



Full wwPDB EM Validation Report ⓘ

Jun 18, 2026 – 10:25 am BST

PDB ID : 6ZMW / pdb_00006zmw
EMDB ID : EMD-11302
Title : Structure of a human 48S translational initiation complex
Authors : Brito Querido, J.; Sokabe, M.; Kraatz, S.; Gordiyenko, Y.; Skehel, M.; Fraser, C.; Ramakrishnan, V.
Deposited on : 2020-07-04
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

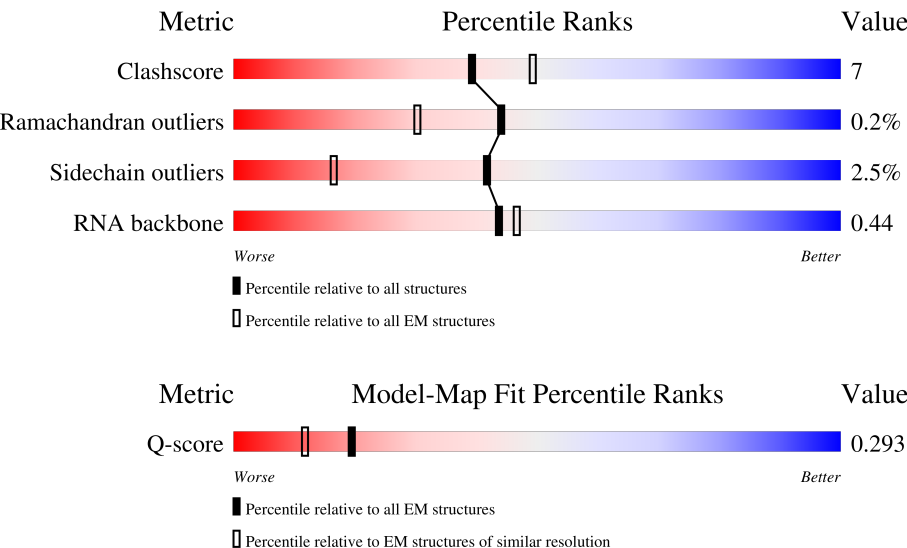
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.70 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	2	325	
2	1	814	
3	6	374	

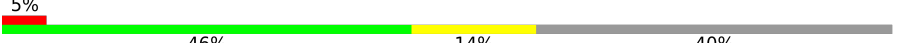
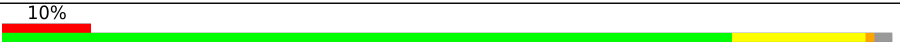
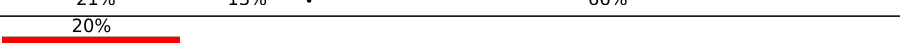
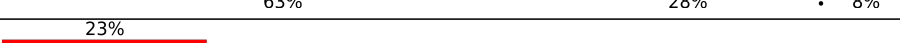
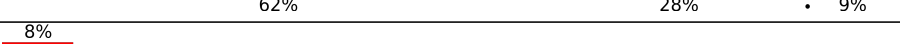
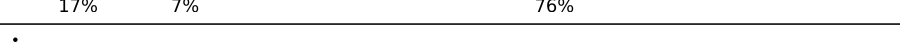
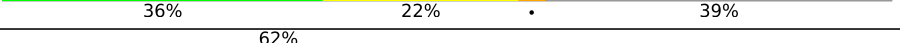
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Mol	Chain	Length	Quality of chain
4	4	357	
5	u	1382	
6	v	445	
7	S	249	
8	y	913	
9	8	352	
10	G	194	
11	H	84	
12	K	83	
13	L	293	
14	O	264	
15	N	295	
16	Q	115	
17	P	151	
18	I	151	
19	x	548	
20	3	218	
21	5	564	
22	7	28	
23	9	25	
24	A	1869	
25	B	158	
26	C	263	
27	D	194	
28	E	143	

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Mol	Chain	Length	Quality of chain
29	F	59	
30	r	315	
31	J	130	
32	R	208	
33	T	133	
34	V	204	
35	Y	146	
36	Z	243	
37	a	165	
38	b	145	
39	c	317	
40	d	145	
41	e	125	
42	f	152	
43	i	56	
44	k	156	
45	m	132	
46	n	69	
47	o	320	
48	p	113	
49	q	144	
50	z	258	
51	M	135	
52	h	119	
53	s	333	

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Mol	Chain	Length	Quality of chain
54	w	75	97% 41% 53% 5%
55	t	472	71% 72% 25%
56	j	406	55% 71% 23% 5%
57	g	1310	11% 12% 5% 83%

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 118155 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Eukaryotic translation initiation factor 3 subunit I.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	2	304	Total	C	N	O	0	0
			1493	885	304	304		

- Molecule 2 is a protein called Eukaryotic translation initiation factor 3 subunit B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	588	Total	C	N	O	S	0	0
			3258	1986	633	634	5		

- Molecule 3 is a protein called Eukaryotic translation initiation factor 3 subunit M.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	6	350	Total	C	N	O	S	0	0
			1917	1159	376	380	2		

- Molecule 4 is a protein called Eukaryotic translation initiation factor 3 subunit F.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	4	257	Total	C	N	O	0	0
			1272	757	257	258		

- Molecule 5 is a protein called Eukaryotic translation initiation factor 3 subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	u	706	Total	C	N	O	S	1	0
			5383	3379	982	999	23		

- Molecule 6 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	v	384	Total	C	N	O	S	0	0
			2635	1657	477	489	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	S	230	Total	C	N	O	S	0	0
			1862	1164	371	320	7		

- Molecule 8 is a protein called Eukaryotic translation initiation factor 3 subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	y	697	Total	C	N	O	S	0	0
			5470	3437	980	1018	35		

- Molecule 9 is a protein called Eukaryotic translation initiation factor 3 subunit H.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	317	Total	C	N	O	S	0	0
			1571	936	317	318			

- Molecule 10 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	177	Total	C	N	O	S	0	0
			1430	917	260	252	1		

- Molecule 11 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	81	Total	C	N	O	S	0	0
			631	397	116	111	7		

- Molecule 12 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	81	Total	C	N	O	S	0	0
			617	380	114	118	5		

- Molecule 13 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	220	Total	C	N	O	S	0	0
			1707	1104	292	301	10		

- Molecule 14 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	211	Total	C	N	O	S	0	0
			1715	1088	307	306	14		

- Molecule 15 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	207	Total	C	N	O	S	0	0
			1633	1040	288	297	8		

- Molecule 16 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	99	Total	C	N	O	S	0	0
			792	492	165	130	5		

- Molecule 17 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	133	Total	C	N	O	S	0	0
			997	610	196	185	6		

- Molecule 18 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	I	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 19 is a protein called Eukaryotic translation initiation factor 3 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	x	421	Total	C	N	O	S	0	0
			2831	1746	521	555	9		

- Molecule 20 is a protein called Eukaryotic translation initiation factor 3 subunit K.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	3	213	Total	C	N	O	0	0
			1057	631	213	213		

- Molecule 21 is a protein called Eukaryotic translation initiation factor 3 subunit L.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	5	319	Total	C	N	O	0	0
			1581	943	319	319		

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	7	28	Total	C	O	P	0	0
			336	140	168	28		

- Molecule 23 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	9	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 24 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	A	1719	Total	C	N	O	P	0	0
			36670	16380	6574	11998	1718		

- Molecule 25 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B	142	Total	C	N	O	S	0	0
			1166	743	218	199	6		

- Molecule 26 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	C	256	Total	C	N	O	S	0	0
			2035	1302	378	347	8		

- Molecule 27 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	D	177	Total	C	N	O	S	0	0
			1477	941	295	239	2		

- Molecule 28 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	E	140	Total	C	N	O	S	0	0
			1087	687	215	182	3		

- Molecule 29 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	F	47	Total	C	N	O	S	0	0
			378	231	85	61	1		

- Molecule 30 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	r	275	Total	C	N	O	S	0	0
			2215	1398	387	418	12		

- Molecule 31 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	J	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 32 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	R	198	Total	C	N	O	S	0	0
			1627	1021	322	279	5		

- Molecule 33 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	T	125	Total	C	N	O	S	0	0
			1015	642	199	169	5		

- Molecule 34 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	V	184	Total	C	N	O	S	0	0
			1461	914	276	264	7		

- Molecule 35 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Y	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 36 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Z	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 37 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	a	99	Total	C	N	O	S	0	0
			834	544	149	135	6		

- Molecule 38 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	b	110	Total	C	N	O	S	0	0
			913	580	168	158	7		

- Molecule 39 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	c	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 40 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	d	142	Total	C	N	O	S	0	0
			1105	692	213	197	3		

- Molecule 41 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	e	66	Total	C	N	O	S	0	0
			523	338	93	91	1		

- Molecule 42 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	f	142	Total	C	N	O	S	0	0
			1176	737	239	199	1		

- Molecule 43 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	i	50	Total	C	N	O	S	0	0
			419	262	85	67	5		

- Molecule 44 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	k	53	Total	C	N	O	S	0	0
			435	276	82	70	7		

- Molecule 45 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	m	122	Total	C	N	O	S	0	0
			950	596	168	177	9		

- Molecule 46 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	n	63	Total	C	N	O	S	0	0
			498	302	101	93	2		

- Molecule 47 is a protein called Eukaryotic translation initiation factor 3 subunit G.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	o	77	Total	C	N	O	0	0
			616	389	111	116		

- Molecule 48 is a protein called Eukaryotic translation initiation factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	p	85	Total	C	N	O	S	0	0
			691	438	125	126	2		

- Molecule 49 is a protein called Eukaryotic translation initiation factor 1A, X-chromosomal.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q	88	Total	C	N	O	S	0	0
			714	451	129	130	4		

- Molecule 50 is a protein called Eukaryotic translation initiation factor 3 subunit J.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	z	160	Total	C	N	O		0	0
			795	475	160	160			

- Molecule 51 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	M	131	Total	C	N	O	S	0	0
			1064	668	198	194	4		

- Molecule 52 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	h	103	Total	C	N	O	S	0	0
			817	511	155	147	4		

- Molecule 53 is a protein called Eukaryotic translation initiation factor 2 subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	s	138	Total	C	N	O	S	0	0
			1123	709	206	199	9		

- Molecule 54 is a RNA chain called Initiator Met-tRNA-i.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	w	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 55 is a protein called Eukaryotic translation initiation factor 2 subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	t	356	Total	C	N	O	0	0
			1750	1038	356	356		

- Molecule 56 is a protein called Eukaryotic initiation factor 4A-I.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	j	384	Total	C	N	O	S	0	0
			3073	1940	533	581	19		

- Molecule 57 is a protein called Eukaryotic translation initiation factor 4 gamma 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	g	224	Total	C	N	O	S	0	0
			1848	1168	324	341	15		

- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
58	Q	1	Total	Zn	0
			1	1	
58	k	1	Total	Zn	0
			1	1	

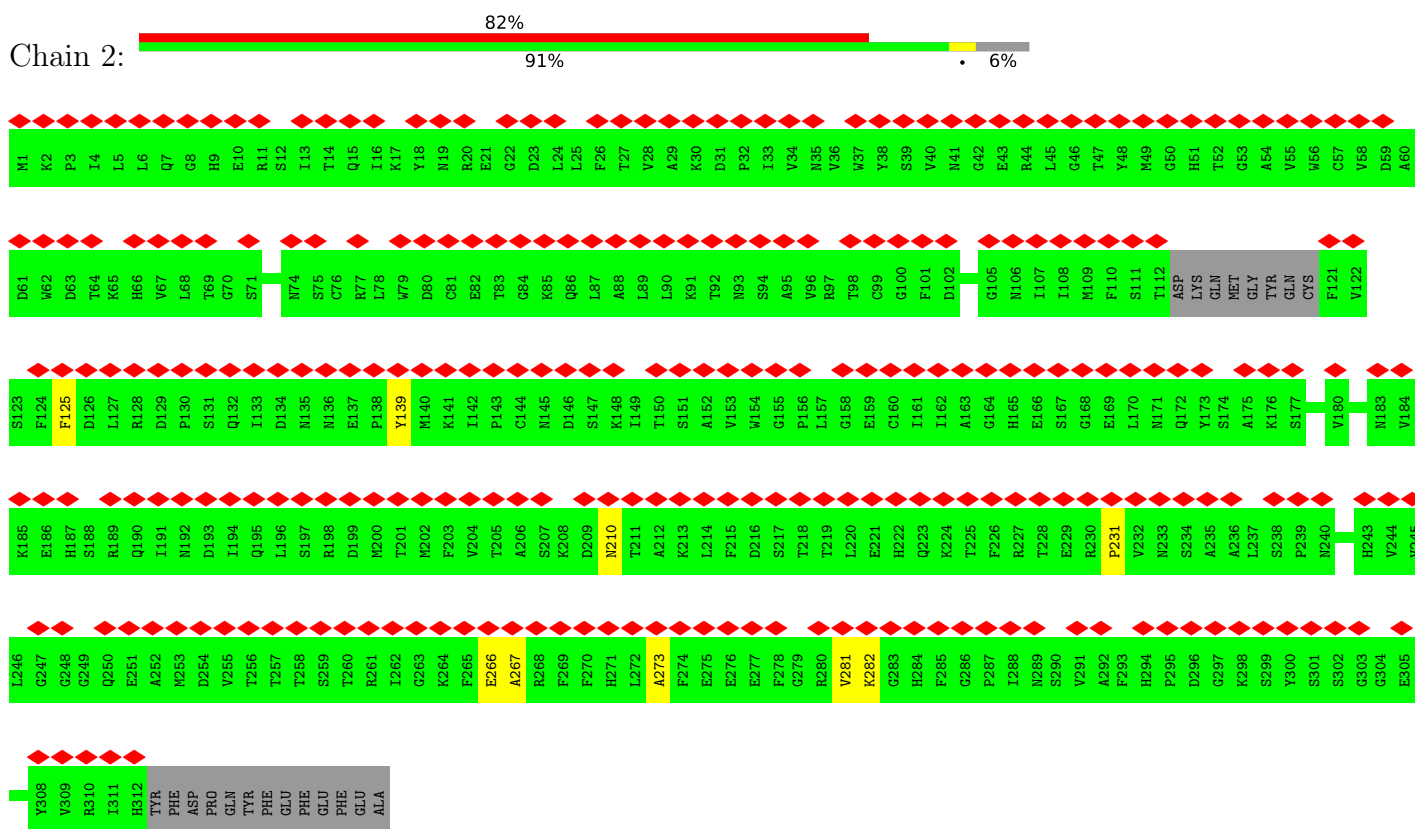
- Molecule 59 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
59	A	87	Total	Mg	0
			87	87	
59	d	1	Total	Mg	0
			1	1	
59	f	1	Total	Mg	0
			1	1	

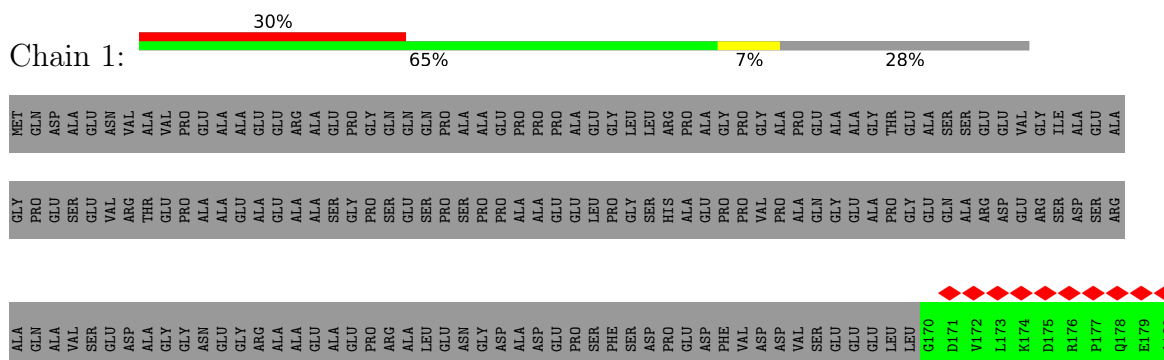
3 Residue-property plots

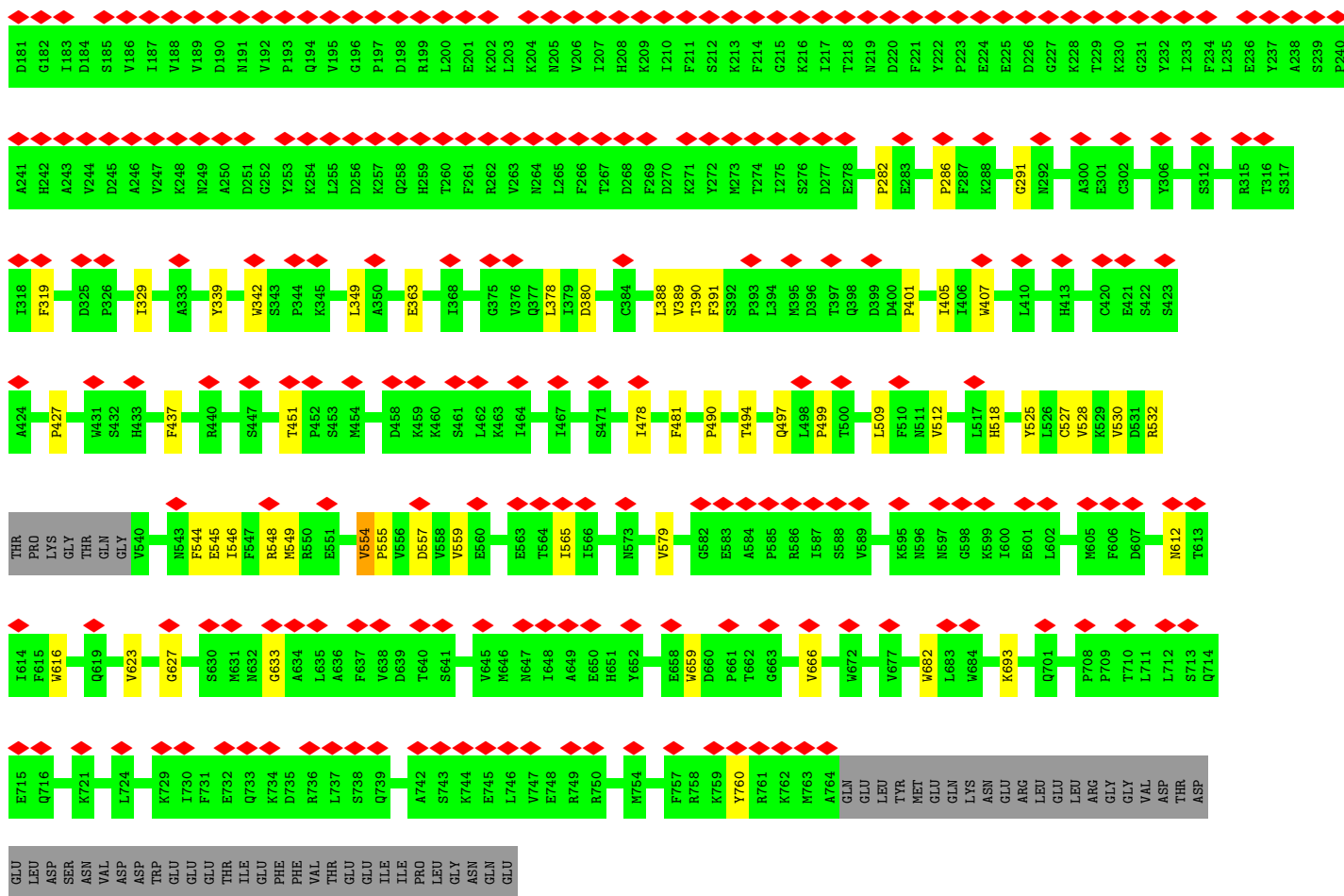
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Eukaryotic translation initiation factor 3 subunit I

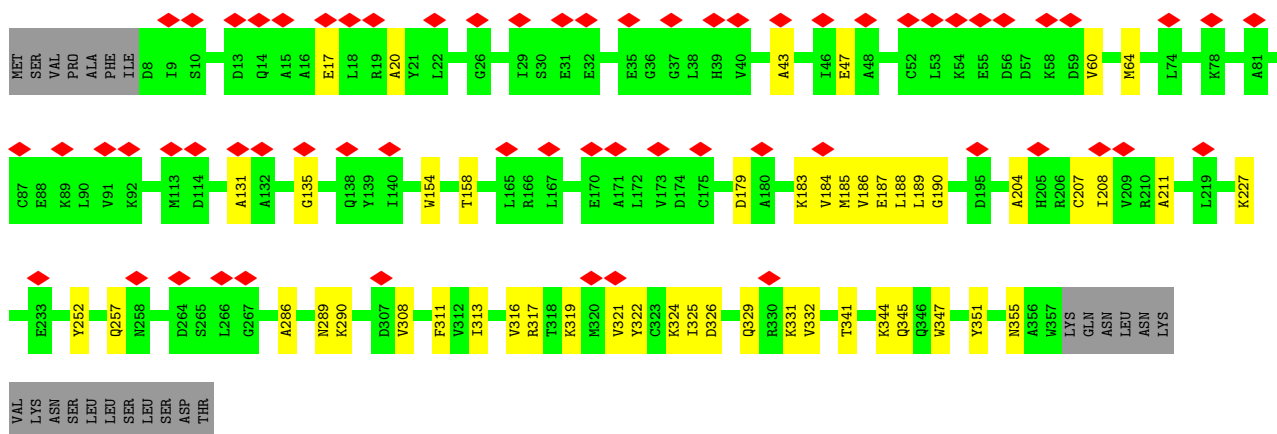
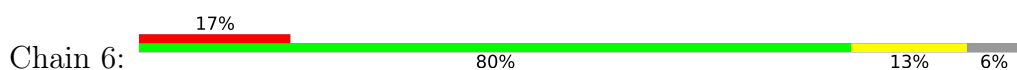


- Molecule 2: Eukaryotic translation initiation factor 3 subunit B





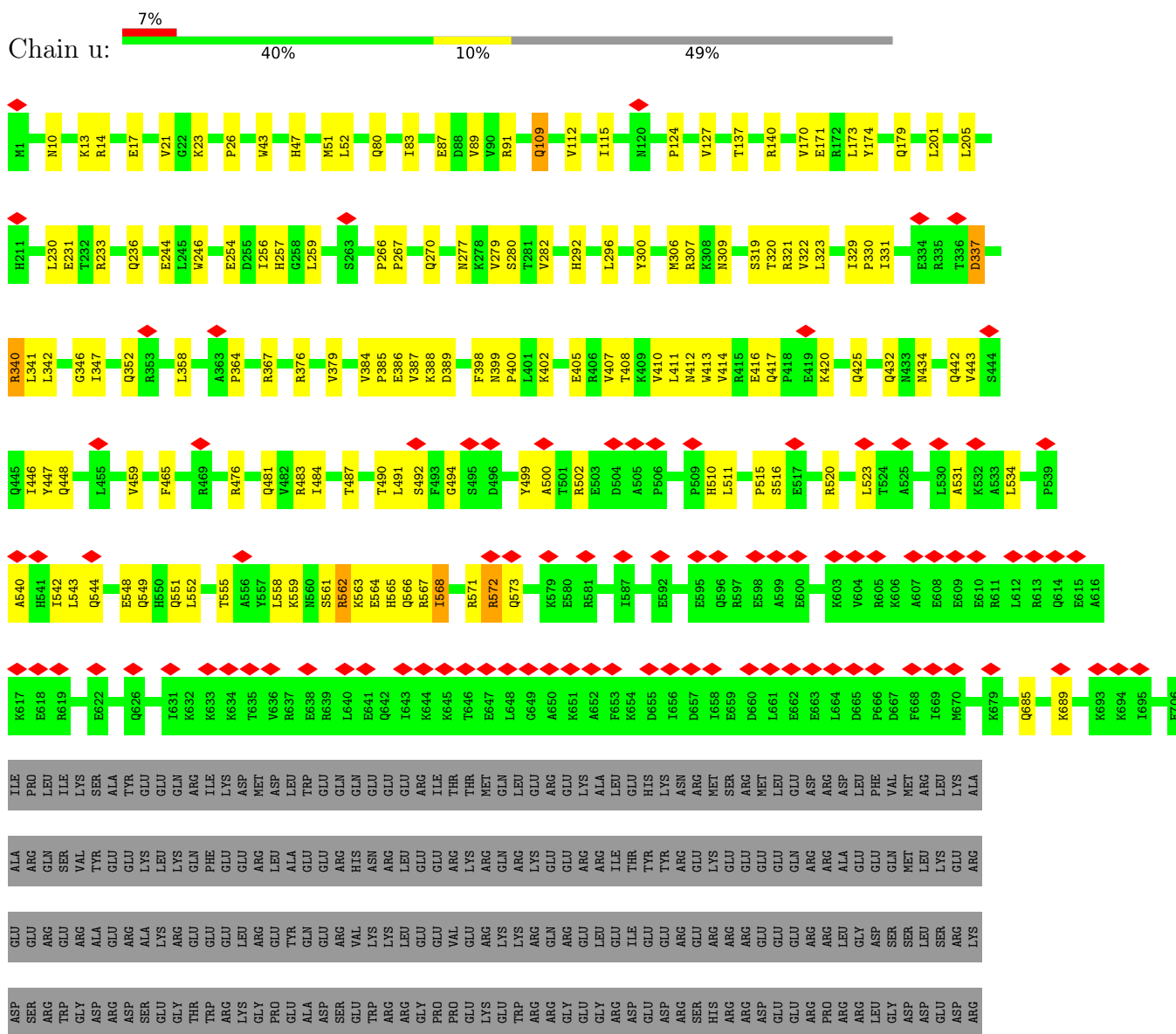
• Molecule 3: Eukaryotic translation initiation factor 3 subunit M



• Molecule 4: Eukaryotic translation initiation factor 3 subunit F



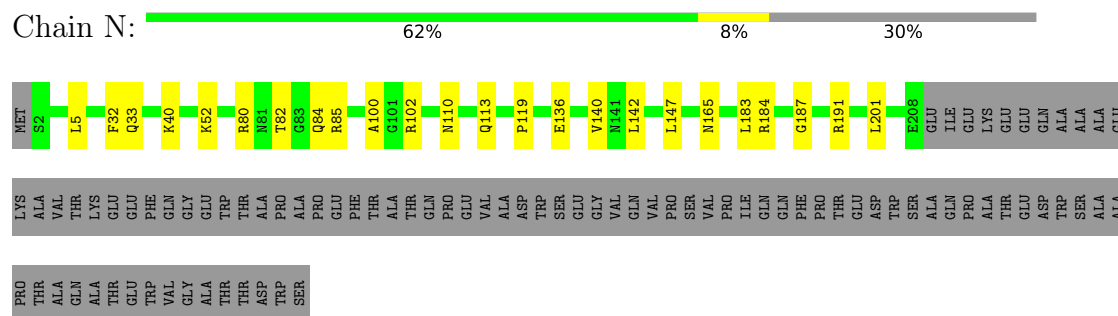
- Molecule 5: Eukaryotic translation initiation factor 3 subunit A



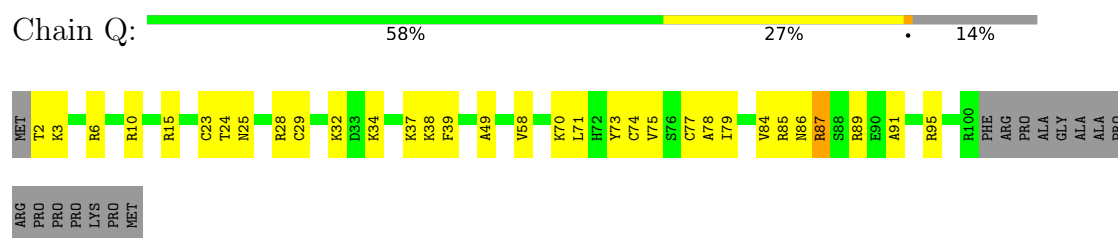
WORLDWIDE
PDB
PROTEIN DATA BANK



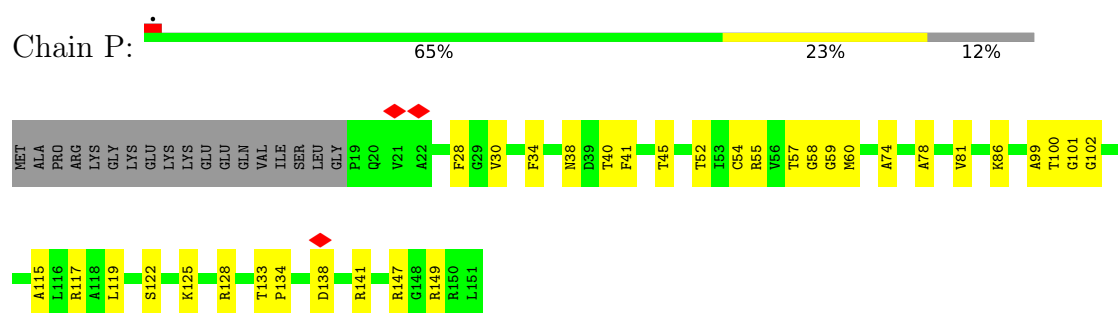
- Molecule 15: 40S ribosomal protein SA



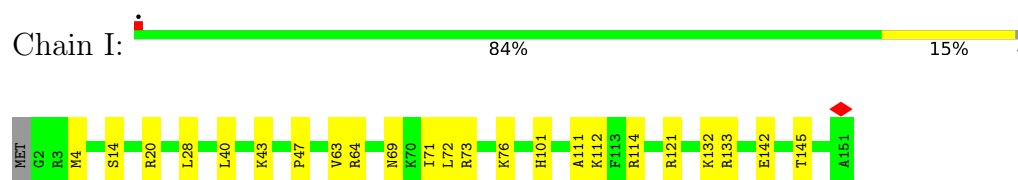
- Molecule 16: 40S ribosomal protein S26



- Molecule 17: 40S ribosomal protein S14



- Molecule 18: 40S ribosomal protein S13



- Molecule 19: Eukaryotic translation initiation factor 3 subunit D



A1579	U1463	U1360	A1260	A1170	C1026	C927	U844	G	G	A521	A604	G	G	G	A525	G377	G	C201
A1580	C1464	U1371	C1261	G1171	A1027	G928	G845	A	G	A525	A605	G	G	G	A525	U378	G	G202
G1587	G1473	U1372	U1263	A1183	C1031	C930	G846	U	G	A528	G606	G	G	G	A528	C379	C	G203
A1589	A1474	C1374	C1268	G1184	G1032	G933	U847	C	G	A533	U607	G	G	G	A533	G380	G	G204
A1594	A1476	U1378	C1272	G1187	A1055	G934	A849	U	G	A533	C382	C	G	G	A533	C382	C	G206
		A1378	C1273	A1194	A1060	U943	C850	U	C	A533	U612	G	U	U	A533	G383	G	G207
		A1379	C1274	A1195	C948	U943	C851	U	C	A533	G613	G	C	C	A533	U384	G	G208
		A1396	G1275	A1195	G949	C948	C852	U	C	A533	G614	G	C	C	A533	U384	G	U214
		U1397	A1276	G1203	U1061	G949	G860	C	G	A533	C615	G	C	C	A533	C386	G	
		G1398	A1277	A1204	A1062	C950	A861	U	C	A533	C624	G	C	C	A533	C386	G	C223
		A1402	A1278			A955		G	C	A533	G625	G	C	C	A533	C386	G	A224
		C1403			G1065	A955	A869	G	C	A533	G625	G	C	C	A533	C386	G	G225
		U1404	C1283	G1207	A1080	G959	A870	A	G	A533	U626	G	C	C	A533	C386	G	A
		A1405	G1284	A1208	U1081	G959	U871	G	A	A533	U627	G	C	C	A533	C386	G	U
		G1406	G1285	A1209	A872	G959	U871	U	G	A533	A628	G	C	C	A533	C386	G	C
		U1407	G1286		A1082	A963	G873	C	G	A533	A629	G	C	C	A533	C386	G	A
			A1287	C1215	A1083	A964	G874	C	G	A533	U630	G	C	C	A533	C386	G	A
			U1288	C1216	A1084	A965	G875	C	G	A533	U631	G	C	C	A533	C386	G	A
			G1294	A1217	C1085	U969	C876	C	G	A533	A641	G	C	C	A533	C386	G	A
			A1295	C1218	G1091	G970	C877	C	G	A533	A642	G	C	C	A533	C386	G	A
				G1221	C1092	A980	C878	C	G	A533	A643	G	C	C	A533	C386	G	A
				G1222	A1093	A981	C879	C	G	A533	A644	G	C	C	A533	C386	G	A
				A1223	G1097	A982	A886	G	C	A533	A645	G	C	C	A533	C386	G	A
				U1224	U1101	A983	U887	C	C	A533	A646	G	C	C	A533	C386	G	A
				U1225	G1102	A984	U888	C	C	A533	A647	G	C	C	A533	C386	G	A
				G1227		A985	U889	C	C	A533	A648	G	C	C	A533	C386	G	A
				U1228	C1109	A986	U890	C	C	A533	A649	G	C	C	A533	C386	G	A
				G1229	U1112	A987	U891	C	C	A533	A650	G	C	C	A533	C386	G	A
				C1230	U1113	A988	U892	C	C	A533	A651	G	C	C	A533	C386	G	A
				U1231	A1114	A989	U893	C	C	A533	A652	G	C	C	A533	C386	G	A
				G1233	U1115	A990	U894	C	C	A533	A653	G	C	C	A533	C386	G	A
					C1116	A991	U895	C	C	A533	A654	G	C	C	A533	C386	G	A
					C1117	A992	U896	C	C	A533	A655	G	C	C	A533	C386	G	A
					U1119	A993	U897	C	C	A533	A656	G	C	C	A533	C386	G	A
					U1120	A994	U898	C	C	A533	A657	G	C	C	A533	C386	G	A
						A995	U899	C	C	A533	A658	G	C	C	A533	C386	G	A
						G999	U900	C	C	A533	A659	G	C	C	A533	C386	G	A
						U1002		C	C	A533	A660	G	C	C	A533	C386	G	A
						G1005	A903	C	C	A533	A661	G	C	C	A533	C386	G	A
						C1006	A904	C	C	A533	A662	G	C	C	A533	C386	G	A
						C1007		C	C	A533	A663	G	C	C	A533	C386	G	A
						A1008	G909	C	C	A533	A664	G	C	C	A533	C386	G	A
						A1009		C	C	A533	A665	G	C	C	A533	C386	G	A
						G1010	C912	C	C	A533	A666	G	C	C	A533	C386	G	A
						A1011	A913	C	C	A533	A667	G	C	C	A533	C386	G	A
						A1012	U914	C	C	A533	A668	G	C	C	A533	C386	G	A
						U1013		C	C	A533	A669	G	C	C	A533	C386	G	A
						G1014	A919	C	C	A533	A670	G	C	C	A533	C386	G	A
						U1015	G921	C	C	A533	A671	G	C	C	A533	C386	G	A
						U1016	A922	C	C	A533	A672	G	C	C	A533	C386	G	A
						U1017	G923	C	C	A533	A673	G	C	C	A533	C386	G	A
						U1021	G924	C	C	A533	A674	G	C	C	A533	C386	G	A
						U1022	G925	C	C	A533	A675	G	C	C	A533	C386	G	A
						U1023	A926	C	C	A533	A676	G	C	C	A533	C386	G	A
								C	C	A533	A677	G	C	C	A533	C386	G	A
								C	C	A533	A678	G	C	C	A533	C386	G	A
								C	C	A533	A679	G	C	C	A533	C386	G	A
								C	C	A533	A680	G	C	C	A533	C386	G	A
								C	C	A533	A681	G	C	C	A533	C386	G	A
								C	C	A533	A682	G	C	C	A533	C386	G	A
								C	C	A533	A683	G	C	C	A533	C386	G	A
								C	C	A533	A684	G	C	C	A533	C386	G	A
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								C	C	A533	A689	G	C	C	A533	C386	G	A
								C	C	A533	A690	G	C	C	A533	C386	G	A
								C	C	A533	A691	G	C	C	A533	C386	G	A
								C	C	A533	A692	G	C	C	A533	C386	G	A
								C	C	A533	A693	G	C	C	A533	C386	G	A
								C	C	A533	A694	G	C	C	A533	C386	G	A
								C	C	A533	A695	G	C	C	A533	C386	G	A
								C	C	A533	A696	G	C	C	A533	C386	G	A
								C	C	A533	A697	G	C	C	A533	C386	G	A
								C	C	A533	A698	G	C	C	A533	C386	G	A
								C	C	A533	A699	G	C	C	A533	C386	G	A
								C	C	A533	A700	G	C	C	A533	C386	G	A
								C	C	A533	A701	G	C	C	A533	C386	G	A
								C	C	A533	A702	G	C	C	A533	C386	G	A
								C	C	A533	A703	G	C	C	A533	C386	G	A
								C	C	A533	A704	G	C	C	A533	C386	G	A
								C	C	A533	A705	G	C	C	A533	C386	G	A
								C	C	A533	A706	G	C	C	A533	C386	G	A
								C	C	A533	A707	G	C	C	A533	C386	G	A
								C	C	A533	A708	G	C	C	A533	C386	G	A
								C	C	A533	A709	G	C	C	A533	C386	G	A
								C	C	A533	A710	G	C	C	A533	C386	G	A
								C	C	A533	A711	G	C	C	A533	C386	G	A
								C	C	A533	A712	G	C	C	A533	C386	G	A
								C	C	A533	A713	G	C	C	A533	C386	G	A
								C	C	A533	A714	G	C	C	A533	C386	G	A
								C	C	A533	A715	G	C	C	A533	C386	G	A
								C	C	A533	A716	G	C	C	A533	C386	G	A
								C	C	A533	A717	G	C	C	A533	C386	G	A
								C	C	A533	A718	G	C	C	A533	C386	G	A
								C	C	A533	A719	G	C	C	A533	C386	G	A
								C	C	A533	A720	G	C	C	A533	C386	G	A
								C	C	A533	A721	G	C	C	A533	C386	G	A
								C	C	A533	A722	G	C	C	A533	C386	G	A
								C	C	A533	A723	G	C	C	A533	C386	G	A
								C	C	A533	A724	G	C	C	A533	C386	G	A
								C	C	A533	A725	G	C	C	A533	C386	G	A
								C	C	A533	A726	G	C	C	A533	C386	G	A
								C	C	A533	A727	G	C	C	A533	C386	G	A
								C	C	A533	A728	G	C	C	A533	C386	G	A
								C	C	A533	A729	G	C	C	A533	C386	G	A
								C	C	A533	A730	G	C	C	A533	C386	G	A
								C	C	A533	A731	G						



- Molecule 25: 40S ribosomal protein S11

Chain B: 77% 13% 10%



- Molecule 26: 40S ribosomal protein S4, X isoform

Chain C: 87% 10% 1%



- Molecule 27: 40S ribosomal protein S9

Chain D: 76% 14% 9%



- Molecule 28: 40S ribosomal protein S23

Chain E: 86% 12% 1%

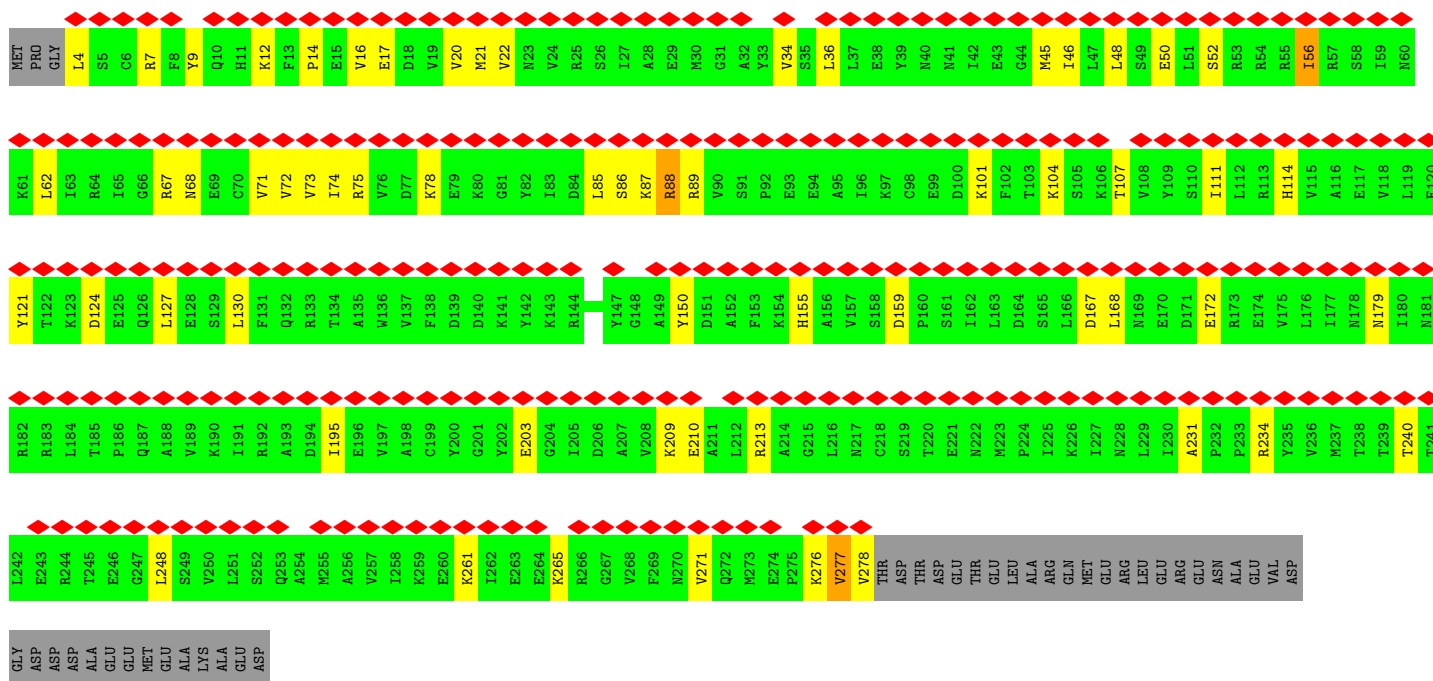
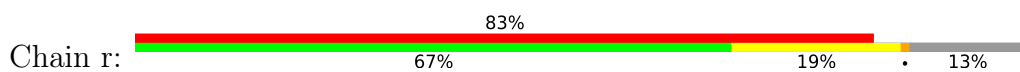


- Molecule 29: 40S ribosomal protein S30

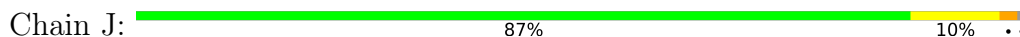
Chain F: 71% 7% 20%



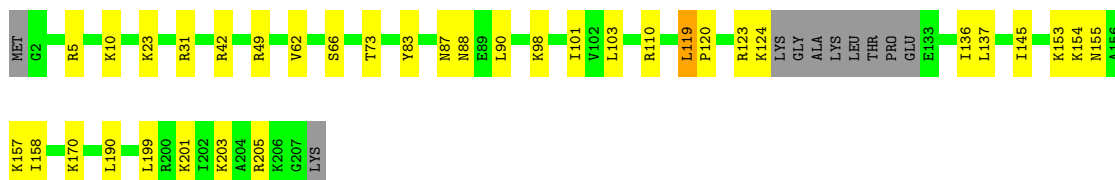
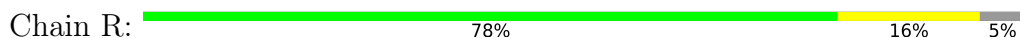
- Molecule 30: Eukaryotic translation initiation factor 2 subunit 1



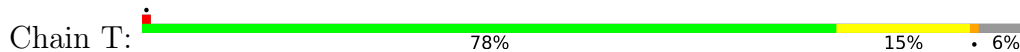
- Molecule 31: 40S ribosomal protein S15a



- Molecule 32: 40S ribosomal protein S8

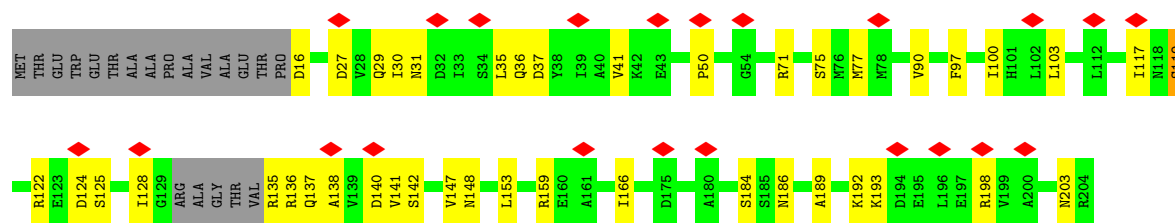


- Molecule 33: 40S ribosomal protein S24

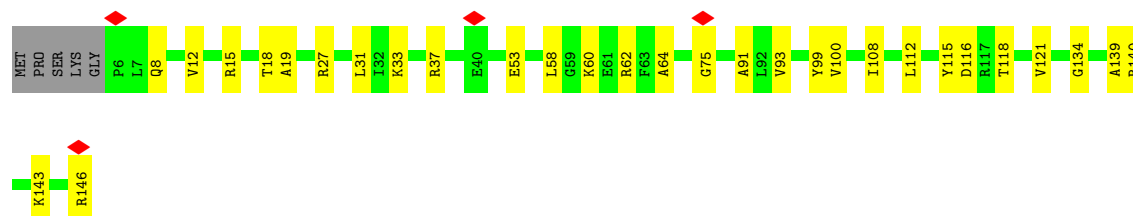
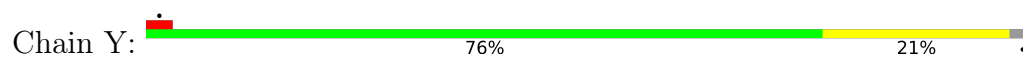


- Molecule 34: 40S ribosomal protein S5

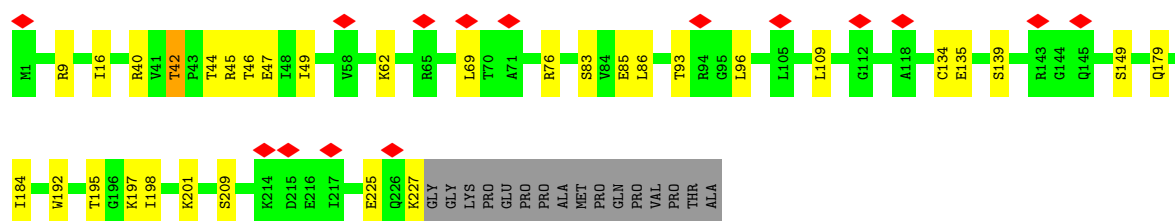
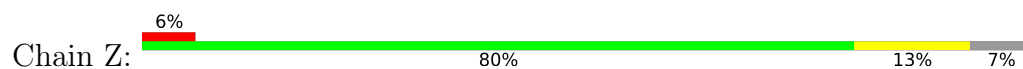




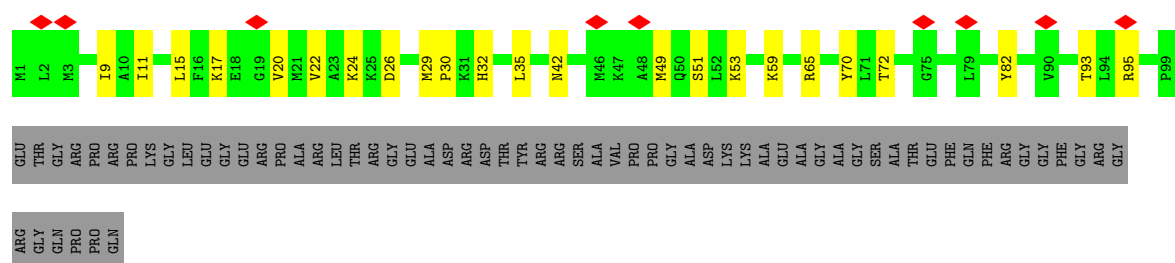
- Molecule 35: 40S ribosomal protein S16



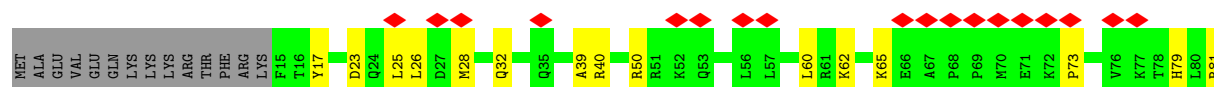
- Molecule 36: 40S ribosomal protein S3

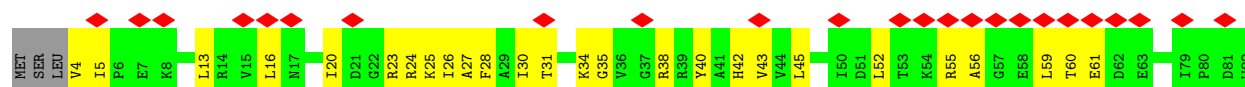


- Molecule 37: 40S ribosomal protein S10



- Molecule 38: 40S ribosomal protein S15



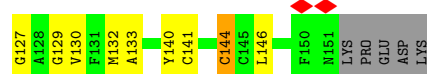
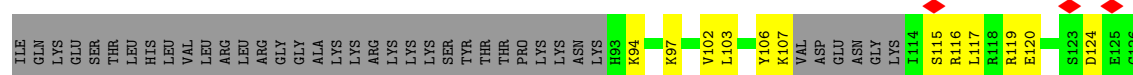
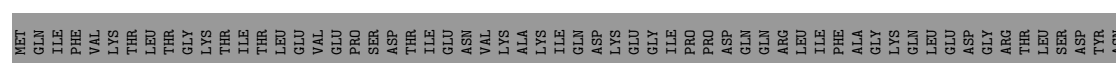




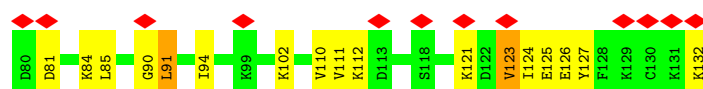
- Molecule 43: 40S ribosomal protein S29



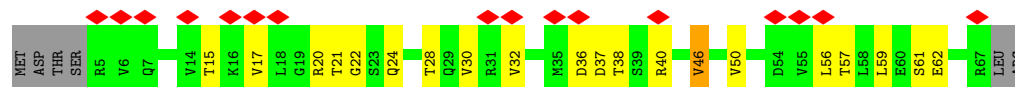
- Molecule 44: Ubiquitin-40S ribosomal protein S27a



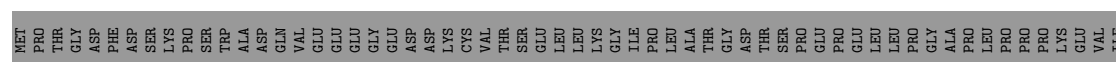
- Molecule 45: 40S ribosomal protein S12

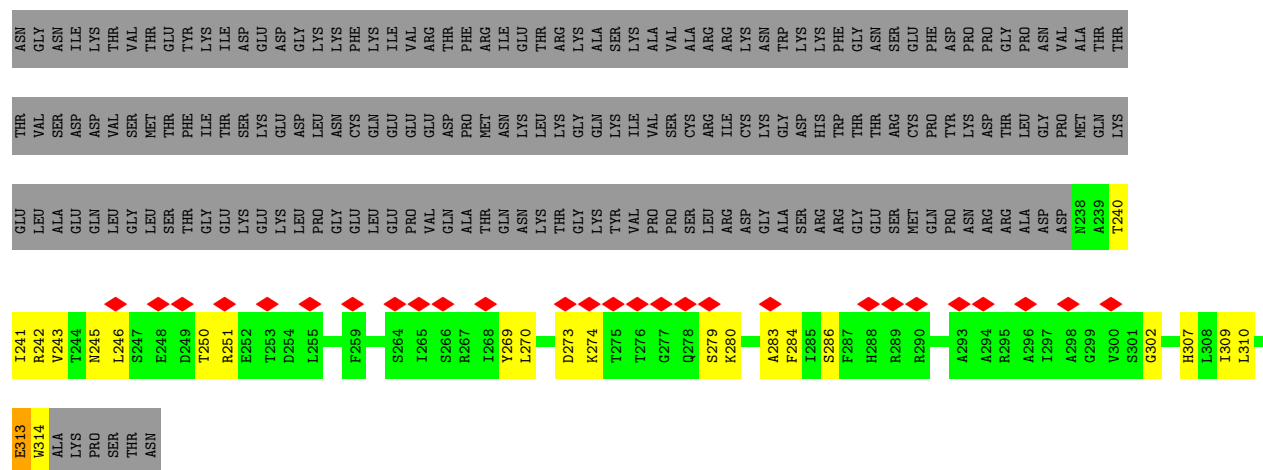


- Molecule 46: 40S ribosomal protein S28

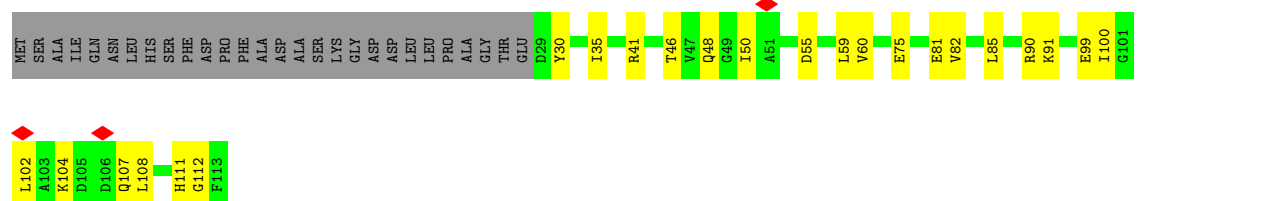


- Molecule 47: Eukaryotic translation initiation factor 3 subunit G

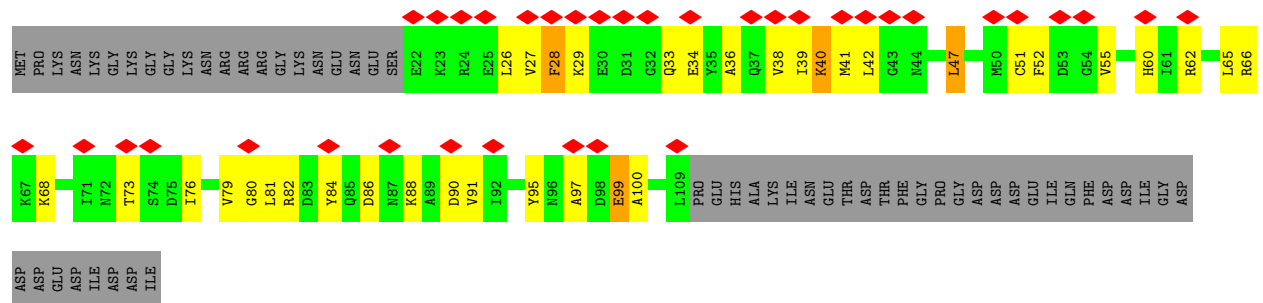




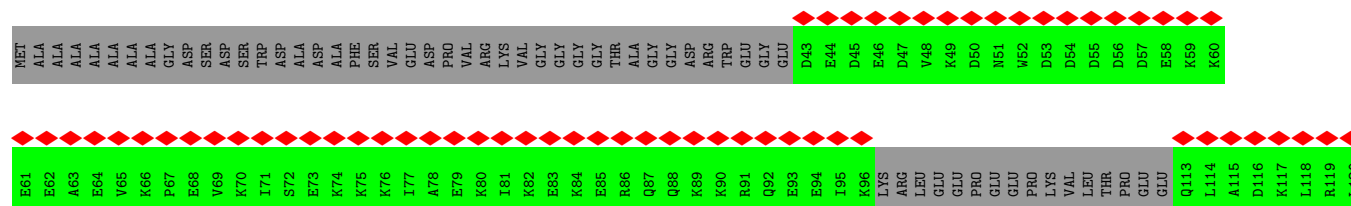
• Molecule 48: Eukaryotic translation initiation factor 1

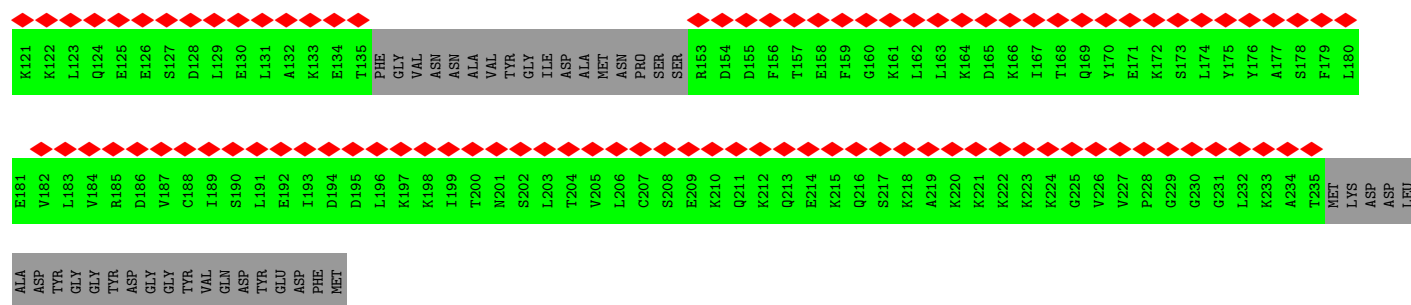


• Molecule 49: Eukaryotic translation initiation factor 1A, X-chromosomal

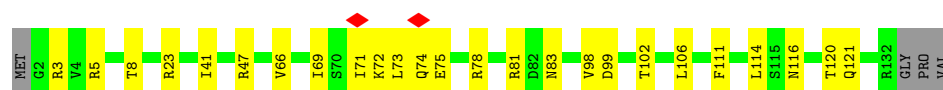
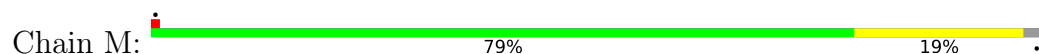


• Molecule 50: Eukaryotic translation initiation factor 3 subunit J

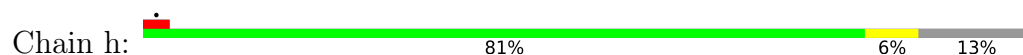




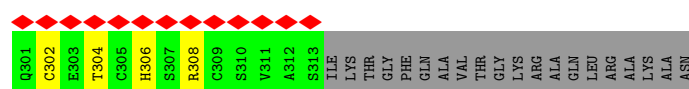
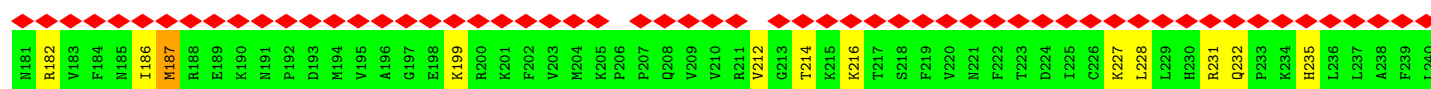
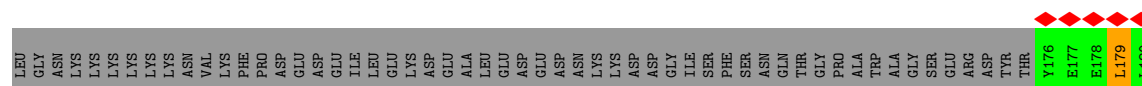
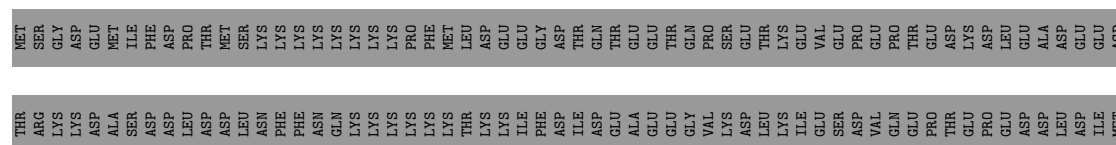
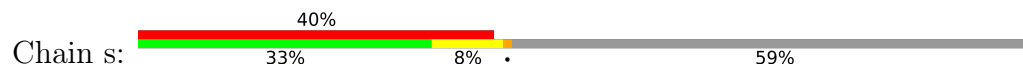
- Molecule 51: 40S ribosomal protein S17



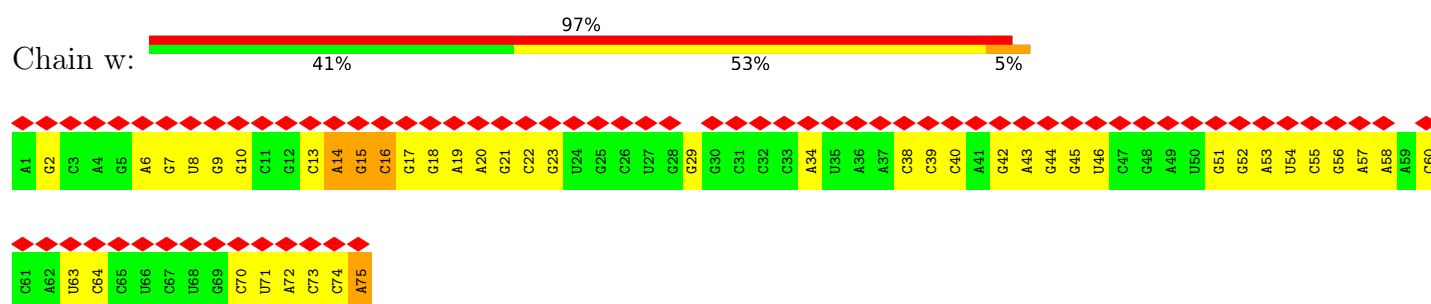
- Molecule 52: 40S ribosomal protein S20



- Molecule 53: Eukaryotic translation initiation factor 2 subunit 2



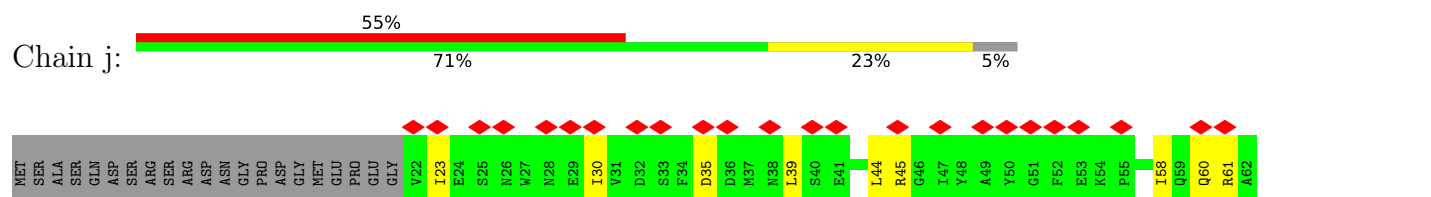
- Molecule 54: Initiator Met-tRNA-i

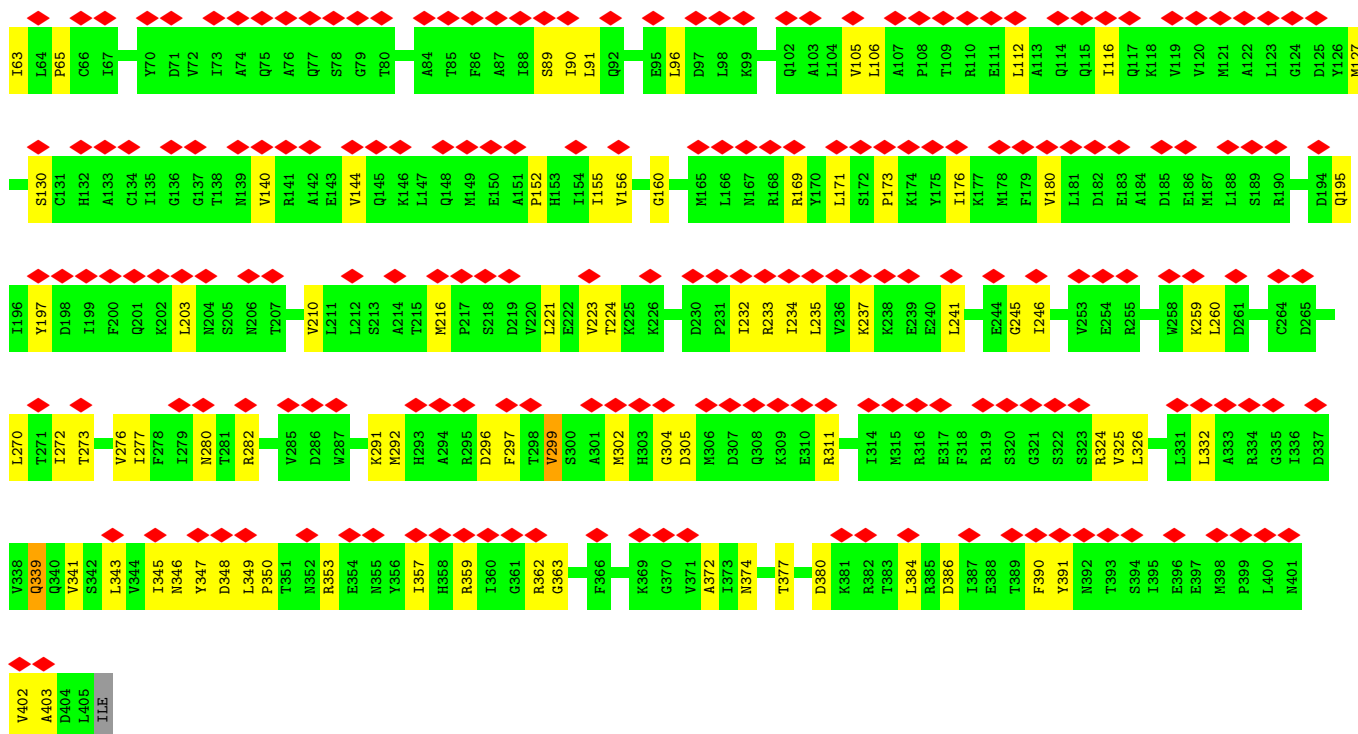


• Molecule 55: Eukaryotic translation initiation factor 2 subunit 3

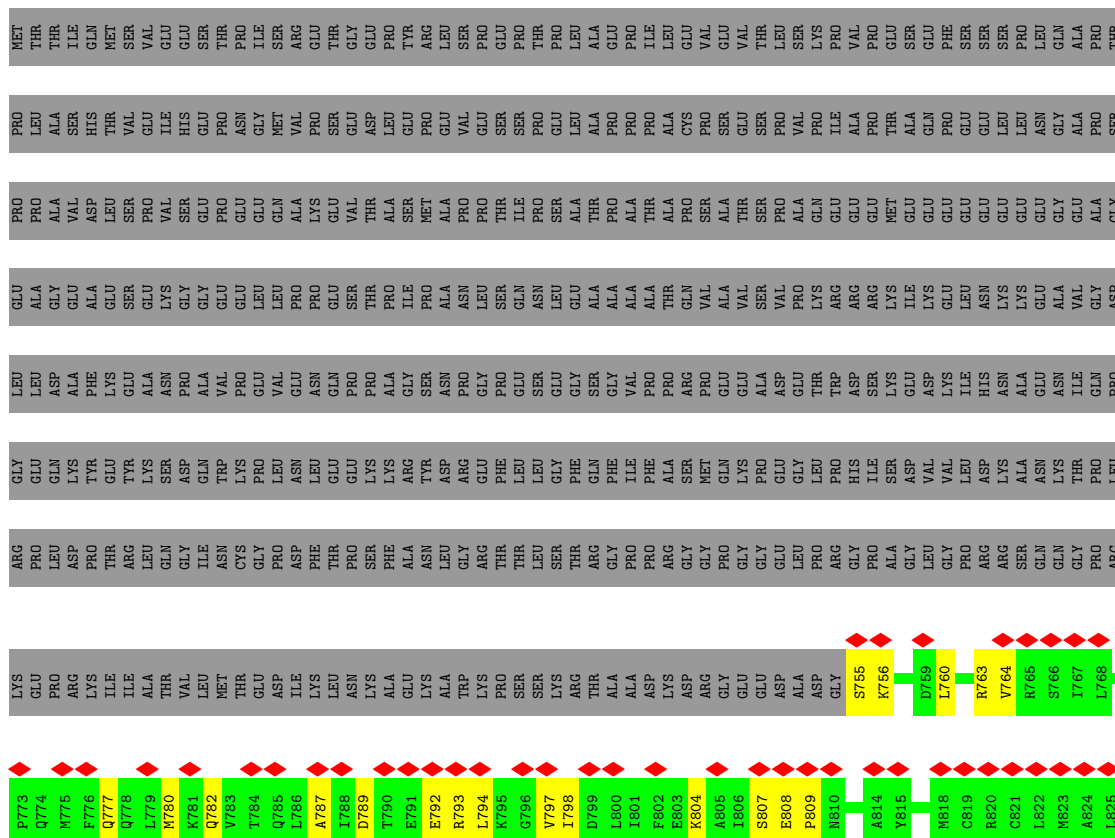


• Molecule 56: Eukaryotic initiation factor 4A-I





● Molecule 57: Eukaryotic translation initiation factor 4 gamma 1



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	37870	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 ($e^-/\text{\AA}^2$)	107	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.339	Depositor
Minimum map value	-0.216	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	537.0, 537.0, 537.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.074, 1.074, 1.074	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, OMC, MA6, UR3, 6MZ, 5MU, OMG, PSU, 5MC, MG, OMU, JMH, A2M

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	2	0.22	0/1491	0.90	0/2068
2	1	0.29	0/3279	0.94	0/4534
3	6	0.25	0/1926	0.82	1/2669 (0.0%)
4	4	0.24	0/1269	0.82	0/1762
5	u	0.31	0/5475	0.77	0/7432
6	v	0.29	0/2672	0.81	0/3647
7	S	0.30	0/1885	0.69	0/2510
8	y	0.28	0/5557	0.70	0/7503
9	8	0.26	0/1569	0.93	0/2183
10	G	0.35	0/1451	0.79	0/1942
11	H	0.37	0/644	0.68	0/864
12	K	0.38	0/623	0.64	0/833
13	L	0.45	0/1743	0.82	1/2354 (0.0%)
14	O	0.34	0/1742	0.64	0/2330
15	N	0.39	0/1670	0.60	1/2271 (0.0%)
16	Q	0.43	0/805	0.78	0/1079
17	P	0.37	0/1010	0.82	1/1353 (0.1%)
18	I	0.43	0/1232	0.70	0/1656
19	x	0.29	0/2874	0.82	1/3925 (0.0%)
20	3	0.27	0/1055	0.92	0/1469
21	5	0.27	0/1575	0.88	2/2187 (0.1%)
22	7	0.36	0/363	1.03	0/556
23	9	0.29	0/231	0.64	0/294
24	A	0.41	0/40313	0.61	6/62824 (0.0%)
25	B	0.38	0/1186	0.52	0/1585
26	C	0.35	0/2077	0.56	0/2796
27	D	0.38	0/1502	0.63	0/2008
28	E	0.38	0/1105	0.58	0/1476
29	F	0.32	0/380	0.52	0/496
30	r	0.25	0/2247	0.72	0/3029
31	J	0.41	0/1051	0.64	0/1406
32	R	0.33	0/1654	0.63	0/2203

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	T	0.31	0/1032	0.55	0/1371
34	V	0.26	0/1481	0.76	1/1988 (0.1%)
35	Y	0.30	0/1142	0.78	0/1528
36	Z	0.28	0/1793	0.67	0/2414
37	a	0.28	0/859	0.76	0/1159
38	b	0.28	0/929	0.76	0/1241
39	c	0.30	0/2493	0.75	0/3394
40	d	0.29	0/1123	0.79	0/1504
41	e	0.30	0/529	0.80	0/712
42	f	0.29	0/1194	0.80	0/1599
43	i	0.27	0/429	0.66	0/568
44	k	0.40	0/444	1.05	0/588
45	m	0.36	0/960	0.89	0/1286
46	n	0.32	0/500	0.80	0/669
47	o	0.31	0/628	0.87	0/846
48	p	0.29	0/701	0.76	0/936
49	q	0.24	0/722	0.74	0/963
50	z	0.23	0/792	0.87	0/1101
51	M	0.32	0/1078	0.71	0/1447
52	h	0.30	0/827	0.78	0/1110
53	s	0.26	0/1142	0.79	0/1534
54	w	0.24	0/1795	0.68	0/2798
55	t	0.23	0/1745	0.89	3/2417 (0.1%)
56	j	0.35	0/3119	0.90	0/4210
57	g	0.40	0/1869	0.99	5/2494 (0.2%)
All	All	0.35	0/122982	0.72	22/175121 (0.0%)

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1631	U	C5'-C4'-C3'	-6.79	105.81	116.00
57	g	855	LYS	N-CA-CB	6.75	121.90	110.49
17	P	138	ASP	N-CA-CB	-5.62	102.50	110.58
15	N	102	ARG	CA-CB-CG	-5.53	103.03	114.10
24	A	1311	C	C5'-C4'-C3'	-5.52	107.72	116.00
55	t	247	PRO	CA-C-N	5.47	131.99	121.54
55	t	247	PRO	C-N-CA	5.47	131.99	121.54
19	x	480	ILE	CG1-CB-CG2	-5.43	94.41	110.70
24	A	1207	G	N9-C1'-C2'	5.41	120.11	112.00
24	A	996	A	O4'-C1'-N9	5.40	116.61	108.50
57	g	855	LYS	N-CA-C	-5.39	99.32	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	t	168	PRO	N-CA-C	5.22	123.22	112.47
24	A	1600	G	P-O3'-C3'	5.14	127.91	120.20
34	V	198	ARG	CB-CG-CD	-5.13	99.49	111.30
3	6	227	LYS	N-CA-C	-5.13	98.47	109.81
57	g	988	SER	CA-C-N	5.09	131.26	121.54
57	g	988	SER	C-N-CA	5.09	131.26	121.54
21	5	499	ASN	CA-C-N	5.08	135.06	125.66
21	5	499	ASN	C-N-CA	5.08	135.06	125.66
57	g	763	ARG	N-CA-C	5.05	116.59	111.14
13	L	194	ARG	CG-CD-NE	5.03	123.07	112.00
24	A	1600	G	C4'-C3'-O3'	5.02	116.93	109.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2	1493	0	677	5	0
2	1	3258	0	1917	28	0
3	6	1917	0	1096	30	0
4	4	1272	0	564	6	0
5	u	5383	0	5085	101	0
6	v	2635	0	2207	49	0
7	S	1862	0	2018	43	0
8	y	5470	0	5329	72	0
9	8	1571	0	683	7	0
10	G	1430	0	1520	30	0
11	H	631	0	657	10	0
12	K	617	0	622	11	0
13	L	1707	0	1794	26	0
14	O	1715	0	1785	29	0
15	N	1633	0	1640	16	0
16	Q	792	0	844	23	0
17	P	997	0	1021	24	0
18	I	1208	0	1294	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	x	2831	0	2199	44	0
20	3	1057	0	475	9	0
21	5	1581	0	689	5	0
22	7	336	0	169	1	0
23	9	230	0	276	4	0
24	A	36670	0	18540	357	0
25	B	1166	0	1233	14	0
26	C	2035	0	2138	15	0
27	D	1477	0	1589	19	0
28	E	1087	0	1154	11	0
29	F	378	0	417	4	0
30	r	2215	0	2266	36	0
31	J	1034	0	1080	13	0
32	R	1627	0	1706	23	0
33	T	1015	0	1086	15	0
34	V	1461	0	1511	30	0
35	Y	1124	0	1193	22	0
36	Z	1765	0	1865	20	0
37	a	834	0	861	17	0
38	b	913	0	952	21	0
39	c	2436	0	2393	42	0
40	d	1105	0	1138	15	0
41	e	523	0	573	13	0
42	f	1176	0	1233	31	0
43	i	419	0	415	10	0
44	k	435	0	435	15	0
45	m	950	0	987	23	0
46	n	498	0	525	14	0
47	o	616	0	600	14	0
48	p	691	0	706	11	0
49	q	714	0	735	22	0
50	z	795	0	341	0	0
51	M	1064	0	1118	11	0
52	h	817	0	882	7	0
53	s	1123	0	1157	19	0
54	w	1604	0	816	13	0
55	t	1750	0	806	6	0
56	j	3073	0	3114	57	0
57	g	1848	0	1924	50	0
58	Q	1	0	0	0	0
58	k	1	0	0	0	0
59	A	87	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	d	1	0	0	0	0
59	f	1	0	0	0	0
All	All	118155	0	92050	1339	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 7.

All (1339) 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)
24:A:1091:C:HO2'	31:J:2:VAL:N	1.81	0.79
24:A:925:G:H1	24:A:1017:U:H3	1.29	0.79
13:L:202:THR:HG22	27:D:54:ARG:HH12	1.48	0.76
19:x:359:ARG:H	19:x:375:CYS:HB2	1.52	0.73
39:c:87:LEU:HB2	39:c:101:PHE:HB2	1.67	0.73
7:S:135:PRO:HB2	7:S:141:ILE:HG12	1.71	0.73
3:6:308:VAL:HA	3:6:311:PHE:HB3	1.70	0.72
8:y:831:LEU:HG	8:y:844:MET:HB2	1.71	0.72
24:A:1033:G:H1	24:A:1080:A:HO2'	1.35	0.72
17:P:57:THR:HB	17:P:60:MET:HG3	1.71	0.72
24:A:1283:C:H42	45:m:102:LYS:HB3	1.56	0.71
6:v:290:ASP:HB3	6:v:293:THR:HB	1.73	0.71
45:m:79:VAL:HG21	45:m:85:LEU:HB2	1.73	0.70
24:A:928:G:H1	24:A:1013:U:H3	1.37	0.70
25:B:4:ILE:HG13	25:B:5:GLN:HE21	1.56	0.70
49:q:33:GLN:HG2	49:q:80:GLY:HA2	1.75	0.69
3:6:290:LYS:HA	3:6:331:LYS:H	1.58	0.69
25:B:104:LYS:O	28:E:11:ARG:NH2	2.26	0.69
18:I:121:ARG:HH12	24:A:925:G:H5'	1.57	0.69
37:a:59:LYS:HG2	37:a:72:THR:HG22	1.73	0.69
42:f:34:LYS:HB3	42:f:100:ALA:HA	1.76	0.68
8:y:421:GLY:HA2	8:y:440:VAL:HA	1.76	0.68
2:1:565:ILE:HD11	2:1:579:VAL:HB	1.76	0.68
7:S:142:ARG:HA	7:S:147:LEU:HB2	1.76	0.68
39:c:174:VAL:HB	39:c:188:HIS:HB2	1.75	0.68
57:g:855:LYS:HD2	57:g:892:ARG:HA	1.76	0.67
56:j:260:LEU:HD22	56:j:291:LYS:HD2	1.76	0.67
45:m:81:ASP:HB3	45:m:84:LYS:HB2	1.76	0.67
57:g:881:LYS:HB3	57:g:885:GLU:HB2	1.76	0.67
24:A:1606:G:H1	24:A:1632:G:HO2'	1.42	0.67
36:Z:42:THR:HG22	36:Z:45:ARG:H	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:g:807:SER:O	57:g:893:ARG:NH1	2.27	0.67
8:y:64:ILE:HG12	8:y:109:ILE:HD11	1.76	0.67
5:u:405:GLU:HA	5:u:408:THR:HG22	1.75	0.67
10:G:117:PRO:HB2	10:G:120:ARG:HG3	1.76	0.66
24:A:72:C:O2'	24:A:74:G:N2	2.29	0.66
56:j:90:ILE:HD11	56:j:180:VAL:HG21	1.77	0.66
18:I:64:ARG:NH2	24:A:919:A:OP2	2.28	0.66
24:A:751:G:H22	24:A:789:G:H5''	1.60	0.66
24:A:887:U:H2'	24:A:888:U:H2'	1.78	0.66
24:A:1488:C:O2'	24:A:1490:G:OP2	2.14	0.66
24:A:1252:C:N4	35:Y:146:ARG:O	2.28	0.65
13:L:123:ARG:NH1	24:A:1358:U:OP2	2.29	0.65
44:k:119:ARG:HG3	44:k:132:MET:HB2	1.78	0.65
47:o:269:TYR:HB3	47:o:284:PHE:HB2	1.78	0.65
5:u:329:ILE:HB	5:u:367:ARG:HH11	1.62	0.65
24:A:528:A:N1	24:A:557:U:O2'	2.30	0.65
57:g:903:GLY:HA3	57:g:938:LEU:HD11	1.78	0.65
14:O:162:ARG:NH1	24:A:1005:G:OP2	2.30	0.65
56:j:23:ILE:HG12	56:j:216:MET:HG3	1.79	0.65
24:A:1831:A:H2'	24:A:1832:6MZ:H8	1.78	0.64
19:x:391:ILE:HG22	19:x:446:TYR:HB2	1.79	0.64
5:u:296:LEU:HB3	5:u:322:VAL:HG23	1.80	0.64
8:y:68:ARG:HH12	8:y:109:ILE:HA	1.62	0.64
17:P:149:ARG:NH1	24:A:1065:G:OP1	2.31	0.64
24:A:752:G:N2	24:A:793:G:O2'	2.31	0.64
24:A:1156:U:OP1	31:J:71:LYS:NZ	2.31	0.64
55:t:418:SER:H	55:t:427:ILE:HA	1.60	0.64
57:g:855:LYS:HD3	57:g:895:SER:HB2	1.81	0.64
16:Q:95:ARG:HD2	24:A:1866:A:H5'	1.80	0.63
46:n:20:ARG:HA	46:n:28:THR:HA	1.80	0.63
36:Z:62:LYS:HD2	37:a:95:ARG:HH22	1.63	0.63
49:q:41:MET:HG2	49:q:47:LEU:HD13	1.81	0.63
57:g:922:LYS:O	57:g:926:ASN:ND2	2.31	0.63
19:x:452:VAL:HG22	19:x:465:ILE:HG22	1.80	0.63
41:e:101:SER:HB3	41:e:108:ILE:HD12	1.80	0.63
2:1:546:ILE:HB	2:1:557:ASP:HB2	1.81	0.62
10:G:106:ARG:NH1	24:A:861:A:N1	2.43	0.62
12:K:17:CYS:SG	12:K:18:SER:N	2.72	0.62
16:Q:32:LYS:NZ	24:A:987:A:OP1	2.32	0.62
24:A:839:C:H41	33:T:10:ARG:HA	1.63	0.62
2:1:319:PHE:HA	2:1:329:ILE:H	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:145:LYS:NZ	24:A:1348:G:OP1	2.32	0.62
6:v:206:GLN:NE2	19:x:21:VAL:O	2.31	0.62
7:S:49:VAL:HB	7:S:115:LYS:HB3	1.80	0.62
39:c:5:MET:HE2	39:c:312:VAL:HB	1.81	0.62
24:A:835:C:H5''	24:A:836:G:H5'	1.80	0.62
7:S:63:MET:HG2	7:S:98:ARG:HD2	1.82	0.61
24:A:1550:G:H3'	24:A:1579:A:H61	1.65	0.61
15:N:147:LEU:O	15:N:165:ASN:ND2	2.33	0.61
19:x:289:LEU:HD23	19:x:316:ALA:HB1	1.82	0.61
39:c:165:ILE:HB	39:c:177:TRP:HB2	1.82	0.61
49:q:65:LEU:HD22	49:q:68:LYS:HD2	1.82	0.61
29:F:80:LEU:N	49:q:82:ARG:O	2.34	0.61
37:a:65:ARG:NH2	43:i:21:CYS:O	2.33	0.61
24:A:888:U:H3	24:A:900:C:H42	1.49	0.61
3:6:351:TYR:O	3:6:355:ASN:ND2	2.33	0.61
7:S:58:LYS:HA	7:S:107:SER:HB2	1.81	0.61
46:n:37:ASP:HB3	46:n:40:ARG:HH11	1.66	0.61
5:u:400:PRO:HD3	5:u:442:GLN:HE21	1.65	0.61
6:v:220:PHE:O	6:v:229:ARG:NH2	2.34	0.61
24:A:838:G:O2'	24:A:840:C:OP2	2.19	0.61
24:A:1616:U:O4	38:b:40:ARG:NH1	2.34	0.61
24:A:1752:C:O2'	24:A:1782:G:N2	2.33	0.61
5:u:124:PRO:HA	5:u:127:VAL:HG22	1.81	0.60
14:O:175:GLU:O	14:O:179:ASN:ND2	2.34	0.60
24:A:1825:A:N7	49:q:66:ARG:NH1	2.49	0.60
2:1:659:TRP:HA	2:1:666:VAL:HA	1.81	0.60
21:5:206:LYS:HA	21:5:269:LEU:H	1.66	0.60
24:A:535:G:N2	24:A:536:A:N7	2.49	0.60
42:f:13:LEU:HB2	42:f:20:ILE:HB	1.84	0.60
56:j:272:ILE:HD12	56:j:343:LEU:HB2	1.83	0.60
2:1:478:ILE:HD12	2:1:497:GLN:HG2	1.84	0.60
24:A:926:A:H61	24:A:1015:U:H3	1.49	0.60
5:u:137:THR:HA	5:u:140:ARG:HG3	1.83	0.60
6:v:247:GLN:HG2	6:v:250:CYS:HB2	1.82	0.60
12:K:56:CYS:SG	12:K:57:GLY:N	2.75	0.60
24:A:1610:G:N7	42:f:132:ARG:NH2	2.49	0.60
30:r:114:HIS:HB3	30:r:179:ASN:HD22	1.66	0.60
32:R:87:ASN:HB3	32:R:90:LEU:HG	1.84	0.60
56:j:61:ARG:HB3	56:j:234:ILE:HD13	1.84	0.60
24:A:1441:U:O2	24:A:1443:C:N4	2.35	0.59
30:r:4:LEU:HB2	30:r:124:ASP:HB3	1.82	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:1710:C:O2	24:A:1824:A:N6	2.35	0.59
16:Q:74:CYS:SG	16:Q:75:VAL:N	2.75	0.59
5:u:91:ARG:HH21	5:u:173:LEU:HD22	1.65	0.59
5:u:307:ARG:HD2	5:u:309:ASN:HB2	1.85	0.59
24:A:1541:G:N3	40:d:12:GLN:NE2	2.51	0.59
18:I:121:ARG:NH2	24:A:925:G:OP1	2.35	0.59
24:A:199:C:H2'	24:A:200:G:H21	1.66	0.59
24:A:1624:U:O4	38:b:40:ARG:NH2	2.35	0.59
9:8:31:SER:HA	9:8:37:LYS:HA	1.85	0.59
27:D:113:GLN:OE1	27:D:154:GLN:NE2	2.35	0.59
24:A:1639:G:N2	54:w:40:C:O2'	2.36	0.59
35:Y:8:GLN:HB2	35:Y:27:ARG:HB2	1.84	0.59
10:G:116:ARG:NH2	24:A:687:C:O2'	2.36	0.59
24:A:1208:A:O2'	24:A:1835:A:N7	2.35	0.59
24:A:1474:A:H5''	35:Y:121:VAL:HG13	1.84	0.59
44:k:130:VAL:HA	45:m:36:ARG:HH22	1.68	0.59
17:P:86:LYS:NZ	17:P:122:SER:O	2.34	0.58
18:I:132:LYS:NZ	24:A:1021:U:OP1	2.36	0.58
42:f:27:ALA:HB2	42:f:52:LEU:HD22	1.84	0.58
56:j:296:ASP:OD2	57:g:782:GLN:NE2	2.35	0.58
19:x:378:ASP:HB2	19:x:393:ILE:H	1.68	0.58
24:A:922:A:OP2	31:J:28:ARG:NH1	2.36	0.58
5:u:51:MET:HB3	5:u:89:VAL:HG21	1.85	0.58
57:g:938:LEU:O	57:g:942:ILE:N	2.35	0.58
2:1:291:GLY:HA3	2:1:363:GLU:H	1.67	0.58
24:A:844:U:OP1	26:C:240:ARG:NH2	2.36	0.58
43:i:16:GLN:O	43:i:27:ARG:NH1	2.37	0.58
57:g:933:GLU:HA	57:g:978:MET:HE1	1.85	0.58
26:C:204:SER:OG	26:C:205:PHE:N	2.37	0.58
5:u:230:LEU:HD12	5:u:256:ILE:HG23	1.86	0.58
14:O:214:LYS:NZ	24:A:943:U:OP1	2.37	0.58
15:N:80:ARG:NH2	15:N:82:THR:OG1	2.36	0.58
24:A:537:C:O2	24:A:546:G:N2	2.35	0.58
24:A:615:C:H5'	49:q:62:ARG:HH22	1.69	0.58
7:S:168:LYS:O	24:A:67:C:N4	2.36	0.58
10:G:145:ARG:NH2	31:J:49:GLU:OE2	2.36	0.58
19:x:31:GLN:OE1	19:x:67:SER:N	2.36	0.58
31:J:80:ASP:N	31:J:80:ASP:OD1	2.37	0.58
32:R:101:ILE:HD12	32:R:190:LEU:HD11	1.85	0.58
35:Y:31:LEU:HD11	35:Y:33:LYS:HE2	1.85	0.58
41:e:51:ASP:OD1	41:e:51:ASP:N	2.30	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:o:273:ASP:HA	47:o:280:LYS:HE2	1.84	0.58
13:L:76:LYS:NZ	13:L:80:GLU:OE1	2.36	0.58
14:O:139:CYS:SG	14:O:140:VAL:N	2.76	0.58
24:A:54:A:H5'	33:T:108:LYS:HZ3	1.67	0.58
44:k:132:MET:HG2	44:k:141:CYS:HB2	1.85	0.58
15:N:84:GLN:HG2	15:N:100:ALA:HB1	1.85	0.57
39:c:67:SER:OG	39:c:108:VAL:O	2.22	0.57
20:3:170:LEU:O	20:3:174:MET:N	2.36	0.57
33:T:80:ASP:OD1	33:T:80:ASP:N	2.36	0.57
39:c:28:PRO:O	39:c:47:ARG:NH1	2.37	0.57
5:u:201:LEU:O	5:u:233:ARG:NH2	2.37	0.57
7:S:23:LYS:HD3	7:S:41:LEU:HA	1.85	0.57
16:Q:49:ALA:HB2	17:P:117:ARG:HD2	1.86	0.57
17:P:40:THR:HG23	17:P:58:GLY:HA3	1.86	0.57
43:i:41:GLN:NE2	52:h:69:PRO:O	2.36	0.57
53:s:212:VAL:HG23	53:s:214:THR:H	1.69	0.57
56:j:350:PRO:HG3	56:j:359:ARG:HD2	1.86	0.57
2:1:548:ARG:HB2	2:1:555:PRO:HD2	1.85	0.57
5:u:561:SER:O	5:u:565:HIS:N	2.37	0.57
24:A:790:C:OP1	24:A:791:C:O2'	2.23	0.57
24:A:1285:G:OP2	45:m:61:TYR:OH	2.19	0.57
35:Y:58:LEU:HB3	35:Y:62:ARG:HD2	1.86	0.57
56:j:140:VAL:HG22	56:j:144:VAL:HB	1.87	0.57
8:y:570:LEU:HD22	8:y:612:THR:HG21	1.86	0.57
13:L:182:CYS:SG	13:L:183:LYS:N	2.77	0.57
6:v:372:VAL:HG23	6:v:384:ILE:HD13	1.85	0.57
6:v:400:PRO:HB2	8:y:848:GLU:HB3	1.86	0.57
24:A:1396:A:O2'	24:A:1398:G:N7	2.31	0.57
24:A:1606:G:O6	42:f:38:ARG:NH2	2.36	0.57
34:V:142:SER:HB2	46:n:50:VAL:HG22	1.87	0.57
5:u:21:VAL:HG21	14:O:187:LYS:HG3	1.87	0.57
7:S:170:ARG:HG3	24:A:72:C:H42	1.68	0.57
35:Y:8:GLN:HG3	35:Y:27:ARG:HE	1.68	0.57
56:j:346:ASN:ND2	56:j:374:ASN:OD1	2.37	0.57
5:u:417:GLN:HB3	5:u:420:LYS:HB3	1.85	0.57
8:y:722:GLU:OE1	8:y:742:LYS:NZ	2.37	0.57
24:A:831:G:N7	33:T:11:LYS:NZ	2.49	0.57
24:A:1566:G:OP2	40:d:102:ARG:NH1	2.38	0.57
38:b:108:LYS:HB2	38:b:111:MET:HE3	1.85	0.57
6:v:246:ILE:HD11	19:x:26:ARG:HH12	1.70	0.57
8:y:147:LYS:NZ	24:A:394:G:N7	2.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:x:417:ARG:N	34:V:37:ASP:OD1	2.35	0.57
24:A:201:C:H5''	24:A:202:G:H21	1.70	0.57
8:y:52:ALA:HA	8:y:55:LYS:HE2	1.86	0.57
34:V:71:ARG:NH1	34:V:148:ASN:OD1	2.38	0.57
56:j:160:GLY:HA2	56:j:195:GLN:HG2	1.87	0.57
12:K:1:MET:HE3	13:L:166:ARG:HH11	1.68	0.56
24:A:643:A:OP1	27:D:38:ARG:NH1	2.38	0.56
2:1:525:TYR:OH	2:1:548:ARG:NH2	2.38	0.56
6:v:405:ILE:HG12	8:y:855:LEU:HD21	1.88	0.56
14:O:59:SER:OG	14:O:63:LYS:NZ	2.34	0.56
19:x:44:ASP:OD1	19:x:47:GLY:N	2.38	0.56
24:A:948:C:H2'	24:A:949:G:H8	1.70	0.56
56:j:45:ARG:NH1	57:g:981:ASP:OD1	2.30	0.56
6:v:208:LEU:HD21	6:v:246:ILE:HB	1.87	0.56
53:s:296:ARG:HH11	54:w:70:C:H5	1.51	0.56
7:S:188:LYS:NZ	24:A:142:C:OP2	2.38	0.56
8:y:602:ASP:OD1	8:y:602:ASP:N	2.38	0.56
26:C:102:ILE:HD12	26:C:239:PRO:HD3	1.88	0.56
34:V:122:ARG:HD2	46:n:57:THR:HG21	1.87	0.56
40:d:35:ASP:N	40:d:35:ASP:OD1	2.36	0.56
56:j:235:LEU:HD21	56:j:237:LYS:HE3	1.88	0.56
56:j:302:MET:HE2	56:j:326:LEU:HD11	1.87	0.56
5:u:109:GLN:HA	5:u:112:VAL:HG12	1.87	0.56
24:A:546:G:N2	24:A:547:G:O6	2.39	0.56
7:S:74:ARG:NH1	7:S:96:SER:OG	2.38	0.56
36:Z:225:GLU:OE2	36:Z:227:LYS:NZ	2.39	0.56
37:a:15:LEU:HD22	37:a:49:MET:HE1	1.87	0.56
53:s:212:VAL:HG13	53:s:216:LYS:HE3	1.86	0.56
5:u:319:SER:HB3	5:u:379:VAL:HB	1.88	0.56
10:G:154:ILE:HB	10:G:185:VAL:HG12	1.86	0.56
13:L:168:GLY:N	13:L:179:THR:O	2.39	0.56
19:x:34:SER:OG	19:x:57:ASN:ND2	2.38	0.56
24:A:1839:U:O4'	24:A:1863:A:N6	2.37	0.56
30:r:52:SER:HA	30:r:88:ARG:HB3	1.87	0.56
22:7:7:A:H5''	22:7:8:A:H5'	1.87	0.56
39:c:90:TRP:HA	39:c:97:THR:HA	1.88	0.56
49:q:36:ALA:H	49:q:52:PHE:HB3	1.70	0.56
53:s:182:ARG:O	53:s:186:ILE:N	2.39	0.56
55:t:167:GLN:O	55:t:169:GLN:N	2.34	0.56
24:A:1203:G:H2'	24:A:1204:A:C8	2.40	0.56
16:Q:25:ASN:ND2	16:Q:77:CYS:SG	2.79	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:1275:G:O4'	24:A:1506:A:N6	2.38	0.55
2:1:682:TRP:HA	2:1:693:LYS:HA	1.88	0.55
19:x:479:GLN:NE2	34:V:30:ILE:O	2.39	0.55
24:A:553:U:O4	24:A:555:A:N6	2.39	0.55
30:r:86:SER:OG	30:r:87:LYS:N	2.38	0.55
17:P:57:THR:HG22	17:P:59:GLY:H	1.69	0.55
24:A:545:A:O2'	24:A:546:G:O4'	2.23	0.55
24:A:1656:G:H1	24:A:1668:U:H3	1.54	0.55
24:A:1757:G:H8	24:A:1777:G:H1	1.54	0.55
39:c:79:LEU:HD11	39:c:87:LEU:HD23	1.87	0.55
39:c:272:GLN:NE2	39:c:284:PRO:O	2.39	0.55
56:j:299:VAL:HA	56:j:325:VAL:HB	1.88	0.55
56:j:304:GLY:O	56:j:311:ARG:NH2	2.39	0.55
24:A:1522:A:OP1	42:f:144:ARG:NH2	2.32	0.55
5:u:270:GLN:HB2	5:u:306:MET:HE1	1.89	0.55
7:S:170:ARG:NH1	24:A:71:G:O6	2.40	0.55
8:y:735:GLU:HA	8:y:738:VAL:HG12	1.87	0.55
24:A:588:G:H4'	24:A:589:G:H5'	1.87	0.55
24:A:1551:U:OP1	36:Z:9:ARG:NH2	2.40	0.55
37:a:24:LYS:O	37:a:42:ASN:ND2	2.37	0.55
24:A:1609:C:H5''	42:f:131:VAL:HG22	1.89	0.55
56:j:324:ARG:NH2	57:g:808:GLU:OE1	2.40	0.55
5:u:337:ASP:OD1	5:u:337:ASP:N	2.40	0.55
5:u:544:GLN:O	5:u:548:GLU:N	2.40	0.55
17:P:54:CYS:SG	17:P:55:ARG:N	2.79	0.55
24:A:641:A:OP1	27:D:40:LYS:NZ	2.38	0.55
30:r:46:ILE:HG12	30:r:85:LEU:HB2	1.89	0.55
24:A:1454:A:O4'	51:M:3:ARG:NH2	2.40	0.55
27:D:170:PRO:O	27:D:175:ARG:NH1	2.40	0.55
11:H:30:SER:OG	11:H:31:TYR:N	2.38	0.55
40:d:73:GLY:O	40:d:94:ARG:NH1	2.39	0.55
4:4:263:ILE:O	4:4:265:LEU:N	2.40	0.54
6:v:205:LEU:HB2	19:x:23:GLU:HG2	1.87	0.54
19:x:307:ASN:HA	19:x:312:LEU:HD13	1.87	0.54
24:A:1226:G:N1	24:A:1639:G:OP2	2.34	0.54
39:c:146:SER:OG	39:c:147:HIS:N	2.40	0.54
51:M:106:LEU:HB3	51:M:111:PHE:HB2	1.89	0.54
6:v:263:THR:HG21	6:v:328:CYS:HB2	1.89	0.54
24:A:1232:U:H2'	24:A:1233:G:C8	2.42	0.54
24:A:1473:G:N1	24:A:1476:A:OP2	2.38	0.54
39:c:124:SER:OG	39:c:126:ASP:OD2	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:544:PHE:HB2	2:1:559:VAL:HB	1.90	0.54
5:u:329:ILE:O	5:u:434:ASN:ND2	2.39	0.54
5:u:481:GLN:O	5:u:494:GLY:N	2.40	0.54
6:v:262:ILE:O	6:v:335:ASN:ND2	2.39	0.54
24:A:1422:G:O2'	24:A:1424:G:OP2	2.26	0.54
42:f:98:VAL:HG11	42:f:106:LYS:HG3	1.90	0.54
45:m:50:CYS:HB2	45:m:110:VAL:HG12	1.88	0.54
5:u:300:TYR:HD2	5:u:376:ARG:HH12	1.54	0.54
8:y:694:GLU:OE2	8:y:715:HIS:NE2	2.40	0.54
12:K:43:THR:HG1	12:K:45:ARG:HH21	1.53	0.54
17:P:99:ALA:H	17:P:133:THR:HG22	1.72	0.54
24:A:198:U:O2	24:A:202:G:N2	2.39	0.54
24:A:1599:U:OP2	41:e:46:ASN:ND2	2.40	0.54
24:A:1613:G:OP2	38:b:39:ALA:N	2.41	0.54
36:Z:109:LEU:HD12	36:Z:184:ILE:HD11	1.90	0.54
42:f:20:ILE:HD13	42:f:30:ILE:HG22	1.89	0.54
8:y:144:LYS:HE3	24:A:367:U:H3	1.73	0.54
15:N:140:VAL:HG13	15:N:142:LEU:HG	1.88	0.54
30:r:104:LYS:O	30:r:107:THR:OG1	2.25	0.54
1:2:125:PHE:HA	1:2:139:TYR:H	1.71	0.54
1:2:210:ASN:HA	1:2:231:PRO:HA	1.89	0.54
6:v:349:GLN:OE1	6:v:393:MET:N	2.36	0.54
16:Q:34:LYS:NZ	24:A:1860:A:N7	2.56	0.54
56:j:259:LYS:NZ	56:j:348:ASP:OD2	2.40	0.54
7:S:159:ARG:NH2	7:S:171:THR:O	2.41	0.54
12:K:16:LYS:NZ	13:L:256:TRP:O	2.41	0.54
39:c:107:ASP:N	39:c:107:ASP:OD1	2.41	0.54
48:p:99:GLU:HG2	48:p:100:ILE:HG13	1.90	0.54
49:q:84:TYR:HB2	49:q:88:LYS:HB2	1.90	0.54
55:t:85:ASN:HA	55:t:131:SER:HA	1.90	0.54
24:A:1424:G:H2'	24:A:1425:G:H8	1.73	0.54
44:k:127:GLY:O	45:m:44:LYS:NZ	2.41	0.54
45:m:46:GLN:OE1	45:m:112:LYS:NZ	2.32	0.54
48:p:55:ASP:OD1	48:p:55:ASP:N	2.40	0.54
8:y:831:LEU:HD21	8:y:846:ARG:HB2	1.89	0.53
16:Q:58:VAL:HG21	17:P:28:PHE:HZ	1.73	0.53
24:A:326:C:O2	24:A:328:U:N3	2.38	0.53
24:A:1237:C:O2'	24:A:1522:A:N1	2.41	0.53
42:f:60:THR:OG1	42:f:61:GLU:N	2.41	0.53
55:t:442:ALA:HA	55:t:456:TRP:HA	1.90	0.53
14:O:57:ILE:HG23	14:O:59:SER:H	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:1230:C:HO2'	24:A:1665:G:H1	1.54	0.53
53:s:231:ARG:NE	53:s:274:TYR:OH	2.40	0.53
5:u:558:LEU:O	5:u:562:ARG:N	2.42	0.53
8:y:589:MET:O	8:y:595:GLN:NE2	2.41	0.53
10:G:98:ARG:HG3	24:A:913:A:C6	2.44	0.53
13:L:206:SER:OG	13:L:207:ALA:N	2.41	0.53
28:E:98:ASP:OD1	28:E:140:ARG:NH2	2.41	0.53
30:r:111:ILE:O	30:r:179:ASN:ND2	2.40	0.53
19:x:76:ASP:N	19:x:76:ASP:OD1	2.42	0.53
21:5:210:GLU:O	21:5:214:PHE:N	2.41	0.53
27:D:18:ARG:O	27:D:24:ARG:NH1	2.41	0.53
42:f:38:ARG:O	42:f:42:HIS:ND1	2.30	0.53
56:j:277:ILE:HG12	56:j:345:ILE:HD12	1.91	0.53
5:u:408:THR:HA	5:u:411:LEU:HB2	1.89	0.53
19:x:169:GLU:O	19:x:521:SER:N	2.41	0.53
44:k:124:ASP:OD1	44:k:124:ASP:N	2.38	0.53
46:n:21:THR:OG1	46:n:22:GLY:N	2.42	0.53
7:S:137:ARG:NH2	24:A:146:G:O6	2.40	0.53
8:y:511:TYR:OH	8:y:611:ARG:NH1	2.42	0.53
8:y:781:ARG:HH11	8:y:817:THR:HG21	1.72	0.53
39:c:149:GLU:OE2	51:M:23:ARG:NH1	2.41	0.53
7:S:44:GLU:HG3	7:S:45:TRP:HD1	1.73	0.53
11:H:20:LYS:NZ	24:A:1016:U:OP2	2.41	0.53
20:3:151:GLN:O	20:3:189:ILE:N	2.39	0.53
8:y:358:VAL:HG21	8:y:378:ILE:HD11	1.90	0.53
8:y:449:GLU:OE2	8:y:501:ARG:NH1	2.41	0.53
14:O:182:LYS:O	14:O:186:ASN:ND2	2.41	0.53
15:N:184:ARG:HH11	15:N:191:ARG:HD3	1.74	0.53
20:3:81:ASP:O	20:3:85:CYS:N	2.39	0.53
24:A:982:G:H2'	24:A:983:A:C8	2.44	0.53
24:A:1406:G:H21	24:A:1443:C:H42	1.57	0.53
26:C:199:GLU:OE2	26:C:209:HIS:NE2	2.42	0.53
5:u:548:GLU:O	5:u:552:LEU:N	2.35	0.53
24:A:1245:G:H2'	24:A:1246:A:C8	2.43	0.53
24:A:1597:C:OP2	41:e:85:ARG:NH2	2.41	0.53
26:C:182:MET:HB2	26:C:228:ILE:HD13	1.90	0.53
38:b:73:PRO:HG2	38:b:92:SER:HA	1.91	0.53
6:v:304:ASP:OD1	6:v:304:ASP:N	2.42	0.52
14:O:175:GLU:OE1	14:O:187:LYS:NZ	2.41	0.52
18:I:114:ARG:NH1	24:A:996:A:OP1	2.36	0.52
8:y:330:ILE:O	8:y:334:ASN:ND2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:x:426:LYS:HE2	46:n:38:THR:HA	1.90	0.52
24:A:585:C:H2'	24:A:586:G:C8	2.45	0.52
24:A:1171:G:O2'	24:A:1187:G:O6	2.27	0.52
43:i:40:ARG:NH2	52:h:69:PRO:O	2.42	0.52
44:k:116:ARG:NH1	44:k:120:GLU:OE2	2.41	0.52
24:A:1416:C:OP1	40:d:129:ARG:NE	2.42	0.52
30:r:14:PRO:HG3	30:r:36:LEU:HD21	1.91	0.52
5:u:564:GLU:HA	5:u:567:ARG:HB2	1.92	0.52
7:S:78:SER:HB3	7:S:92:ARG:HG2	1.92	0.52
24:A:539:C:H41	24:A:542:U:H5''	1.75	0.52
7:S:134:GLY:O	24:A:65:C:N4	2.40	0.52
14:O:73:ASP:OD2	17:P:128:ARG:NH1	2.43	0.52
24:A:1657:G:H1	24:A:1667:U:H3	1.56	0.52
7:S:92:ARG:O	24:A:453:C:O2'	2.22	0.52
17:P:141:ARG:NH1	24:A:1856:C:OP1	2.42	0.52
35:Y:146:ARG:NH2	54:w:34:A:OP2	2.42	0.52
7:S:12:CYS:SG	7:S:13:GLN:N	2.82	0.52
5:u:443:VAL:HG22	5:u:447:TYR:HB2	1.91	0.52
19:x:25:PHE:O	19:x:26:ARG:NE	2.43	0.52
20:3:36:GLN:HA	20:3:41:ALA:HB3	1.91	0.52
24:A:1550:G:O2'	24:A:1558:C:O2	2.28	0.52
49:q:80:GLY:N	49:q:90:ASP:O	2.42	0.52
10:G:184:ASP:OD1	10:G:184:ASP:N	2.42	0.52
18:I:76:LYS:NZ	24:A:871:U:OP2	2.39	0.52
24:A:1302:G:N2	24:A:1305:C:OP2	2.43	0.52
24:A:1398:G:O2'	39:c:88:ARG:NH2	2.43	0.52
5:u:564:GLU:O	5:u:568:ILE:N	2.39	0.52
6:v:347:ILE:HG23	8:y:826:ILE:HD12	1.91	0.52
13:L:254:ASP:N	13:L:254:ASP:OD1	2.41	0.52
38:b:60:LEU:HD11	38:b:89:MET:HE3	1.92	0.52
23:9:24:SER:OG	24:A:1719:A:OP1	2.28	0.51
24:A:1672:U:OP1	35:Y:18:THR:OG1	2.23	0.51
56:j:272:ILE:O	56:j:324:ARG:NH2	2.42	0.51
57:g:984:ASP:O	57:g:988:SER:N	2.38	0.51
2:1:481:PHE:HB2	2:1:494:THR:HB	1.92	0.51
7:S:178:ARG:NH1	24:A:145:G:O6	2.40	0.51
8:y:339:ALA:HA	8:y:342:LYS:HD2	1.92	0.51
19:x:479:GLN:OE1	34:V:36:GLN:NE2	2.44	0.51
24:A:373:G:OP1	25:B:137:THR:OG1	2.28	0.51
24:A:1082:A:HO2'	24:A:1842:C:HO2'	1.56	0.51
13:L:183:LYS:HG2	13:L:196:ILE:HA	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:T:117:VAL:HG21	33:T:125:VAL:HG21	1.93	0.51
5:u:112:VAL:HA	5:u:115:ILE:HB	1.92	0.51
8:y:358:VAL:HG22	8:y:374:ILE:HG13	1.92	0.51
12:K:80:SER:OG	12:K:81:LYS:N	2.44	0.51
13:L:70:VAL:HG11	13:L:93:ILE:HG23	1.92	0.51
19:x:481:ASN:ND2	46:n:36:ASP:OD1	2.43	0.51
53:s:289:THR:HB	53:s:300:LEU:HD11	1.93	0.51
2:1:616:TRP:HA	2:1:623:VAL:HA	1.91	0.51
3:6:204:ALA:O	3:6:208:ILE:N	2.43	0.51
13:L:196:ILE:HB	13:L:223:TYR:HB2	1.91	0.51
15:N:136:GLU:OE2	24:A:1378:A:N6	2.43	0.51
24:A:818:A:OP1	27:D:80:ARG:NH2	2.42	0.51
36:Z:86:LEU:O	47:o:307:HIS:ND1	2.34	0.51
11:H:34:ASP:OD2	11:H:82:LYS:NZ	2.35	0.51
24:A:1055:A:N6	24:A:1061:U:OP2	2.43	0.51
35:Y:62:ARG:HD3	35:Y:108:ILE:HG22	1.93	0.51
56:j:105:VAL:HG11	56:j:116:ILE:HG21	1.92	0.51
10:G:31:GLU:HA	10:G:40:LEU:HD23	1.91	0.51
17:P:147:ARG:HH21	24:A:1854:U:H3'	1.75	0.51
24:A:1060:A:O2'	24:A:1062:A:N7	2.38	0.51
25:B:135:SER:OG	25:B:136:LYS:N	2.43	0.51
1:2:267:ALA:N	1:2:281:VAL:O	2.40	0.51
7:S:3:LEU:HB3	7:S:5:ILE:HD11	1.93	0.51
14:O:32:ASP:HA	14:O:46:LYS:HA	1.91	0.51
16:Q:87:ARG:NH2	16:Q:91:ALA:O	2.44	0.51
24:A:681:U:H4'	28:E:9:THR:HG22	1.93	0.51
47:o:243:VAL:HB	47:o:283:ALA:HB3	1.93	0.51
6:v:265:LYS:NZ	6:v:335:ASN:OD1	2.36	0.51
8:y:601:ALA:O	8:y:606:GLN:NE2	2.44	0.51
24:A:1734:G:O2'	24:A:1800:A:N6	2.44	0.51
33:T:29:HIS:NE2	33:T:69:THR:OG1	2.43	0.51
34:V:125:SER:HA	34:V:138:ALA:HA	1.93	0.51
47:o:250:THR:O	47:o:251:ARG:NH1	2.42	0.51
8:y:50:ARG:HH21	8:y:55:LYS:HD2	1.75	0.51
19:x:301:ASP:HB3	19:x:309:PRO:HD3	1.93	0.51
24:A:476:A:N3	24:A:488:U:O2'	2.39	0.51
25:B:66:VAL:HG11	25:B:141:ASN:HD22	1.76	0.51
34:V:35:LEU:HD22	34:V:147:VAL:HG23	1.92	0.51
54:w:22:C:H2'	54:w:23:G:H8	1.76	0.51
2:1:509:LEU:HD21	2:1:532:ARG:HD2	1.93	0.50
8:y:333:LEU:HD13	8:y:374:ILE:HG22	1.91	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:323:C:O2'	24:A:328:U:O4	2.29	0.50
16:Q:6:ARG:NH1	24:A:1147:C:OP1	2.45	0.50
23:9:1:MET:HB2	24:A:1706:G:H5'	1.93	0.50
24:A:1360:U:O2'	24:A:1379:A:OP2	2.25	0.50
24:A:1605:G:N1	24:A:1633:A:OP2	2.37	0.50
24:A:1813:A:H3'	24:A:1814:G:H8	1.77	0.50
47:o:241:ILE:HD13	47:o:314:TRP:HA	1.92	0.50
49:q:76:ILE:HG23	49:q:95:TYR:HB2	1.92	0.50
56:j:30:ILE:HG23	56:j:60:GLN:HB3	1.93	0.50
2:1:518:HIS:HB2	2:1:527:CYS:HB2	1.93	0.50
5:u:567:ARG:HB3	5:u:572:ARG:HA	1.93	0.50
24:A:482:G:N1	24:A:485:A:OP2	2.38	0.50
37:a:29:MET:HB3	37:a:42:ASN:HB2	1.92	0.50
45:m:121:LYS:O	45:m:125:GLU:N	2.35	0.50
54:w:22:C:H2'	54:w:23:G:C8	2.46	0.50
6:v:373:ASN:O	6:v:377:ASN:ND2	2.45	0.50
8:y:468:GLU:HA	8:y:471:GLU:HB2	1.93	0.50
11:H:20:LYS:HG3	11:H:21:LYS:HG2	1.93	0.50
5:u:398:PHE:O	5:u:442:GLN:NE2	2.45	0.50
18:I:133:ARG:HH22	25:B:150:GLY:HA3	1.76	0.50
24:A:10:G:H2'	24:A:11:A:H8	1.76	0.50
24:A:848:U:H2'	24:A:849:A:H8	1.75	0.50
57:g:894:ARG:O	57:g:898:ASN:N	2.39	0.50
57:g:923:LEU:HB3	57:g:935:LEU:HD13	1.94	0.50
5:u:520:ARG:HA	5:u:523:LEU:HD12	1.94	0.50
24:A:1531:A:OP1	40:d:84:ARG:NH2	2.45	0.50
26:C:115:THR:HG22	26:C:117:GLU:H	1.77	0.50
34:V:140:ASP:HB2	46:n:46:VAL:HG12	1.94	0.50
38:b:81:ARG:NH2	38:b:117:GLY:O	2.44	0.50
39:c:20:GLN:HG2	39:c:69:VAL:H	1.76	0.50
39:c:88:ARG:HH11	39:c:97:THR:HG21	1.75	0.50
48:p:48:GLN:HA	48:p:82:VAL:HG12	1.93	0.50
56:j:39:LEU:HD12	56:j:44:LEU:HD13	1.93	0.50
2:1:342:TRP:HA	2:1:349:LEU:HA	1.94	0.50
3:6:322:TYR:HB3	3:6:332:VAL:HA	1.93	0.50
24:A:1708:C:H2'	24:A:1709:G:H8	1.76	0.50
7:S:198:ARG:NE	24:A:126:G:OP1	2.41	0.50
10:G:149:ASP:OD1	10:G:149:ASP:N	2.45	0.50
39:c:35:SER:OG	39:c:36:ARG:N	2.45	0.50
5:u:80:GLN:HA	5:u:83:ILE:HB	1.93	0.50
16:Q:28:ARG:NH1	16:Q:29:CYS:O	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:197:U:H5	24:A:203:G:H1'	1.76	0.50
24:A:1708:C:H2'	24:A:1709:G:C8	2.47	0.50
34:V:124:ASP:HB2	34:V:141:VAL:HG22	1.92	0.50
57:g:764:VAL:HG21	57:g:797:VAL:HG22	1.93	0.50
3:6:326:ASP:OD1	3:6:326:ASP:N	2.42	0.49
3:6:344:LYS:HG3	3:6:351:TYR:HE2	1.76	0.49
5:u:179:GLN:NE2	5:u:231:GLU:OE1	2.44	0.49
5:u:387:VAL:HG12	5:u:410:VAL:HB	1.92	0.49
24:A:1622:U:OP1	42:f:120:HIS:ND1	2.43	0.49
3:6:43:ALA:HB1	3:6:47:GLU:H	1.77	0.49
24:A:877:C:H2'	24:A:878:G:C8	2.47	0.49
24:A:1092:G:H2'	24:A:1093:A:H8	1.77	0.49
24:A:1413:G:H2'	24:A:1414:A:C8	2.46	0.49
25:B:57:ASP:OD1	25:B:84:ARG:NH1	2.46	0.49
28:E:124:LYS:HG2	28:E:129:SER:HA	1.94	0.49
30:r:71:VAL:HG21	30:r:85:LEU:HD13	1.94	0.49
37:a:9:ILE:HG12	37:a:82:TYR:HE1	1.77	0.49
38:b:28:MET:HB2	38:b:32:GLN:HB2	1.94	0.49
39:c:236:ILE:HG12	39:c:252:THR:HG22	1.94	0.49
18:I:142:GLU:HB3	18:I:145:THR:HG22	1.94	0.49
19:x:195:CYS:HA	19:x:359:ARG:HA	1.92	0.49
24:A:534:G:N2	24:A:550:C:O2	2.45	0.49
27:D:107:GLU:O	27:D:113:GLN:NE2	2.39	0.49
14:O:52:THR:HG22	14:O:58:ALA:H	1.77	0.49
18:I:63:VAL:HG11	18:I:71:ILE:HG13	1.94	0.49
24:A:1445:U:H4'	52:h:57:PRO:HG3	1.94	0.49
25:B:75:GLY:HA3	25:B:88:ILE:HD12	1.94	0.49
39:c:83:TRP:HA	39:c:107:ASP:HB3	1.94	0.49
47:o:246:LEU:HD22	47:o:250:THR:HG21	1.93	0.49
57:g:892:ARG:NH1	57:g:928:ASP:OD2	2.45	0.49
57:g:977:PHE:O	57:g:981:ASP:N	2.34	0.49
5:u:319:SER:HA	5:u:322:VAL:HG12	1.93	0.49
6:v:208:LEU:HG	6:v:242:TYR:HD1	1.77	0.49
20:3:8:ARG:O	20:3:12:GLY:N	2.38	0.49
24:A:980:A:H2'	24:A:981:A:C8	2.47	0.49
24:A:1415:C:OP1	40:d:129:ARG:NH2	2.46	0.49
36:Z:49:ILE:HD12	47:o:309:ILE:HD11	1.93	0.49
41:e:50:PHE:HB2	42:f:4:VAL:HG12	1.94	0.49
56:j:353:ARG:HG2	56:j:386:ASP:HB3	1.93	0.49
8:y:833:ALA:HB2	8:y:844:MET:HE3	1.92	0.49
14:O:70:SER:OG	14:O:71:LEU:N	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Q:58:VAL:HG13	17:P:125:LYS:HB3	1.95	0.49
24:A:874:G:H2'	24:A:875:A:H8	1.76	0.49
24:A:1531:A:H4'	24:A:1605:G:H4'	1.93	0.49
24:A:1618:C:O3'	38:b:50:ARG:NH2	2.46	0.49
24:A:1627:C:H5''	40:d:41:LYS:HD2	1.94	0.49
34:V:122:ARG:HG3	46:n:59:LEU:HD13	1.95	0.49
51:M:99:ASP:HB2	51:M:102:THR:HG22	1.95	0.49
53:s:299:PHE:HE1	53:s:308:ARG:HB3	1.78	0.49
54:w:75:A:N6	55:t:68:ARG:O	2.41	0.49
56:j:221:LEU:HA	56:j:224:THR:HB	1.94	0.49
57:g:756:LYS:HA	57:g:793:ARG:HH11	1.77	0.49
14:O:150:ILE:HG12	24:A:1124:C:H5''	1.93	0.49
36:Z:40:ARG:NH1	36:Z:47:GLU:OE1	2.44	0.49
40:d:104:LEU:HD13	40:d:121:ARG:HD2	1.94	0.49
42:f:105:ASN:OD1	42:f:108:ARG:NH1	2.46	0.49
8:y:121:TRP:HZ2	8:y:139:SER:HA	1.78	0.49
24:A:981:A:H2'	24:A:982:G:C8	2.48	0.49
24:A:1311:C:H42	44:k:97:LYS:HE3	1.78	0.49
24:A:1329:U:O2'	24:A:1332:A:OP2	2.24	0.49
30:r:16:VAL:HG22	30:r:17:GLU:HG2	1.95	0.49
38:b:23:ASP:HA	38:b:26:LEU:HD12	1.93	0.49
56:j:246:ILE:HD13	56:j:372:ALA:HB3	1.95	0.49
2:l:549:MET:HA	2:l:554:VAL:HG13	1.95	0.49
24:A:1275:G:O2'	24:A:1321:G:N2	2.39	0.49
25:B:49:GLU:HG2	25:B:118:ARG:HH12	1.78	0.49
42:f:84:LEU:HD12	42:f:95:TYR:HB3	1.94	0.49
12:K:43:THR:OG1	12:K:45:ARG:NH2	2.35	0.49
14:O:101:HIS:O	14:O:101:HIS:ND1	2.46	0.49
19:x:225:HIS:O	19:x:374:ARG:NH2	2.42	0.49
34:V:128:ILE:HD12	34:V:137:GLN:HB3	1.95	0.49
41:e:48:VAL:HG11	42:f:23:ARG:HA	1.93	0.49
45:m:26:LEU:HD22	45:m:90:GLY:HA3	1.95	0.49
56:j:180:VAL:HG22	56:j:210:VAL:HB	1.94	0.49
2:l:378:LEU:N	2:l:391:PHE:O	2.45	0.48
24:A:1617:G:N1	24:A:1620:A:OP2	2.46	0.48
25:B:21:LYS:NZ	32:R:157:LYS:O	2.36	0.48
54:w:14:A:O2'	54:w:16:C:N4	2.46	0.48
5:u:476:ARG:NH1	8:y:794:THR:OG1	2.46	0.48
24:A:1597:C:OP1	42:f:25:LYS:NZ	2.34	0.48
24:A:1758:G:H21	24:A:1775:U:H3	1.60	0.48
36:Z:195:THR:HA	36:Z:201:LYS:HE2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:a:59:LYS:HB2	37:a:70:TYR:HB2	1.94	0.48
57:g:924:LEU:HD13	57:g:958:TYR:HD1	1.77	0.48
5:u:23:LYS:HB3	5:u:26:PRO:HD2	1.96	0.48
6:v:261:VAL:HG23	6:v:262:ILE:HG13	1.96	0.48
8:y:643:LYS:HG3	8:y:650:LEU:HB2	1.94	0.48
10:G:60:ILE:HB	10:G:92:VAL:HG23	1.94	0.48
12:K:64:GLU:HG3	15:N:33:GLN:HE21	1.78	0.48
19:x:432:LEU:HD12	19:x:476:PHE:HZ	1.78	0.48
24:A:1532:C:OP1	24:A:1604:G:O2'	2.28	0.48
57:g:932:LEU:HD22	57:g:979:LEU:HD21	1.95	0.48
7:S:202:ASN:OD1	26:C:148:ARG:NH2	2.36	0.48
8:y:857:LEU:HD13	9:8:258:VAL:HA	1.94	0.48
10:G:99:ARG:O	24:A:913:A:N6	2.47	0.48
18:I:14:SER:HB2	24:A:1016:U:H5''	1.96	0.48
19:x:322:ASN:OD1	19:x:323:PHE:N	2.46	0.48
24:A:10:G:H2'	24:A:11:A:C8	2.48	0.48
24:A:1255:G:OP1	24:A:1256:G:O2'	2.28	0.48
30:r:209:LYS:O	30:r:213:ARG:N	2.44	0.48
54:w:15:G:H1'	54:w:21:G:H1'	1.96	0.48
13:L:144:SER:HB3	13:L:150:ALA:HB2	1.95	0.48
15:N:85:ARG:NH2	15:N:201:LEU:O	2.46	0.48
24:A:677:G:N1	24:A:1027:A:OP2	2.30	0.48
24:A:1741:U:OP1	32:R:42:ARG:NH1	2.45	0.48
53:s:231:ARG:HA	53:s:291:LEU:HD21	1.94	0.48
2:1:380:ASP:N	2:1:389:VAL:O	2.40	0.48
10:G:58:LYS:HE2	10:G:90:LYS:HE2	1.96	0.48
19:x:405:ASN:HD21	46:n:15:THR:HG23	1.78	0.48
24:A:874:G:H2'	24:A:875:A:C8	2.48	0.48
39:c:245:ARG:NH1	39:c:295:GLY:O	2.46	0.48
6:v:93:LYS:O	6:v:97:ASP:N	2.47	0.48
8:y:78:LYS:HA	8:y:81:GLU:HG2	1.94	0.48
8:y:763:GLY:HA2	8:y:767:ASP:HB2	1.95	0.48
10:G:105:THR:HG23	10:G:107:LYS:H	1.79	0.48
24:A:96:C:O2	24:A:473:A:O2'	2.32	0.48
24:A:746:C:N4	24:A:797:C:O2	2.46	0.48
39:c:167:SER:OG	39:c:177:TRP:NE1	2.44	0.48
44:k:106:TYR:HA	44:k:116:ARG:HA	1.95	0.48
2:1:546:ILE:O	2:1:557:ASP:N	2.34	0.48
7:S:167:LYS:NZ	24:A:70:G:OP2	2.34	0.48
8:y:146:ARG:O	8:y:150:ARG:NE	2.46	0.48
10:G:47:ALA:HB3	10:G:63:PHE:HD1	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:123:ARG:HD2	13:L:145:LYS:HE2	1.96	0.48
24:A:747:U:H2'	24:A:748:C:C2	2.49	0.48
24:A:1233:G:N3	24:A:1252:C:O2'	2.41	0.48
24:A:1712:A:H2'	24:A:1713:C:C6	2.48	0.48
30:r:22:VAL:HG23	30:r:36:LEU:HA	1.94	0.48
30:r:104:LYS:HD3	30:r:150:TYR:HB2	1.95	0.48
32:R:66:SER:HA	32:R:73:THR:HA	1.94	0.48
17:P:60:MET:HE3	24:A:955:A:H4'	1.96	0.48
23:9:15:ARG:NH1	24:A:1183:A:OP1	2.47	0.48
24:A:45:A:N1	24:A:480:G:O2'	2.43	0.48
24:A:1113:A:O2'	24:A:1114:U:O4'	2.28	0.48
33:T:5:VAL:O	33:T:43:LYS:NZ	2.45	0.48
39:c:209:SER:OG	39:c:219:TRP:NE1	2.38	0.48
45:m:45:ARG:HG2	45:m:72:HIS:CD2	2.49	0.48
57:g:798:ILE:HG22	57:g:846:ARG:HG2	1.94	0.48
24:A:1010:G:H2'	24:A:1011:A:C8	2.49	0.48
57:g:755:SER:N	57:g:789:ASP:OD1	2.47	0.48
16:Q:2:THR:OG1	16:Q:3:LYS:N	2.47	0.47
24:A:925:G:N2	24:A:1017:U:O2	2.36	0.47
24:A:1398:G:H22	24:A:1448:A:H2	1.62	0.47
24:A:1452:A:O2'	24:A:1475:G:N2	2.47	0.47
40:d:60:THR:HA	40:d:63:HIS:HB2	1.96	0.47
55:t:441:ILE:O	55:t:457:GLY:N	2.47	0.47
3:6:154:TRP:O	3:6:158:THR:N	2.41	0.47
20:3:9:ALA:O	20:3:13:LYS:N	2.42	0.47
13:L:199:PRO:HG2	13:L:202:THR:HG21	1.96	0.47
24:A:533:A:H2'	24:A:534:G:C8	2.50	0.47
24:A:1603:G:OP1	42:f:24:ARG:NH2	2.46	0.47
30:r:45:MET:HE3	30:r:45:MET:HB2	1.75	0.47
41:e:98:LYS:O	41:e:110:THR:N	2.46	0.47
56:j:241:LEU:HA	56:j:363:GLY:HA3	1.95	0.47
37:a:11:ILE:HA	37:a:35:LEU:HD11	1.96	0.47
6:v:331:ASP:N	6:v:331:ASP:OD1	2.48	0.47
9:8:235:SER:O	9:8:240:GLY:N	2.37	0.47
42:f:28:PHE:HE2	42:f:38:ARG:HD3	1.79	0.47
45:m:24:THR:HA	45:m:27:ILE:HG12	1.97	0.47
51:M:120:THR:OG1	51:M:121:GLN:N	2.46	0.47
5:u:685:GLN:O	5:u:689:LYS:N	2.48	0.47
17:P:34:PHE:O	17:P:41:PHE:N	2.47	0.47
24:A:70:G:N2	24:A:80:G:O6	2.48	0.47
24:A:1754:G:H2'	24:A:1755:C:H4'	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:e:63:PRO:HG2	41:e:96:LEU:HD23	1.96	0.47
57:g:899:ILE:HG21	57:g:923:LEU:HD21	1.96	0.47
3:6:184:VAL:O	3:6:188:LEU:N	2.44	0.47
5:u:171:GLU:HA	5:u:174:TYR:HB3	1.97	0.47
5:u:572:ARG:NH2	9:8:209:HIS:O	2.36	0.47
7:S:186:GLN:OE1	24:A:319:C:N4	2.47	0.47
10:G:43:LEU:HD22	10:G:72:PHE:HD1	1.80	0.47
13:L:172:ASN:OD1	13:L:172:ASN:N	2.47	0.47
14:O:62:LEU:O	14:O:88:THR:OG1	2.24	0.47
18:I:133:ARG:NH1	25:B:150:GLY:O	2.48	0.47
24:A:1827:U:OP1	48:p:41:ARG:NH2	2.47	0.47
32:R:103:LEU:HD22	32:R:170:LYS:HB3	1.95	0.47
39:c:183:LYS:HA	39:c:183:LYS:HD3	1.68	0.47
39:c:256:ILE:HD13	39:c:289:LEU:HD21	1.96	0.47
56:j:91:LEU:HB3	56:j:127:MET:HE1	1.96	0.47
5:u:484:ILE:HG13	8:y:798:VAL:HG22	1.97	0.47
14:O:72:ALA:HB3	17:P:128:ARG:HH12	1.79	0.47
24:A:1142:G:N2	24:A:1145:A:OP2	2.42	0.47
30:r:203:GLU:OE2	30:r:265:LYS:NZ	2.37	0.47
5:u:411:LEU:HD23	5:u:432:GLN:HG2	1.97	0.47
11:H:15:GLU:O	11:H:23:ARG:NE	2.37	0.47
14:O:117:TRP:HB3	14:O:153:THR:HA	1.97	0.47
18:I:121:ARG:NH1	24:A:924:G:O3'	2.48	0.47
24:A:1207:G:N2	24:A:1837:G:H2'	2.30	0.47
24:A:1455:A:OP1	51:M:5:ARG:NH1	2.45	0.47
24:A:1514:G:O2'	38:b:79:HIS:ND1	2.38	0.47
26:C:21:ASP:OD2	26:C:24:THR:OG1	2.32	0.47
51:M:98:VAL:HG13	51:M:102:THR:HG23	1.97	0.47
4:4:124:VAL:HA	4:4:129:VAL:HA	1.96	0.47
8:y:515:ASP:H	8:y:579:HIS:CE1	2.33	0.47
24:A:379:C:O2	32:R:5:ARG:NE	2.34	0.47
24:A:570:C:O2'	33:T:34:THR:O	2.30	0.47
24:A:583:A:H2'	24:A:584:A:C8	2.50	0.47
51:M:74:GLN:O	51:M:78:ARG:N	2.46	0.47
7:S:131:ARG:NE	24:A:167:G:O2'	2.48	0.46
16:Q:85:ARG:NH2	24:A:1209:A:O2'	2.48	0.46
19:x:360:TYR:HE1	19:x:374:ARG:HG3	1.78	0.46
24:A:836:G:OP1	33:T:8:ARG:NH2	2.39	0.46
24:A:1229:G:H4'	24:A:1633:A:H2	1.79	0.46
24:A:1427:C:OP1	40:d:7:LYS:NZ	2.35	0.46
32:R:203:LYS:HE3	32:R:203:LYS:HB2	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Z:96:LEU:HD13	36:Z:198:ILE:HG23	1.97	0.46
56:j:96:LEU:HD21	56:j:127:MET:HB3	1.96	0.46
5:u:500:ALA:HB1	5:u:502:ARG:HB2	1.97	0.46
8:y:422:GLU:HB3	8:y:433:ASN:HD21	1.79	0.46
13:L:222:CYS:SG	13:L:223:TYR:N	2.87	0.46
19:x:447:LEU:HB2	19:x:473:PRO:HG3	1.96	0.46
24:A:1702:G:H2'	24:A:1703:OMC:C6	2.50	0.46
39:c:155:ARG:O	39:c:166:VAL:N	2.45	0.46
42:f:26:ILE:HD13	42:f:56:ALA:HA	1.97	0.46
49:q:79:VAL:HG12	49:q:91:VAL:HG13	1.96	0.46
3:6:325:ILE:HD13	3:6:329:GLN:HB3	1.96	0.46
7:S:57:ASP:OD1	7:S:58:LYS:N	2.48	0.46
11:H:38:PRO:HD3	11:H:77:CYS:HA	1.97	0.46
16:Q:38:LYS:HB3	16:Q:71:LEU:HB2	1.98	0.46
24:A:1309:C:H1'	44:k:133:ALA:HB2	1.98	0.46
34:V:30:ILE:HG21	34:V:36:GLN:HA	1.96	0.46
47:o:302:GLY:HA2	47:o:309:ILE:HG23	1.97	0.46
5:u:411:LEU:HA	5:u:414:VAL:HB	1.97	0.46
7:S:132:ARG:NH1	24:A:151:C:O2'	2.48	0.46
24:A:161:U:H5'	33:T:116:LYS:HB3	1.96	0.46
49:q:38:VAL:HG22	49:q:41:MET:HE2	1.96	0.46
56:j:140:VAL:O	56:j:144:VAL:N	2.49	0.46
56:j:282:ARG:NH1	56:j:305:ASP:OD2	2.49	0.46
5:u:52:LEU:HD12	5:u:89:VAL:HG23	1.97	0.46
5:u:483:ARG:O	5:u:492:SER:N	2.46	0.46
19:x:397:ASN:N	19:x:397:ASN:OD1	2.48	0.46
19:x:446:TYR:OH	34:V:27:ASP:OD1	2.32	0.46
38:b:17:TYR:HB3	38:b:25:LEU:HD11	1.97	0.46
47:o:270:LEU:HD11	47:o:279:SER:HB2	1.97	0.46
48:p:75:GLU:HG3	48:p:81:GLU:HG3	1.98	0.46
57:g:854:ASP:OD1	57:g:922:LYS:NZ	2.47	0.46
6:v:246:ILE:HD13	19:x:24:GLN:HG3	1.96	0.46
8:y:792:LEU:HD21	8:y:807:LEU:HD21	1.97	0.46
10:G:123:THR:HG21	24:A:687:C:H5''	1.98	0.46
24:A:1277:C:H2'	24:A:1278:A:H8	1.81	0.46
24:A:1448:A:OP1	52:h:30:LYS:NZ	2.44	0.46
49:q:62:ARG:NH1	49:q:90:ASP:OD1	2.48	0.46
57:g:900:LYS:HA	57:g:938:LEU:HD13	1.97	0.46
7:S:134:GLY:HA3	7:S:158:VAL:HG11	1.96	0.46
17:P:78:ALA:HB1	17:P:119:LEU:HG	1.98	0.46
24:A:53:C:O2'	24:A:507:G:N7	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:1273:C:OP2	44:k:94:LYS:HE2	2.16	0.46
48:p:30:TYR:HA	48:p:107:GLN:HG3	1.98	0.46
56:j:270:LEU:HB2	56:j:402:VAL:HG12	1.98	0.46
57:g:856:ASP:HB2	57:g:922:LYS:HD2	1.98	0.46
3:6:289:ASN:HA	3:6:332:VAL:HG22	1.98	0.46
6:v:243:LEU:HB3	6:v:249:MET:SD	2.56	0.46
24:A:1643:U:H2'	24:A:1644:C:C6	2.51	0.46
34:V:16:ASP:OD1	34:V:16:ASP:N	2.49	0.46
35:Y:93:VAL:HA	35:Y:108:ILE:HD11	1.98	0.46
3:6:252:TYR:O	3:6:257:GLN:N	2.49	0.46
24:A:562:U:H4'	27:D:132:GLN:HB3	1.98	0.46
24:A:615:C:OP2	28:E:64:SER:OG	2.33	0.46
24:A:683:OMG:HM23	24:A:683:OMG:H1'	1.80	0.46
24:A:750:C:H41	24:A:793:G:H1'	1.80	0.46
39:c:32:LEU:HB2	39:c:71:ILE:HD11	1.97	0.46
39:c:118:ARG:O	39:c:134:THR:OG1	2.34	0.46
43:i:52:PHE:HB3	52:h:80:PHE:HB3	1.97	0.46
2:1:612:ASN:H	2:1:627:GLY:HA2	1.81	0.46
8:y:439:ARG:HH22	8:y:441:ARG:HH21	1.64	0.46
24:A:377:G:H5'	32:R:98:LYS:HD3	1.97	0.46
24:A:1337:C:H2'	24:A:1338:G:H8	1.81	0.46
24:A:1683:C:C2	46:n:24:GLN:HG3	2.50	0.46
32:R:110:ARG:HD3	32:R:123:ARG:HH21	1.82	0.46
35:Y:12:VAL:HG21	35:Y:91:ALA:HA	1.97	0.46
45:m:75:ASN:HB2	45:m:127:TYR:CG	2.51	0.46
4:4:329:SER:O	6:v:401:TYR:OH	2.28	0.45
15:N:183:LEU:O	15:N:187:GLY:N	2.49	0.45
18:I:69:ASN:N	18:I:69:ASN:OD1	2.47	0.45
24:A:447:A:OP1	32:R:49:ARG:NH1	2.49	0.45
24:A:1010:G:H2'	24:A:1011:A:H8	1.80	0.45
24:A:1084:A:OP1	24:A:1858:G:O2'	2.29	0.45
28:E:46:HIS:HB3	28:E:101:LEU:HD11	1.98	0.45
6:v:208:LEU:O	6:v:212:THR:N	2.48	0.45
8:y:785:GLU:HG2	8:y:813:LEU:HD11	1.96	0.45
16:Q:79:ILE:HD11	24:A:1863:A:N3	2.31	0.45
31:J:96:SER:OG	31:J:97:ARG:N	2.49	0.45
45:m:44:LYS:HB3	45:m:46:GLN:HG2	1.98	0.45
49:q:97:ALA:HA	49:q:100:ALA:HB3	1.99	0.45
53:s:214:THR:O	53:s:261:ARG:NH1	2.45	0.45
53:s:231:ARG:HH11	53:s:235:HIS:HB3	1.81	0.45
3:6:344:LYS:HA	3:6:347:TRP:HB2	1.96	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:v:385:ASP:OD2	6:v:390:HIS:N	2.49	0.45
24:A:1403:C:N4	24:A:1433:C:OP1	2.50	0.45
26:C:11:ARG:HA	26:C:28:ALA:HB2	1.99	0.45
28:E:58:GLU:OE2	49:q:60:HIS:ND1	2.49	0.45
32:R:124:LYS:HD2	32:R:124:LYS:HA	1.66	0.45
46:n:61:SER:OG	46:n:62:GLU:N	2.48	0.45
53:s:179:LEU:HA	53:s:182:ARG:HB2	1.98	0.45
54:w:13:C:H2'	54:w:14:A:H4'	1.98	0.45
2:l:437:PHE:HA	2:l:451:THR:H	1.81	0.45
3:6:131:ALA:HB3	3:6:135:GLY:HA3	1.97	0.45
5:u:567:ARG:HA	5:u:573:GLN:HG3	1.98	0.45
7:S:2:LYS:HB2	7:S:108:VAL:HG23	1.98	0.45
10:G:17:ASP:O	10:G:21:SER:N	2.44	0.45
15:N:110:ASN:HB3	15:N:113:GLN:HG3	1.98	0.45
24:A:43:U:OP2	24:A:485:A:N6	2.49	0.45
24:A:830:A:OP2	24:A:846:G:N2	2.49	0.45
38:b:111:MET:HA	42:f:117:ILE:HD11	1.99	0.45
45:m:69:CYS:SG	45:m:76:LEU:HD21	2.57	0.45
56:j:349:LEU:HD21	56:j:384:LEU:HD13	1.98	0.45
2:l:390:THR:O	2:l:405:ILE:N	2.40	0.45
5:u:515:PRO:O	5:u:520:ARG:NH2	2.49	0.45
7:S:195:LYS:NZ	24:A:126:G:OP2	2.48	0.45
8:y:318:PHE:HA	8:y:356:LEU:HD21	1.99	0.45
19:x:381:MET:HB2	19:x:391:ILE:HD13	1.98	0.45
24:A:1458:G:OP1	39:c:278:SER:OG	2.34	0.45
27:D:93:LYS:HB2	27:D:96:TYR:HD2	1.82	0.45
36:Z:93:THR:HG21	36:Z:96:LEU:HD12	1.99	0.45
36:Z:197:LYS:HE2	36:Z:197:LYS:HB2	1.81	0.45
56:j:63:ILE:HA	56:j:89:SER:HB3	1.97	0.45
3:6:316:VAL:HG23	3:6:321:VAL:HA	1.99	0.45
5:u:561:SER:HA	5:u:564:GLU:HB2	1.99	0.45
9:8:49:ILE:O	9:8:53:TYR:N	2.49	0.45
15:N:32:PHE:CD1	24:A:1097:G:H4'	2.51	0.45
24:A:1268:C:H4'	38:b:100:LYS:HG3	1.98	0.45
27:D:137:VAL:HG22	27:D:157:ILE:HG12	1.99	0.45
3:6:207:CYS:O	3:6:211:ALA:N	2.50	0.45
8:y:596:ASP:OD1	8:y:596:ASP:N	2.49	0.45
24:A:1650:A:H5''	35:Y:139:ALA:HB2	1.99	0.45
32:R:119:LEU:HD21	32:R:153:LYS:HG2	1.99	0.45
33:T:41:ARG:NH1	33:T:52:PRO:O	2.42	0.45
34:V:153:LEU:HB3	34:V:189:ALA:HB1	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Z:16:ILE:HD11	43:i:36:LEU:HD23	1.98	0.45
38:b:25:LEU:HD22	38:b:87:PRO:HG3	1.98	0.45
49:q:79:VAL:HA	49:q:91:VAL:HA	1.99	0.45
5:u:389:ASP:OD1	5:u:389:ASP:N	2.49	0.45
5:u:562:ARG:O	5:u:566:GLN:NE2	2.50	0.45
14:O:180:ASP:N	14:O:180:ASP:OD1	2.49	0.45
24:A:202:G:H5'	24:A:203:G:H5''	1.99	0.45
24:A:1261:C:O2	24:A:1618:C:N4	2.49	0.45
26:C:44:LEU:HD21	26:C:70:ILE:HG21	1.98	0.45
31:J:42:MET:HE2	31:J:42:MET:HB3	1.91	0.45
5:u:549:GLN:HA	5:u:552:LEU:HB3	1.99	0.45
16:Q:73:TYR:HB3	16:Q:78:ALA:HB2	1.98	0.45
19:x:448:LYS:HE3	19:x:448:LYS:HB3	1.72	0.45
24:A:11:A:O2'	24:A:12:U:H5'	2.16	0.45
24:A:562:U:H2'	24:A:563:G:C8	2.52	0.45
24:A:1524:G:O2'	54:w:29:G:H4'	2.17	0.45
37:a:26:ASP:OD2	37:a:29:MET:N	2.50	0.45
39:c:153:CYS:HB3	39:c:198:VAL:HG12	1.98	0.45
44:k:144:CYS:SG	44:k:146:LEU:HB2	2.57	0.45
45:m:33:ARG:HE	45:m:33:ARG:HB2	1.65	0.45
57:g:792:GLU:O	57:g:793:ARG:NH2	2.46	0.45
7:S:203:LYS:HB2	7:S:203:LYS:HE3	1.77	0.45
10:G:52:GLU:HA	10:G:58:LYS:HG3	1.99	0.45
24:A:1183:A:H2'	24:A:1184:G:H8	1.82	0.45
24:A:1221:G:H2'	24:A:1222:G:C8	2.52	0.45
35:Y:19:ALA:HB2	35:Y:75:GLY:HA3	1.98	0.45
39:c:230:LEU:HD13	39:c:259:TRP:CG	2.52	0.45
48:p:104:LYS:HD3	48:p:104:LYS:HA	1.80	0.45
5:u:416:GLU:O	5:u:425:GLN:NE2	2.50	0.44
5:u:516:SER:O	5:u:516:SER:OG	2.33	0.44
24:A:115:U:O2'	24:A:381:C:O2	2.31	0.44
24:A:383:G:O2'	25:B:133:PRO:O	2.34	0.44
24:A:1358:U:H2'	24:A:1359:U:C6	2.52	0.44
24:A:1754:G:OP1	24:A:1780:G:N1	2.47	0.44
6:v:339:PHE:HA	6:v:342:GLU:HB3	1.99	0.44
18:I:4:MET:HE3	18:I:4:MET:HB2	1.84	0.44
24:A:223:C:H2'	24:A:224:A:H8	1.82	0.44
24:A:1752:C:H6	24:A:1779:G:H1	1.64	0.44
26:C:143:ASP:OD1	26:C:143:ASP:N	2.50	0.44
30:r:127:LEU:HA	30:r:130:LEU:HB2	1.98	0.44
30:r:265:LYS:HE2	30:r:265:LYS:HB2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:f:16:LEU:HA	42:f:16:LEU:HD23	1.86	0.44
49:q:26:LEU:HG	49:q:99:GLU:HB2	2.00	0.44
15:N:52:LYS:HB3	15:N:52:LYS:HE2	1.88	0.44
17:P:78:ALA:HA	17:P:81:VAL:HG12	1.99	0.44
24:A:380:G:OP1	32:R:31:ARG:NH1	2.45	0.44
24:A:584:A:H2'	24:A:585:C:C6	2.52	0.44
24:A:678:U:OP2	24:A:1026:C:N4	2.41	0.44
24:A:897:U:N3	24:A:899:U:O4	2.50	0.44
27:D:84:ILE:HG13	27:D:86:VAL:HG13	1.99	0.44
34:V:184:SER:OG	34:V:186:ASN:OD1	2.34	0.44
36:Z:45:ARG:HD2	36:Z:85:GLU:HG3	1.99	0.44
51:M:41:ILE:HD12	51:M:47:ARG:HG2	1.99	0.44
57:g:916:MET:O	57:g:920:VAL:HG22	2.17	0.44
5:u:407:VAL:HG22	5:u:411:LEU:HD13	2.00	0.44
5:u:465:PHE:HE1	8:y:806:THR:HB	1.82	0.44
5:u:562:ARG:HA	5:u:562:ARG:HD3	1.64	0.44
16:Q:23:CYS:SG	16:Q:24:THR:N	2.90	0.44
24:A:113:G:H22	24:A:292:A:H2'	1.82	0.44
24:A:1536:G:H2'	24:A:1537:A:C8	2.53	0.44
37:a:20:VAL:HG13	37:a:93:THR:HG21	1.98	0.44
49:q:28:PHE:HD1	49:q:29:LYS:HG2	1.81	0.44
57:g:787:ALA:HB1	57:g:794:LEU:HD13	1.99	0.44
1:2:266:GLU:HA	1:2:282:LYS:HA	2.00	0.44
2:1:512:VAL:HG13	2:1:530:VAL:HG13	2.00	0.44
5:u:567:ARG:O	5:u:572:ARG:N	2.50	0.44
13:L:194:ARG:HD2	24:A:1154:U:O2'	2.18	0.44
24:A:116:OMU:H6	24:A:116:OMU:O5'	2.17	0.44
24:A:543:C:H1'	47:o:274:LYS:HE3	1.98	0.44
24:A:1705:C:H2'	24:A:1706:G:C8	2.52	0.44
3:6:286:ALA:HA	3:6:332:VAL:HG21	1.98	0.44
5:u:205:LEU:HD11	5:u:259:LEU:HD21	2.00	0.44
5:u:280:SER:OG	5:u:321:ARG:NH1	2.51	0.44
7:S:72:ARG:NH2	24:A:467:G:O5'	2.51	0.44
16:Q:84:VAL:HG12	24:A:1867:U:C4	2.53	0.44
24:A:223:C:H2'	24:A:224:A:C8	2.52	0.44
24:A:1491:G:H2'	24:A:1492:U:C6	2.53	0.44
30:r:231:ALA:HB3	30:r:234:ARG:HB3	1.99	0.44
44:k:129:GLY:HA3	45:m:40:LYS:HA	2.00	0.44
45:m:49:LEU:HB3	45:m:111:VAL:HB	1.98	0.44
56:j:105:VAL:HB	56:j:156:VAL:HG22	1.99	0.44
5:u:266:PRO:HA	5:u:267:PRO:HD3	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:u:555:THR:O	5:u:559:LYS:N	2.44	0.44
8:y:580:SER:OG	8:y:623:GLN:OE1	2.35	0.44
10:G:44:ASN:OD1	10:G:44:ASN:N	2.50	0.44
11:H:80:ARG:HB3	19:x:78:SER:HA	2.00	0.44
13:L:178:HIS:ND1	13:L:221:ASP:OD1	2.51	0.44
17:P:74:ALA:HB1	17:P:115:ALA:HB2	1.99	0.44
24:A:322:C:N4	24:A:323:C:O2	2.50	0.44
24:A:582:U:O2'	24:A:583:A:H5'	2.17	0.44
24:A:692:G:H2'	24:A:693:A:C8	2.53	0.44
24:A:934:G:H22	24:A:1008:A:H2	1.65	0.44
24:A:1446:A:H5''	52:h:58:THR:HG23	1.99	0.44
24:A:1531:A:N6	24:A:1638:G:O6	2.51	0.44
39:c:109:LEU:H	39:c:124:SER:HA	1.83	0.44
39:c:217:MET:HG2	39:c:229:THR:HG23	1.99	0.44
56:j:353:ARG:HD2	56:j:390:PHE:HB2	1.99	0.44
5:u:386:GLU:HG2	5:u:413:TRP:CG	2.53	0.44
5:u:567:ARG:HE	5:u:572:ARG:HG3	1.83	0.44
21:5:387:HIS:O	21:5:391:ARG:N	2.38	0.44
24:A:583:A:H2'	24:A:584:A:H8	1.83	0.44
24:A:1263:U:O4	24:A:1518:C:N4	2.51	0.44
24:A:1416:C:H4'	40:d:132:ASP:HB3	1.98	0.44
28:E:123:VAL:HG12	28:E:124:LYS:HG3	1.99	0.44
32:R:23:LYS:HB2	32:R:23:LYS:HE3	1.81	0.44
39:c:154:VAL:HG23	39:c:167:SER:HB3	1.99	0.44
45:m:14:VAL:HG21	45:m:126:GLU:HG3	1.98	0.44
56:j:155:ILE:HG13	56:j:171:LEU:HD21	1.99	0.44
57:g:771:LEU:HD12	57:g:771:LEU:HA	1.89	0.44
2:1:528:VAL:HB	2:1:545:GLU:HB2	1.99	0.44
6:v:229:ARG:HA	6:v:229:ARG:HD3	1.67	0.44
19:x:365:LEU:HD22	19:x:369:ILE:HG21	2.00	0.44
24:A:1101:U:H2'	24:A:1102:G:C8	2.52	0.44
26:C:45:ILE:HA	26:C:61:VAL:HG11	2.00	0.44
42:f:35:GLY:HA3	42:f:99:LEU:HA	1.99	0.44
48:p:90:ARG:HD2	48:p:112:GLY:HA2	2.00	0.44
11:H:36:LYS:N	11:H:78:SER:O	2.46	0.43
13:L:190:SER:OG	24:A:14:C:OP1	2.36	0.43
24:A:1228:A:H2'	24:A:1229:G:C8	2.53	0.43
24:A:1405:A:H2'	24:A:1406:G:O4'	2.18	0.43
24:A:1707:U:H2'	24:A:1708:C:C6	2.53	0.43
31:J:30:CYS:HB2	31:J:61:ILE:HG13	1.99	0.43
32:R:10:LYS:HE3	32:R:10:LYS:HB3	1.85	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:u:244:GLU:OE1	5:u:246:TRP:NE1	2.46	0.43
5:u:341:LEU:HD11	5:u:347:ILE:HG13	2.00	0.43
6:v:353:ILE:HG12	6:v:371:ILE:HG13	2.00	0.43
7:S:186:GLN:NE2	24:A:333:G:O6	2.52	0.43
14:O:28:LYS:HA	14:O:50:THR:HA	2.00	0.43
14:O:115:LYS:HG2	24:A:1869:A:C5	2.53	0.43
16:Q:23:CYS:SG	16:Q:74:CYS:N	2.89	0.43
20:3:174:MET:O	20:3:178:GLY:N	2.51	0.43
24:A:116:OMU:HM23	24:A:116:OMU:H1'	1.81	0.43
24:A:185:G:H1	24:A:214:U:H3	1.66	0.43
32:R:88:ASN:OD1	32:R:205:ARG:NH1	2.51	0.43
32:R:158:ILE:HD12	32:R:158:ILE:HA	1.81	0.43
36:Z:46:THR:N	36:Z:83:SER:O	2.49	0.43
57:g:760:LEU:HD22	57:g:793:ARG:HD2	2.01	0.43
2:1:490:PRO:HG3	27:D:159:PHE:HE2	1.83	0.43
5:u:320:THR:HG21	5:u:384:VAL:HG23	2.00	0.43
6:v:367:ALA:O	6:v:371:ILE:HG12	2.18	0.43
13:L:180:VAL:HG22	13:L:219:ILE:HD13	2.00	0.43
14:O:195:LYS:HB3	14:O:195:LYS:HE2	1.86	0.43
27:D:122:SER:OG	27:D:123:ILE:N	2.52	0.43
5:u:446:ILE:HG23	5:u:447:TYR:HD2	1.83	0.43
5:u:551:GLN:O	5:u:555:THR:N	2.41	0.43
5:u:555:THR:HA	5:u:558:LEU:HB2	2.00	0.43
6:v:273:VAL:O	6:v:277:LEU:N	2.38	0.43
8:y:815:LEU:HA	8:y:818:VAL:HG12	1.99	0.43
9:8:212:ASN:O	9:8:216:TRP:N	2.49	0.43
24:A:521:A:OP1	27:D:45:ARG:NH1	2.50	0.43
24:A:851:C:H5''	24:A:852:G:H5'	2.00	0.43
24:A:1272:C:N4	24:A:1508:A:OP1	2.51	0.43
32:R:199:LEU:HD23	32:R:199:LEU:HA	1.81	0.43
34:V:75:SER:O	34:V:75:SER:OG	2.34	0.43
36:Z:192:TRP:NE1	36:Z:201:LYS:O	2.40	0.43
37:a:17:LYS:HE2	37:a:17:LYS:HB3	1.87	0.43
39:c:254:PRO:HA	39:c:285:GLN:HA	2.00	0.43
40:d:138:VAL:O	40:d:142:ASN:N	2.51	0.43
56:j:273:THR:O	56:j:324:ARG:NE	2.52	0.43
15:N:184:ARG:NH1	15:N:191:ARG:O	2.52	0.43
24:A:472:C:O2'	24:A:474:G:OP1	2.32	0.43
28:E:24:ASP:HB3	28:E:27:TYR:HB3	2.00	0.43
30:r:74:ILE:HG22	30:r:75:ARG:HG3	1.99	0.43
31:J:102:ILE:HB	31:J:113:HIS:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:120:PRO:HD3	32:R:137:LEU:HD11	1.99	0.43
53:s:199:LYS:HD2	53:s:199:LYS:HA	1.80	0.43
56:j:130:SER:HB3	56:j:152:PRO:HA	1.99	0.43
57:g:777:GLN:HA	57:g:780:MET:HE2	2.01	0.43
57:g:938:LEU:HA	57:g:938:LEU:HD12	1.78	0.43
5:u:233:ARG:HG3	5:u:236:GLN:NE2	2.34	0.43
5:u:385:PRO:O	5:u:388:LYS:NZ	2.51	0.43
6:v:267:VAL:HG13	6:v:270:ARG:HG3	2.00	0.43
8:y:95:SER:OG	8:y:96:ILE:N	2.51	0.43
17:P:34:PHE:HE1	17:P:100:THR:HA	1.82	0.43
24:A:1523:C:H42	42:f:137:LYS:HG3	1.83	0.43
24:A:1588:A:H2'	24:A:1589:A:C8	2.53	0.43
24:A:1674:G:H4'	34:V:77:MET:HE1	2.01	0.43
35:Y:58:LEU:HD11	35:Y:112:LEU:HD11	2.00	0.43
48:p:91:LYS:HA	48:p:91:LYS:HD3	1.81	0.43
51:M:114:LEU:HD23	51:M:114:LEU:HA	1.83	0.43
51:M:116:ASN:OD1	51:M:116:ASN:N	2.47	0.43
7:S:22:ARG:HG2	7:S:25:ARG:HH21	1.82	0.43
11:H:24:LEU:HD11	31:J:53:ILE:HG12	2.00	0.43
14:O:62:LEU:HD13	14:O:91:VAL:HG11	2.01	0.43
24:A:129:C:H4'	24:A:130:G:H5'	2.00	0.43
24:A:580:U:H2'	24:A:581:U:C6	2.54	0.43
24:A:750:C:N4	24:A:793:G:O2'	2.52	0.43
32:R:201:LYS:HA	32:R:201:LYS:HD2	1.77	0.43
42:f:26:ILE:HG12	42:f:59:LEU:HD11	2.01	0.43
56:j:65:PRO:HB3	56:j:232:ILE:HG13	2.01	0.43
3:6:319:LYS:HA	3:6:319:LYS:HD3	1.90	0.43
24:A:1692:U:H2'	24:A:1693:G:C8	2.53	0.43
43:i:22:ARG:HD2	43:i:38:MET:HE2	2.01	0.43
56:j:197:TYR:HE1	56:j:223:VAL:HG22	1.84	0.43
57:g:809:PRO:HB3	57:g:900:LYS:HD2	2.01	0.43
5:u:10:ASN:HA	5:u:13:LYS:HD2	2.01	0.43
5:u:280:SER:O	5:u:292:HIS:ND1	2.47	0.43
24:A:17:C:O2'	24:A:1194:A:N1	2.51	0.43
24:A:507:G:OP1	33:T:108:LYS:NZ	2.37	0.43
24:A:1310:U:O4	44:k:97:LYS:HE2	2.19	0.43
30:r:210:GLU:HA	30:r:213:ARG:HB2	2.01	0.43
39:c:91:ASP:OD2	39:c:93:THR:OG1	2.35	0.43
5:u:277:ASN:HA	5:u:280:SER:HB3	2.01	0.43
28:E:134:TYR:O	29:F:87:ARG:NH2	2.52	0.43
30:r:9:TYR:OH	30:r:101:LYS:NZ	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6:183:LYS:O	3:6:187:GLU:N	2.50	0.42
5:u:342:LEU:HA	5:u:346:GLY:HA2	2.00	0.42
6:v:322:ASP:HB3	6:v:325:LEU:HD12	2.00	0.42
10:G:98:ARG:HG3	24:A:913:A:N6	2.34	0.42
24:A:563:G:N7	27:D:172:ARG:NH2	2.53	0.42
24:A:1808:U:H2'	24:A:1809:A:C8	2.53	0.42
30:r:167:ASP:N	30:r:167:ASP:OD1	2.51	0.42
34:V:119:SER:HA	34:V:193:LYS:HE2	2.00	0.42
46:n:17:VAL:HA	46:n:30:VAL:HG12	2.00	0.42
56:j:259:LYS:HB3	56:j:347:TYR:CZ	2.54	0.42
10:G:158:LEU:HD23	10:G:158:LEU:HA	1.90	0.42
14:O:28:LYS:HD3	14:O:48:LEU:HD13	2.00	0.42
16:Q:39:PHE:HD1	16:Q:70:LYS:HD2	1.84	0.42
19:x:315:GLU:O	19:x:319:ILE:HG12	2.19	0.42
24:A:1543:U:OP1	35:Y:37:ARG:NH2	2.53	0.42
24:A:1750:C:N3	24:A:1751:C:N4	2.67	0.42
24:A:1849:G:H2'	24:A:1850:MA6:C8	2.48	0.42
27:D:127:ARG:HD3	29:F:105:ARG:HD3	2.01	0.42
37:a:29:MET:HA	37:a:30:PRO:HD3	1.89	0.42
42:f:89:ASP:HB3	42:f:93:GLY:H	1.85	0.42
56:j:35:ASP:OD2	57:g:973:SER:N	2.52	0.42
56:j:292:MET:HB3	56:j:297:PHE:HB2	2.00	0.42
57:g:881:LYS:HE3	57:g:883:GLU:HB2	2.00	0.42
57:g:888:ARG:HA	57:g:891:ALA:HB3	2.00	0.42
57:g:913:GLU:OE1	57:g:917:HIS:NE2	2.51	0.42
3:6:17:GLU:HA	3:6:20:ALA:HB3	2.02	0.42
3:6:186:VAL:O	3:6:190:GLY:N	2.52	0.42
5:u:487:THR:HA	8:y:840:GLN:HE22	1.84	0.42
16:Q:89:ARG:NH1	24:A:1145:A:O3'	2.52	0.42
24:A:1013:U:OP1	24:A:1129:G:O2'	2.37	0.42
24:A:1217:A:H2'	24:A:1218:C:C6	2.54	0.42
34:V:31:ASN:HB2	34:V:117:ILE:HD13	2.02	0.42
35:Y:134:GLY:HA3	35:Y:140:ARG:HA	2.01	0.42
39:c:33:SER:HB3	39:c:43:TRP:HE1	1.84	0.42
39:c:57:ARG:HD3	39:c:95:GLY:HA3	2.02	0.42
39:c:130:LYS:HB3	39:c:130:LYS:HE2	1.83	0.42
47:o:242:ARG:N	47:o:313:GLU:O	2.50	0.42
53:s:227:LYS:HE3	53:s:227:LYS:HB3	1.63	0.42
4:4:93:ARG:O	4:4:130:GLU:HA	2.19	0.42
6:v:408:THR:HB	8:y:858:GLN:HB3	2.01	0.42
7:S:175:LYS:HG3	24:A:77:A:H2	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:I:28:LEU:HD23	18:I:28:LEU:HA	1.89	0.42
24:A:116:OMU:HN3	24:A:347:G:H1	1.67	0.42
30:r:50:GLU:OE1	30:r:88:ARG:NH2	2.53	0.42
30:r:56:ILE:HD11	30:r:62:LEU:HD11	2.02	0.42
30:r:155:HIS:O	30:r:159:ASP:N	2.47	0.42
30:r:276:LYS:NZ	30:r:277:VAL:O	2.47	0.42
36:Z:134:CYS:SG	36:Z:135:GLU:N	2.93	0.42
48:p:111:HIS:HB2	53:s:244:LEU:HG	2.01	0.42
5:u:352:GLN:HG2	5:u:364:PRO:HB3	2.00	0.42
6:v:383:LYS:HZ1	21:5:468:THR:H	1.67	0.42
7:S:2:LYS:HD2	24:A:156:G:H5''	2.02	0.42
8:y:139:SER:HB3	24:A:368:U:H2'	2.00	0.42
13:L:93:ILE:H	13:L:93:ILE:HG13	1.71	0.42
13:L:94:ILE:HG21	13:L:162:ILE:HD12	2.01	0.42
17:P:102:GLY:O	17:P:106:LYS:NZ	2.47	0.42
24:A:174:OMC:HM23	24:A:174:OMC:H1'	1.81	0.42
24:A:1513:C:H5'	43:i:7:TYR:O	2.19	0.42
30:r:114:HIS:NE2	54:w:53:A:N3	2.59	0.42
35:Y:116:ASP:OD1	35:Y:118:THR:OG1	2.35	0.42
5:u:14[B]:ARG:NH2	5:u:17:GLU:OE1	2.52	0.42
6:v:128:LEU:O	6:v:132:TYR:N	2.50	0.42
6:v:233:ILE:HD11	6:v:273:VAL:HB	2.01	0.42
6:v:259:THR:O	6:v:263:THR:N	2.48	0.42
8:y:602:ASP:HB3	19:x:73:HIS:CG	2.55	0.42
11:H:20:LYS:HA	11:H:23:ARG:NH1	2.34	0.42
19:x:304:ASN:OD1	19:x:311:ASN:ND2	2.52	0.42
20:3:154:ASP:O	20:3:158:LEU:N	2.43	0.42
24:A:196:C:O2	24:A:203:G:O2'	2.36	0.42
24:A:1710:C:H42	24:A:1823:A:H61	1.67	0.42
30:r:78:LYS:HE2	30:r:78:LYS:HB3	1.90	0.42
38:b:62:LYS:HA	38:b:65:LYS:HG2	2.02	0.42
39:c:234:ASP:H	39:c:252:THR:HB	1.83	0.42
56:j:116:ILE:HB	56:j:156:VAL:HG11	2.02	0.42
57:g:922:LYS:HD3	57:g:925:LYS:HD2	2.01	0.42
6:v:231:ASN:HA	6:v:235:LEU:HB2	2.02	0.42
7:S:98:ARG:NH1	7:S:101:ILE:O	2.52	0.42
26:C:21:ASP:OD1	26:C:21:ASP:N	2.46	0.42
30:r:67:ARG:HH22	54:w:21:G:H4'	1.85	0.42
35:Y:8:GLN:HA	35:Y:99:TYR:CZ	2.55	0.42
53:s:302:CYS:O	53:s:306:HIS:N	2.37	0.42
56:j:339:GLN:HG3	56:j:341:VAL:HG23	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:v:261:VAL:HG21	6:v:274:LEU:HG	2.01	0.42
8:y:83:PHE:HA	8:y:86:LEU:HD12	2.02	0.42
24:A:1441:U:H1'	24:A:1443:C:H41	1.85	0.42
30:r:21:MET:HG3	30:r:68:ASN:HB2	2.02	0.42
33:T:68:LYS:HE2	33:T:68:LYS:HB3	1.86	0.42
34:V:50:PRO:HG2	34:V:90:VAL:HG13	2.01	0.42
45:m:33:ARG:HD2	45:m:91:LEU:HD23	2.02	0.42
56:j:23:ILE:HD12	56:j:233:ARG:HB3	2.01	0.42
2:1:388:LEU:N	2:1:407:TRP:O	2.45	0.42
3:6:185:MET:O	3:6:189:LEU:N	2.47	0.42
5:u:552:LEU:HA	5:u:555:THR:HB	2.01	0.42
13:L:82:TYR:CZ	13:L:164:PRO:HD3	2.55	0.42
19:x:472:LYS:HE3	34:V:29:GLN:HE21	1.85	0.42
24:A:158:A:H61	24:A:467:G:H1'	1.85	0.42
24:A:444:G:N2	24:A:447:A:OP2	2.51	0.42
24:A:1251:A:N6	35:Y:146:ARG:OXT	2.40	0.42
24:A:1677:U:O4	24:A:1678:A2M:N6	2.53	0.42
34:V:119:SER:O	34:V:119:SER:OG	2.38	0.42
37:a:53:LYS:HE3	37:a:53:LYS:HB3	1.91	0.42
38:b:85:ILE:HG21	38:b:111:MET:HG3	2.01	0.42
41:e:49:LEU:HD13	42:f:5:ILE:HA	2.01	0.42
44:k:133:ALA:N	44:k:140:TYR:O	2.53	0.42
45:m:44:LYS:HE2	45:m:44:LYS:HB2	1.88	0.42
57:g:854:ASP:O	57:g:895:SER:OG	2.30	0.42
3:6:313:ILE:HA	3:6:316:VAL:HG12	2.02	0.42
6:v:269:LYS:HE2	6:v:269:LYS:HB2	1.63	0.42
7:S:149:LYS:HD2	7:S:149:LYS:HA	1.86	0.42
8:y:386:ASN:OD1	8:y:386:ASN:N	2.52	0.42
8:y:672:PRO:HD2	8:y:675:LEU:HD13	2.02	0.42
12:K:3:ASN:ND2	12:K:7:GLU:OE2	2.51	0.42
24:A:1114:U:O2'	24:A:1119:A:N6	2.53	0.42
24:A:1831:A:H2'	24:A:1832:6MZ:C8	2.49	0.42
26:C:126:VAL:HG22	26:C:139:LEU:HD13	2.02	0.42
31:J:43:LYS:HD2	31:J:43:LYS:HA	1.87	0.42
36:Z:76:ARG:HB2	37:a:22:VAL:HG11	2.01	0.42
49:q:42:LEU:HD12	49:q:42:LEU:HA	1.86	0.42
54:w:38:C:H2'	54:w:39:C:C6	2.55	0.42
56:j:176:ILE:HG21	56:j:203:LEU:HD13	2.01	0.42
56:j:280:ASN:OD1	56:j:359:ARG:NH2	2.37	0.42
57:g:920:VAL:HG12	57:g:923:LEU:HD12	2.02	0.42
3:6:341:THR:HG21	4:4:302:ASN:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:u:323:LEU:HD12	5:u:323:LEU:HA	1.91	0.41
5:u:540:ALA:O	5:u:544:GLN:N	2.33	0.41
8:y:439:ARG:HH12	8:y:441:ARG:HE	1.67	0.41
8:y:673:PHE:HA	8:y:676:HIS:ND1	2.35	0.41
15:N:40:LYS:HB2	15:N:40:LYS:HE3	1.90	0.41
24:A:557:U:H2'	24:A:558:G:C8	2.54	0.41
24:A:663:C:OP2	28:E:3:LYS:NZ	2.45	0.41
24:A:1337:C:H2'	24:A:1338:G:C8	2.54	0.41
24:A:1374:5MC:O2'	24:A:1464:C:O2	2.31	0.41
24:A:1406:G:H2'	24:A:1407:U:C6	2.55	0.41
24:A:1512:C:O2'	43:i:7:TYR:O	2.38	0.41
24:A:1598:G:OP1	41:e:80:ARG:NH2	2.48	0.41
25:B:8:ARG:O	32:R:83:TYR:OH	2.34	0.41
39:c:31:ILE:HG23	39:c:45:LEU:HD11	2.01	0.41
44:k:107:LYS:HD3	44:k:115:SER:H	1.85	0.41
56:j:324:ARG:HG3	57:g:772:THR:HG22	2.02	0.41
2:l:544:PHE:CZ	2:l:565:ILE:HG12	2.55	0.41
5:u:279:VAL:HA	5:u:282:VAL:HG12	2.02	0.41
5:u:481:GLN:HG2	5:u:499:TYR:CD2	2.55	0.41
7:S:164:LYS:NZ	24:A:69:C:OP1	2.45	0.41
8:y:552:CYS:HB3	8:y:556:TYR:CZ	2.55	0.41
15:N:119:PRO:HG2	15:N:142:LEU:HD11	2.02	0.41
24:A:579:C:H2'	24:A:580:U:C6	2.55	0.41
39:c:201:SER:HB3	39:c:206:LEU:HB2	2.02	0.41
46:n:32:VAL:HG11	46:n:56:LEU:HD12	2.01	0.41
49:q:40:LYS:HA	49:q:40:LYS:HD2	1.72	0.41
57:g:777:GLN:HG2	57:g:780:MET:HE2	2.01	0.41
6:v:369:ARG:HA	6:v:372:VAL:HG12	2.02	0.41
8:y:421:GLY:N	8:y:440:VAL:HG13	2.35	0.41
13:L:214:LEU:HD23	13:L:214:LEU:HA	1.91	0.41
18:I:43:LYS:HB3	18:I:43:LYS:HE2	1.79	0.41
24:A:897:U:H5'	24:A:898:U:O4'	2.21	0.41
24:A:1033:G:N1	24:A:1080:A:O2'	2.35	0.41
26:C:124:CYS:HB3	26:C:141:THR:HB	2.02	0.41
30:r:7:ARG:H	30:r:7:ARG:HG2	1.70	0.41
47:o:246:LEU:HD23	47:o:246:LEU:HA	1.86	0.41
56:j:237:LYS:HE2	56:j:237:LYS:HB3	1.81	0.41
56:j:245:GLY:HA3	56:j:362:ARG:HD2	2.02	0.41
8:y:83:PHE:HA	8:y:86:LEU:HB2	2.02	0.41
10:G:81:ARG:HE	10:G:81:ARG:HB2	1.54	0.41
10:G:144:ILE:HG23	10:G:154:ILE:HG12	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:101:GLY:HA3	17:P:134:PRO:HG2	2.02	0.41
19:x:35:LYS:H	19:x:35:LYS:HG3	1.53	0.41
19:x:394:LYS:HD2	19:x:447:LEU:HD11	2.01	0.41
24:A:1515:G:N2	38:b:99:GLY:O	2.53	0.41
24:A:1535:U:O4	34:V:159:ARG:NH1	2.53	0.41
24:A:1849:G:H2'	24:A:1850:MA6:H8	2.02	0.41
29:F:103:THR:HA	29:F:107:LYS:HB2	2.01	0.41
35:Y:53:GLU:OE2	35:Y:115:TYR:OH	2.32	0.41
42:f:40:TYR:HA	42:f:43:VAL:HG12	2.01	0.41
3:6:179:ASP:O	3:6:183:LYS:N	2.53	0.41
5:u:43:TRP:O	5:u:47:HIS:ND1	2.54	0.41
7:S:53:SER:O	7:S:53:SER:OG	2.36	0.41
17:P:30:VAL:N	17:P:45:THR:O	2.53	0.41
17:P:38:ASN:ND2	24:A:959:G:OP2	2.44	0.41
18:I:47:PRO:HG2	18:I:72:LEU:HD12	2.02	0.41
24:A:145:G:H2'	24:A:146:G:C8	2.55	0.41
27:D:78:LEU:HD22	27:D:92:MET:HA	2.03	0.41
41:e:58:LEU:HD12	41:e:73:VAL:HG21	2.02	0.41
7:S:44:GLU:HG3	7:S:45:TRP:CD1	2.54	0.41
8:y:594:LEU:HD22	8:y:598:ILE:HD13	2.03	0.41
10:G:27:LEU:HD22	10:G:45:ILE:HD11	2.02	0.41
14:O:82:ARG:HH11	14:O:191:ASP:HB3	1.84	0.41
20:3:173:TRP:O	20:3:177:TYR:N	2.52	0.41
24:A:159:A2M:HM'3	24:A:159:A2M:H1'	1.93	0.41
24:A:1736:G:H2'	24:A:1737:G:C8	2.56	0.41
32:R:154:LYS:HD3	32:R:154:LYS:HA	1.86	0.41
36:Z:69:LEU:HD23	36:Z:69:LEU:HA	1.90	0.41
56:j:276:VAL:HG23	56:j:341:VAL:HG11	2.03	0.41
56:j:353:ARG:O	56:j:391:TYR:OH	2.24	0.41
3:6:345:GLN:NE2	4:4:299:SER:O	2.54	0.41
8:y:750:LYS:HD2	8:y:750:LYS:HA	1.74	0.41
8:y:806:THR:O	8:y:810:MET:N	2.43	0.41
10:G:168:HIS:CE1	10:G:169:LYS:HE2	2.56	0.41
18:I:111:ALA:HA	18:I:114:ARG:HB2	2.01	0.41
21:5:201:ARG:O	21:5:205:ALA:N	2.50	0.41
25:B:111:VAL:HG12	25:B:140:PHE:HB2	2.02	0.41
35:Y:60:LYS:O	35:Y:64:ALA:N	2.54	0.41
47:o:245:ASN:HB3	47:o:310:LEU:HA	2.03	0.41
53:s:187:MET:HE3	53:s:187:MET:HB2	1.91	0.41
56:j:270:LEU:HA	56:j:403:ALA:HA	2.02	0.41
3:6:317:ARG:NH1	5:u:399:ASN:OD1	2.40	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:u:254:GLU:HG3	5:u:358:LEU:HD21	2.02	0.41
6:v:302:ASN:OD1	6:v:302:ASN:N	2.54	0.41
6:v:393:MET:N	6:v:393:MET:SD	2.93	0.41
9:8:41:ILE:HA	9:8:78:ILE:H	1.86	0.41
10:G:27:LEU:O	10:G:31:GLU:N	2.53	0.41
16:Q:10:ARG:HH22	24:A:1859:A:P	2.44	0.41
23:9:2:ARG:HB3	23:9:5:TRP:CD1	2.56	0.41
24:A:550:C:O2'	24:A:551:U:O4'	2.31	0.41
24:A:664:A:O2'	24:A:670:A:N1	2.49	0.41
24:A:860:G:H21	31:J:107:SER:HG	1.64	0.41
24:A:1678:A2M:HM'3	24:A:1678:A2M:H1'	1.86	0.41
53:s:216:LYS:HG2	53:s:257:VAL:HG13	2.02	0.41
57:g:855:LYS:HE2	57:g:896:LEU:HG	2.02	0.41
5:u:17:GLU:OE2	14:O:75:GLN:NE2	2.54	0.41
5:u:87:GLU:HG2	5:u:170:VAL:HG23	2.02	0.41
5:u:483:ARG:N	5:u:492:SER:O	2.44	0.41
5:u:531:ALA:HA	5:u:534:LEU:HB3	2.01	0.41
6:v:307:GLY:HA2	6:v:311:LYS:HB2	2.02	0.41
8:y:151:ASP:OD1	8:y:151:ASP:N	2.54	0.41
8:y:459:MET:HB3	8:y:672:PRO:HB3	2.02	0.41
8:y:499:VAL:HA	8:y:502:ILE:HG22	2.01	0.41
8:y:792:LEU:HD13	8:y:792:LEU:HA	1.94	0.41
8:y:813:LEU:HD23	8:y:813:LEU:HA	1.86	0.41
24:A:70:G:H21	24:A:79:A:H62	1.69	0.41
24:A:290:U:O2'	24:A:292:A:N7	2.52	0.41
24:A:928:G:H2'	24:A:929:G:C8	2.55	0.41
24:A:1261:C:O2	43:i:10:HIS:NE2	2.50	0.41
27:D:87:LEU:HD12	27:D:87:LEU:HA	1.91	0.41
30:r:56:ILE:HD12	30:r:56:ILE:HA	1.84	0.41
34:V:103:LEU:HD23	34:V:103:LEU:HA	1.79	0.41
36:Z:209:SER:O	36:Z:209:SER:OG	2.35	0.41
37:a:35:LEU:HD23	37:a:35:LEU:HA	1.87	0.41
38:b:83:MET:HB3	38:b:116:LEU:HD12	2.03	0.41
39:c:5:MET:SD	39:c:270:LEU:HD21	2.61	0.41
41:e:82:SER:OG	42:f:55:ARG:NH1	2.54	0.41
48:p:35:ILE:HD11	48:p:90:ARG:HB2	2.03	0.41
53:s:214:THR:HA	53:s:261:ARG:HH11	1.86	0.41
53:s:296:ARG:HA	53:s:296:ARG:HD2	1.82	0.41
56:j:377:THR:H	56:j:380:ASP:HB2	1.85	0.41
57:g:906:PHE:HD1	57:g:942:ILE:HD11	1.86	0.41
5:u:233:ARG:HA	5:u:236:GLN:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:u:408:THR:O	5:u:412:ASN:N	2.53	0.41
6:v:339:PHE:HA	6:v:339:PHE:HD1	1.72	0.41
10:G:73:GLN:HA	10:G:76:GLN:HB2	2.02	0.41
10:G:143:ARG:HH22	31:J:53:ILE:HG23	1.86	0.41
14:O:42:ARG:HA	14:O:42:ARG:HD2	1.95	0.41
19:x:472:LYS:HE2	19:x:472:LYS:HB2	1.85	0.41
24:A:581:U:H2'	24:A:582:U:C6	2.55	0.41
30:r:168:LEU:HD13	30:r:172:GLU:HB3	2.02	0.41
34:V:136:ARG:O	34:V:203:ASN:ND2	2.54	0.41
34:V:192:LYS:HA	34:V:192:LYS:HD2	1.86	0.41
52:h:26:SER:HB3	52:h:32:LEU:HD22	2.02	0.41
6:v:249:MET:HB2	6:v:281:ILE:HG12	2.02	0.40
6:v:344:PHE:CE1	6:v:351:ILE:HG22	2.56	0.40
8:y:515:ASP:HB3	8:y:579:HIS:HE1	1.86	0.40
24:A:536:A:H3'	24:A:537:C:H4'	2.02	0.40
24:A:1444:U:P	35:Y:15:ARG:HH22	2.44	0.40
24:A:1644:C:H2'	24:A:1645:C:C6	2.56	0.40
30:r:21:MET:HE2	30:r:21:MET:HB2	1.94	0.40
57:g:892:ARG:HH11	57:g:930:GLU:H	1.69	0.40
1:2:273:ALA:HB3	2:1:760:TYR:HA	2.03	0.40
6:v:261:VAL:HG11	6:v:274:LEU:HD21	2.01	0.40
8:y:70:ALA:HA	8:y:73:ILE:HG22	2.02	0.40
8:y:493:LYS:HE3	8:y:493:LYS:HB3	1.90	0.40
12:K:41:LYS:HA	15:N:5:LEU:HD12	2.03	0.40
14:O:52:THR:O	14:O:52:THR:OG1	2.35	0.40
16:Q:32:LYS:O	16:Q:37:LYS:NZ	2.53	0.40
18:I:101:HIS:ND1	24:A:1007:C:O2'	2.44	0.40
19:x:288:LEU:HB2	19:x:317:THR:HG21	2.04	0.40
19:x:412:LYS:HD3	19:x:416:GLN:HB3	2.02	0.40
30:r:261:LYS:HB2	30:r:261:LYS:HE2	1.89	0.40
34:V:97:PHE:HA	34:V:100:ILE:HD12	2.03	0.40
34:V:128:ILE:O	34:V:135:ARG:NH2	2.44	0.40
37:a:32:HIS:HB3	37:a:35:LEU:HB2	2.03	0.40
40:d:116:ASP:OD1	40:d:117:GLN:N	2.46	0.40
56:j:270:LEU:HD23	56:j:343:LEU:HD13	2.03	0.40
57:g:942:ILE:HD12	57:g:942:ILE:HA	1.85	0.40
5:u:490:THR:OG1	5:u:491:LEU:N	2.54	0.40
7:S:16:ILE:HD12	7:S:16:ILE:HA	1.99	0.40
8:y:439:ARG:HH12	8:y:441:ARG:HH21	1.68	0.40
10:G:66:VAL:HB	24:A:913:A:H1'	2.02	0.40
10:G:83:LEU:HD23	10:G:83:LEU:HA	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:1240:A:C4	38:b:100:LYS:HD3	2.57	0.40
24:A:1405:A:H61	24:A:1441:U:H3	1.70	0.40
33:T:81:TYR:O	33:T:85:ASN:ND2	2.43	0.40
38:b:108:LYS:NZ	42:f:116:LYS:HG2	2.36	0.40
45:m:42:LEU:HD12	45:m:42:LEU:HA	1.88	0.40
49:q:34:GLU:HB2	49:q:52:PHE:CG	2.57	0.40
5:u:257:HIS:CD2	5:u:358:LEU:HA	2.56	0.40
5:u:542:ILE:HG23	5:u:543:LEU:HD12	2.02	0.40
7:S:32:MET:O	7:S:65:GLN:NE2	2.54	0.40
18:I:40:LEU:HD23	18:I:40:LEU:HA	1.91	0.40
18:I:69:ASN:HB3	18:I:73:ARG:NH2	2.37	0.40
18:I:112:LYS:NZ	24:A:1031:A2M:O3'	2.55	0.40
24:A:1253:A:O2'	24:A:1666:C:O3'	2.39	0.40
24:A:1301:A:O2'	24:A:1303:C:OP1	2.32	0.40
24:A:1323:U:H2'	24:A:1324:G:C8	2.57	0.40
24:A:1703:OMC:HM23	24:A:1703:OMC:H1'	1.85	0.40
24:A:1844:U:H2'	24:A:1845:A:C8	2.57	0.40
30:r:7:ARG:HD3	30:r:12:LYS:HG3	2.03	0.40
33:T:44:LEU:HD23	33:T:44:LEU:HA	1.93	0.40
41:e:57:LYS:HE3	41:e:57:LYS:HB3	1.97	0.40
42:f:45:LEU:HD23	42:f:45:LEU:HA	1.92	0.40
57:g:939:LEU:HD13	57:g:982:VAL:HG11	2.04	0.40
3:6:60:VAL:O	3:6:64:MET:N	2.53	0.40
3:6:324:LYS:HB2	5:u:447:TYR:HA	2.03	0.40
5:u:399:ASN:HB3	5:u:402:LYS:HZ3	1.87	0.40
5:u:510:HIS:ND1	5:u:511:LEU:HG	2.37	0.40
5:u:571:ARG:HD2	5:u:571:ARG:HA	1.80	0.40
12:K:32:ILE:HD12	12:K:34:MET:HB2	2.04	0.40
14:O:199:LYS:HD3	14:O:199:LYS:HA	1.70	0.40
24:A:517:OMC:HM23	24:A:517:OMC:H1'	1.81	0.40
24:A:1092:G:H2'	24:A:1093:A:C8	2.57	0.40
24:A:1749:G:H2'	24:A:1750:C:C6	2.56	0.40
40:d:122:LYS:HB2	40:d:122:LYS:HE3	1.90	0.40
45:m:75:ASN:ND2	45:m:123:VAL:O	2.54	0.40
49:q:27:VAL:HG13	49:q:95:TYR:HE1	1.86	0.40
57:g:760:LEU:HD21	57:g:797:VAL:HG23	2.02	0.40
57:g:899:ILE:HA	57:g:919:CYS:SG	2.62	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2	300/325 (92%)	277 (92%)	23 (8%)	0	100	100
2	1	584/814 (72%)	541 (93%)	36 (6%)	7 (1%)	10	40
3	6	348/374 (93%)	296 (85%)	52 (15%)	0	100	100
4	4	251/357 (70%)	217 (86%)	31 (12%)	3 (1%)	10	40
5	u	705/1382 (51%)	656 (93%)	47 (7%)	2 (0%)	36	65
6	v	380/445 (85%)	331 (87%)	49 (13%)	0	100	100
7	S	228/249 (92%)	222 (97%)	6 (3%)	0	100	100
8	y	691/913 (76%)	645 (93%)	44 (6%)	2 (0%)	36	65
9	8	313/352 (89%)	264 (84%)	48 (15%)	1 (0%)	36	65
10	G	171/194 (88%)	158 (92%)	13 (8%)	0	100	100
11	H	79/84 (94%)	73 (92%)	6 (8%)	0	100	100
12	K	79/83 (95%)	75 (95%)	4 (5%)	0	100	100
13	L	218/293 (74%)	205 (94%)	13 (6%)	0	100	100
14	O	209/264 (79%)	193 (92%)	16 (8%)	0	100	100
15	N	205/295 (70%)	189 (92%)	16 (8%)	0	100	100
16	Q	97/115 (84%)	92 (95%)	5 (5%)	0	100	100
17	P	131/151 (87%)	116 (88%)	15 (12%)	0	100	100
18	I	148/151 (98%)	141 (95%)	7 (5%)	0	100	100
19	x	415/548 (76%)	373 (90%)	42 (10%)	0	100	100
20	3	209/218 (96%)	203 (97%)	5 (2%)	1 (0%)	24	56
21	5	307/564 (54%)	299 (97%)	8 (3%)	0	100	100
23	9	22/25 (88%)	22 (100%)	0	0	100	100
25	B	138/158 (87%)	135 (98%)	3 (2%)	0	100	100
26	C	254/263 (97%)	250 (98%)	4 (2%)	0	100	100
27	D	175/194 (90%)	174 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	E	138/143 (96%)	133 (96%)	5 (4%)	0	100	100
29	F	43/59 (73%)	42 (98%)	1 (2%)	0	100	100
30	r	273/315 (87%)	250 (92%)	23 (8%)	0	100	100
31	J	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
32	R	194/208 (93%)	186 (96%)	8 (4%)	0	100	100
33	T	123/133 (92%)	122 (99%)	1 (1%)	0	100	100
34	V	180/204 (88%)	170 (94%)	10 (6%)	0	100	100
35	Y	139/146 (95%)	131 (94%)	8 (6%)	0	100	100
36	Z	225/243 (93%)	218 (97%)	7 (3%)	0	100	100
37	a	97/165 (59%)	93 (96%)	4 (4%)	0	100	100
38	b	108/145 (74%)	105 (97%)	3 (3%)	0	100	100
39	c	311/317 (98%)	295 (95%)	16 (5%)	0	100	100
40	d	140/145 (97%)	133 (95%)	7 (5%)	0	100	100
41	e	64/125 (51%)	59 (92%)	5 (8%)	0	100	100
42	f	140/152 (92%)	136 (97%)	4 (3%)	0	100	100
43	i	48/56 (86%)	45 (94%)	3 (6%)	0	100	100
44	k	49/156 (31%)	43 (88%)	6 (12%)	0	100	100
45	m	120/132 (91%)	117 (98%)	3 (2%)	0	100	100
46	n	61/69 (88%)	58 (95%)	3 (5%)	0	100	100
47	o	75/320 (23%)	72 (96%)	3 (4%)	0	100	100
48	p	83/113 (74%)	80 (96%)	3 (4%)	0	100	100
49	q	86/144 (60%)	76 (88%)	10 (12%)	0	100	100
50	z	154/258 (60%)	140 (91%)	14 (9%)	0	100	100
51	M	129/135 (96%)	121 (94%)	7 (5%)	1 (1%)	16	48
52	h	101/119 (85%)	94 (93%)	7 (7%)	0	100	100
53	s	136/333 (41%)	119 (88%)	17 (12%)	0	100	100
55	t	346/472 (73%)	334 (96%)	8 (2%)	4 (1%)	10	40
56	j	382/406 (94%)	365 (96%)	15 (4%)	2 (0%)	24	56
57	g	220/1310 (17%)	207 (94%)	9 (4%)	4 (2%)	6	34
All	All	10949/15464 (71%)	10216 (93%)	706 (6%)	27 (0%)	44	72

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	1	282	PRO
4	4	264	GLY
9	8	154	PRO
55	t	167	GLN
55	t	168	PRO
55	t	248	ARG
57	g	827	VAL
2	1	339	TYR
51	M	83	ASN
56	j	339	GLN
57	g	855	LYS
57	g	989	ASN
2	1	427	PRO
2	1	499	PRO
4	4	263	ILE
5	u	340	ARG
8	y	849	PRO
55	t	247	PRO
4	4	320	PRO
8	y	313	GLU
57	g	854	ASP
2	1	286	PRO
2	1	401	PRO
5	u	330	PRO
20	3	206	ASP
2	1	633	GLY
56	j	173	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	1	97/702 (14%)	96 (99%)	1 (1%)	68	74
3	6	49/335 (15%)	49 (100%)	0	100	100
5	u	528/1259 (42%)	518 (98%)	10 (2%)	50	65
6	v	206/406 (51%)	200 (97%)	6 (3%)	37	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	S	200/218 (92%)	197 (98%)	3 (2%)	57	68
8	y	564/811 (70%)	559 (99%)	5 (1%)	70	75
10	G	159/174 (91%)	159 (100%)	0	100	100
11	H	73/76 (96%)	72 (99%)	1 (1%)	59	70
12	K	65/67 (97%)	65 (100%)	0	100	100
13	L	186/225 (83%)	181 (97%)	5 (3%)	39	59
14	O	192/231 (83%)	191 (100%)	1 (0%)	81	80
15	N	173/243 (71%)	173 (100%)	0	100	100
16	Q	86/98 (88%)	83 (96%)	3 (4%)	32	54
17	P	104/119 (87%)	103 (99%)	1 (1%)	68	74
18	I	130/131 (99%)	129 (99%)	1 (1%)	73	76
19	x	206/494 (42%)	199 (97%)	7 (3%)	32	55
23	9	23/24 (96%)	23 (100%)	0	100	100
25	B	129/142 (91%)	128 (99%)	1 (1%)	73	76
26	C	220/225 (98%)	218 (99%)	2 (1%)	70	75
27	D	158/168 (94%)	155 (98%)	3 (2%)	50	65
28	E	112/115 (97%)	110 (98%)	2 (2%)	51	67
29	F	38/48 (79%)	37 (97%)	1 (3%)	40	60
30	r	247/280 (88%)	232 (94%)	15 (6%)	17	44
31	J	112/113 (99%)	108 (96%)	4 (4%)	31	54
32	R	172/180 (96%)	167 (97%)	5 (3%)	37	57
33	T	107/115 (93%)	104 (97%)	3 (3%)	38	58
34	V	156/170 (92%)	153 (98%)	3 (2%)	50	65
35	Y	117/121 (97%)	115 (98%)	2 (2%)	53	67
36	Z	190/202 (94%)	185 (97%)	5 (3%)	40	60
37	a	90/136 (66%)	89 (99%)	1 (1%)	65	73
38	b	100/130 (77%)	100 (100%)	0	100	100
39	c	272/275 (99%)	263 (97%)	9 (3%)	33	55
40	d	112/115 (97%)	107 (96%)	5 (4%)	24	49
41	e	58/103 (56%)	56 (97%)	2 (3%)	32	55
42	f	123/132 (93%)	121 (98%)	2 (2%)	55	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	i	44/49 (90%)	44 (100%)	0	100	100
44	k	47/140 (34%)	43 (92%)	4 (8%)	10	35
45	m	104/108 (96%)	96 (92%)	8 (8%)	12	38
46	n	56/62 (90%)	55 (98%)	1 (2%)	51	67
47	o	64/277 (23%)	61 (95%)	3 (5%)	23	48
48	p	74/96 (77%)	67 (90%)	7 (10%)	8	31
49	q	75/123 (61%)	65 (87%)	10 (13%)	4	20
51	M	119/122 (98%)	111 (93%)	8 (7%)	15	42
52	h	94/107 (88%)	94 (100%)	0	100	100
53	s	128/304 (42%)	119 (93%)	9 (7%)	14	41
56	j	339/357 (95%)	332 (98%)	7 (2%)	47	64
57	g	210/1121 (19%)	206 (98%)	4 (2%)	50	65
All	All	6908/11249 (61%)	6738 (98%)	170 (2%)	42	61

All (170) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	l	554	VAL
5	u	109	GLN
5	u	331	ILE
5	u	337	ASP
5	u	340	ARG
5	u	448	GLN
5	u	459	VAL
5	u	562	ARG
5	u	563	LYS
5	u	568	ILE
5	u	572	ARG
6	v	205	LEU
6	v	237	LEU
6	v	243	LEU
6	v	246	ILE
6	v	252	HIS
6	v	392	VAL
7	S	44	GLU
7	S	153	VAL
7	S	158	VAL
8	y	77	THR

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Mol	Chain	Res	Type
8	y	102	VAL
8	y	116	TYR
8	y	140	THR
8	y	841	THR
11	H	25	VAL
13	L	115	GLN
13	L	116	THR
13	L	120	GLN
13	L	227	ARG
13	L	230	THR
14	O	210	VAL
16	Q	15	ARG
16	Q	86	ASN
16	Q	87	ARG
17	P	52	THR
18	I	20	ARG
19	x	57	ASN
19	x	368	ASP
19	x	385	ASN
19	x	466	LEU
19	x	470	GLN
19	x	471	PHE
19	x	475	GLU
25	B	114	SER
26	C	12	VAL
26	C	139	LEU
27	D	3	VAL
27	D	154	GLN
27	D	155	LYS
28	E	105	PHE
28	E	125	VAL
29	F	103	THR
30	r	20	VAL
30	r	34	VAL
30	r	48	LEU
30	r	56	ILE
30	r	72	VAL
30	r	73	VAL
30	r	88	ARG
30	r	89	ARG
30	r	121	TYR
30	r	195	ILE

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Mol	Chain	Res	Type
30	r	240	THR
30	r	248	LEU
30	r	271	VAL
30	r	277	VAL
30	r	278	VAL
31	J	2	VAL
31	J	25	VAL
31	J	30	CYS
31	J	80	ASP
32	R	62	VAL
32	R	119	LEU
32	R	136	ILE
32	R	145	ILE
32	R	155	ASN
33	T	27	VAL
33	T	80	ASP
33	T	100	LYS
34	V	41	VAL
34	V	119	SER
34	V	166	ILE
35	Y	100	VAL
35	Y	143	LYS
36	Z	42	THR
36	Z	44	THR
36	Z	139	SER
36	Z	149	SER
36	Z	179	GLN
37	a	51	SER
39	c	72	SER
39	c	107	ASP
39	c	113	PHE
39	c	134	THR
39	c	148	SER
39	c	199	THR
39	c	265	ILE
39	c	275	ILE
39	c	277	THR
40	d	34	VAL
40	d	63	HIS
40	d	66	LEU
40	d	96	SER
40	d	123	LEU

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Mol	Chain	Res	Type
41	e	51	ASP
41	e	58	LEU
42	f	31	THR
42	f	83	PHE
44	k	102	VAL
44	k	103	LEU
44	k	117	LEU
44	k	144	CYS
45	m	62	VAL
45	m	66	GLU
45	m	74	ILE
45	m	91	LEU
45	m	94	ILE
45	m	123	VAL
45	m	124	ILE
45	m	132	LYS
46	n	46	VAL
47	o	240	THR
47	o	286	SER
47	o	313	GLU
48	p	46	THR
48	p	50	ILE
48	p	59	LEU
48	p	60	VAL
48	p	85	LEU
48	p	102	LEU
48	p	108	LEU
49	q	28	PHE
49	q	39	ILE
49	q	40	LYS
49	q	47	LEU
49	q	51	CYS
49	q	55	VAL
49	q	73	THR
49	q	81	LEU
49	q	86	ASP
49	q	99	GLU
51	M	8	THR
51	M	66	VAL
51	M	69	ILE
51	M	71	ILE
51	M	72	LYS

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Mol	Chain	Res	Type
51	M	73	LEU
51	M	75	GLU
51	M	81	ARG
53	s	179	LEU
53	s	187	MET
53	s	228	LEU
53	s	232	GLN
53	s	244	LEU
53	s	275	ILE
53	s	279	VAL
53	s	290	ILE
53	s	304	THR
56	j	58	ILE
56	j	106	LEU
56	j	112	LEU
56	j	169	ARG
56	j	299	VAL
56	j	332	LEU
56	j	357	ILE
57	g	804	LYS
57	g	827	VAL
57	g	854	ASP
57	g	919	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (56) such sidechains are listed below:

Mol	Chain	Res	Type
5	u	79	GLN
5	u	200	ASN
5	u	212	HIS
5	u	219	ASN
5	u	221	ASN
5	u	236	GLN
5	u	270	GLN
5	u	288	ASN
5	u	392	ASN
5	u	442	GLN
5	u	448	GLN
5	u	512	GLN
5	u	566	GLN
6	v	377	ASN
8	y	118	ASN

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Mol	Chain	Res	Type
8	y	433	ASN
8	y	460	GLN
8	y	467	GLN
8	y	520	GLN
8	y	701	HIS
8	y	717	GLN
8	y	852	GLN
15	N	33	GLN
15	N	193	HIS
16	Q	17	HIS
16	Q	43	ASN
18	I	36	GLN
19	x	57	ASN
19	x	470	GLN
25	B	94	HIS
25	B	112	HIS
26	C	142	HIS
26	C	201	HIS
28	E	16	HIS
28	E	23	HIS
28	E	61	GLN
30	r	179	ASN
30	r	181	ASN
31	J	70	ASN
31	J	120	HIS
32	R	167	GLN
34	V	36	GLN
35	Y	11	GLN
35	Y	29	ASN
36	Z	145	GLN
38	b	32	GLN
42	f	73	ASN
51	M	74	GLN
51	M	118	GLN
52	h	81	GLN
52	h	85	HIS
53	s	221	ASN
53	s	292	GLN
56	j	248	GLN
57	g	898	ASN
57	g	980	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
22	7	27/28 (96%)	20 (74%)	0
24	A	1710/1869 (91%)	415 (24%)	42 (2%)
54	w	74/75 (98%)	33 (44%)	0
All	All	1811/1972 (91%)	468 (25%)	42 (2%)

All (468) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
22	7	4	A
22	7	5	A
22	7	7	A
22	7	9	A
22	7	10	A
22	7	11	A
22	7	12	A
22	7	13	A
22	7	14	A
22	7	15	A
22	7	16	A
22	7	17	A
22	7	18	A
22	7	20	A
22	7	21	A
22	7	22	A
22	7	24	A
22	7	25	A
22	7	26	A
22	7	27	A
24	A	2	A
24	A	4	C
24	A	9	U
24	A	10	G
24	A	11	A
24	A	12	U
24	A	17	C
24	A	23	G
24	A	33	G
24	A	41	G
24	A	42	A
24	A	44	U
24	A	46	A

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Mol	Chain	Res	Type
24	A	56	G
24	A	58	C
24	A	59	U
24	A	62	G
24	A	64	A
24	A	65	C
24	A	67	C
24	A	68	A
24	A	72	C
24	A	73	C
24	A	74	G
24	A	78	C
24	A	82	G
24	A	103	A
24	A	110	U
24	A	114	G
24	A	115	U
24	A	126	G
24	A	129	C
24	A	130	G
24	A	140	U
24	A	142	C
24	A	143	U
24	A	147	A
24	A	155	G
24	A	158	A
24	A	160	U
24	A	163	U
24	A	168	C
24	A	173	A
24	A	180	G
24	A	182	C
24	A	184	G
24	A	190	G
24	A	198	U
24	A	200	G
24	A	202	G
24	A	203	G
24	A	204	G
24	A	206	G
24	A	208	G
24	A	288	G

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Mol	Chain	Res	Type
24	A	291	G
24	A	292	A
24	A	294	U
24	A	295	C
24	A	306	C
24	A	307	G
24	A	308	G
24	A	309	G
24	A	314	U
24	A	318	A
24	A	319	C
24	A	320	G
24	A	321	C
24	A	323	C
24	A	324	C
24	A	325	C
24	A	326	C
24	A	327	G
24	A	328	U
24	A	329	G
24	A	332	G
24	A	347	G
24	A	362	C
24	A	363	A
24	A	364	A
24	A	368	U
24	A	369	C
24	A	370	G
24	A	382	C
24	A	385	G
24	A	386	C
24	A	409	C
24	A	418	A
24	A	421	G
24	A	447	A
24	A	448	A
24	A	449	A
24	A	450	C
24	A	452	G
24	A	465	A
24	A	471	G
24	A	472	C

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Mol	Chain	Res	Type
24	A	473	A
24	A	474	G
24	A	476	A
24	A	482	G
24	A	487	U
24	A	492	C
24	A	508	A
24	A	512	A
24	A	516	A
24	A	525	A
24	A	533	A
24	A	534	G
24	A	536	A
24	A	537	C
24	A	538	U
24	A	539	C
24	A	540	U
24	A	541	U
24	A	542	U
24	A	543	C
24	A	544	G
24	A	545	A
24	A	546	G
24	A	547	G
24	A	550	C
24	A	553	U
24	A	554	A
24	A	556	U
24	A	557	U
24	A	558	G
24	A	559	G
24	A	563	G
24	A	564	A
24	A	566	U
24	A	568	C
24	A	576	A
24	A	583	A
24	A	589	G
24	A	590	A
24	A	591	U
24	A	598	G
24	A	604	A

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Mol	Chain	Res	Type
24	A	606	G
24	A	607	U
24	A	608	C
24	A	614	C
24	A	624	C
24	A	626	G
24	A	627	U
24	A	628	A
24	A	629	A
24	A	631	U
24	A	643	A
24	A	655	A
24	A	659	G
24	A	660	C
24	A	662	G
24	A	664	A
24	A	668	A2M
24	A	669	A
24	A	671	A
24	A	672	A
24	A	673	G
24	A	687	C
24	A	688	U
24	A	689	U
24	A	690	G
24	A	693	A
24	A	694	G
24	A	734	C
24	A	736	C
24	A	748	C
24	A	749	U
24	A	751	G
24	A	752	G
24	A	753	C
24	A	790	C
24	A	791	C
24	A	797	C
24	A	798	G
24	A	799	U
24	A	801	U
24	A	810	A
24	A	811	A

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Mol	Chain	Res	Type
24	A	821	G
24	A	827	A
24	A	830	A
24	A	836	G
24	A	837	A
24	A	838	G
24	A	839	C
24	A	840	C
24	A	841	G
24	A	845	G
24	A	869	A
24	A	870	A
24	A	872	A
24	A	873	G
24	A	878	G
24	A	880	G
24	A	886	A
24	A	888	U
24	A	889	U
24	A	890	U
24	A	891	G
24	A	892	U
24	A	894	G
24	A	895	G
24	A	896	U
24	A	897	U
24	A	898	U
24	A	899	U
24	A	900	C
24	A	903	A
24	A	904	A
24	A	909	G
24	A	912	C
24	A	913	A
24	A	914	U
24	A	920	A
24	A	922	A
24	A	930	C
24	A	933	G
24	A	943	U
24	A	950	C
24	A	963	A

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Mol	Chain	Res	Type
24	A	965	U
24	A	969	U
24	A	970	G
24	A	989	C
24	A	990	A
24	A	991	G
24	A	992	A
24	A	999	G
24	A	1002	U
24	A	1017	U
24	A	1023	A
24	A	1061	U
24	A	1062	A
24	A	1083	A
24	A	1085	C
24	A	1109	C
24	A	1112	U
24	A	1113	A
24	A	1114	U
24	A	1115	U
24	A	1116	C
24	A	1117	C
24	A	1120	U
24	A	1138	C
24	A	1153	C
24	A	1154	U
24	A	1170	A
24	A	1195	A
24	A	1207	G
24	A	1208	A
24	A	1209	A
24	A	1215	C
24	A	1216	C
24	A	1217	A
24	A	1224	G
24	A	1242	U
24	A	1243	PSU
24	A	1245	G
24	A	1248	U
24	A	1250	A
24	A	1251	A
24	A	1253	A

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Mol	Chain	Res	Type
24	A	1256	G
24	A	1257	G
24	A	1259	A
24	A	1274	G
24	A	1275	G
24	A	1283	C
24	A	1284	A
24	A	1286	G
24	A	1288	U
24	A	1294	G
24	A	1295	A
24	A	1301	A
24	A	1302	G
24	A	1303	C
24	A	1308	U
24	A	1318	G
24	A	1322	G
24	A	1326	U
24	A	1342	U
24	A	1356	G
24	A	1357	A
24	A	1358	U
24	A	1371	U
24	A	1372	U
24	A	1378	A
24	A	1397	U
24	A	1402	A
24	A	1406	G
24	A	1417	C
24	A	1418	C
24	A	1419	C
24	A	1420	G
24	A	1421	A
24	A	1422	G
24	A	1423	C
24	A	1424	G
24	A	1433	C
24	A	1435	C
24	A	1436	C
24	A	1437	C
24	A	1438	A
24	A	1454	A

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Mol	Chain	Res	Type
24	A	1455	A
24	A	1463	U
24	A	1488	C
24	A	1489	A
24	A	1490	G
24	A	1497	G
24	A	1498	A
24	A	1519	U
24	A	1520	G
24	A	1521	C
24	A	1522	A
24	A	1533	A
24	A	1534	C
24	A	1544	C
24	A	1553	C
24	A	1556	A
24	A	1570	G
24	A	1580	A
24	A	1587	G
24	A	1588	A
24	A	1594	A
24	A	1598	G
24	A	1599	U
24	A	1600	G
24	A	1601	A
24	A	1602	U
24	A	1603	G
24	A	1604	G
24	A	1618	C
24	A	1619	A
24	A	1621	U
24	A	1623	A
24	A	1624	U
24	A	1639	G
24	A	1644	C
24	A	1648	G
24	A	1654	G
24	A	1663	A
24	A	1665	G
24	A	1671	G
24	A	1686	G
24	A	1695	A

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Mol	Chain	Res	Type
24	A	1699	A
24	A	1700	C
24	A	1701	C
24	A	1702	G
24	A	1711	U
24	A	1712	A
24	A	1715	A
24	A	1719	A
24	A	1721	U
24	A	1722	G
24	A	1733	U
24	A	1744	G
24	A	1749	G
24	A	1750	C
24	A	1752	C
24	A	1753	C
24	A	1754	G
24	A	1755	C
24	A	1756	C
24	A	1757	G
24	A	1758	G
24	A	1759	G
24	A	1760	G
24	A	1772	C
24	A	1773	C
24	A	1774	C
24	A	1775	U
24	A	1776	G
24	A	1777	G
24	A	1778	C
24	A	1779	G
24	A	1780	G
24	A	1781	A
24	A	1782	G
24	A	1783	C
24	A	1784	G
24	A	1800	A
24	A	1804	U
24	A	1805	G
24	A	1808	U
24	A	1809	A
24	A	1813	A

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Mol	Chain	Res	Type
24	A	1822	A
24	A	1823	A
24	A	1824	A
24	A	1825	A
24	A	1829	G
24	A	1831	A
24	A	1834	A
24	A	1835	A
24	A	1837	G
24	A	1838	U
24	A	1839	U
24	A	1841	C
24	A	1849	G
24	A	1851	MA6
24	A	1853	C
24	A	1860	A
24	A	1861	G
24	A	1862	G
24	A	1863	A
24	A	1864	U
24	A	1865	C
24	A	1866	A
24	A	1867	U
24	A	1868	U
54	w	2	G
54	w	6	A
54	w	7	G
54	w	8	U
54	w	9	G
54	w	10	G
54	w	14	A
54	w	15	G
54	w	16	C
54	w	17	G
54	w	18	G
54	w	19	A
54	w	20	A
54	w	42	G
54	w	43	A
54	w	44	G
54	w	45	G
54	w	46	U

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Mol	Chain	Res	Type
54	w	51	G
54	w	52	G
54	w	54	U
54	w	55	C
54	w	56	G
54	w	57	A
54	w	58	A
54	w	60	C
54	w	63	U
54	w	64	C
54	w	71	U
54	w	72	A
54	w	73	C
54	w	74	C
54	w	75	A

All (42) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
24	A	1	U
24	A	9	U
24	A	291	G
24	A	368	U
24	A	370	G
24	A	687	C
24	A	688	U
24	A	689	U
24	A	797	C
24	A	798	G
24	A	912	C
24	A	913	A
24	A	988	C
24	A	989	C
24	A	990	A
24	A	1250	A
24	A	1357	A
24	A	1434	C
24	A	1519	U
24	A	1520	G
24	A	1521	C
24	A	1598	G
24	A	1599	U

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Mol	Chain	Res	Type
24	A	1600	G
24	A	1601	A
24	A	1603	G
24	A	1699	A
24	A	1700	C
24	A	1701	C
24	A	1753	C
24	A	1759	G
24	A	1775	U
24	A	1781	A
24	A	1834	A
24	A	1860	A
24	A	1861	G
24	A	1862	G
24	A	1863	A
24	A	1864	U
24	A	1865	C
24	A	1866	A
24	A	1867	U

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

28 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$
24	PSU	A	119	24	18,21,22	0.97	1 (5%)	22,30,33	0.69	0
24	OMG	A	683	24	23,26,27	0.37	0	33,38,41	0.58	0
24	OMG	A	644	24	23,26,27	0.44	0	33,38,41	0.45	0
24	OMC	A	1703	24	19,22,23	0.44	0	26,31,34	0.49	0
24	OMC	A	517	24	19,22,23	0.46	0	26,31,34	0.41	0
24	MA6	A	1850	24	23,26,27	0.43	0	34,38,41	0.78	1 (2%)
24	A2M	A	484	24	22,25,26	0.22	0	31,36,39	0.42	0
24	OMC	A	174	59,24	19,22,23	0.43	0	26,31,34	0.44	0
24	OMU	A	116	24	19,22,23	0.39	0	26,31,34	0.51	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	PSU	A	612	24	18,21,22	1.10	2 (11%)	22,30,33	0.75	1 (4%)
24	A2M	A	668	59,24	22,25,26	0.27	0	31,36,39	0.54	0
24	JMH	A	1219	59,24	18,22,23	0.64	0	21,32,35	0.65	0
24	OMG	A	509	59,24	23,26,27	0.43	0	33,38,41	0.50	0
24	A2M	A	166	24	22,25,26	0.17	0	31,36,39	0.63	0
24	PSU	A	1243	24	18,21,22	1.00	1 (5%)	22,30,33	0.70	0
24	MA6	A	1851	24	23,26,27	0.45	0	34,38,41	0.84	1 (2%)
24	6MZ	A	1832	59,24	22,25,26	0.50	0	30,36,39	0.55	0
24	A2M	A	1678	24	22,25,26	0.18	0	31,36,39	0.43	0
24	A2M	A	1031	24	22,25,26	0.20	0	31,36,39	0.51	0
24	OMU	A	121	24	19,22,23	0.44	0	26,31,34	0.51	0
24	PSU	A	1081	24	18,21,22	1.04	2 (11%)	22,30,33	0.82	0
24	A2M	A	159	24	22,25,26	0.20	0	31,36,39	0.43	0
24	5MC	A	1374	24	18,22,23	0.44	0	26,32,35	0.61	0
24	UR3	A	1830	24	19,22,23	0.41	0	26,32,35	1.00	2 (7%)
24	PSU	A	822	24	18,21,22	1.04	2 (11%)	22,30,33	0.84	1 (4%)
24	PSU	A	823	24	18,21,22	1.05	1 (5%)	22,30,33	0.68	0
24	A2M	A	27	59,24	22,25,26	0.22	0	31,36,39	0.46	0
24	5MU	A	814	24	19,22,23	0.45	0	28,32,35	0.50	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	PSU	A	119	24	-	0/7/25/26	0/2/2/2
24	OMG	A	683	24	-	0/9/27/28	0/3/3/3
24	OMG	A	644	24	-	1/9/27/28	0/3/3/3
24	OMC	A	1703	24	-	0/9/27/28	0/2/2/2
24	OMC	A	517	24	-	0/9/27/28	0/2/2/2
24	MA6	A	1850	24	-	3/11/29/30	0/3/3/3
24	A2M	A	484	24	-	0/9/27/28	0/3/3/3
24	OMC	A	174	59,24	-	0/9/27/28	0/2/2/2
24	OMU	A	116	24	-	0/9/27/28	0/2/2/2
24	PSU	A	612	24	-	0/7/25/26	0/2/2/2
24	A2M	A	668	59,24	-	2/9/27/28	0/3/3/3
24	JMH	A	1219	59,24	-	0/7/25/26	0/2/2/2
24	OMG	A	509	59,24	-	0/9/27/28	0/3/3/3
24	A2M	A	166	24	-	0/9/27/28	0/3/3/3
24	PSU	A	1243	24	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	MA6	A	1851	24	-	5/11/29/30	0/3/3/3
24	6MZ	A	1832	59,24	-	2/9/27/28	0/3/3/3
24	A2M	A	1678	24	-	0/9/27/28	0/3/3/3
24	A2M	A	1031	24	-	0/9/27/28	0/3/3/3
24	OMU	A	121	24	-	0/9/27/28	0/2/2/2
24	PSU	A	1081	24	-	1/7/25/26	0/2/2/2
24	A2M	A	159	24	-	2/9/27/28	0/3/3/3
24	5MC	A	1374	24	-	0/7/25/26	0/2/2/2
24	UR3	A	1830	24	-	2/7/25/26	0/2/2/2
24	PSU	A	822	24	-	0/7/25/26	0/2/2/2
24	PSU	A	823	24	-	0/7/25/26	0/2/2/2
24	A2M	A	27	59,24	-	0/9/27/28	0/3/3/3
24	5MU	A	814	24	-	0/7/25/26	0/2/2/2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1243	PSU	C6-C5	3.37	1.39	1.35
24	A	823	PSU	C6-C5	3.35	1.39	1.35
24	A	119	PSU	C6-C5	3.23	1.39	1.35
24	A	612	PSU	C6-C5	3.22	1.39	1.35
24	A	1081	PSU	C6-C5	3.20	1.39	1.35
24	A	822	PSU	C6-C5	3.14	1.39	1.35
24	A	612	PSU	O4'-C1'	-2.52	1.40	1.43
24	A	1081	PSU	O4'-C1'	-2.31	1.40	1.43
24	A	822	PSU	O4'-C1'	-2.26	1.40	1.43

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1850	MA6	C2-N1-C6	3.06	118.98	111.75
24	A	1851	MA6	C2-N1-C6	3.05	118.95	111.75
24	A	822	PSU	O4'-C1'-C2'	2.28	108.36	105.14
24	A	1830	UR3	C6-N1-C2	-2.25	119.77	121.79
24	A	612	PSU	O4'-C1'-C2'	2.23	108.29	105.14
24	A	1830	UR3	C1'-N1-C2	2.16	120.63	116.99

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	A	1832	6MZ	N1-C6-N6-C9
24	A	1850	MA6	C5-C6-N6-C10
24	A	1850	MA6	N1-C6-N6-C10
24	A	1851	MA6	O4'-C4'-C5'-O5'
24	A	1851	MA6	C5-C6-N6-C10
24	A	668	A2M	O4'-C4'-C5'-O5'
24	A	1851	MA6	C3'-C4'-C5'-O5'
24	A	668	A2M	C3'-C4'-C5'-O5'
24	A	1851	MA6	N1-C6-N6-C10
24	A	1830	UR3	O4'-C1'-N1-C2
24	A	159	A2M	C3'-C4'-C5'-O5'
24	A	1830	UR3	O4'-C1'-N1-C6
24	A	159	A2M	O4'-C4'-C5'-O5'
24	A	1850	MA6	C5-C6-N6-C9
24	A	1851	MA6	C5-C6-N6-C9
24	A	644	OMG	C4'-C5'-O5'-P
24	A	1081	PSU	C4'-C5'-O5'-P
24	A	1832	6MZ	C5-C6-N6-C9

There are no ring outliers.

11 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	A	683	OMG	1	0
24	A	1703	OMC	2	0
24	A	517	OMC	1	0
24	A	1850	MA6	2	0
24	A	174	OMC	1	0
24	A	116	OMU	3	0
24	A	1832	6MZ	2	0
24	A	1678	A2M	2	0
24	A	1031	A2M	1	0
24	A	159	A2M	1	0
24	A	1374	5MC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 91 ligands modelled in this entry, 91 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

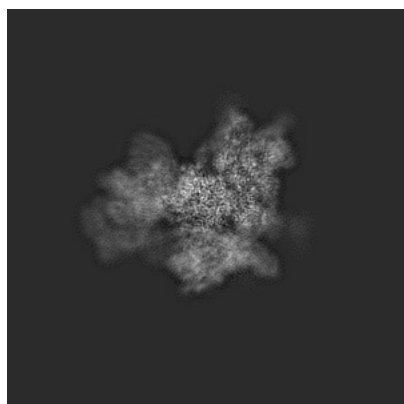
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11302. These allow visual inspection of the internal detail of the map and identification of artifacts.

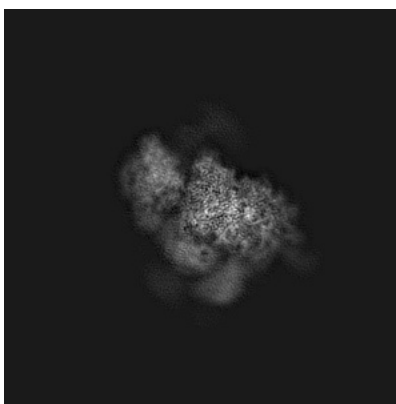
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

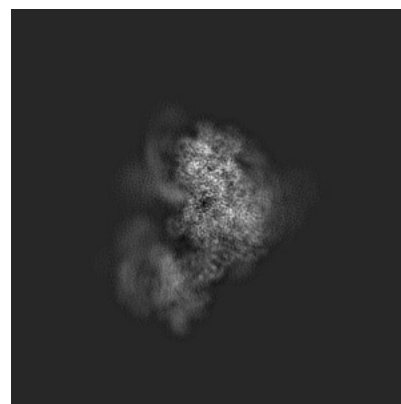
6.1.1 Primary map



X

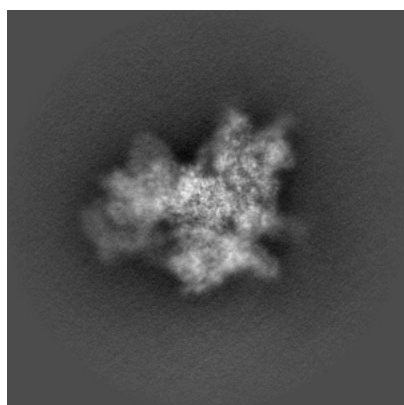


Y

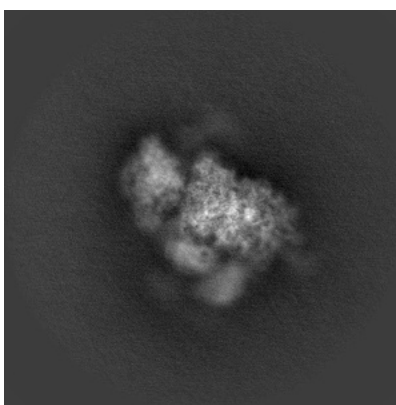


Z

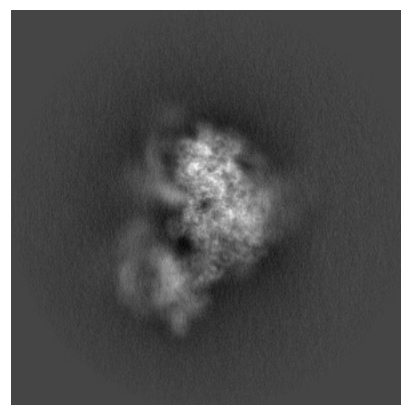
6.1.2 Raw map



X



Y

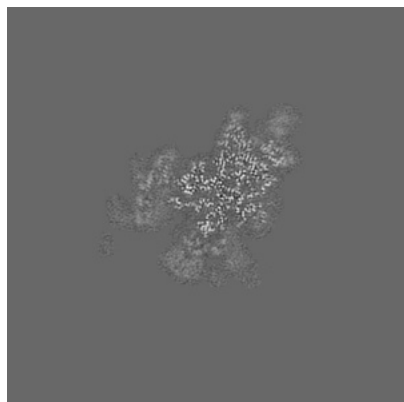


Z

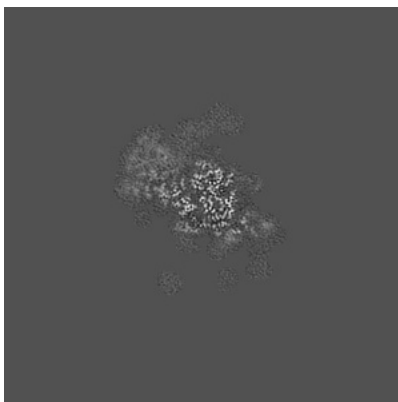
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

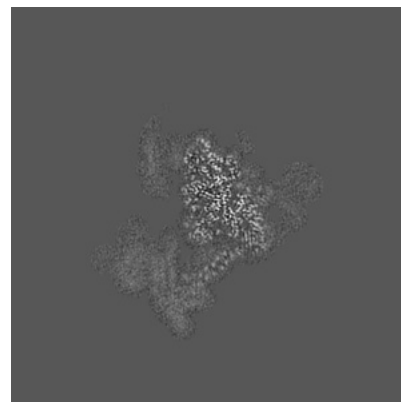
6.2.1 Primary map



X Index: 250

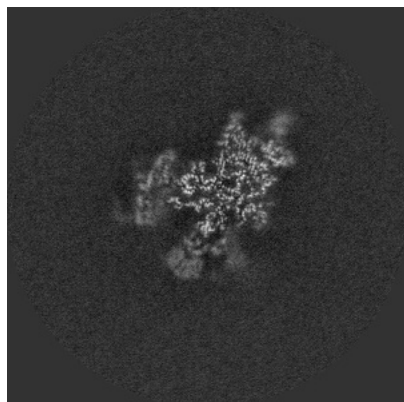


Y Index: 250

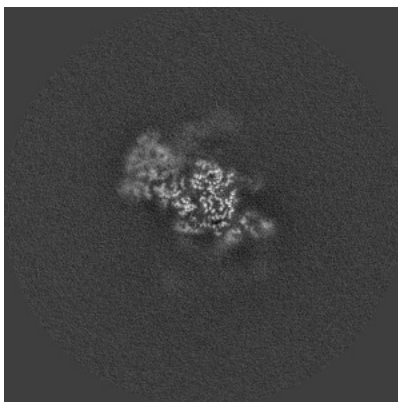


Z Index: 250

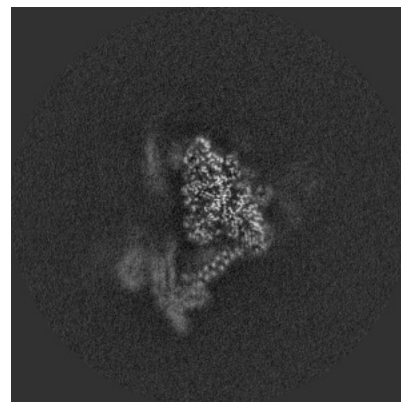
6.2.2 Raw map



X Index: 250



Y Index: 250

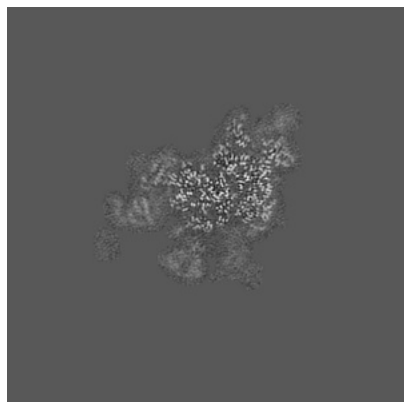


Z Index: 250

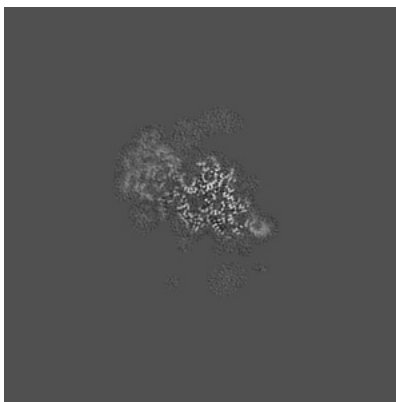
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

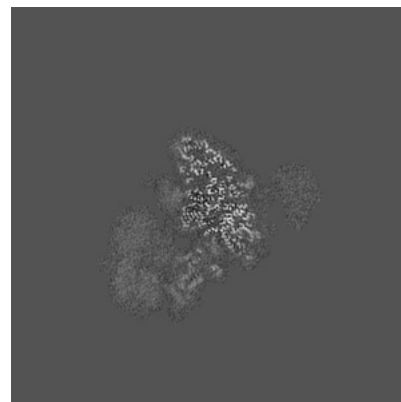
6.3.1 Primary map



X Index: 244

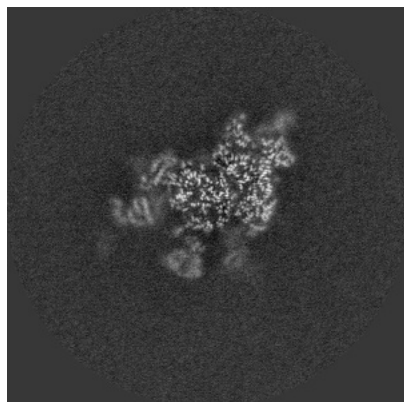


Y Index: 244

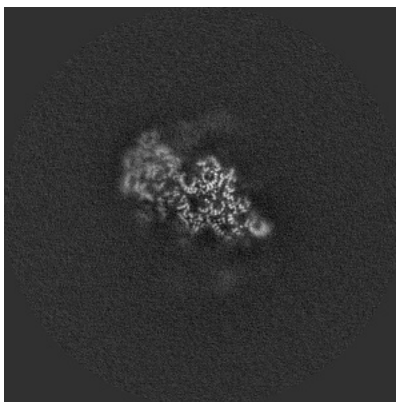


Z Index: 271

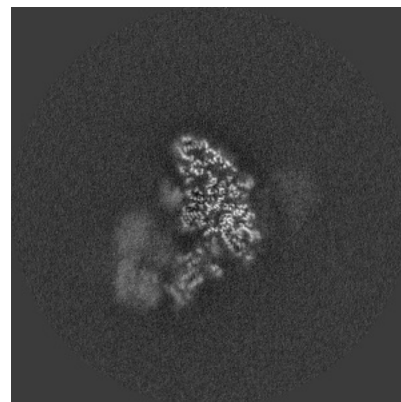
6.3.2 Raw map



X Index: 244



Y Index: 244

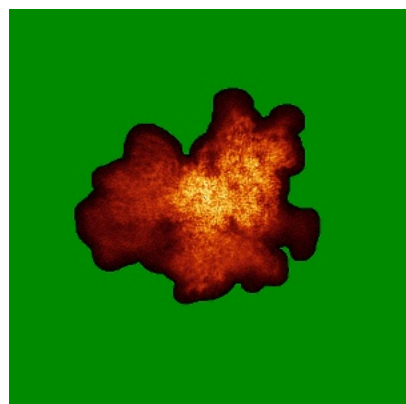


Z Index: 271

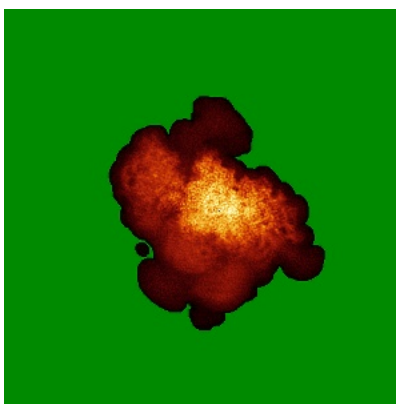
The images above show the largest variance slices of the map in three orthogonal directions.

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

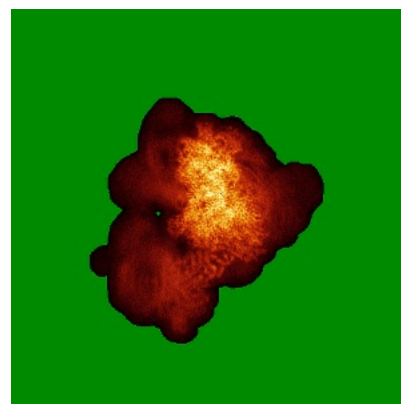
6.4.1 Primary map



X

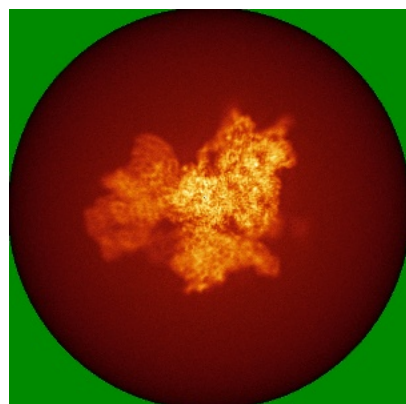


Y

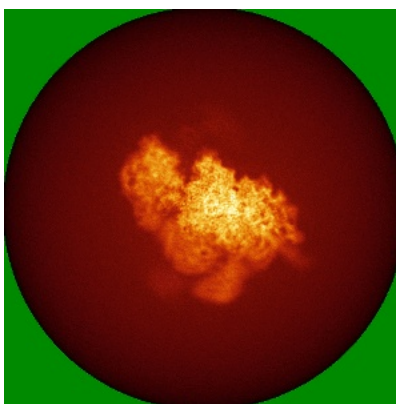


Z

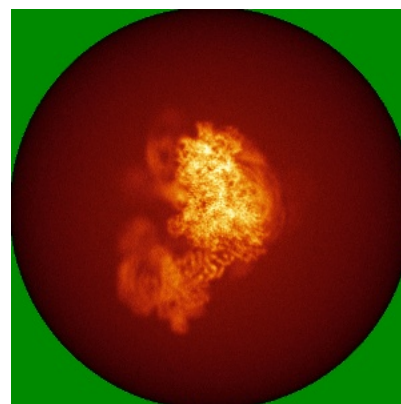
6.4.2 Raw map



X



Y

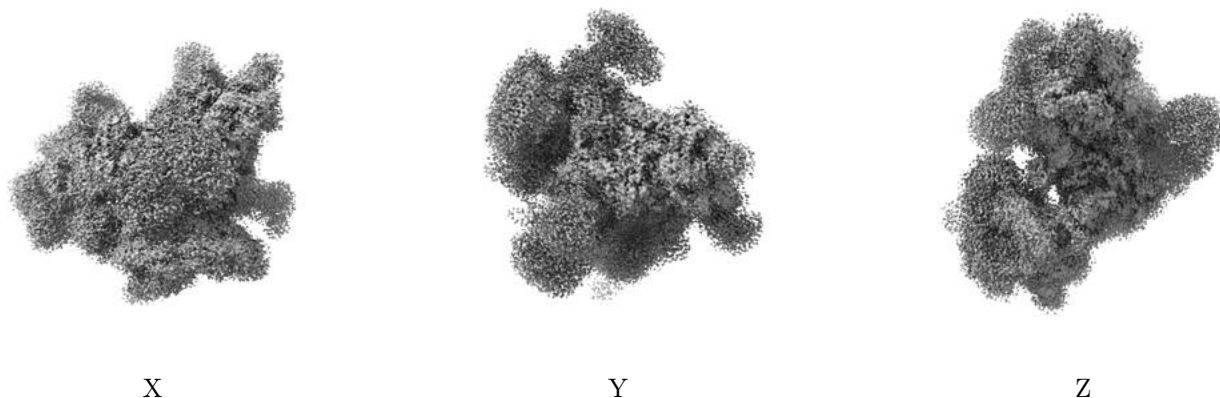


Z

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

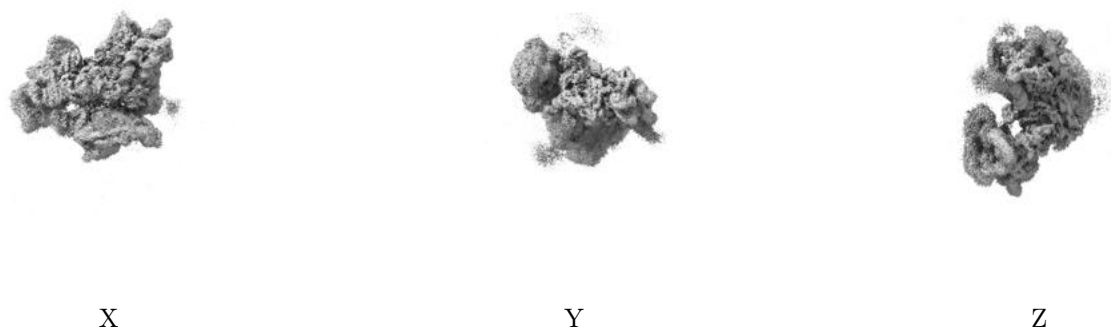
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

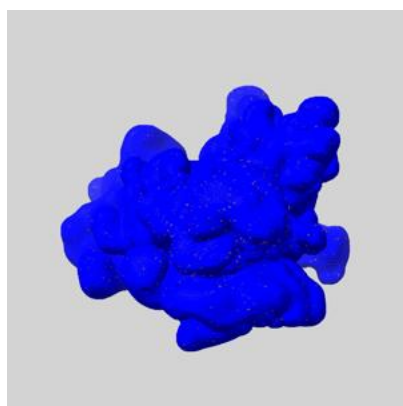
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

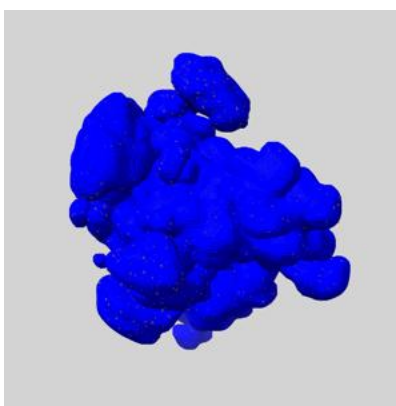
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

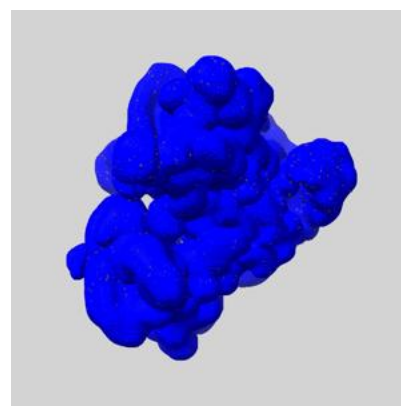
6.6.1 emd_11302_msk_1.map [i](#)



X



Y

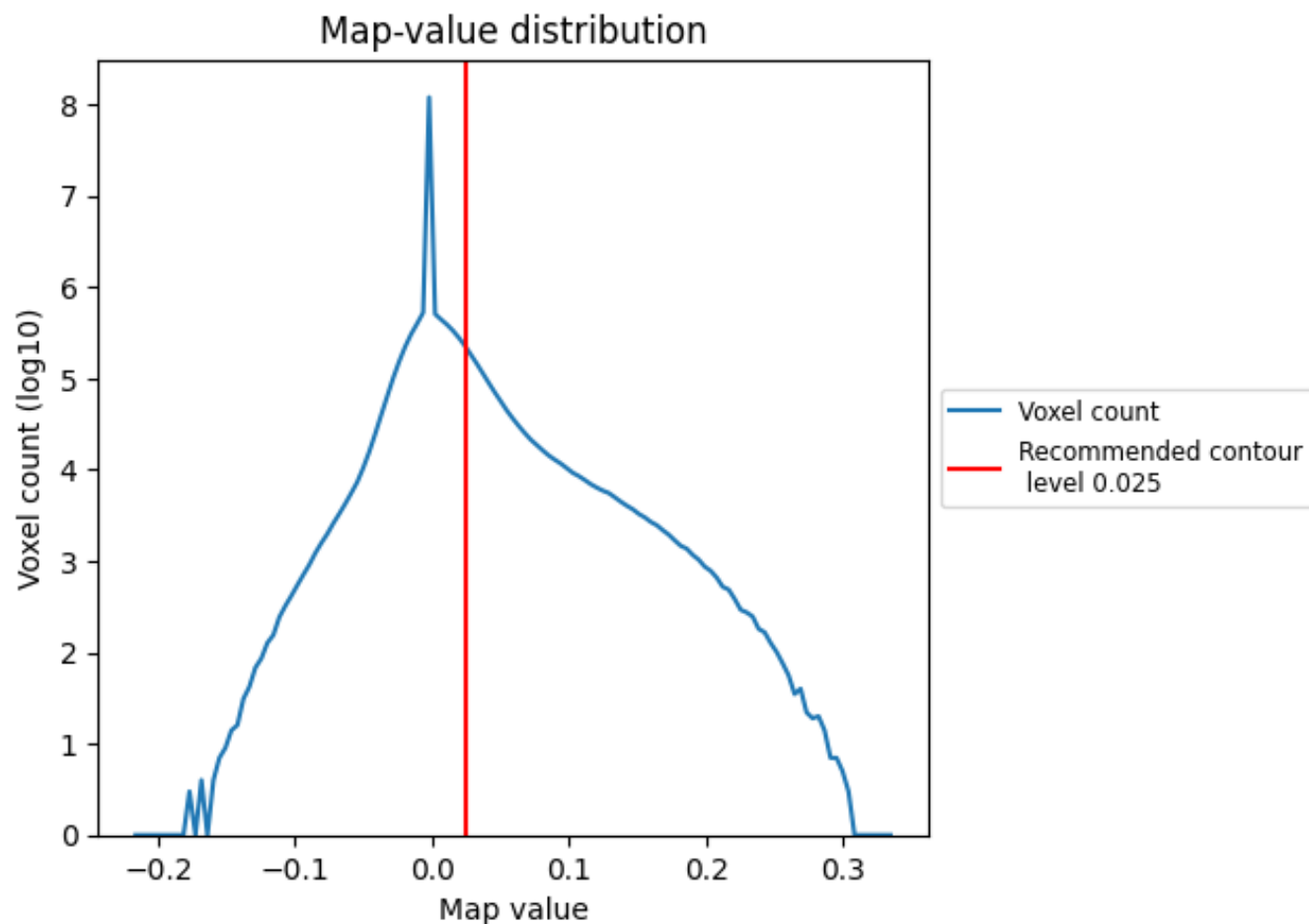


Z

7 Map analysis [i](#)

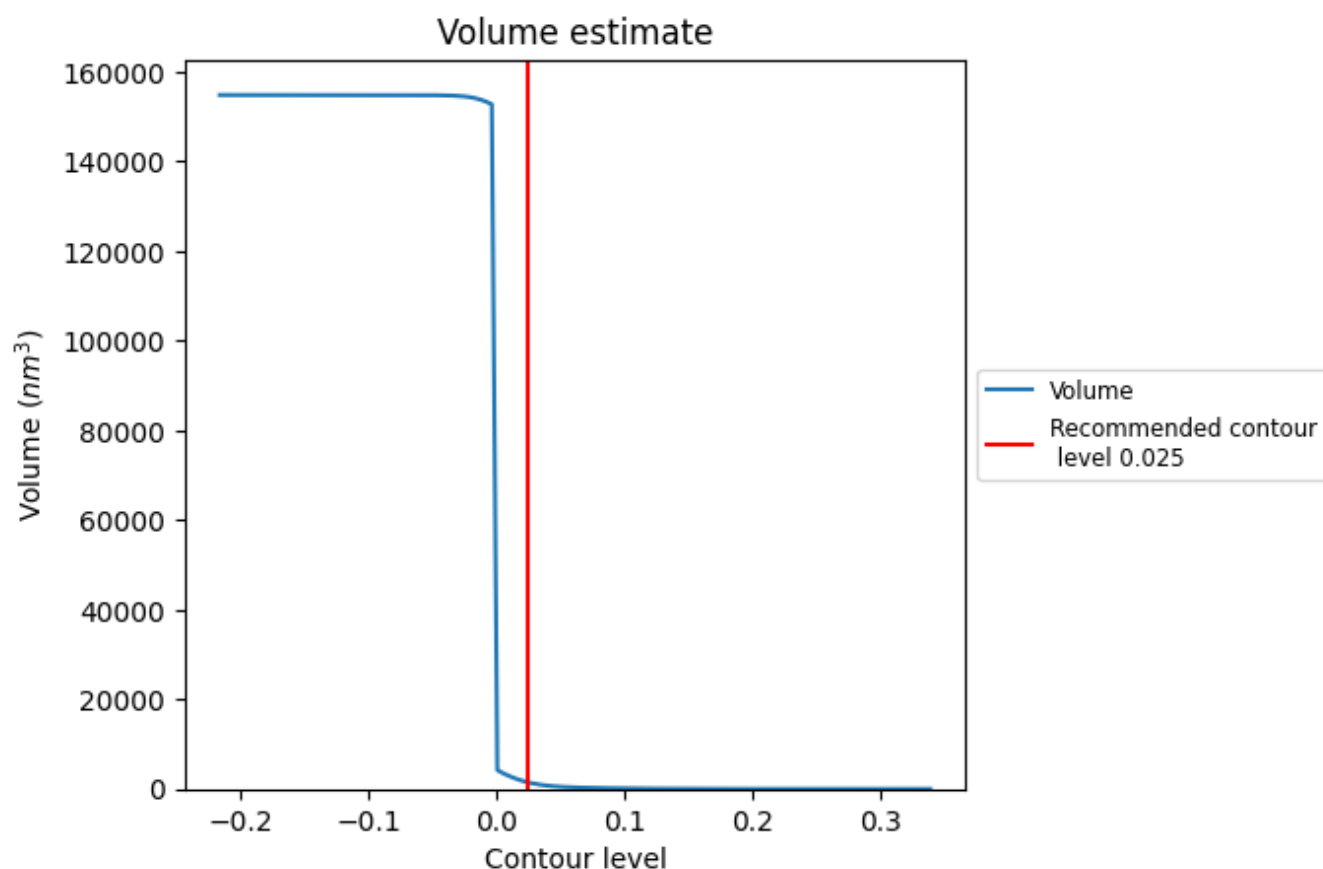
This section contains the results of statistical analysis of the map.

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.

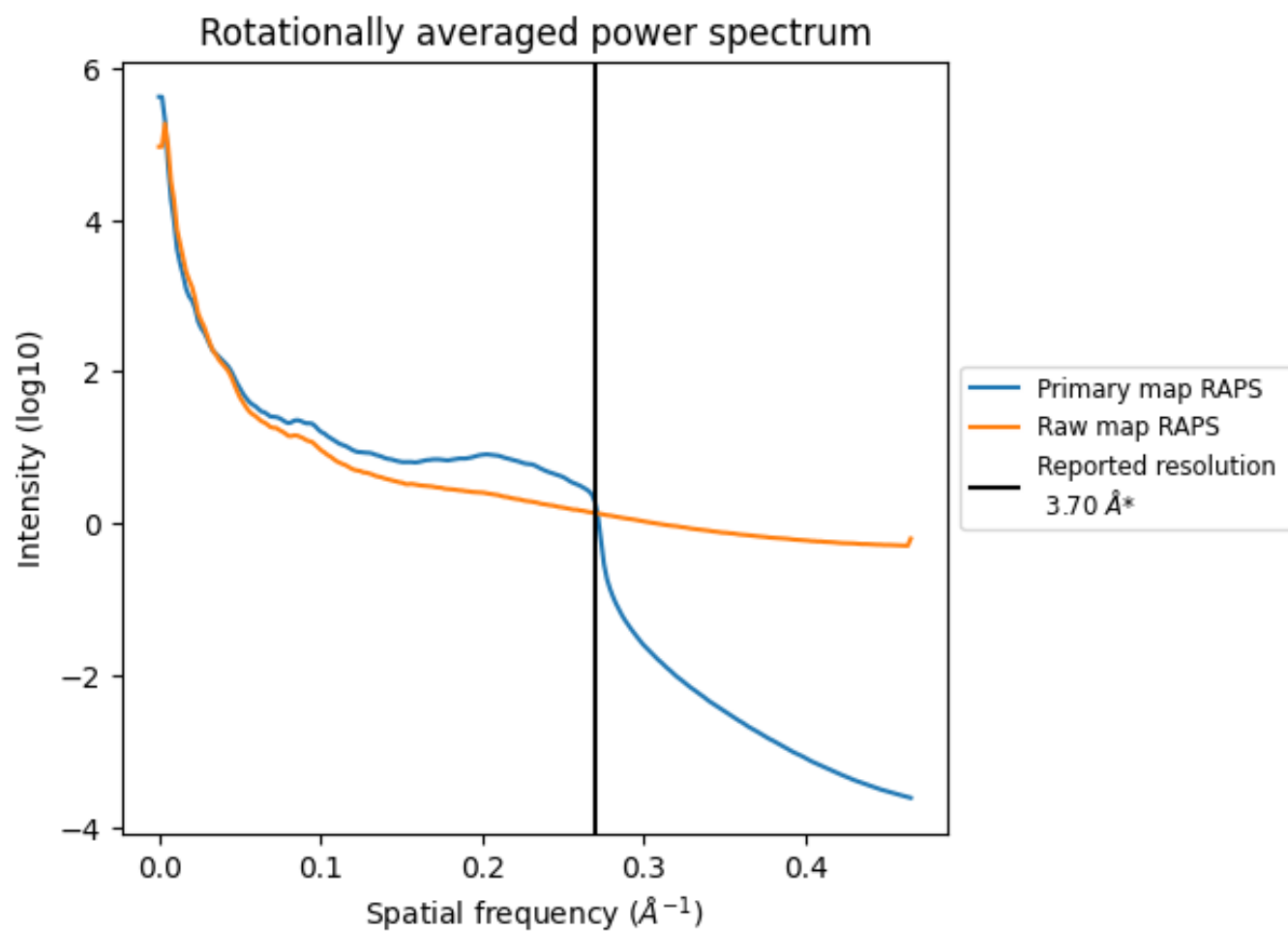
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1449 nm³; this corresponds to an approximate mass of 1309 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

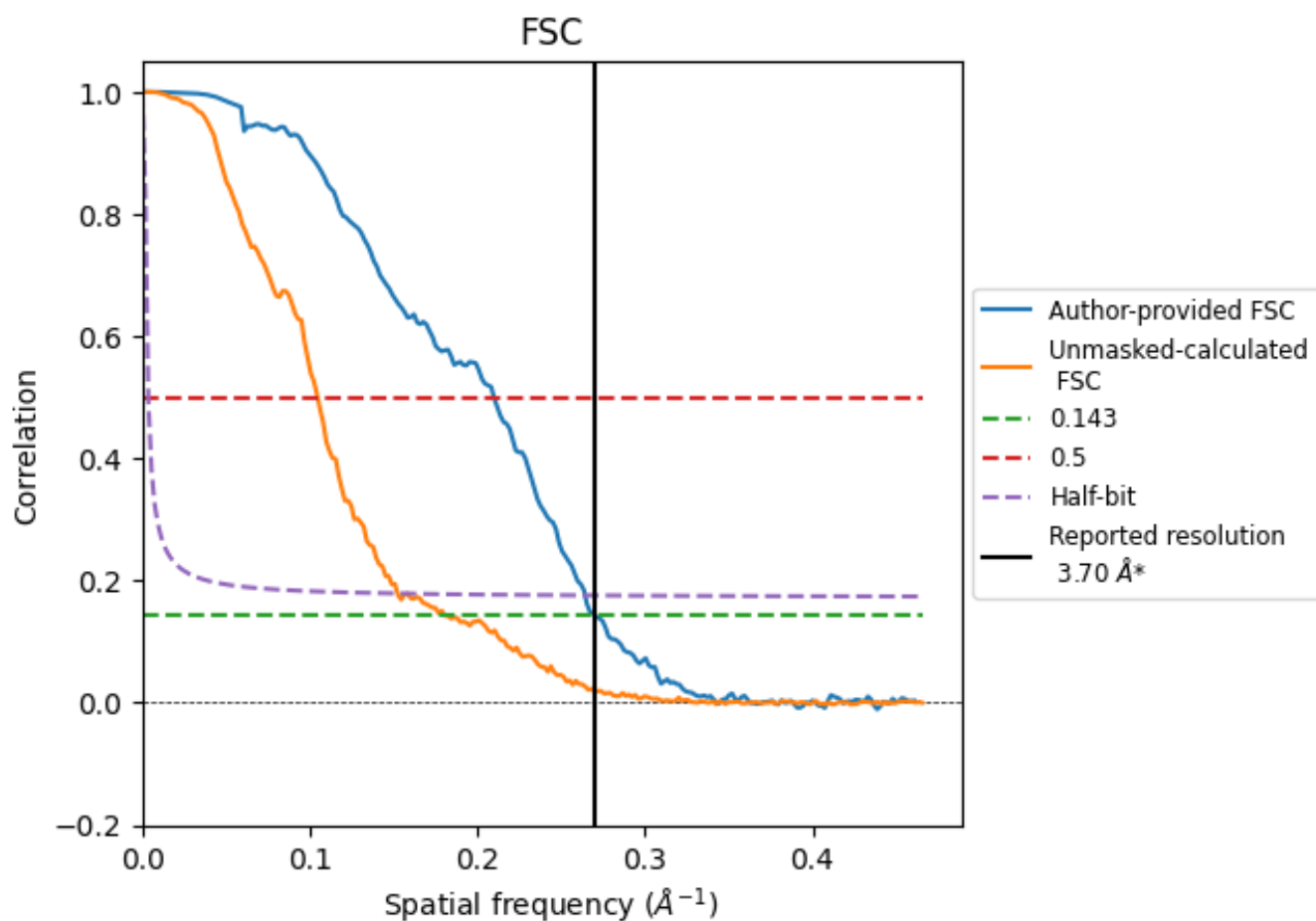


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.270 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

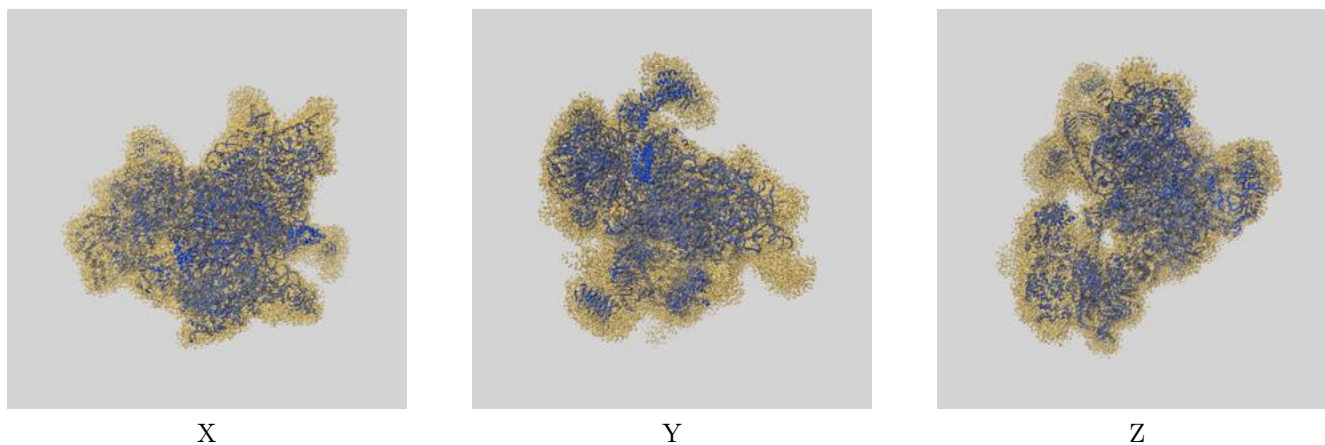
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.70	4.76	3.78
Unmasked-calculated*	5.54	9.55	6.56

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.54 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

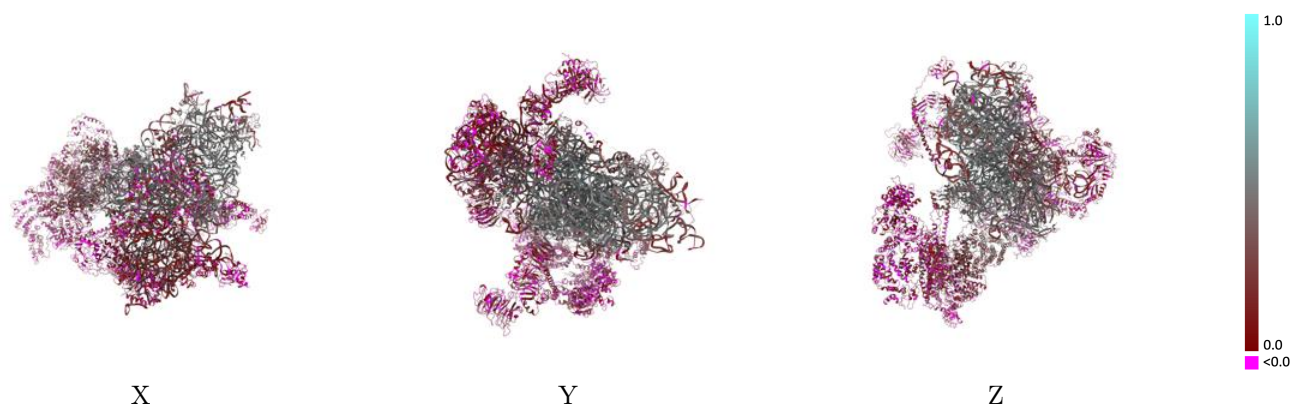
This section contains information regarding the fit between EMDB map EMD-11302 and PDB model 6ZMW. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



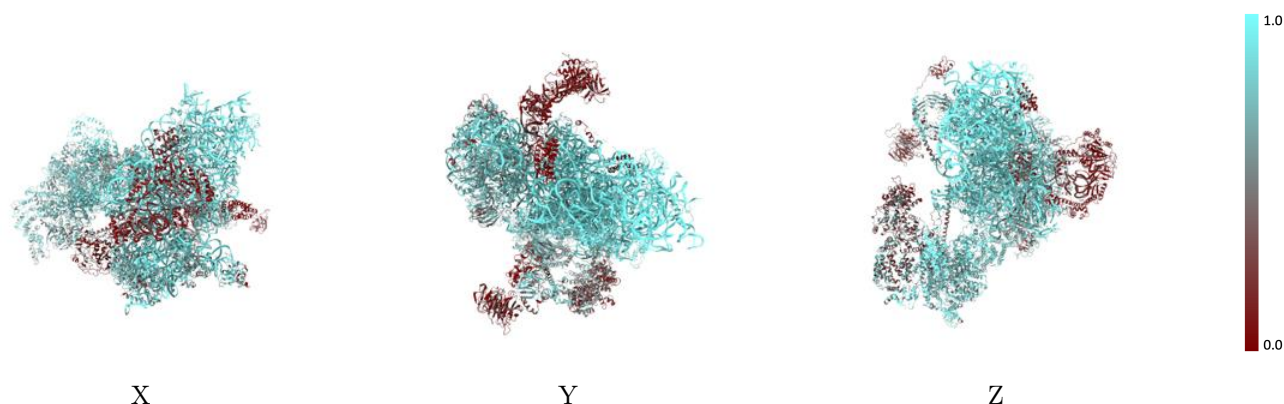
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



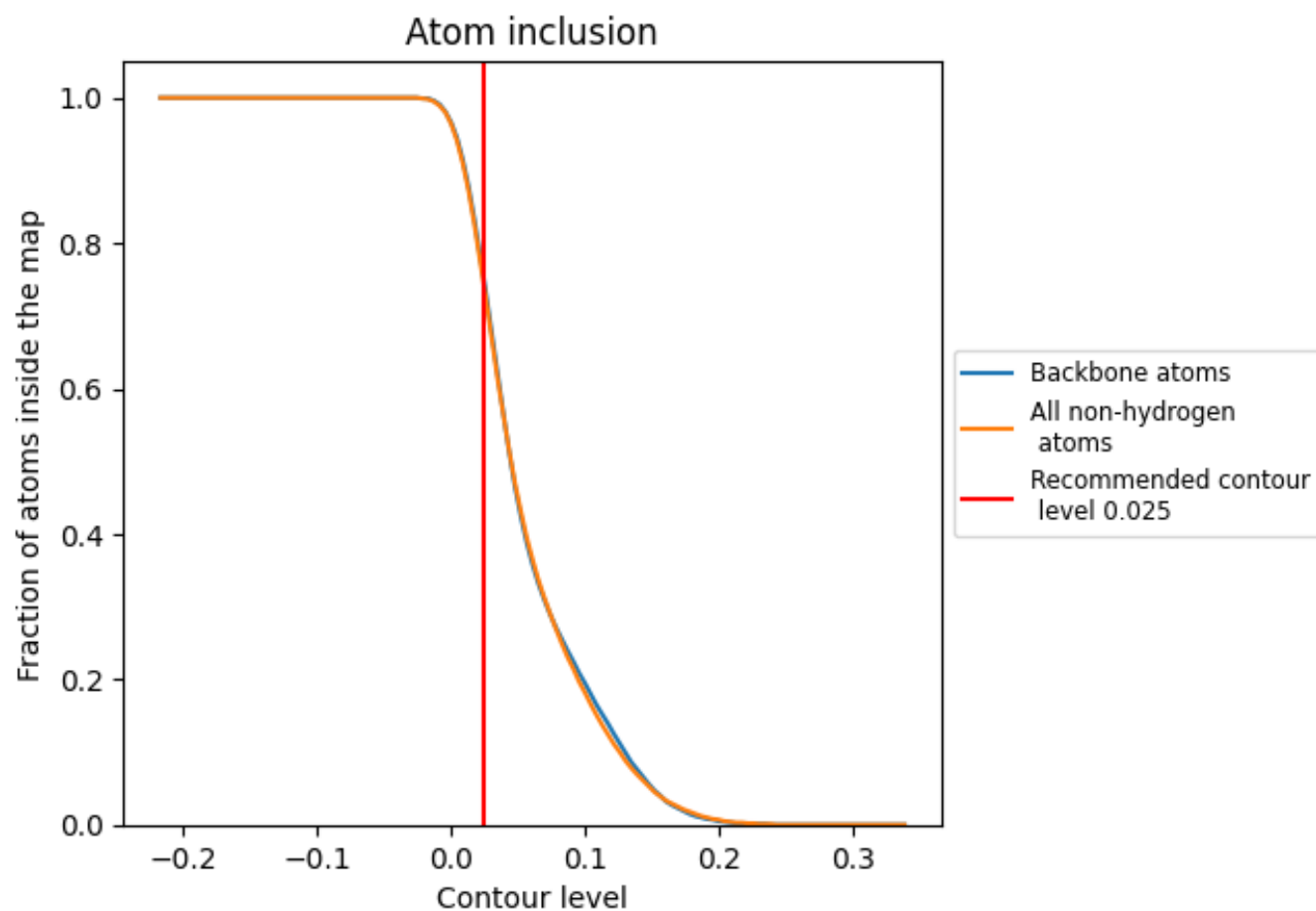
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 74% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7430	 0.2930
1	 0.5380	 0.1670
2	 0.1960	 0.1120
3	 0.6320	 0.1030
4	 0.6660	 0.1060
5	 0.6180	 0.1130
6	 0.7170	 0.1180
7	 0.2230	 0.1670
8	 0.6360	 0.1240
9	 0.8180	 0.4460
A	 0.9520	 0.3820
B	 0.9230	 0.4960
C	 0.9230	 0.5070
D	 0.9080	 0.4880
E	 0.9250	 0.5170
F	 0.9120	 0.4880
G	 0.8600	 0.4030
H	 0.8970	 0.4780
I	 0.9040	 0.4790
J	 0.9110	 0.5190
K	 0.8870	 0.4740
L	 0.8660	 0.4630
M	 0.8020	 0.3830
N	 0.9090	 0.4780
O	 0.8840	 0.4420
P	 0.8680	 0.4280
Q	 0.9070	 0.4850
R	 0.9180	 0.4460
S	 0.9230	 0.4040
T	 0.9260	 0.4690
V	 0.6710	 0.1900
Y	 0.7280	 0.2530
Z	 0.7390	 0.3100
a	 0.7030	 0.1760
b	 0.5820	 0.0970



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Chain	Atom inclusion	Q-score
c	 0.7180	 0.1900
d	 0.6890	 0.1350
e	 0.6250	 0.1070
f	 0.6540	 0.1310
g	 0.3190	 0.0700
h	 0.7650	 0.3260
i	 0.8130	 0.2940
j	 0.3680	 0.0680
k	 0.6610	 0.0570
m	 0.5900	 0.0640
n	 0.5540	 0.1890
o	 0.5360	 0.1060
p	 0.7190	 0.3500
q	 0.4400	 0.2350
r	 0.1020	 0.1310
s	 0.0940	 0.1190
t	 0.1420	 0.1150
u	 0.7290	 0.2270
v	 0.7640	 0.1550
w	 0.1860	 0.1340
x	 0.3490	 0.1270
y	 0.6920	 0.2760
z	 0.0810	 0.1120