3/3/3
84	P5P	r3	17(A)	84	-	3/3/25/26	0/3/3/3
87	DBB	A	3	87	-	0/3/4/6	-
84	Y5P	r3	2	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	34	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	50	84	-	4/7/33/34	0/2/2/2
84	P5P	r3	23	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	18	84	-	2/3/25/26	0/3/3/3
84	P5P	r3	30	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	46	84	-	1/3/25/26	0/3/3/3
84	Y5P	r3	41	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	65	84	-	1/7/33/34	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
84	P5P	r3	66	84	-	2/3/25/26	0/3/3/3
84	P5P	r3	3	84	-	3/3/25/26	0/3/3/3
84	P5P	r3	26	84	-	2/3/25/26	0/3/3/3
84	P5P	r3	21	84	-	3/3/25/26	0/3/3/3
84	Y5P	r3	67	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	38	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	13	84	-	5/7/33/34	0/2/2/2
83	Y5P	r1	47	83	-	5/7/33/34	0/2/2/2
84	P5P	r3	51	84	-	2/3/25/26	0/3/3/3
87	MHW	A	1	87	-	0/2/2/4	0/1/1/1
83	Y5P	r1	48	83	-	1/7/33/34	0/2/2/2
84	Y5P	r3	27	84	-	1/7/33/34	0/2/2/2
87	MHV	A	6	87	-	0/1/12/14	0/1/1/1
83	Y5P	r1	46	83	-	5/7/33/34	0/2/2/2
87	004	A	7	87	-	1/4/6/8	0/1/1/1
84	Y5P	r3	63	84	-	3/7/33/34	0/2/2/2
84	Y5P	r3	56	84	-	4/7/33/34	0/2/2/2
84	Y5P	r3	16	84	-	2/7/33/34	0/2/2/2
84	P5P	r3	8	84	-	0/3/25/26	0/3/3/3
84	Y5P	r3	24	84	-	1/7/33/34	0/2/2/2
84	Y5P	r3	20	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	4	84	-	3/3/25/26	0/3/3/3
84	Y5P	r3	60	84	-	1/7/33/34	0/2/2/2
84	P5P	r3	45	84	-	0/3/25/26	0/3/3/3
84	P5P	r3	19	84	-	2/3/25/26	0/3/3/3
84	P5P	r3	31	84	-	2/3/25/26	0/3/3/3
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	5	MHU	1	0
87	A	1	MHW	1	0
87	A	7	004	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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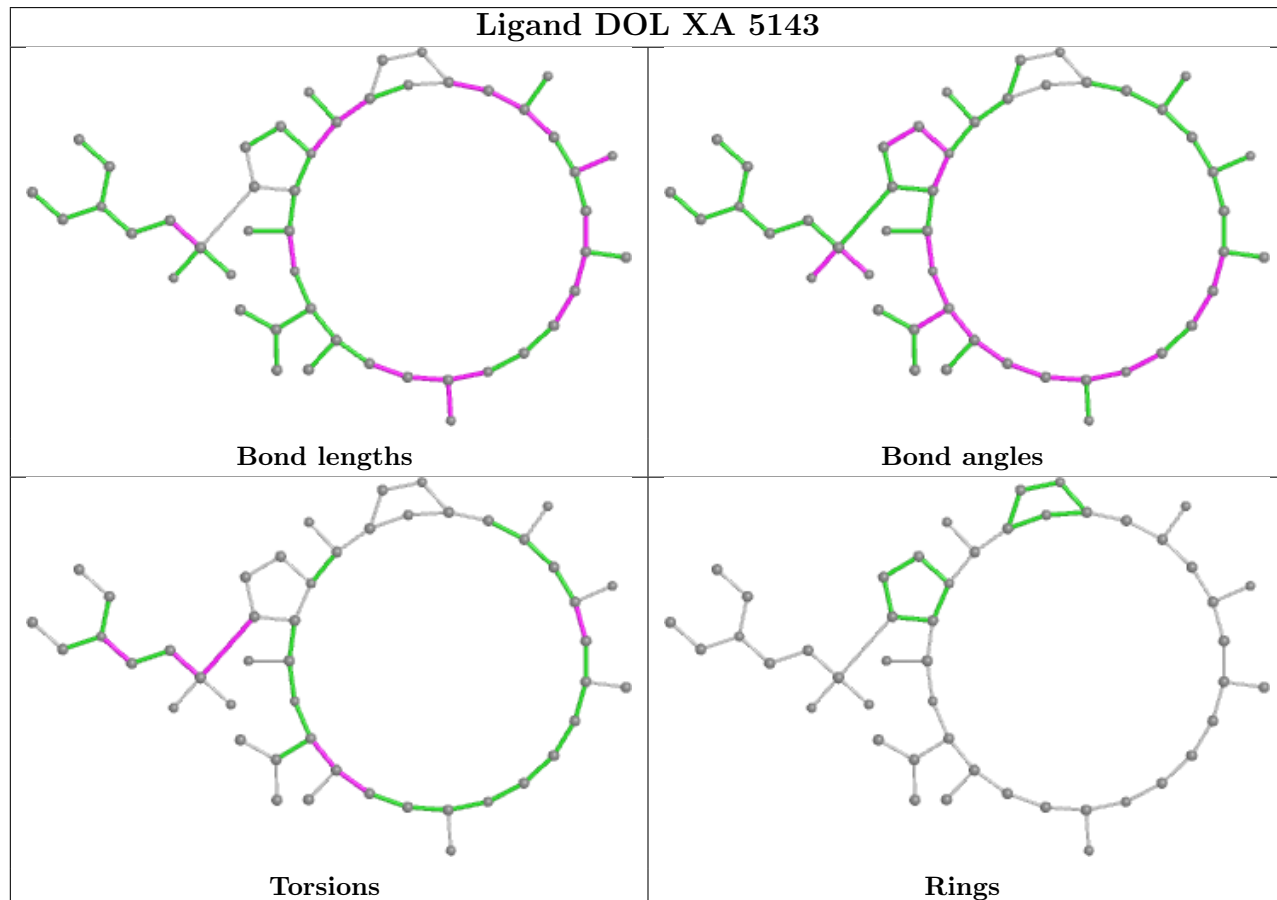
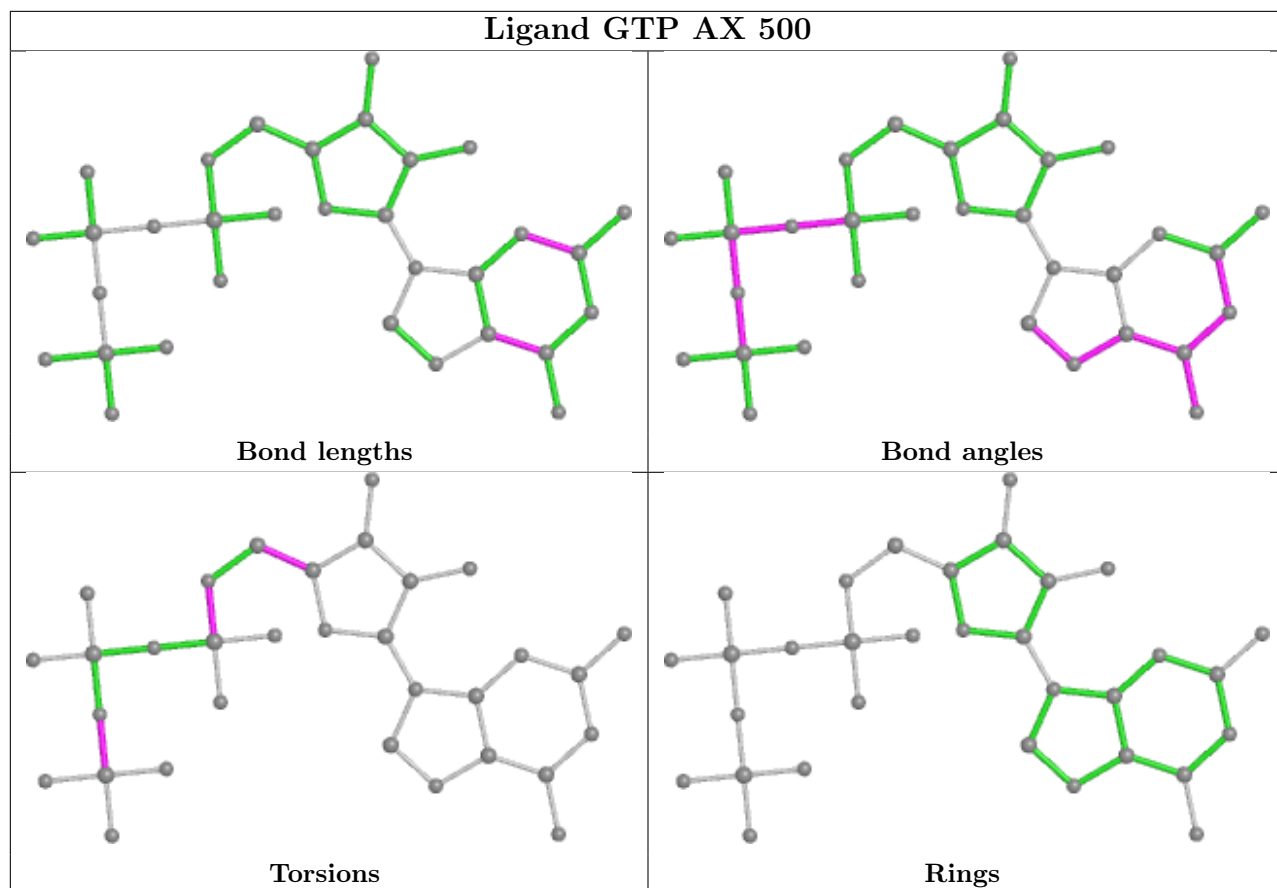
Mol	Chain	Res	Type	Atoms
90	XA	5143	DOL	C43-C42-S39-C2
90	XA	5143	DOL	C43-C42-S39-O41
90	XA	5143	DOL	C29-C30-C32-C33
90	XA	5143	DOL	C31-C30-C32-C33
91	AX	500	GTP	PB-O3B-PG-O3G
91	AX	500	GTP	C5'-O5'-PA-O3A
90	XA	5143	DOL	C3-C2-S39-O41
91	AX	500	GTP	O4'-C4'-C5'-O5'
90	XA	5143	DOL	C31-C30-C32-O36
91	AX	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.



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

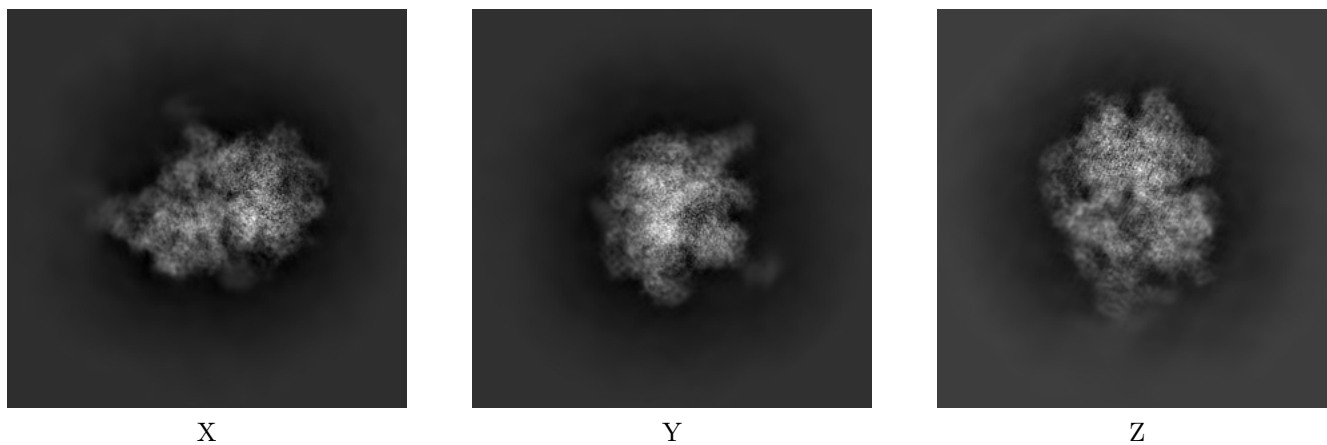
6 Map visualisation [i](#)

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](#)

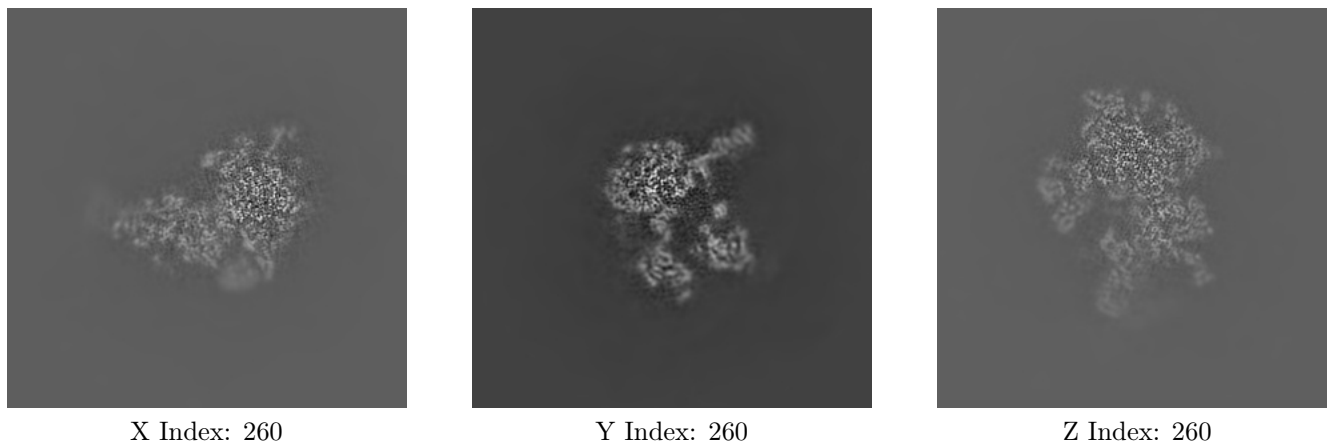
6.1.1 Primary map



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

6.2 Central slices [i](#)

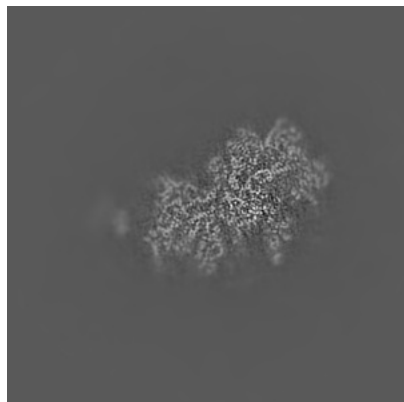
6.2.1 Primary map



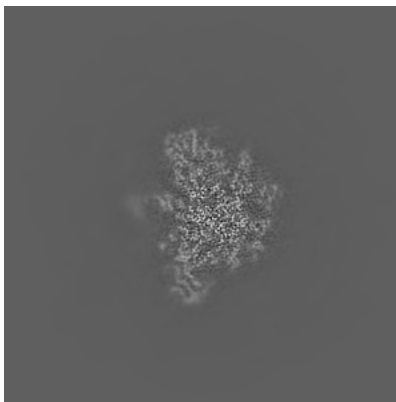
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

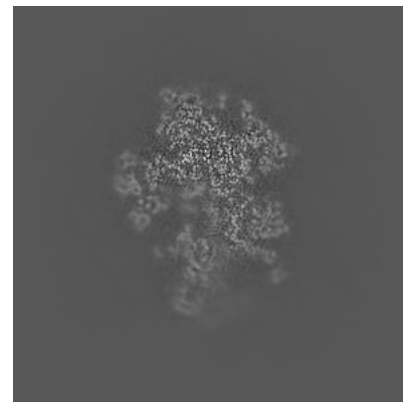
6.3.1 Primary map



X Index: 282



Y Index: 320

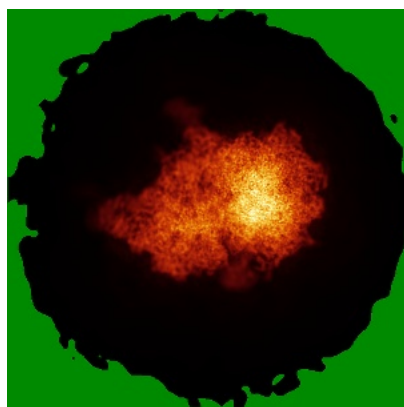


Z Index: 257

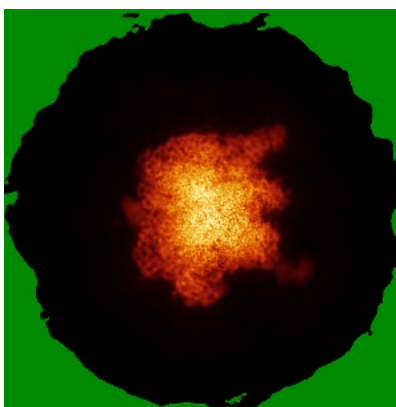
The images above show the largest variance slices of the map in three orthogonal directions.

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

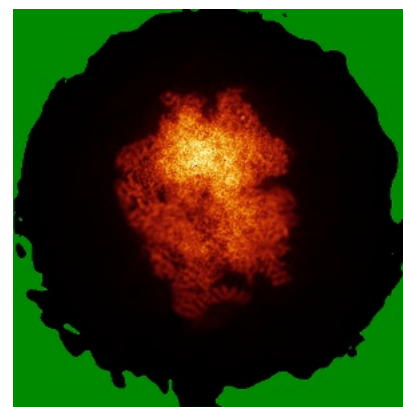
6.4.1 Primary map



X



Y

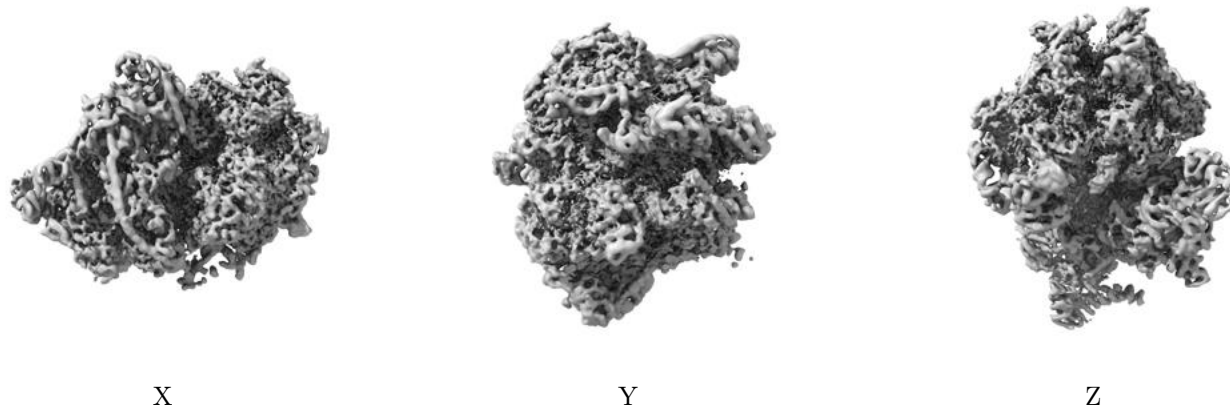


Z

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.

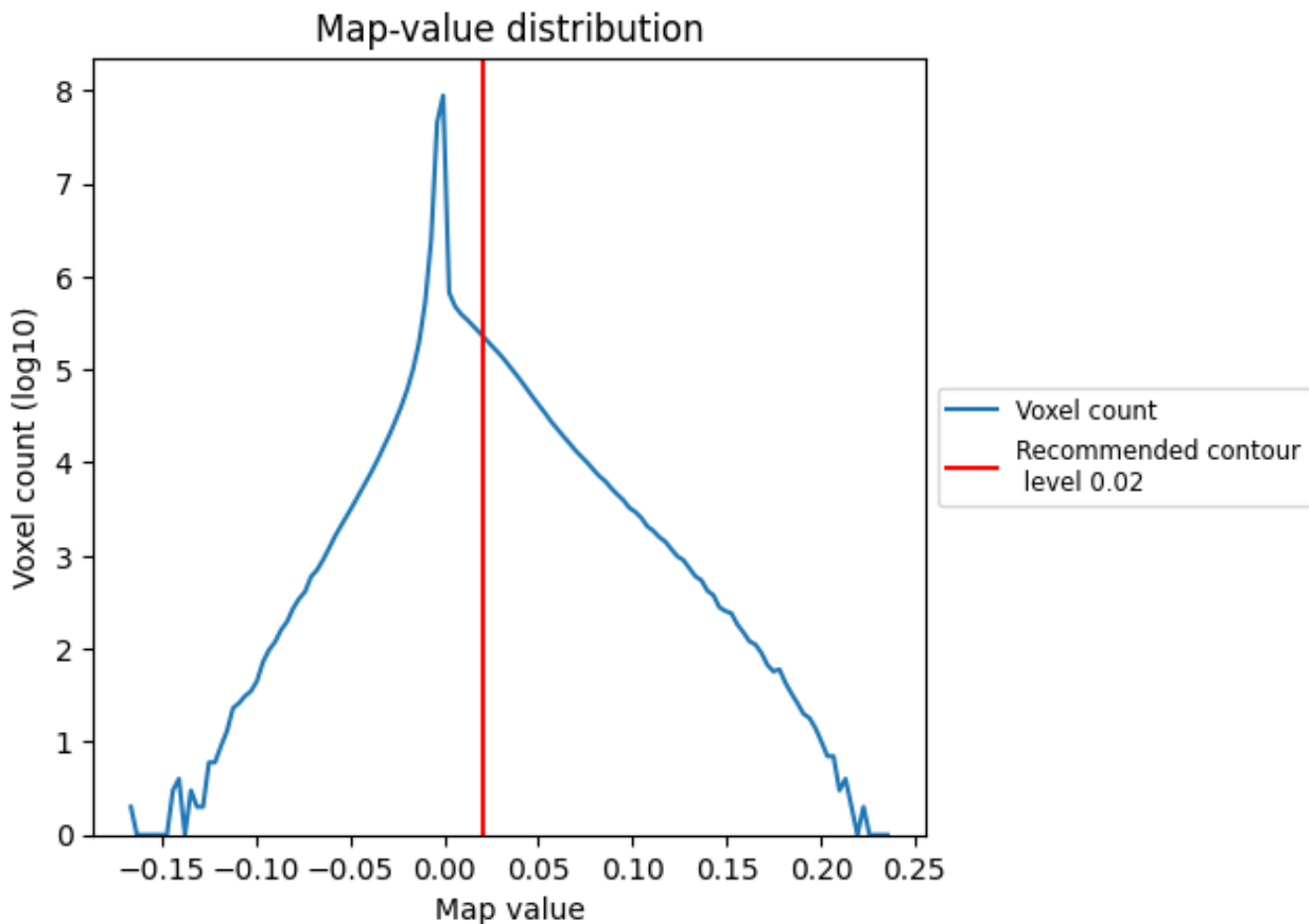
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

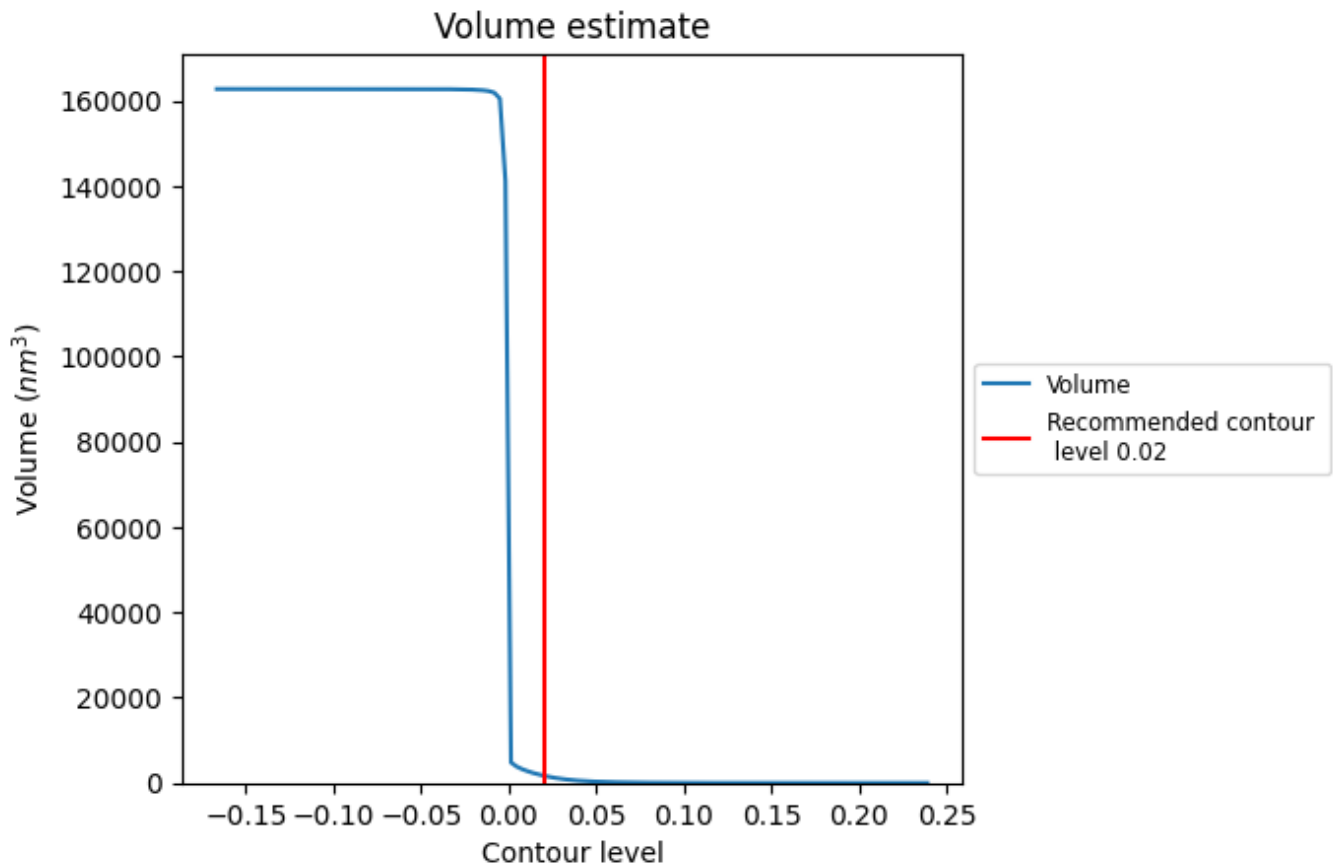
This section contains the results of statistical analysis of the map.

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.

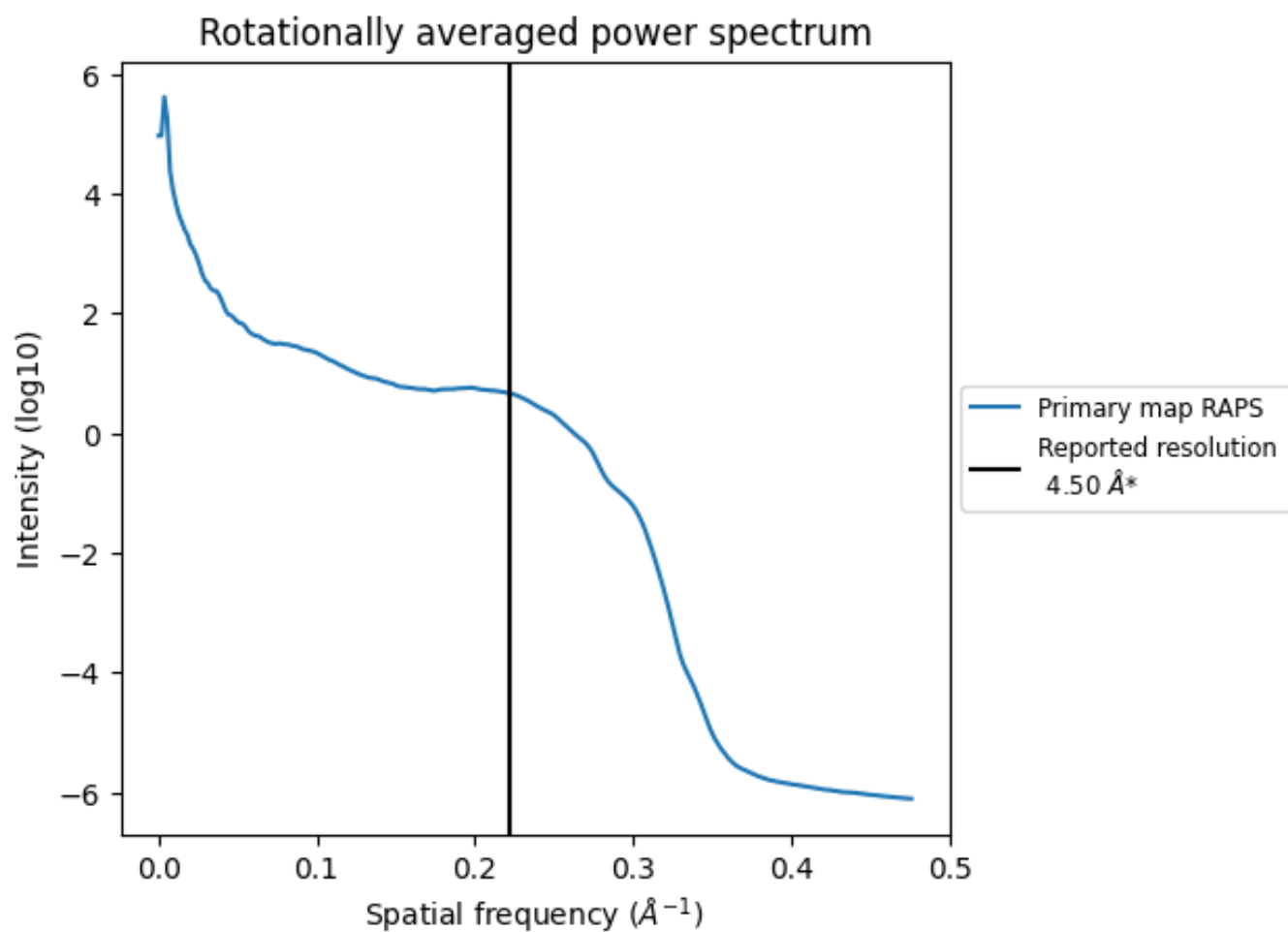
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1693 nm^3 ; 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.222\AA^{-1}

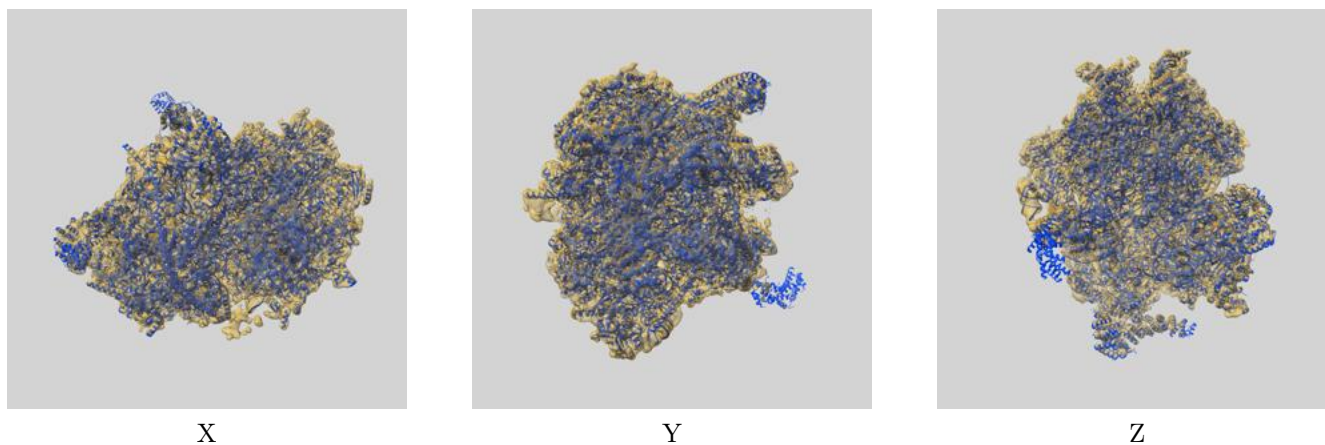
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

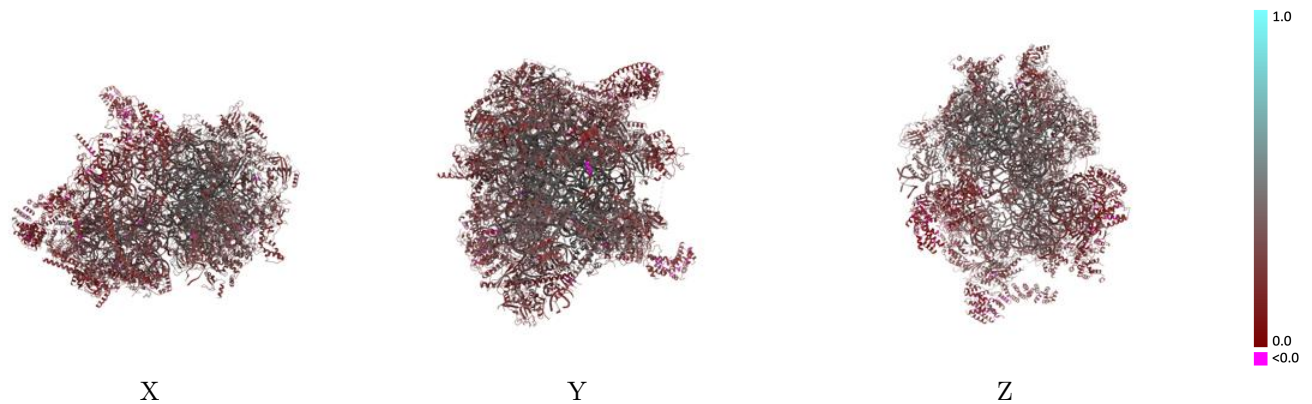
This section contains information regarding the fit between EMDB map EMD-11392 and PDB model 6ZSB. Per-residue inclusion information can be found in section 3 on page 22.

9.1 Map-model overlay [i](#)



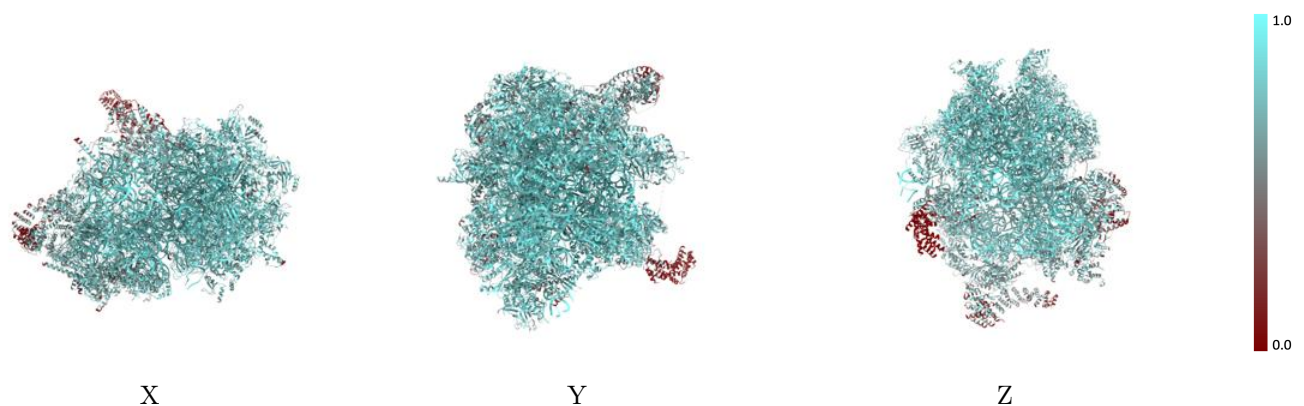
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



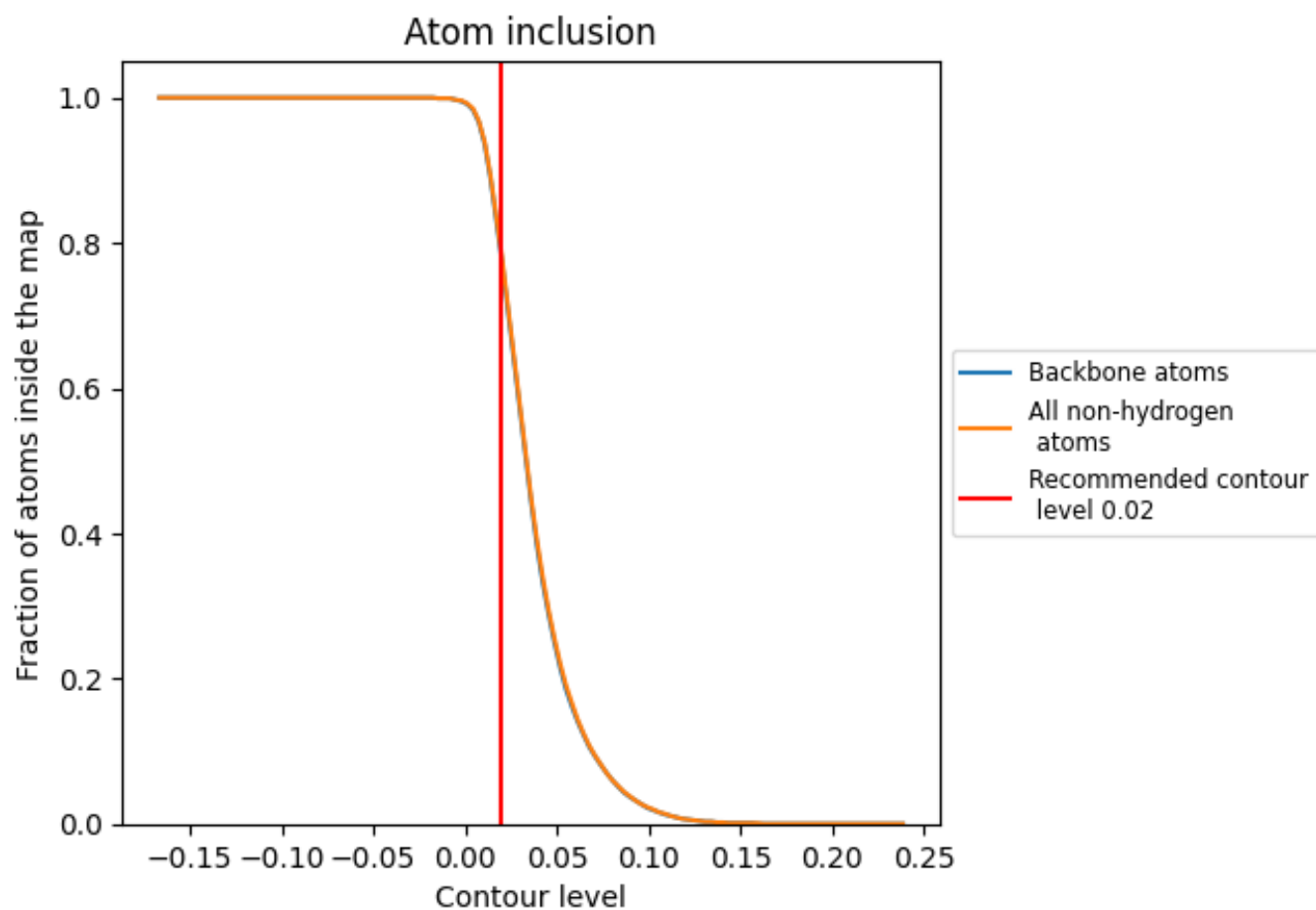
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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