



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 01:11 AM UTC

PDB ID : 8QSJ / pdb_00008qsj
EMDB ID : EMD-17720
Title : Human mitoribosomal large subunit assembly intermediate 2 with GTPBP7
Authors : Ritter, C.; Nguyen, T.G.; Kummer, E.
Deposited on : 2023-10-10
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

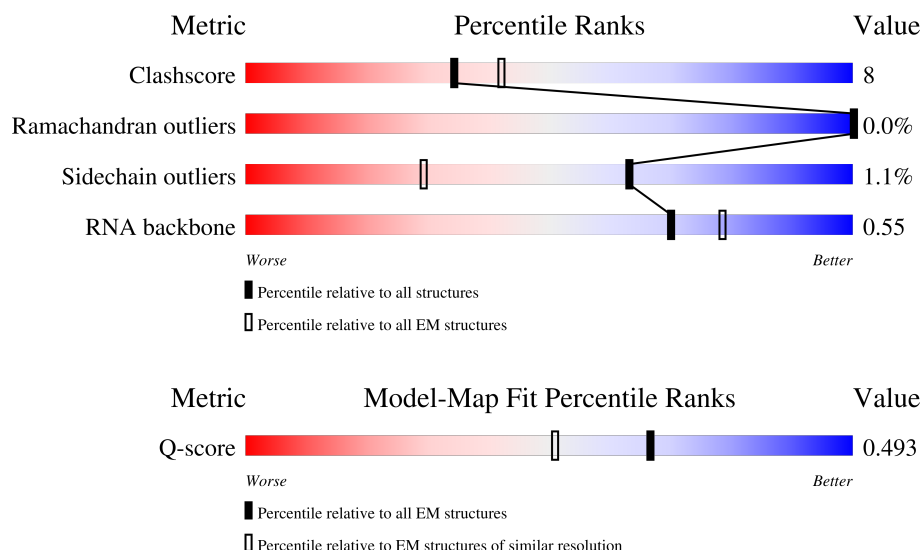
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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

Mol	Chain	Length	Quality of chain
1	0	188	
2	1	65	
3	2	92	

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Mol	Chain	Length	Quality of chain
4	3	188	
5	4	103	
6	5	423	
7	6	380	
8	7	338	
9	8	206	
10	9	137	
11	A	1603	
12	B	72	
13	D	305	
14	E	348	
15	F	311	
16	H	267	
17	I	261	
18	J	192	
19	K	178	
20	L	145	
21	M	296	
22	N	251	
23	O	175	
24	P	180	
25	Q	292	
26	R	149	
27	S	205	
28	T	206	

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Mol	Chain	Length	Quality of chain
29	U	153	
30	V	216	
31	W	148	
32	X	256	
33	Y	250	
34	Z	161	
35	a	142	
36	b	215	
37	c	332	
38	d	306	
39	e	279	
40	f	212	
41	g	166	
42	h	158	
43	i	128	
44	j	123	
45	k	112	
46	l	138	
47	m	128	
48	o	102	
49	p	206	
50	q	222	
51	r	196	
52	s	439	
53	u	234	

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Mol	Chain	Length	Quality of chain
54	v	70	
55	w	156	
56	x	384	
57	y	381	
58	z	334	

2 Entry composition

There are 64 unique types of molecules in this entry. The entry contains 108265 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 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	110	Total	C	N	O	S	0	0
			898	554	176	162	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	55	Total	C	N	O	S	0	0
			455	290	87	76	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	233	83	60	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	95	Total	C	N	O	S	0	0
			832	539	162	128	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	37	Total	C	N	O	S	0	0
			333	212	71	47	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	394	Total	C	N	O	S	0	0
			3210	2073	560	566	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	354	Total	C	N	O	S	0	0
			2948	1881	525	533	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	294	Total	C	N	O	S	0	0
			2390	1529	405	438	18		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	102	Total	C	N	O	S	0	0
			860	543	152	163	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	9	124	Total	C	N	O	S	0	0
			997	644	170	181	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A	1418	Total	C	N	O	P	0	0
			30108	13514	5446	9730	1418		

- Molecule 12 is a RNA chain called tRNA-Val.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	B	72	Total	C	N	O	P	0	0
			1522	683	269	498	72		

- Molecule 13 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D	240	Total	C	N	O	S	0	0
			1872	1165	378	320	9		

- Molecule 14 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	E	305	Total	C	N	O	S	0	0
			2406	1545	418	432	11		

- Molecule 15 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	F	252	Total	C	N	O	S	0	0
			2031	1305	370	350	6		

- Molecule 16 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	97	Total	C	N	O		0	0
			802	508	155	139			

- Molecule 17 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	165	Total	C	N	O	S	0	0
			1338	863	242	223	10		

- Molecule 18 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	137	Total	C	N	O	S	0	0
			1040	665	189	184	2		

- Molecule 19 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	177	Total	C	N	O	S	0	0
			1455	936	259	253	7		

- Molecule 20 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	115	Total	C	N	O	S	0	0
			890	559	171	155	5		

- Molecule 21 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	291	Total	C	N	O	S	0	0
			2327	1483	430	408	6		

- Molecule 22 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	194	Total	C	N	O	S	0	0
			1583	1014	291	269	9		

- Molecule 23 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	154	Total	C	N	O	S	0	0
			1259	792	241	219	7		

- Molecule 24 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	144	Total	C	N	O	S	0	0
			1173	733	224	211	5		

- Molecule 25 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	221	Total	C	N	O	S	0	0
			1843	1179	327	328	9		

- Molecule 26 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	140	Total	C	N	O	S	0	0
			1154	732	231	187	4		

- Molecule 27 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	161	Total	C	N	O	S	0	0
			1293	835	227	227	4		

- Molecule 28 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	166	Total	C	N	O	S	0	0
			1369	875	254	233	7		

- Molecule 29 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	152	Total	C	N	O	S	0	0
			1251	788	234	226	3		

- Molecule 30 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	204	Total	C	N	O	S	0	0
			1667	1062	296	301	8		

- Molecule 31 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	W	106	Total	C	N	O	S	0	0
			835	536	157	139	3		

- Molecule 32 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	X	244	Total	C	N	O	S	0	0
			2044	1322	352	365	5		

- Molecule 33 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Y	181	Total	C	N	O	S	0	0
			1556	995	298	259	4		

- Molecule 34 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	122	Total	C	N	O	S	0	0
			996	636	186	171	3		

- Molecule 35 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	a	100	Total	C	N	O	S	0	0
			840	529	152	154	5		

- Molecule 36 is a protein called Large ribosomal subunit protein mL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	b	150	Total	C	N	O	S	0	0
			1189	739	230	217	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	2	ACE	-	acetylation	UNP Q8N983

- Molecule 37 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	c	286	Total	C	N	O	S	0	0
			2299	1470	397	423	9		

- Molecule 38 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	d	249	Total	C	N	O	S	0	0
			2039	1306	352	367	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	e	228	Total	C	N	O	S	0	0
			1848	1174	326	342	6		

- Molecule 40 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	f	150	Total	C	N	O	S	0	0
			1196	764	197	231	4		

- Molecule 41 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	g	134	Total	C	N	O	S	0	0
			1113	719	193	199	2		

- Molecule 42 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	h	110	Total	C	N	O	S	0	0
			895	568	156	168	3		

- Molecule 43 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	i	97	Total	C	N	O	S	0	0
			828	532	165	127	4		

- Molecule 44 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	j	90	Total	C	N	O	S	0	0
			722	449	140	131	2		

- Molecule 45 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	k	80	Total	C	N	O	S	0	0
			627	392	116	114	5		

- Molecule 46 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	l	23	Total	C	N	O	0	0
			221	137	52	32		

- Molecule 47 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	m	35	Total	C	N	O	S	0	0
			292	187	55	48	2		

- Molecule 48 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	o	94	Total	C	N	O	S	0	0
			798	501	165	129	3		

- Molecule 49 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	p	147	Total	C	N	O	S	0	0
			1205	748	228	225	4		

- Molecule 50 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	q	141	Total	C	N	O	S	0	0
			1177	732	229	211	5		

- Molecule 51 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	r	146	Total	C	N	O	S	0	0
			1203	764	232	199	8		

- Molecule 52 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	s	386	Total	C	N	O	S	0	0
			3155	2023	559	559	14		

- Molecule 53 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	u	126	Total	C	N	O	S	0	0
			1044	671	172	191	10		

- Molecule 54 is a protein called MIEF1 upstream open reading frame protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	v	69	Total	C	N	O		0	0
			588	372	116	100			

- Molecule 55 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	w	79	Total	C	N	O	S	0	0
			638	410	95	128	5		

- Molecule 56 is a protein called 5-methylcytosine rRNA methyltransferase NSUN4.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	x	338	Total	C	N	O	S	0	0
			2676	1703	467	489	17		

- Molecule 57 is a protein called Transcription termination factor 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	y	244	Total	C	N	O	S	0	0
			1980	1264	342	362	12		

- Molecule 58 is a protein called Mitochondrial ribosome-associated GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	z	311	Total	C	N	O	S	0	0
			2443	1549	445	433	16		

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

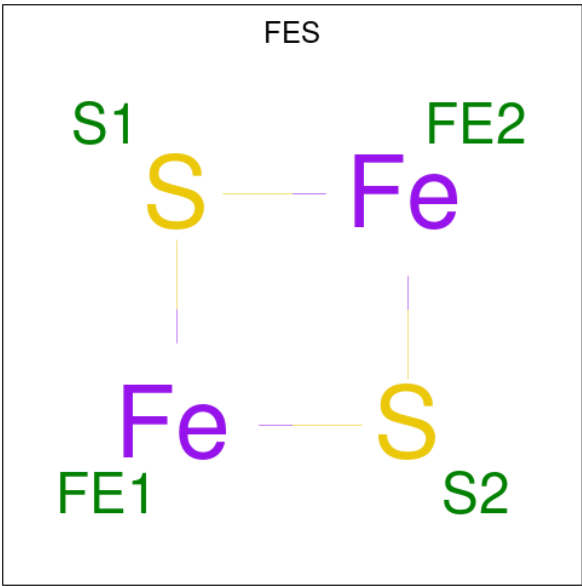
Mol	Chain	Residues	Atoms		AltConf
59	0	1	Total	Zn	0
			1	1	
59	4	1	Total	Zn	0
			1	1	

- Molecule 60 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
60	A	35	Total	Mg	0
			35	35	
60	M	1	Total	Mg	0
			1	1	
60	g	1	Total	Mg	0
			1	1	
60	z	1	Total	Mg	0
			1	1	

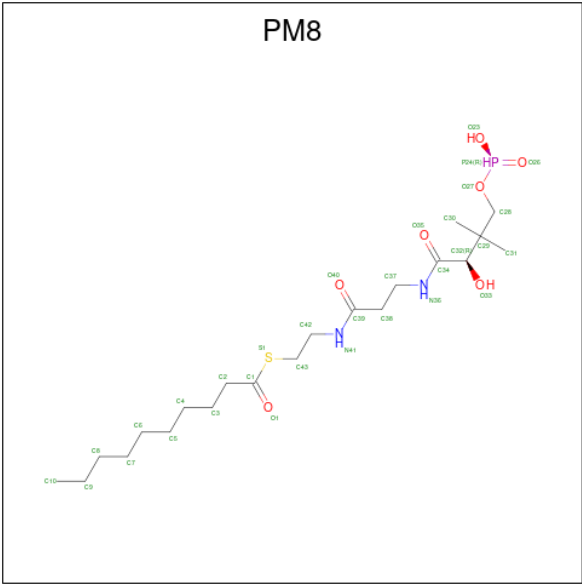
- Molecule 61 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂) (labeled

as "Ligand of Interest" by depositor).



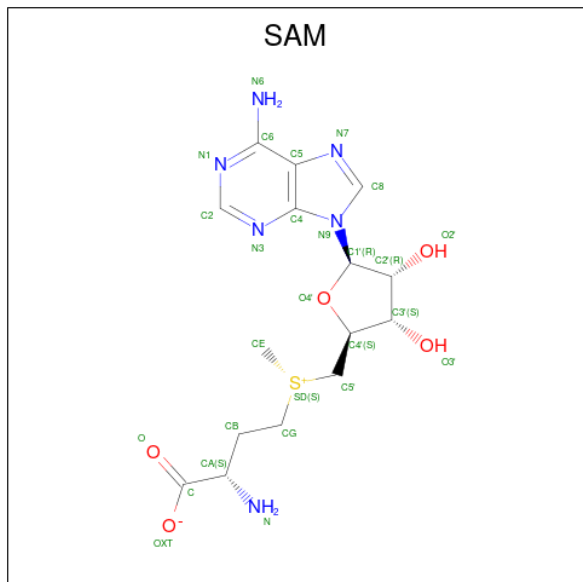
Mol	Chain	Residues	Atoms			AltConf
61	r	1	Total	Fe	S	0
			4	2	2	

- Molecule 62 is S-(2-{[N-(2-HYDROXY-4-{[HYDROXY(OXIDO)PHOSPHINO]OXY}-3,3-DIMETHYLBUTANOYL)-BETA-ALANYL]AMINO}ETHYL) DECANETHIOATE (CCD ID: PM8) (formula: C₂₁H₄₁N₂O₇PS) (labeled as "Ligand of Interest" by depositor).



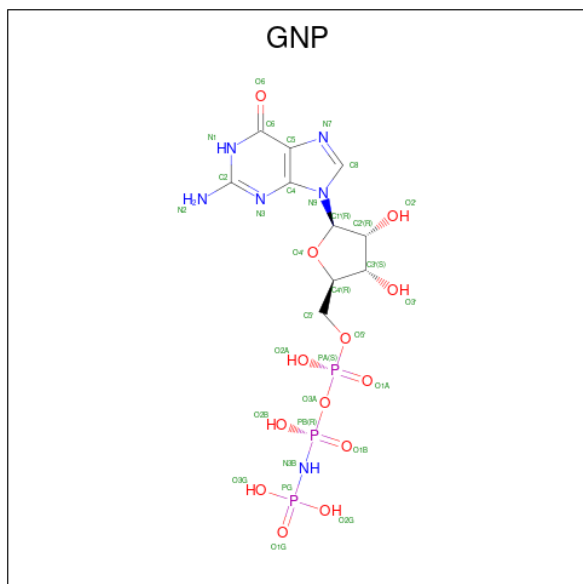
Mol	Chain	Residues	Atoms					AltConf	
62	w	1	Total	C	N	O	P	S	0
			32	21	2	7	1	1	

- Molecule 63 is S-ADENOSYLMETHIONINE (CCD ID: SAM) (formula: $C_{15}H_{22}N_6O_5S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
63	x	1	Total	C	N	O	S	0
			27	15	6	5	1	

- Molecule 64 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).

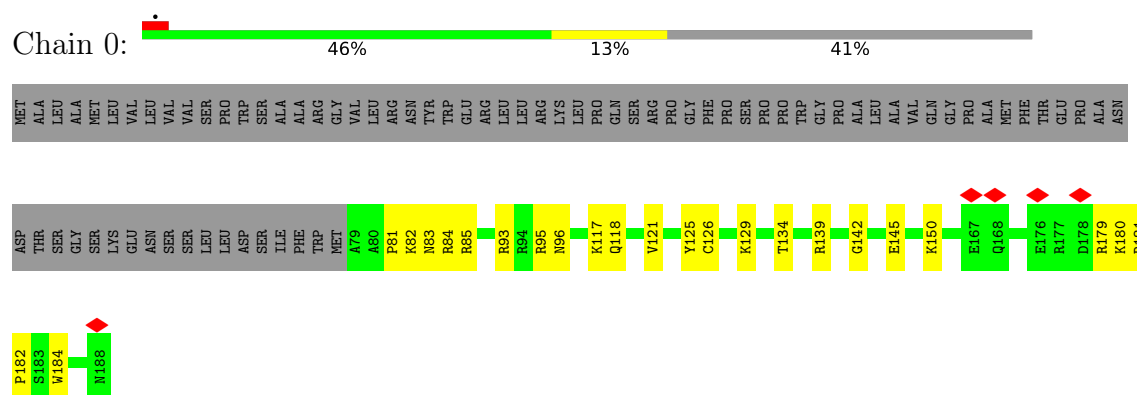


Mol	Chain	Residues	Atoms					AltConf
64	z	1	Total	C	N	O	P	0
			32	10	6	13	3	

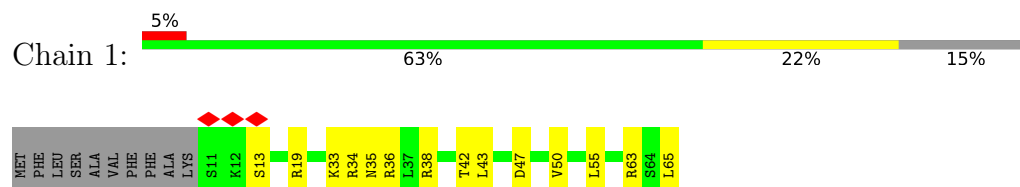
3 Residue-property plots

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.

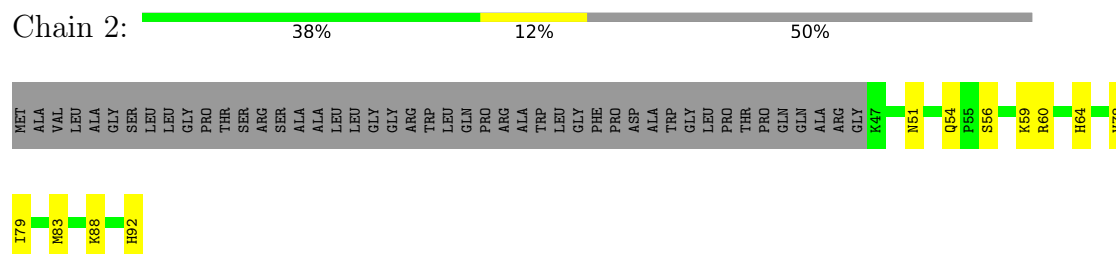
- Molecule 1: 39S ribosomal protein L32, mitochondrial



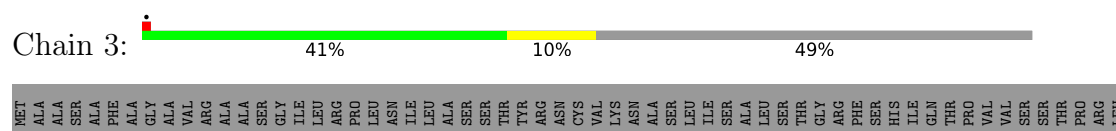
- Molecule 2: 39S ribosomal protein L33, mitochondrial



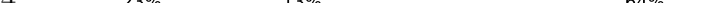
- Molecule 3: 39S ribosomal protein L34, mitochondrial



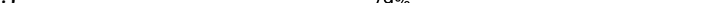
- Molecule 4: 39S ribosomal protein L35, mitochondrial

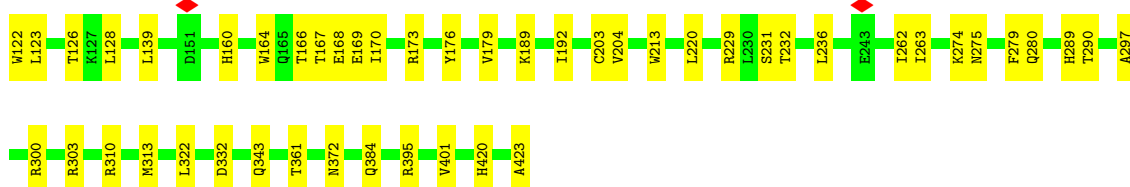




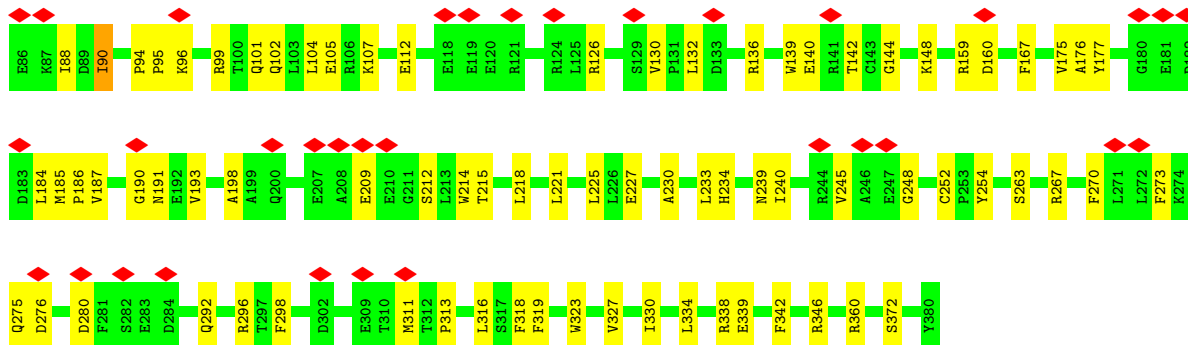
- Chain 4:  23% 13% 64%



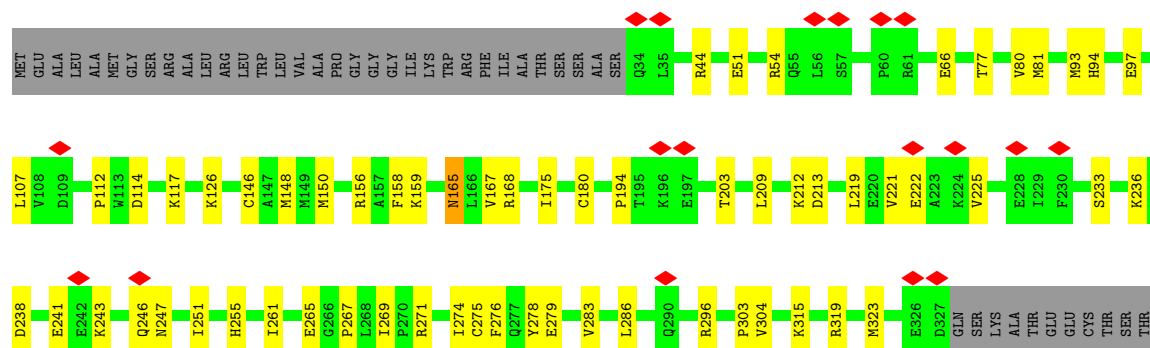
- Chain 5:  79% 14% 7%



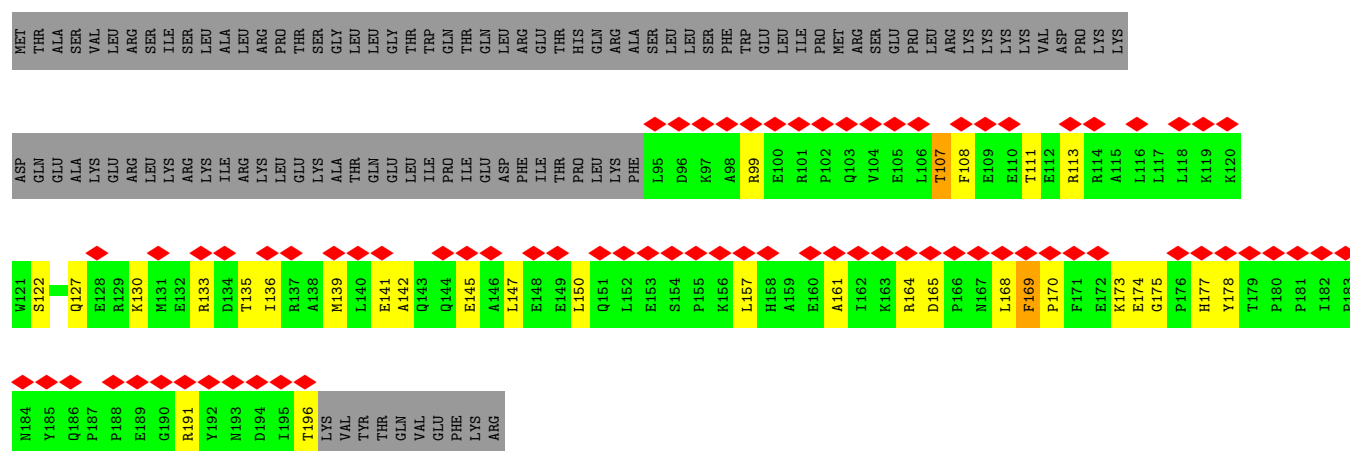
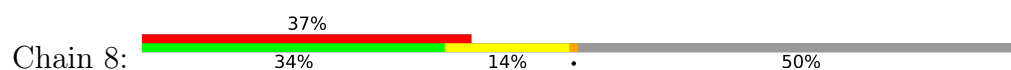
- Chain 6:  12% 69% 24% 7%



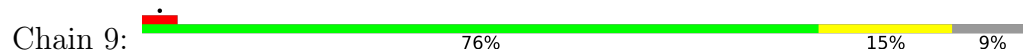
- 



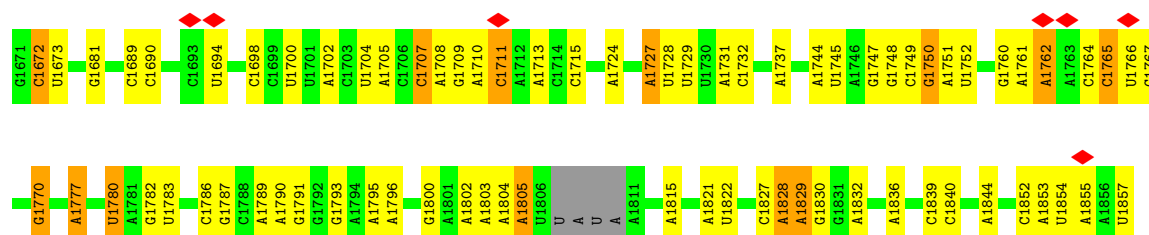
• Molecule 9: 39S ribosomal protein L40, mitochondrial



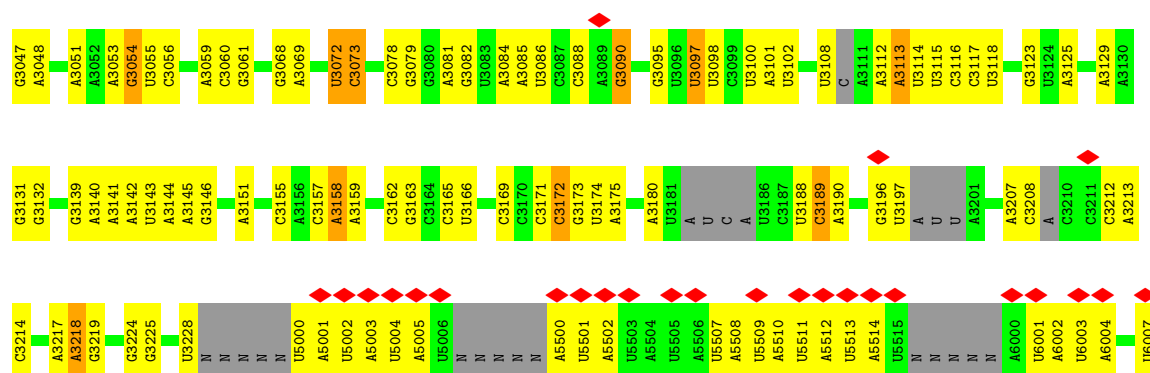
• Molecule 10: 39S ribosomal protein L41, mitochondrial



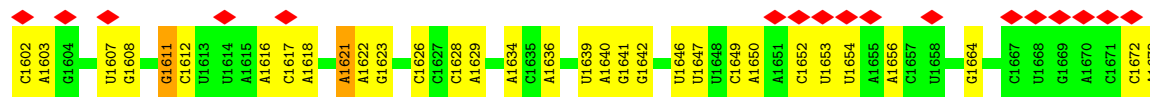
• Molecule 11: 16S rRNA



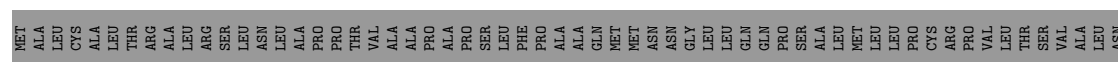




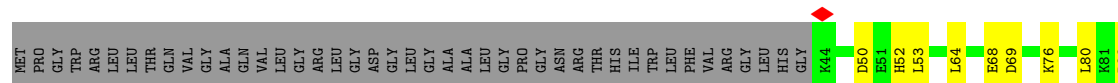
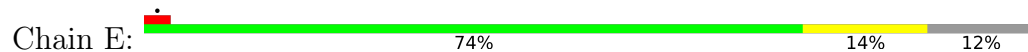
• Molecule 12: tRNA-Val



• Molecule 13: 39S ribosomal protein L2, mitochondrial



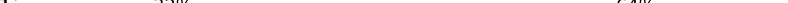
• Molecule 14: 39S ribosomal protein L3, mitochondrial

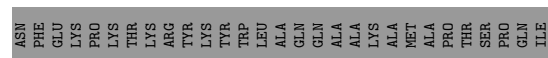


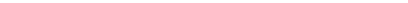
• Molecule 15: 39S ribosomal protein L4, mitochondrial

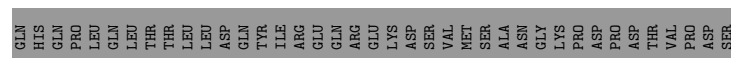
Frequency	Percentage
Daily	62%
Weekly	19%
Monthly	19%

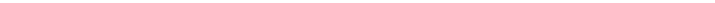


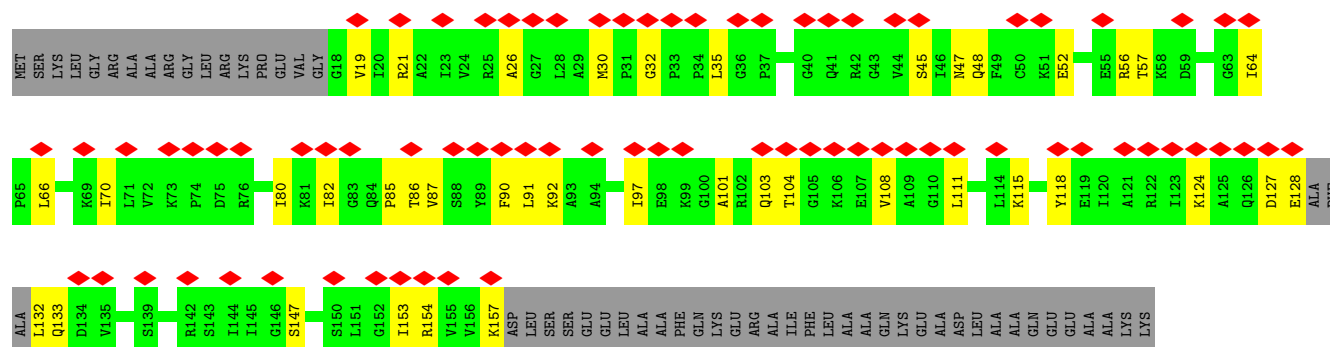
- Chain H:  5% 32% 64%



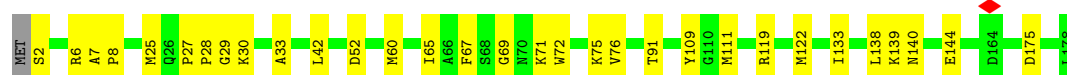
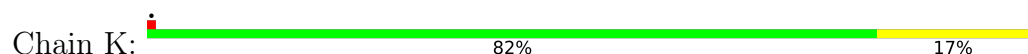
- Chain I: 



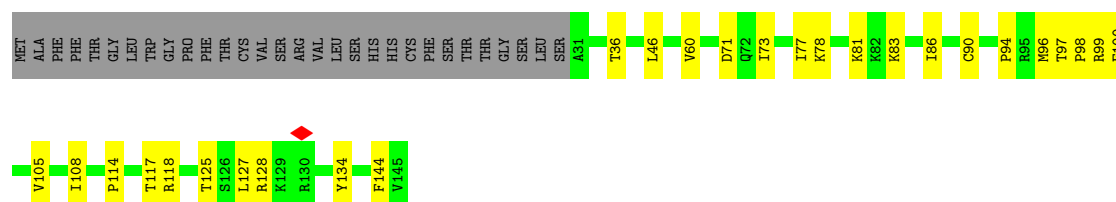
- Chain J: 



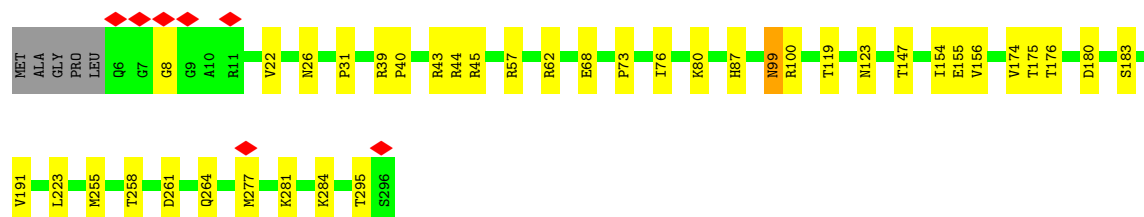
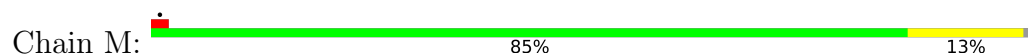
- Molecule 19: 39S ribosomal protein L13, mitochondrial



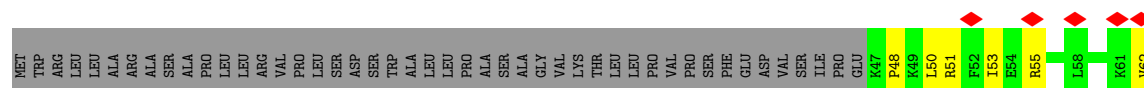
- Molecule 20: 39S ribosomal protein L14, mitochondrial

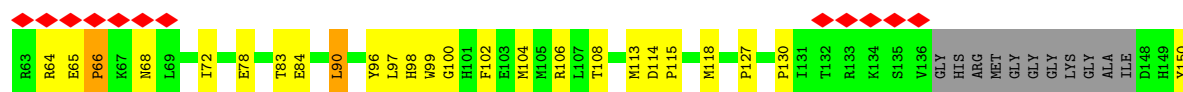


- Molecule 21: 39S ribosomal protein L15, mitochondrial



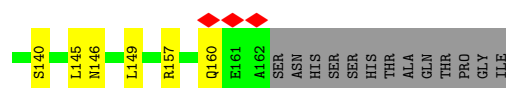
- Molecule 22: 39S ribosomal protein L16, mitochondrial





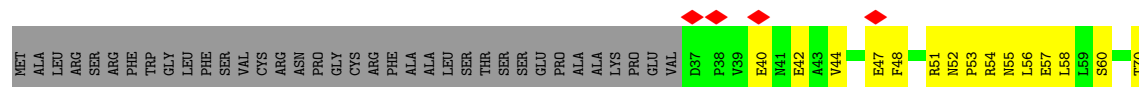
- Molecule 23: 39S ribosomal protein L17, mitochondrial

Chain O: 68% 20% 12%



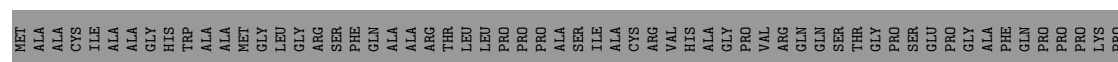
- Molecule 24: 39S ribosomal protein L18, mitochondrial

Chain P: 6% 57% 23% 20%



- Molecule 25: 39S ribosomal protein L19, mitochondrial

Chain Q: 65% 10% 24%



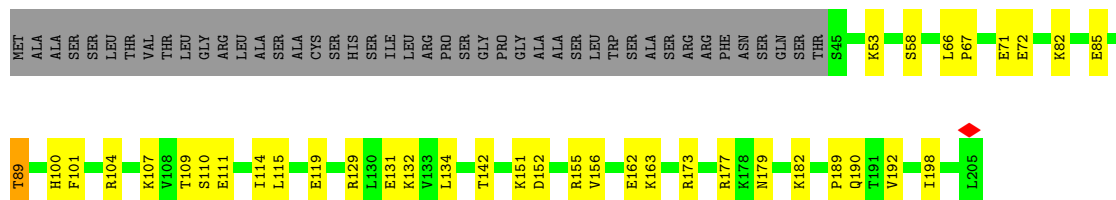
- Molecule 26: 39S ribosomal protein L20, mitochondrial

Chain R: 87% 7% 6%



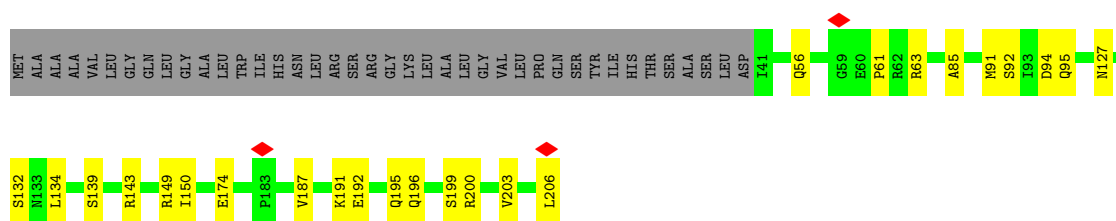
- Molecule 27: 39S ribosomal protein L21, mitochondrial

Chain S: 



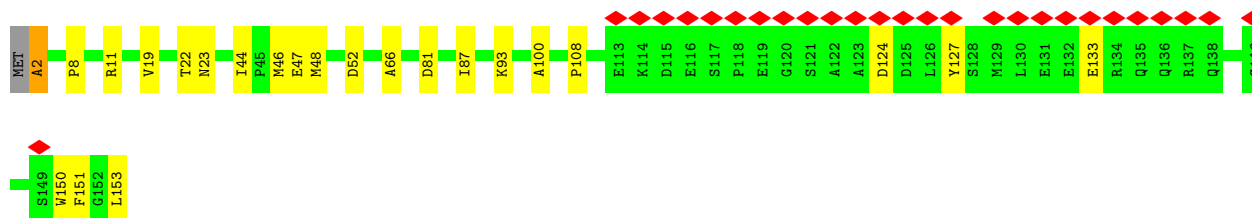
- Molecule 28: 39S ribosomal protein L22, mitochondrial

Chain T: 



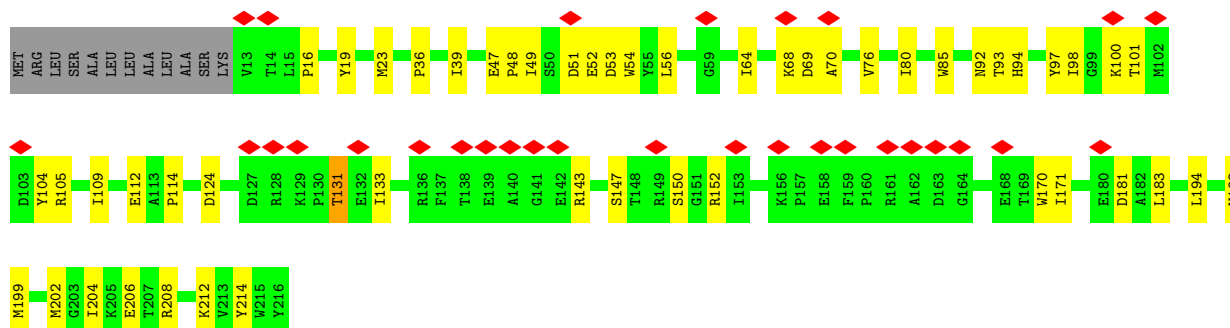
- Molecule 29: 39S ribosomal protein L23, mitochondrial

Chain U: 



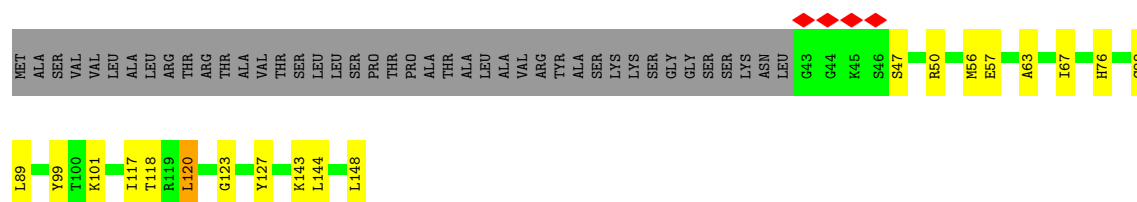
- Molecule 30: 39S ribosomal protein L24, mitochondrial

Chain V: 

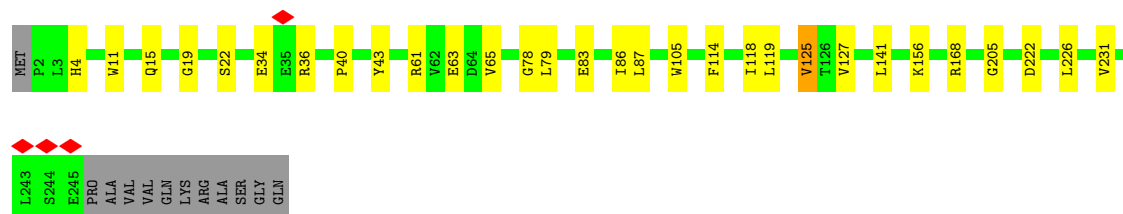
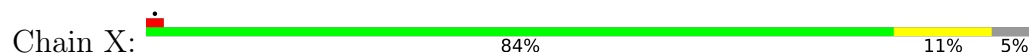


- Molecule 31: 39S ribosomal protein L27, mitochondrial

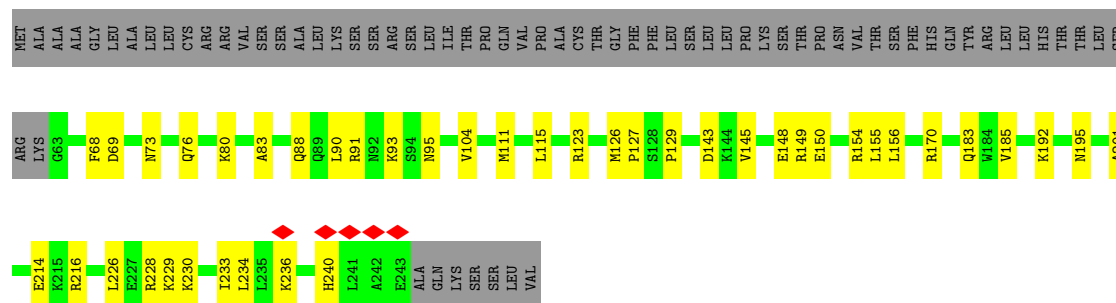
Chain W: 



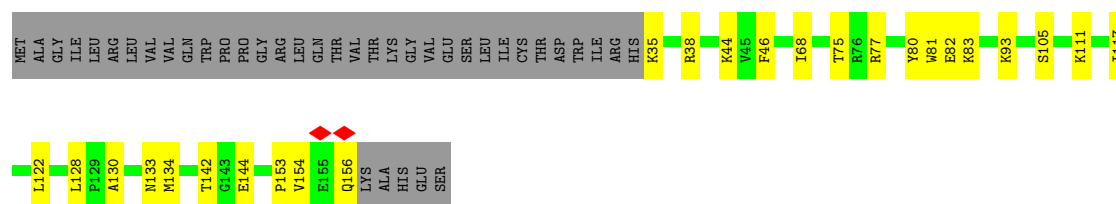
- Molecule 32: 39S ribosomal protein L28, mitochondrial



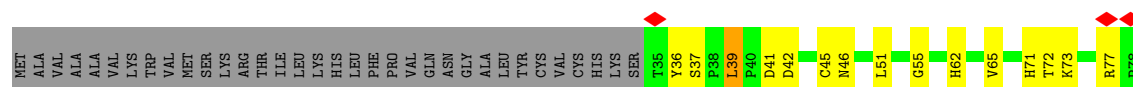
- Molecule 33: 39S ribosomal protein L47, mitochondrial

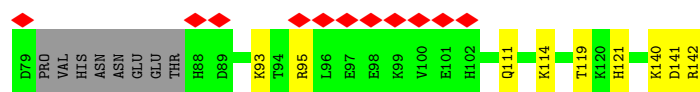


- Molecule 34: 39S ribosomal protein L30, mitochondrial



- Molecule 35: 39S ribosomal protein L42, mitochondrial





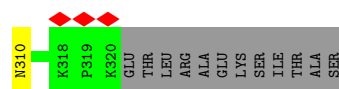
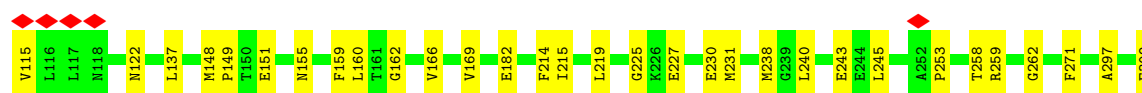
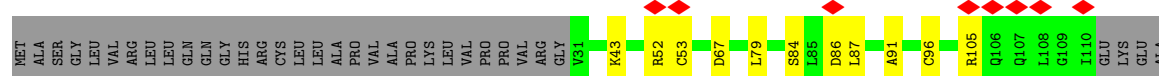
- Molecule 36: Large ribosomal subunit protein mL43

Chain b: 53% 17% 30%



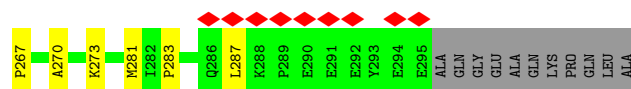
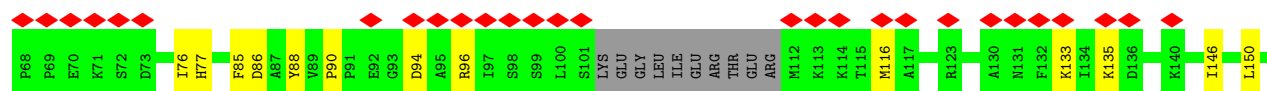
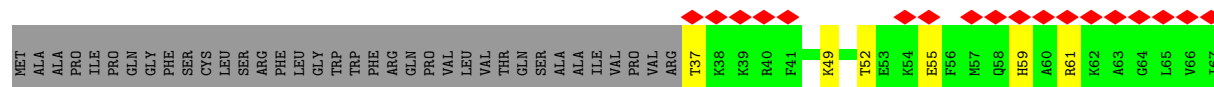
- Molecule 37: 39S ribosomal protein L44, mitochondrial

Chain c: 5% 73% 13% 14%

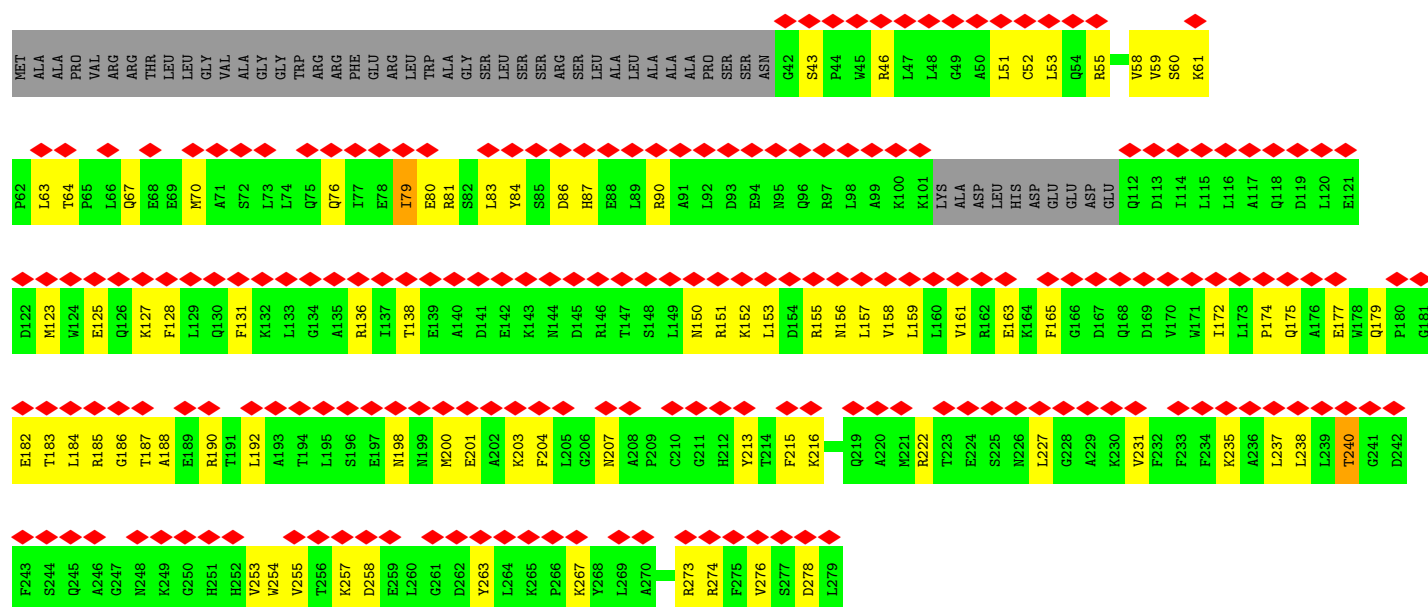


- Molecule 38: 39S ribosomal protein L45, mitochondrial

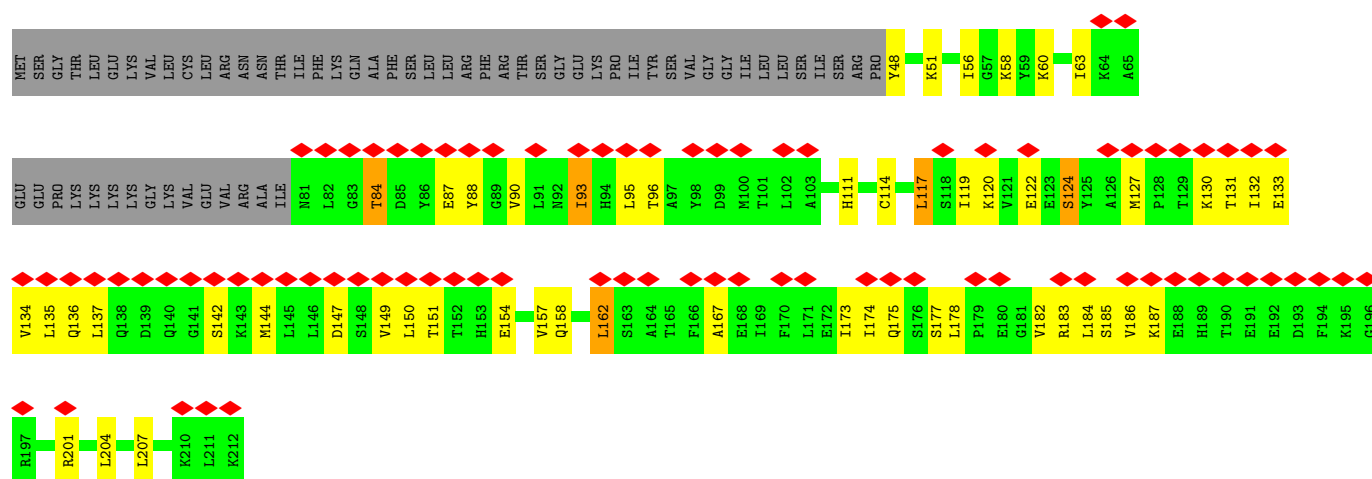
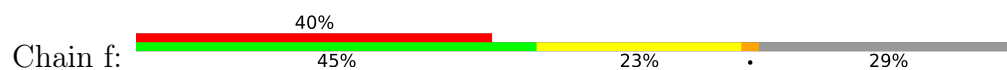
Chain d: 21% 64% 17% 19%



- Molecule 39: 39S ribosomal protein L46, mitochondrial



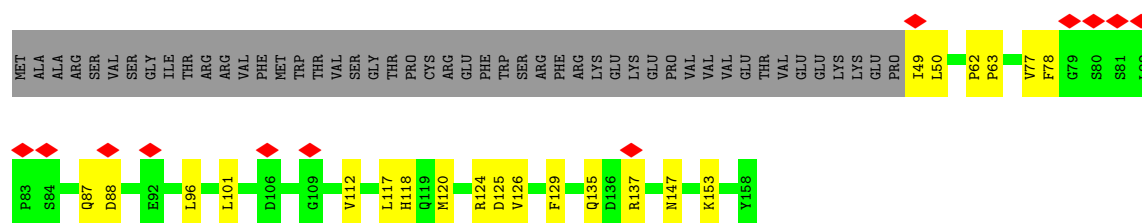
- Molecule 40: 39S ribosomal protein L48, mitochondrial



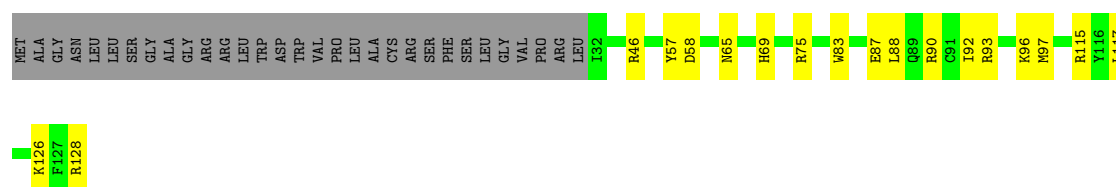
- Molecule 41: 39S ribosomal protein L49, mitochondrial



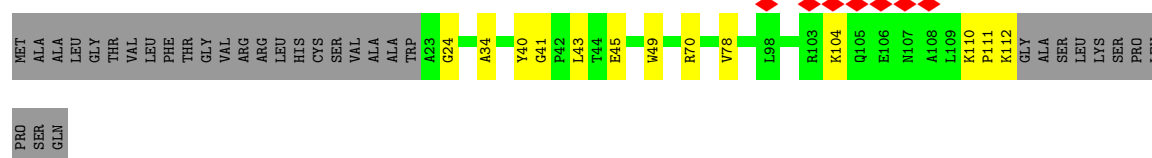
- Molecule 42: 39S ribosomal protein L50, mitochondrial



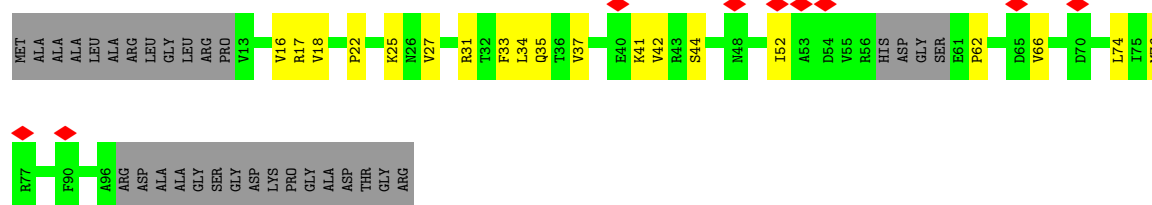
- Molecule 43: 39S ribosomal protein L51, mitochondrial



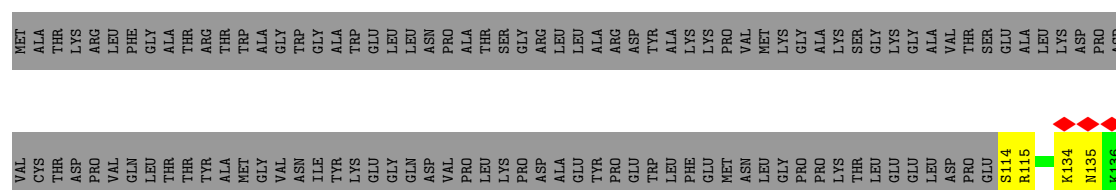
- Molecule 44: 39S ribosomal protein L52, mitochondrial



- Molecule 45: 39S ribosomal protein L53, mitochondrial

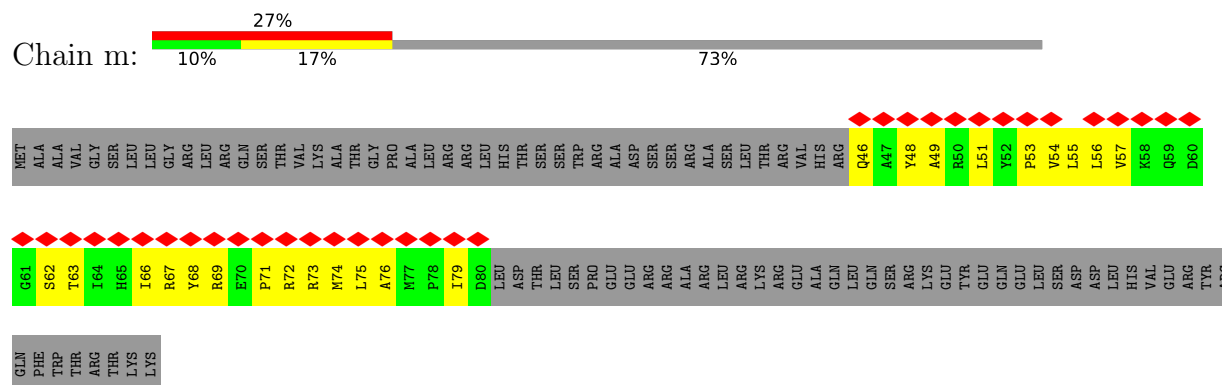


- Molecule 46: 39S ribosomal protein L54, mitochondrial

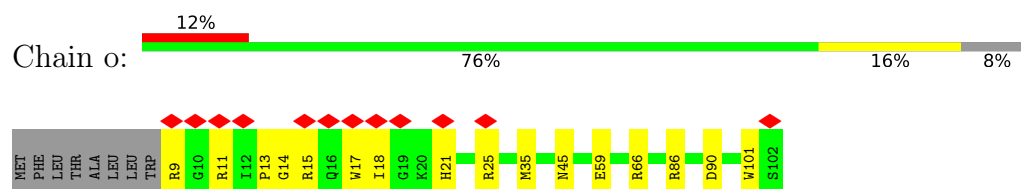


LEU

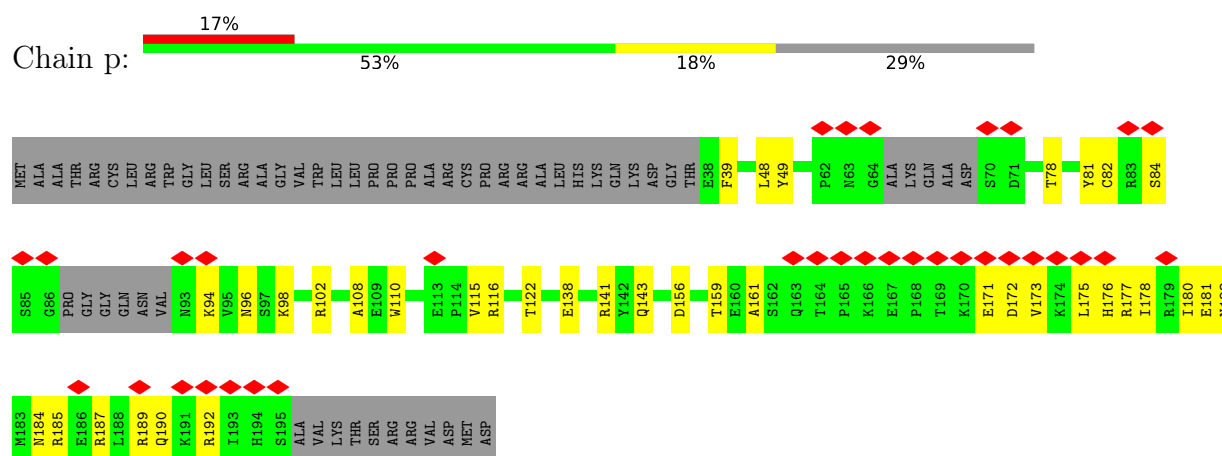
- Molecule 47: 39S ribosomal protein L55, mitochondrial



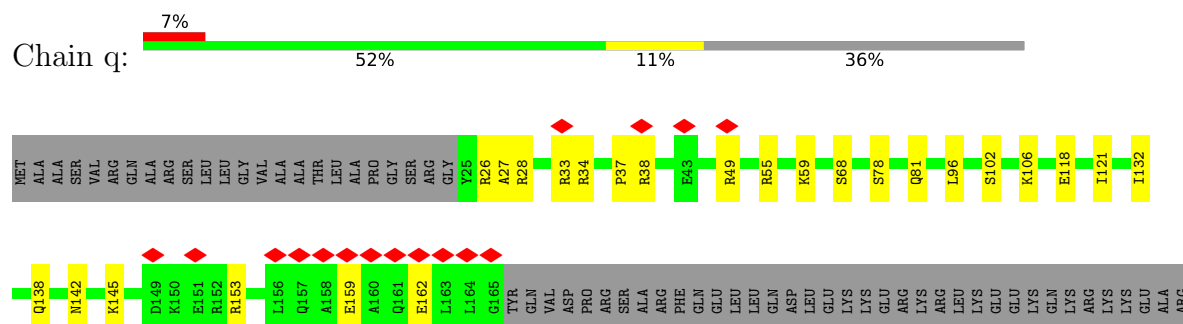
- Molecule 48: Ribosomal protein 63, mitochondrial



- Molecule 49: Peptidyl-tRNA hydrolase ICT1, mitochondrial



- Molecule 50: Growth arrest and DNA damage-inducible proteins-interacting protein 1



ALA
ALA
ALA
LEU
LYS
ALA
ALA
VAL
ALA
ALA
GLN
ASP
PRO
ALA
ALA
GLY
ALA
PRO
SER
SER

- Molecule 51: 39S ribosomal protein S18a, mitochondrial

Chain r:  59% 16% 26%

MET
ALA
ALA
LEU
LYS
ALA
LEU
VAL
SER
GLY
CYS
PRO
ARG
LEU
LEU
ALA
GLY
F35
V39
E40
T41
GLN
GLY
LYS
THR
T47
I48
I49
E59
S60
N65
P66
S67
Q68
Q69
C70
R74

K78
H79
F92
L100
P101
R102
C108
Q109
E110
K114
K120
R124
R134
LEU
PRO
GLU
GLY
VAL
VAL
PRO
LYS
SER
SER
PRO
LEU
PRO
ALA
ARG
GLY
F35
V39
E40
T41
GLN
GLY
LYS
THR
T47
I48
I49
E59
S60
N65
P66
S67
Q68
Q69
C70
R74

- Molecule 52: 39S ribosomal protein S30, mitochondrial

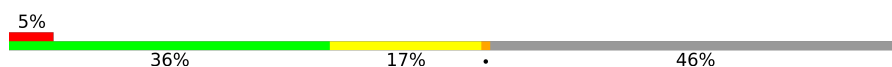
Chain s:  74% 14% 12%

MET
ALA
ALA
ALA
CYS
TRP
ARG
PRO
LEU
LEU
ARG
GLY
PRO
ARG
LEU
LEU
HIS
THR
ALA
ASN
ALA
ALA
ALA
THR
ALA
THR
GLU
THR
THR
CYS
GLN
ASP
VAL
ALA
T39
P40
V41
R59
D77
Q87
K90
Y91
T97
D103
F109
G117
L118
P119

A123
E124
P125
PRO
GLU
PRO
GLU
PRO
GLU
PRO
GLU
P135
A136
L137
L142
Q152
F155
Y156
R161
R162
V163
H164
R165
E168
L174
P175
H191
A197
D201
H207
V211
R212
E215
R223
G224
R225
L229
R230
D234
P237
N238
N239

Q240
I243
Q246
L271
P272
L273
Y278
E279
V280
H281
K287
F299
H300
K305
D318
P354
L374
N375
T376
L377
A378
L379
Q385
N386
R389
W394
G395
E403
T404
I405
E406
D407
L426
R427
R428
E431
E432
K433
SER
GLN
LEU
LEU
GLU
ASN

- Molecule 53: Mitochondrial assembly of ribosomal large subunit protein 1

Chain u:  5% 36% 17% 46%

MET
GLY
PRO
GLY
GLY
ARG
VAL
ALA
LEU
LEU
ALA
PRO
LEU
MET
TRP
ASN
ARG
ARG
VAL
VAL
SER
GLY
ASP
VAL
ALA
GLY
SER
ALA
VAL
GLY
PRO
GLY
F92
D93
I94
D95
N96
N97
V98
R102
Q103
E104
V111
S131
H134
L135
M138
A139
K144
H148
L149
K150
C151
K152

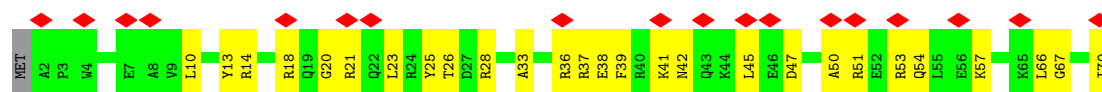
LEU
HIS
SER
GLU
PRO
GLY
GLY
LEU
GLU
GLU
ARG
ALA
GLY
THR
VAL
ASN
GLY
GLY
ARG
PRO
GLU
SER
ASP
ALA
ALA
HIS
THR
GLY
PRO
K91
F92
D93
I94
D95
N96
N97
V98
R102
Q103
E104
V111
S131
H134
L135
M138
A139
K144
H148
L149
K150
C151
K152

I159
D163
T164
D166
W167
C169
V170
D171
S174
L179
M180
F186
I187
Y188
E189
L190
E191
K192
L193
W194
T196
L197
R198
S198
Y199
D200
D201
Q202
A207
P208
E209
T210
E213
T216
LEU
GLY
ILE
GLU
ASP
ASP
THR
SER
SER
VAL
THR
PRO
VAL
GLU
LEU
LYS

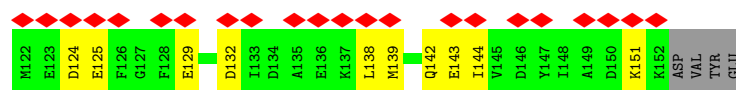
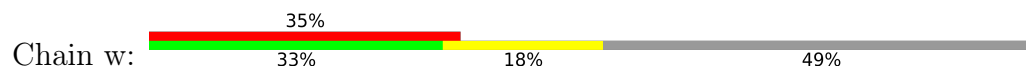
CYS
GLU

- Molecule 54: MIEF1 upstream open reading frame protein

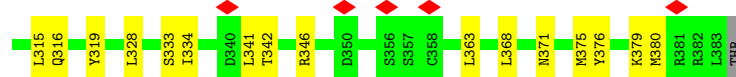
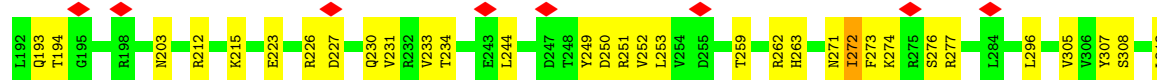
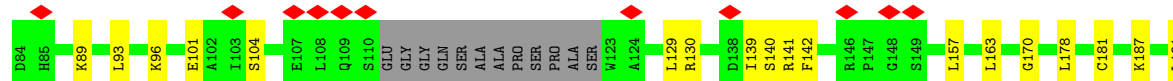
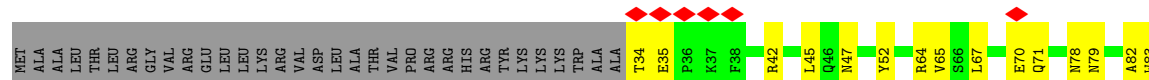
Chain v:  26% 60% 39%



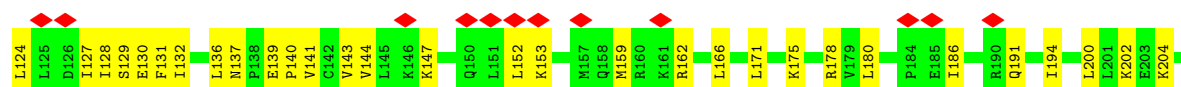
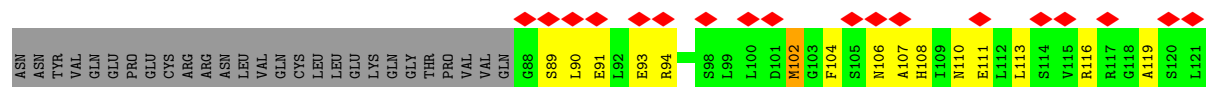
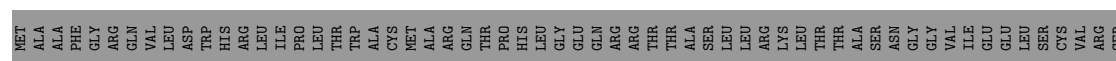
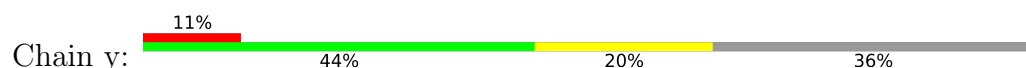
- Molecule 55: Acyl carrier protein, mitochondrial

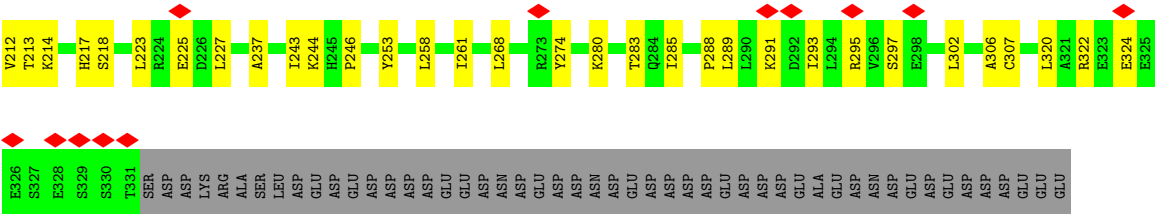


- Molecule 56: 5-methylcytosine rRNA methyltransferase NSUN4

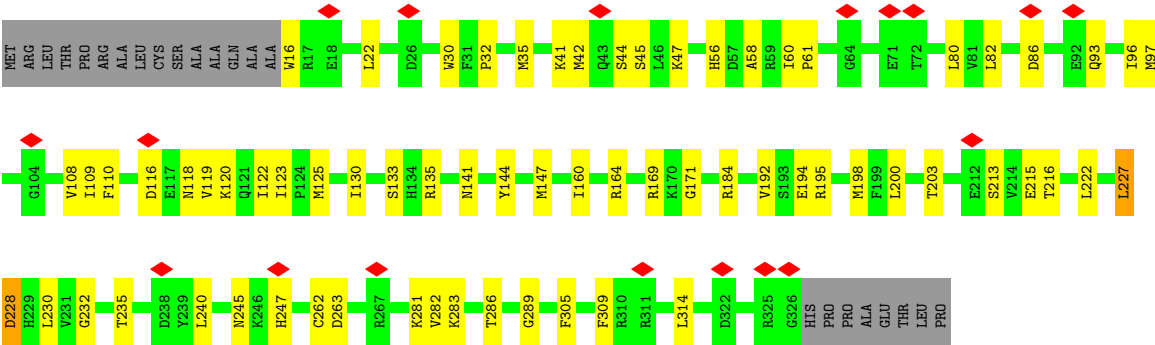


- Molecule 57: Transcription termination factor 4, mitochondrial





• Molecule 58: Mitochondrial ribosome-associated GTPase 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	68901	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	6.009	Depositor
Minimum map value	-2.665	Depositor
Average map value	-0.004	Depositor
Map value standard deviation	0.204	Depositor
Recommended contour level	0.814	Depositor
Map size ($\text{\AA}$)	518.4, 518.4, 518.4	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GNP, MG, FES, AYA, ZN, PM8, SAC, SAM, ACE

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.07	0/913	0.20	0/1224
2	1	0.07	0/460	0.23	0/610
3	2	0.07	0/383	0.20	0/507
4	3	0.08	0/853	0.22	0/1136
5	4	0.09	0/341	0.23	0/451
6	5	0.08	0/3305	0.20	0/4502
7	6	0.08	0/3043	0.22	0/4140
8	7	0.07	0/2447	0.21	0/3310
9	8	0.10	0/880	0.32	0/1188
10	9	0.07	0/1025	0.21	0/1379
11	A	0.09	0/33679	0.20	0/52392
12	B	0.07	0/1700	0.16	0/2641
13	D	0.09	0/1910	0.26	0/2569
14	E	0.08	0/2475	0.22	0/3355
15	F	0.08	0/2090	0.21	0/2842
16	H	0.08	0/816	0.24	0/1097
17	I	0.21	0/1368	0.40	0/1849
18	J	0.10	0/1054	0.28	0/1419
19	K	0.08	0/1490	0.21	0/2021
20	L	0.08	0/905	0.26	0/1218
21	M	0.08	0/2381	0.22	0/3212
22	N	0.10	0/1624	0.28	0/2185
23	O	0.07	0/1283	0.19	0/1727
24	P	0.09	0/1199	0.26	0/1623
25	Q	0.08	0/1884	0.22	0/2535
26	R	0.07	0/1175	0.17	0/1572
27	S	0.08	0/1320	0.25	0/1789
28	T	0.07	0/1403	0.20	0/1886
29	U	0.08	0/1274	0.20	0/1723
30	V	0.08	0/1712	0.21	0/2322
31	W	0.07	0/857	0.20	0/1155
32	X	0.07	0/2099	0.19	0/2837

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Y	0.08	0/1593	0.21	0/2136
34	Z	0.08	0/1021	0.21	0/1378
35	a	0.08	0/866	0.22	0/1174
36	b	0.12	0/1211	0.24	0/1639
37	c	0.07	0/2347	0.20	0/3171
38	d	0.09	0/2095	0.24	0/2834
39	e	0.08	0/1885	0.23	0/2542
40	f	0.08	0/1216	0.25	0/1638
41	g	0.09	0/1151	0.25	0/1569
42	h	0.08	0/918	0.23	0/1249
43	i	0.09	0/850	0.22	0/1135
44	j	0.08	0/737	0.20	0/992
45	k	0.09	0/635	0.26	0/855
46	l	0.06	0/226	0.16	0/299
47	m	0.10	0/298	0.28	0/402
48	o	0.07	0/819	0.19	0/1097
49	p	0.07	0/1223	0.22	0/1641
50	q	0.08	0/1208	0.22	0/1633
51	r	0.10	0/1238	0.30	0/1676
52	s	0.07	0/3239	0.20	0/4400
53	u	0.09	0/1069	0.28	0/1447
54	v	0.10	0/597	0.28	0/796
55	w	0.14	0/647	0.32	0/871
56	x	0.08	0/2737	0.22	0/3714
57	y	0.08	0/2011	0.24	0/2702
58	z	0.09	0/2484	0.26	0/3349
All	All	0.09	0/113669	0.22	0/160755

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

Mol	Chain	#Chirality outliers	#Planarity outliers
9	8	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	8	169	PHE	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	898	0	916	19	0
2	1	455	0	498	10	0
3	2	377	0	406	9	0
4	3	832	0	883	14	0
5	4	333	0	352	12	0
6	5	3210	0	3206	39	0
7	6	2948	0	2841	78	0
8	7	2390	0	2397	39	0
9	8	860	0	852	35	0
10	9	997	0	987	21	0
11	A	30108	0	15303	437	0
12	B	1522	0	776	21	0
13	D	1872	0	1932	24	0
14	E	2406	0	2415	30	0
15	F	2031	0	2065	47	0
16	H	802	0	846	8	0
17	I	1338	0	1417	31	0
18	J	1040	0	1121	25	0
19	K	1455	0	1452	25	0
20	L	890	0	941	21	0
21	M	2327	0	2395	31	0
22	N	1583	0	1607	38	0
23	O	1259	0	1294	21	0
24	P	1173	0	1165	32	0
25	Q	1843	0	1878	20	0
26	R	1154	0	1214	9	0
27	S	1293	0	1365	31	0
28	T	1369	0	1410	20	0
29	U	1251	0	1232	19	0
30	V	1667	0	1674	37	0
31	W	835	0	858	17	0
32	X	2044	0	2060	20	0
33	Y	1556	0	1597	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	Z	996	0	1044	20	0
35	a	840	0	810	22	0
36	b	1189	0	1188	26	0
37	c	2299	0	2320	29	0
38	d	2039	0	2035	42	0
39	e	1848	0	1849	61	0
40	f	1196	0	1212	44	0
41	g	1113	0	1097	16	0
42	h	895	0	881	17	0
43	i	828	0	857	15	0
44	j	722	0	722	12	0
45	k	627	0	636	13	0
46	l	221	0	227	4	0
47	m	292	0	305	23	0
48	o	798	0	804	17	0
49	p	1205	0	1223	27	0
50	q	1177	0	1154	22	0
51	r	1203	0	1219	28	0
52	s	3155	0	3139	36	0
53	u	1044	0	1035	36	0
54	v	588	0	604	23	0
55	w	638	0	636	18	0
56	x	2676	0	2652	52	0
57	y	1980	0	2066	54	0
58	z	2443	0	2545	50	0
59	0	1	0	0	0	0
59	4	1	0	0	0	0
60	A	35	0	0	0	0
60	M	1	0	0	0	0
60	g	1	0	0	0	0
60	z	1	0	0	0	0
61	r	4	0	0	1	0
62	w	32	0	39	2	0
63	x	27	0	22	1	0
64	z	32	0	13	0	0
All	All	108265	0	93689	1614	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 8.

All (1614) 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)
11:A:2994:U:O2	11:A:3068:G:O6	1.82	0.96
11:A:2721:G:H1	11:A:3097:U:H3	1.18	0.92
12:B:1607:U:H3	12:B:1664:G:H1	1.16	0.92
57:y:139:GLU:HG3	57:y:140:PRO:HD3	1.62	0.81
57:y:102:MET:HG2	57:y:132:ILE:HD12	1.65	0.78
42:h:101:LEU:HD21	42:h:120:MET:HE1	1.67	0.77
13:D:296:VAL:HG13	13:D:297:LYS:HG2	1.67	0.77
6:5:126:THR:HG22	6:5:372:ASN:HB2	1.65	0.77
17:I:66:PRO:HG3	51:r:67:SER:HB2	1.68	0.76
17:I:97:ALA:HB3	17:I:154:LEU:HB2	1.68	0.76
39:e:185:ARG:HD2	39:e:207:ASN:HA	1.67	0.75
11:A:2499:U:OP2	11:A:2504:A:N6	2.19	0.75
20:L:86:ILE:HG22	20:L:105:VAL:HG12	1.67	0.75
40:f:114:CYS:HB2	40:f:119:ILE:HD11	1.68	0.75
47:m:56:LEU:HG	47:m:66:ILE:HG21	1.69	0.75
15:F:220:ASP:HB3	15:F:226:MET:HE1	1.67	0.74
7:6:273:PHE:HB3	7:6:311:MET:HE2	1.69	0.74
11:A:2187:C:O2'	18:J:103:GLN:O	2.06	0.74
21:M:44:ARG:HG3	21:M:45:ARG:HG3	1.69	0.74
19:K:33:ALA:HA	19:K:111:MET:HE1	1.71	0.73
30:V:109:ILE:HD12	38:d:76:ILE:HG21	1.70	0.73
11:A:3172:C:O2'	11:A:3173:G:N2	2.22	0.73
54:v:33:ALA:HB1	54:v:37:ARG:HH21	1.52	0.72
11:A:2485:U:H3	11:A:2650:C:H42	1.37	0.72
28:T:150:ILE:HG22	38:d:52:THR:HG21	1.72	0.71
20:L:96:MET:HE2	25:Q:168:ASN:HD22	1.55	0.71
38:d:182:ARG:HB2	38:d:223:ALA:HB3	1.71	0.70
11:A:3082:G:N2	11:A:3085:A:OP2	2.24	0.70
22:N:64:ARG:NH1	22:N:68:ASN:OD1	2.24	0.70
45:k:27:VAL:HG12	45:k:62:PRO:HG3	1.71	0.70
45:k:41:LYS:HD3	45:k:42:VAL:HG13	1.74	0.70
5:4:86:GLY:H	11:A:3189:C:H5'	1.55	0.70
6:5:169:GLU:HG2	6:5:170:ILE:HG13	1.74	0.70
50:q:159:GLU:HA	50:q:162:GLU:HB3	1.73	0.70
11:A:1777:A:N6	11:A:1780:U:OP2	2.25	0.70
13:D:285:LYS:HA	13:D:285:LYS:HE2	1.72	0.70
53:u:92:PHE:H	53:u:150:LYS:HE3	1.55	0.70
14:E:107:MET:HG2	14:E:121:LEU:HD21	1.74	0.70
11:A:2367:A:N3	33:Y:123:ARG:NH2	2.39	0.69
6:5:115:GLU:HB2	6:5:119:GLN:HB2	1.74	0.69
11:A:3072:U:H1'	11:A:3073:C:H5'	1.74	0.69
20:L:118:ARG:HH21	53:u:193:LEU:HB3	1.58	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:N:218:ILE:HG23	22:N:223:MET:HB2	1.75	0.69
7:6:215:THR:HB	7:6:273:PHE:HB2	1.74	0.69
40:f:124:SER:HB2	40:f:157:VAL:HG22	1.74	0.69
40:f:147:ASP:O	47:m:72:ARG:NH2	2.27	0.68
17:I:93:ASN:HD22	17:I:155:VAL:HG12	1.57	0.68
29:U:124:ASP:HB3	29:U:127:TYR:HB3	1.74	0.68
39:e:203:LYS:HB3	39:e:237:LEU:HB3	1.74	0.68
55:w:144:ILE:HD12	55:w:144:ILE:H	1.58	0.68
11:A:1673:U:O2'	28:T:143:ARG:NH1	2.26	0.68
21:M:155:GLU:OE2	21:M:175:THR:OG1	2.12	0.68
39:e:257:LYS:HD3	39:e:278:ASP:HB2	1.75	0.68
7:6:330:ILE:HG23	7:6:334:LEU:HD12	1.76	0.68
11:A:2063:G:N2	31:W:56:MET:SD	2.67	0.68
7:6:239:ASN:H	7:6:275:GLN:HE22	1.39	0.68
11:A:2830:A:N6	11:A:2837:A:OP2	2.27	0.68
50:q:138:GLN:O	50:q:142:ASN:ND2	2.27	0.68
14:E:68:GLU:OE1	14:E:154:ARG:NH2	2.26	0.68
49:p:84:SER:HB3	49:p:98:LYS:HB2	1.76	0.68
1:0:139:ARG:NH1	11:A:2322:C:OP1	2.27	0.67
11:A:2470:G:HO2'	20:L:36:THR:HG1	1.40	0.67
7:6:215:THR:OG1	7:6:275:GLN:NE2	2.27	0.67
11:A:2636:G:H5''	58:z:171:GLY:HA2	1.76	0.67
36:b:88:SER:O	36:b:92:LYS:NZ	2.22	0.67
11:A:1884:G:H1'	11:A:1895:C:H1'	1.77	0.67
11:A:2015:G:H22	11:A:2037:U:H5''	1.59	0.67
18:J:70:ILE:HB	18:J:80:ILE:HG12	1.76	0.67
15:F:70:ARG:HA	15:F:196:PRO:HD3	1.76	0.67
15:F:252:SER:O	15:F:256:HIS:ND1	2.28	0.67
32:X:61:ARG:NH2	32:X:63:GLU:OE2	2.29	0.66
11:A:1765:C:N3	33:Y:228:ARG:NH1	2.43	0.66
30:V:181:ASP:O	33:Y:93:LYS:NZ	2.29	0.66
8:7:114:ASP:HB2	8:7:117:LYS:HB2	1.77	0.66
56:x:363:LEU:HD23	56:x:376:TYR:HB2	1.77	0.66
6:5:166:THR:OG1	6:5:168:GLU:OE2	2.13	0.66
11:A:2531:U:O4	13:D:246:ARG:NH2	2.28	0.66
20:L:118:ARG:NH2	53:u:189:GLU:O	2.28	0.66
11:A:1886:G:N7	15:F:170:ARG:NH2	2.43	0.66
39:e:185:ARG:HH12	39:e:204:PHE:HB3	1.61	0.66
11:A:2416:U:OP2	52:s:165:ARG:NH2	2.29	0.65
53:u:197:ARG:HG2	54:v:66:LEU:HB3	1.77	0.65
11:A:5000:U:H2'	11:A:5001:A:H8	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:s:191:HIS:O	52:s:428:ARG:NH2	2.30	0.65
51:r:108:CYS:HB2	61:r:201:FES:S1	2.36	0.65
36:b:72:VAL:HG13	36:b:90:HIS:HB2	1.79	0.64
57:y:289:LEU:HD12	57:y:291:LYS:HE2	1.77	0.64
6:5:173:ARG:NH2	11:A:2395:A:OP1	2.31	0.64
25:Q:182:ARG:HG3	25:Q:187:LEU:HD11	1.78	0.64
11:A:2081:U:H2'	11:A:2082:G:C8	2.33	0.64
11:A:2103:A:HO2'	34:Z:35:LYS:N	1.95	0.64
13:D:113:ARG:O	13:D:147:ARG:NH2	2.29	0.64
7:6:160:ASP:OD2	7:6:267:ARG:NH2	2.31	0.64
8:7:112:PRO:HB2	8:7:267:PRO:HG2	1.78	0.64
11:A:2740:A:N3	11:A:2921:A:O2'	2.29	0.64
6:5:395:ARG:NH2	11:A:1934:U:OP1	2.31	0.64
11:A:2145:G:N3	27:S:104:ARG:NH2	2.46	0.64
58:z:222:LEU:HD21	58:z:240:LEU:HB2	1.80	0.64
1:0:96:ASN:OD1	11:A:2708:C:O2'	2.14	0.64
11:A:2872:C:O2'	31:W:88:CYS:SG	2.55	0.64
21:M:284:LYS:NZ	41:g:41:SER:OG	2.31	0.64
4:3:108:LYS:NZ	11:A:1745:U:O4	2.31	0.64
4:3:163:THR:HG23	4:3:165:PHE:H	1.63	0.64
11:A:1787:G:N2	11:A:1790:A:OP2	2.28	0.64
25:Q:121:THR:HG22	25:Q:171:VAL:HA	1.79	0.64
39:e:183:THR:HG23	39:e:186:GLY:H	1.62	0.64
49:p:108:ALA:O	49:p:116:ARG:NH1	2.31	0.64
55:w:105:MET:SD	55:w:105:MET:N	2.71	0.64
36:b:126:ILE:O	37:c:310:ASN:ND2	2.31	0.63
39:e:53:LEU:HD23	39:e:159:LEU:HD22	1.80	0.63
7:6:323:TRP:NE1	7:6:339:GLU:OE2	2.32	0.63
33:Y:126:MET:HB3	33:Y:129:PRO:HG3	1.79	0.63
38:d:267:PRO:HG2	38:d:270:ALA:HB2	1.81	0.63
9:8:164:ARG:NH2	40:f:84:THR:O	2.31	0.63
11:A:2933:G:N2	11:A:2936:U:O2	2.31	0.63
36:b:28:ARG:NH1	36:b:78:GLU:OE1	2.31	0.63
39:e:53:LEU:HD11	39:e:238:LEU:HB2	1.80	0.63
15:F:181:LYS:HB3	15:F:187:LEU:HB2	1.81	0.63
39:e:138:THR:OG1	39:e:150:ASN:O	2.15	0.63
28:T:127:ASN:O	38:d:230:ARG:NH2	2.31	0.63
2:1:19:ARG:NH1	11:A:2906:C:N3	2.46	0.62
9:8:99:ARG:HH22	47:m:49:ALA:HA	1.63	0.62
11:A:2093:U:O2	11:A:2266:U:O2'	2.17	0.62
11:A:2243:A:H5''	51:r:188:SER:HB3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:O:140:SER:O	23:O:146:ASN:ND2	2.31	0.62
57:y:128:ILE:HD13	57:y:141:VAL:HG11	1.80	0.62
11:A:2692:G:N1	11:A:2696:A:OP2	2.30	0.62
50:q:102:SER:OG	50:q:106:LYS:NZ	2.32	0.62
9:8:196:THR:OG1	40:f:130:LYS:NZ	2.31	0.62
45:k:76:MET:HG3	51:r:49:ILE:HD11	1.80	0.62
58:z:164:ARG:NH1	58:z:171:GLY:O	2.31	0.62
39:e:51:LEU:HD12	39:e:188:ALA:HB1	1.82	0.62
56:x:47:ASN:HD22	56:x:273:PHE:HE2	1.45	0.62
8:7:276:PHE:HB2	8:7:304:VAL:HG22	1.81	0.62
15:F:103:GLN:HE22	15:F:249:ASN:HB2	1.64	0.62
28:T:91:MET:HE3	28:T:95:GLN:HG2	1.80	0.62
34:Z:142:THR:OG1	34:Z:144:GLU:OE1	2.17	0.62
11:A:2737:U:O2'	11:A:3084:A:N3	2.32	0.62
7:6:292:GLN:NE2	24:P:40:GLU:OE2	2.32	0.62
11:A:2003:A:OP2	11:A:2734:A:O2'	2.17	0.62
18:J:48:GLN:HE22	18:J:52:GLU:HG2	1.64	0.62
18:J:127:ASP:O	18:J:132:LEU:N	2.32	0.62
28:T:149:ARG:HA	38:d:52:THR:HG23	1.82	0.62
9:8:164:ARG:NH2	40:f:87:GLU:O	2.31	0.62
27:S:107:LYS:HD2	28:T:206:LEU:HD11	1.82	0.62
30:V:23:MET:HE3	30:V:114:PRO:HG3	1.81	0.61
39:e:155:ARG:NH1	39:e:258:ASP:OD2	2.31	0.61
11:A:2994:U:H2'	11:A:2995:G:H8	1.64	0.61
12:B:1634:A:O2'	40:f:111:HIS:ND1	2.34	0.61
11:A:2248:U:OP1	26:R:99:ARG:NH2	2.28	0.61
18:J:26:ALA:HB1	18:J:57:THR:HG23	1.82	0.61
58:z:44:SER:O	58:z:47:LYS:NZ	2.33	0.61
11:A:2822:C:O2'	11:A:2915:C:OP2	2.18	0.61
15:F:188:HIS:HB2	15:F:260:VAL:HG12	1.81	0.61
23:O:157:ARG:O	23:O:160:GLN:NE2	2.32	0.61
29:U:108:PRO:HD2	33:Y:68:PHE:HE2	1.66	0.61
30:V:16:PRO:HD2	30:V:19:TYR:HB2	1.81	0.61
11:A:3146:G:N2	14:E:268:GLU:OE2	2.33	0.61
18:J:115:LYS:HD2	18:J:118:TYR:HD2	1.64	0.61
19:K:27:PRO:HG2	19:K:30:LYS:HB2	1.81	0.61
10:9:53:ILE:HG22	10:9:56:MET:H	1.65	0.61
11:A:2994:U:H2'	11:A:2995:G:C8	2.36	0.61
39:e:60:SER:O	39:e:136:ARG:NH1	2.33	0.61
9:8:99:ARG:NH1	39:e:84:TYR:O	2.33	0.61
11:A:2279:U:OP2	43:i:46:ARG:NH1	2.31	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:D:299:PRO:HD2	56:x:42:ARG:HH12	1.66	0.61
17:I:95:MET:HB2	17:I:159:PRO:HB3	1.82	0.61
18:J:108:VAL:HG21	18:J:154:ARG:HG3	1.81	0.61
10:9:82:GLU:O	33:Y:88:GLN:NE2	2.33	0.60
42:h:88:ASP:OD1	42:h:124:ARG:NH1	2.33	0.60
4:3:152:LYS:NZ	11:A:2091:A:OP2	2.32	0.60
27:S:101:PHE:HE2	44:j:49:TRP:HB3	1.66	0.60
11:A:2055:U:H2'	11:A:2056:G:H8	1.66	0.60
12:B:1607:U:H2'	12:B:1608:G:C8	2.36	0.60
15:F:243:ILE:HG22	50:q:27:ALA:HB2	1.84	0.60
11:A:1789:A:N3	11:A:1915:C:O2'	2.32	0.60
17:I:66:PRO:HG3	51:r:67:SER:CB	2.31	0.60
31:W:67:ILE:N	31:W:89:LEU:O	2.32	0.60
55:w:82:ARG:NH2	55:w:125:GLU:OE1	2.34	0.60
57:y:162:ARG:NH1	57:y:191:GLN:OE1	2.34	0.60
13:D:257:ILE:O	13:D:262:ARG:NH1	2.33	0.60
57:y:237:ALA:HB1	57:y:243:ILE:HD11	1.84	0.60
11:A:1994:A:H61	11:A:2736:C:H4'	1.67	0.60
36:b:73:PRO:HB2	36:b:89:ILE:HB	1.84	0.60
37:c:259:ARG:HB2	37:c:271:PHE:HB2	1.84	0.60
56:x:78:ASN:OD1	56:x:193:GLN:NE2	2.35	0.60
37:c:91:ALA:O	37:c:122:ASN:ND2	2.33	0.60
11:A:2067:C:O2'	40:f:60:LYS:NZ	2.28	0.60
11:A:2146:A:O3'	26:R:100:LYS:NZ	2.35	0.60
11:A:2294:A:OP2	21:M:39:ARG:NH2	2.35	0.60
11:A:1822:U:O2	11:A:2707:A:O2'	2.20	0.59
13:D:111:ARG:NH2	13:D:165:ASN:OD1	2.32	0.59
42:h:120:MET:HE3	42:h:126:VAL:HB	1.83	0.59
16:H:78:ARG:NH1	32:X:87:LEU:O	2.35	0.59
40:f:201:ARG:NH2	56:x:233:VAL:O	2.33	0.59
11:A:5507:U:H2'	11:A:5508:A:C8	2.36	0.59
17:I:100:GLN:NE2	45:k:35:GLN:OE1	2.30	0.59
21:M:31:PRO:HG2	48:o:86:ARG:HH21	1.65	0.59
29:U:46:MET:HA	29:U:93:LYS:HE2	1.84	0.59
55:w:90:TYR:HE1	55:w:92:LYS:HB3	1.67	0.59
58:z:164:ARG:HG2	58:z:192:VAL:HA	1.84	0.59
6:5:229:ARG:NH1	6:5:231:SER:OG	2.34	0.59
9:8:113:ARG:NH2	39:e:76:GLN:OE1	2.35	0.59
19:K:67:PHE:HB3	19:K:71:LYS:HB2	1.84	0.59
32:X:156:LYS:NZ	32:X:205:GLY:O	2.34	0.59
11:A:2180:A:O2'	11:A:2206:C:O3'	2.21	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:2239:A:OP2	19:K:75:LYS:NZ	2.35	0.59
57:y:113:LEU:HG	57:y:116:ARG:HH12	1.66	0.59
7:6:198:ALA:O	7:6:254:TYR:OH	2.21	0.59
36:b:15:LEU:HD11	37:c:169:VAL:HA	1.85	0.59
30:V:68:LYS:HE2	30:V:92:ASN:HA	1.85	0.59
38:d:116:MET:SD	38:d:116:MET:N	2.75	0.59
56:x:274:LYS:HG3	56:x:276:SER:H	1.68	0.59
58:z:135:ARG:NH1	58:z:141:ASN:O	2.36	0.59
7:6:52:ARG:HD2	12:B:1636:A:H4'	1.85	0.59
7:6:225:LEU:HB3	24:P:44:VAL:HG23	1.85	0.59
9:8:191:ARG:HB3	40:f:135:LEU:HD12	1.84	0.59
11:A:2651:A:O2'	58:z:281:LYS:O	2.21	0.59
20:L:118:ARG:NH1	53:u:202:GLN:OE1	2.35	0.59
34:Z:105:SER:OG	48:o:59:GLU:OE2	2.21	0.59
50:q:34:ARG:HD2	50:q:38:ARG:HH22	1.68	0.59
52:s:246:GLN:NE2	52:s:354:PRO:O	2.36	0.59
57:y:258:LEU:HD12	57:y:261:ILE:HD11	1.84	0.59
11:A:2109:A:O2'	22:N:130:PRO:O	2.21	0.59
15:F:195:LEU:HD12	15:F:202:TYR:HE2	1.68	0.59
37:c:105:ARG:NH2	37:c:115:VAL:O	2.35	0.59
56:x:70:GLU:OE2	56:x:141:ARG:NH2	2.36	0.59
27:S:131:GLU:HB3	27:S:151:LYS:HE3	1.85	0.58
58:z:109:ILE:HD11	58:z:125:MET:HE1	1.85	0.58
11:A:1911:C:H2'	11:A:1912:A:H8	1.66	0.58
49:p:96:ASN:ND2	49:p:138:GLU:O	2.35	0.58
53:u:164:THR:OG1	53:u:167:TRP:O	2.19	0.58
56:x:45:LEU:HD21	56:x:64:ARG:HH21	1.67	0.58
11:A:5002:U:H2'	11:A:5003:A:H8	1.68	0.58
58:z:93:GLN:HA	58:z:96:ILE:HD12	1.84	0.58
11:A:1672:C:O2'	28:T:143:ARG:O	2.20	0.58
35:a:140:LYS:NZ	35:a:142:ARG:OXT	2.36	0.58
42:h:135:GLN:HE22	42:h:137:ARG:HG3	1.68	0.58
49:p:180:ILE:O	49:p:184:ASN:ND2	2.34	0.58
57:y:288:PRO:HB2	57:y:293:ILE:HD11	1.83	0.58
11:A:2458:A:OP2	23:O:9:ILE:N	2.36	0.58
36:b:48:GLU:OE2	48:o:101:TRP:NE1	2.35	0.58
52:s:376:THR:HB	52:s:389:ARG:HG3	1.86	0.58
53:u:195:THR:HA	54:v:67:GLY:HA3	1.84	0.58
11:A:2740:A:H2'	11:A:2741:A:C8	2.38	0.58
30:V:93:THR:HG22	30:V:112:GLU:HG3	1.84	0.58
55:w:110:LEU:HB3	55:w:114:ASP:HB3	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:2064:A:OP1	31:W:101:LYS:NZ	2.33	0.58
14:E:69:ASP:OD1	14:E:154:ARG:NH1	2.37	0.58
16:H:117:SER:O	16:H:121:ASN:ND2	2.30	0.58
14:E:76:LYS:HG3	14:E:170:LEU:HD21	1.86	0.58
20:L:114:PRO:O	53:u:188:TYR:OH	2.21	0.58
24:P:60:SER:OG	49:p:177:ARG:NH1	2.37	0.58
9:8:141:GLU:OE1	39:e:274:ARG:NH2	2.37	0.58
11:A:2157:U:OP1	51:r:182:ARG:NH1	2.37	0.58
47:m:54:VAL:HG23	47:m:66:ILE:HG23	1.86	0.58
11:A:1690:C:O2	33:Y:216:ARG:NH1	2.37	0.57
11:A:1884:G:N3	11:A:1895:C:O2'	2.37	0.57
48:o:90:ASP:N	48:o:90:ASP:OD1	2.33	0.57
37:c:67:ASP:OD2	42:h:153:LYS:NZ	2.28	0.57
11:A:2044:A:H2'	11:A:2045:A:H8	1.69	0.57
13:D:213:CYS:HB3	13:D:246:ARG:HB3	1.85	0.57
21:M:255:MET:O	21:M:258:THR:OG1	2.22	0.57
23:O:124:GLU:OE1	23:O:128:ASN:ND2	2.36	0.57
27:S:142:THR:OG1	35:a:62:HIS:NE2	2.36	0.57
52:s:374:LEU:HD21	52:s:377:LEU:HD13	1.87	0.57
54:v:45:LEU:HD23	54:v:45:LEU:H	1.69	0.57
8:7:286:LEU:HD21	8:7:296:ARG:HE	1.69	0.57
40:f:48:TYR:HB3	40:f:51:LYS:HG2	1.87	0.57
58:z:123:ILE:HD12	58:z:198:MET:HE1	1.85	0.57
11:A:1828:A:H4'	11:A:1829:A:C8	2.39	0.57
11:A:2173:G:H2'	11:A:2174:G:H8	1.69	0.57
41:g:87:ARG:HD3	41:g:112:LYS:HE3	1.86	0.57
44:j:41:GLY:H	44:j:45:GLU:HG3	1.69	0.57
28:T:206:LEU:OXT	35:a:142:ARG:NH1	2.37	0.57
39:e:125:GLU:OE1	47:m:73:ARG:NH2	2.37	0.57
29:U:66:ALA:HB2	29:U:100:ALA:HA	1.86	0.57
11:A:2471:G:O2'	11:A:2654:U:O4	2.21	0.57
20:L:90:CYS:O	20:L:99:ARG:NH1	2.36	0.57
35:a:111:GLN:HA	35:a:114:LYS:HE2	1.85	0.57
14:E:52:HIS:HB2	23:O:145:LEU:HD23	1.87	0.57
45:k:66:VAL:HB	45:k:74:LEU:HB3	1.87	0.57
8:7:194:PRO:HG2	8:7:283:VAL:HG21	1.85	0.56
8:7:269:ILE:HD12	8:7:274:ILE:HB	1.87	0.56
9:8:127:GLN:HA	9:8:130:LYS:HB3	1.87	0.56
11:A:2408:U:H2'	11:A:2409:A:H8	1.69	0.56
38:d:164:VAL:HG11	38:d:172:MET:HE1	1.87	0.56
57:y:131:PHE:HD1	57:y:136:LEU:HD12	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:y:302:LEU:HA	57:y:306:ALA:HB3	1.86	0.56
6:5:384:GLN:OE1	11:A:2395:A:O2'	2.23	0.56
21:M:180:ASP:OD1	21:M:180:ASP:N	2.37	0.56
28:T:92:SER:OG	28:T:94:ASP:OD1	2.22	0.56
40:f:96:THR:HG22	40:f:183:ARG:HB3	1.87	0.56
44:j:110:LYS:HD2	44:j:111:PRO:HD2	1.87	0.56
6:5:204:VAL:HG11	6:5:279:PHE:HZ	1.68	0.56
7:6:240:ILE:HD13	7:6:248:GLY:HA3	1.86	0.56
11:A:1727:A:H3'	11:A:1728:U:H5	1.70	0.56
11:A:1762:A:OP2	50:q:33:ARG:NH2	2.38	0.56
11:A:1990:G:OP1	13:D:269:ARG:NH2	2.38	0.56
11:A:2747:U:H2'	11:A:2748:A:H8	1.71	0.56
25:Q:127:SER:OG	25:Q:129:LYS:NZ	2.37	0.56
29:U:44:ILE:HB	29:U:48:MET:HE3	1.87	0.56
2:1:13:SER:O	2:1:36:ARG:NH1	2.38	0.56
7:6:275:GLN:HG2	7:6:311:MET:HE1	1.85	0.56
32:X:86:ILE:HB	32:X:105:TRP:HB2	1.87	0.56
49:p:81:TYR:HB3	49:p:143:GLN:HE21	1.69	0.56
56:x:223:GLU:OE1	56:x:226:ARG:NH2	2.39	0.56
11:A:1911:C:H2'	11:A:1912:A:C8	2.41	0.56
11:A:2512:A:O2'	11:A:2541:C:OP1	2.20	0.56
11:A:2044:A:H2'	11:A:2045:A:C8	2.41	0.56
40:f:136:GLN:HB2	40:f:147:ASP:HB2	1.87	0.56
11:A:1829:A:H2'	11:A:1830:G:H8	1.71	0.56
11:A:2346:U:OP1	52:s:223:ARG:NH2	2.34	0.56
11:A:2453:G:O2'	23:O:116:ASP:OD2	2.21	0.56
10:9:136:LEU:HD12	29:U:19:VAL:HG22	1.87	0.56
11:A:2173:G:H2'	11:A:2174:G:C8	2.41	0.56
15:F:294:PRO:HB3	43:i:65:ASN:HD22	1.70	0.56
19:K:52:ASP:O	28:T:200:ARG:NH1	2.39	0.56
41:g:86:VAL:HG22	41:g:113:VAL:HG22	1.87	0.56
7:6:159:ARG:HH21	24:P:53:PRO:HG3	1.71	0.56
8:7:222:GLU:HA	8:7:251:ILE:HG22	1.88	0.56
22:N:98:HIS:CE1	22:N:100:GLY:H	2.24	0.56
39:e:63:LEU:HG	39:e:67:GLN:HB2	1.87	0.56
57:y:200:LEU:HD22	57:y:227:LEU:HB3	1.87	0.56
11:A:2494:C:H3'	11:A:2495:U:C5	2.40	0.55
11:A:2655:G:N2	11:A:2659:C:O2'	2.39	0.55
40:f:95:LEU:N	40:f:154:GLU:OE2	2.40	0.55
57:y:106:ASN:O	57:y:110:ASN:ND2	2.39	0.55
57:y:200:LEU:HD12	57:y:204:LYS:HB3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:8:165:ASP:HB2	9:8:168:LEU:HG	1.88	0.55
6:5:112:ARG:HH11	11:A:2406:A:H61	1.54	0.55
20:L:60:VAL:HA	20:L:73:ILE:HG22	1.88	0.55
52:s:211:VAL:HG22	52:s:230:ARG:HG2	1.88	0.55
56:x:142:PHE:HB2	56:x:157:LEU:HD11	1.88	0.55
14:E:80:LEU:HD12	14:E:323:GLY:HA3	1.88	0.55
21:M:119:THR:O	21:M:123:ASN:ND2	2.38	0.55
56:x:341:LEU:HD11	56:x:379:LYS:HB3	1.87	0.55
11:A:2191:A:N6	11:A:2198:A:OP1	2.39	0.55
32:X:34:GLU:OE1	32:X:36:ARG:NH1	2.39	0.55
45:k:17:ARG:HG3	45:k:52:ILE:HG23	1.88	0.55
11:A:5000:U:H2'	11:A:5001:A:C8	2.40	0.55
30:V:199:MET:HG3	30:V:204:ILE:HB	1.88	0.55
11:A:2031:A:N6	11:A:2044:A:O2'	2.40	0.55
11:A:3054:G:H2'	11:A:3055:U:C6	2.41	0.55
27:S:53:LYS:NZ	27:S:58:SER:OG	2.40	0.55
32:X:118:ILE:O	32:X:168:ARG:NH1	2.37	0.55
57:y:244:LYS:HD3	57:y:246:PRO:HG2	1.89	0.55
58:z:228:ASP:OD1	58:z:228:ASP:N	2.40	0.55
8:7:158:PHE:O	35:a:93:LYS:NZ	2.36	0.55
11:A:2661:U:H2'	11:A:2662:A:H8	1.72	0.55
40:f:93:ILE:HD11	40:f:157:VAL:HB	1.89	0.55
47:m:54:VAL:HG21	47:m:68:TYR:HB2	1.89	0.55
11:A:1829:A:H2'	11:A:1830:G:C8	2.42	0.55
15:F:103:GLN:HE21	43:i:58:ASP:HB2	1.72	0.55
37:c:52:ARG:NE	37:c:53:CYS:SG	2.80	0.55
37:c:238:MET:HE2	37:c:297:ALA:HB2	1.89	0.55
51:r:102:ARG:NH1	51:r:109:GLN:OE1	2.40	0.55
7:6:190:GLY:N	7:6:318:PHE:O	2.39	0.55
11:A:2358:A:H2'	11:A:2361:G:H2'	1.89	0.55
15:F:102:TRP:HE1	15:F:164:MET:HA	1.72	0.55
18:J:85:PRO:O	18:J:124:LYS:NZ	2.40	0.55
20:L:128:ARG:NH1	53:u:171:ASP:OD2	2.39	0.55
56:x:79:ASN:H	56:x:193:GLN:HE21	1.55	0.55
10:9:83:GLU:OE2	33:Y:91:ARG:NH2	2.40	0.54
11:A:1862:U:H2'	11:A:1863:A:H8	1.71	0.54
17:I:65:LEU:HD22	17:I:66:PRO:HD2	1.88	0.54
7:6:83:ASP:OD1	7:6:83:ASP:N	2.39	0.54
11:A:3019:G:O2'	11:A:3125:A:N1	2.40	0.54
11:A:6007:U:H4'	57:y:178:ARG:HD3	1.89	0.54
18:J:128:GLU:HB3	18:J:133:GLN:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:S:162:GLU:HB3	27:S:192:VAL:HB	1.89	0.54
11:A:2449:G:OP2	52:s:225:ARG:NH2	2.35	0.54
19:K:6:ARG:NH2	37:c:225:GLY:O	2.40	0.54
35:a:119:THR:HG23	35:a:121:HIS:H	1.72	0.54
11:A:2943:G:H5''	48:o:14:GLY:H	1.72	0.54
11:A:6001:U:H2'	11:A:6002:A:H8	1.73	0.54
56:x:101:GLU:O	56:x:104:SER:OG	2.21	0.54
11:A:2453:G:O6	11:A:2672:A:N6	2.41	0.54
29:U:153:LEU:OXT	38:d:240:LYS:NZ	2.36	0.54
30:V:49:ILE:HG21	30:V:54:TRP:HE3	1.73	0.54
39:e:175:GLN:HG2	39:e:231:VAL:HG21	1.89	0.54
5:4:84:ARG:NE	11:A:3188:U:OP2	2.38	0.54
9:8:178:TYR:N	47:m:63:THR:O	2.35	0.54
11:A:2458:A:O2'	14:E:215:PHE:O	2.24	0.54
21:M:180:ASP:OD1	21:M:183:SER:OG	2.23	0.54
25:Q:232:ARG:HB3	25:Q:235:ARG:HG3	1.89	0.54
39:e:192:LEU:O	39:e:198:ASN:ND2	2.40	0.54
40:f:84:THR:OG1	40:f:87:GLU:OE1	2.23	0.54
7:6:177:TYR:HB2	7:6:185:MET:HB3	1.88	0.54
11:A:2100:C:H2'	11:A:2101:C:H6	1.72	0.54
11:A:2101:C:H2'	11:A:2102:A:H8	1.73	0.54
11:A:2230:A:H62	11:A:2975:G:H1'	1.71	0.54
20:L:117:THR:HA	53:u:188:TYR:HE1	1.73	0.54
39:e:179:GLN:NE2	39:e:182:GLU:OE1	2.41	0.54
52:s:137:LEU:HD11	52:s:426:LEU:HD11	1.89	0.54
7:6:209:GLU:OE2	7:6:212:SER:OG	2.26	0.54
11:A:2289:G:O2'	15:F:105:ASN:ND2	2.41	0.54
11:A:2926:A:C5	11:A:3073:C:H5''	2.43	0.54
29:U:48:MET:HG3	29:U:52:ASP:HB2	1.88	0.54
58:z:227:LEU:HB2	58:z:230:LEU:HD23	1.90	0.54
11:A:2186:C:O2'	11:A:2187:C:OP1	2.26	0.54
21:M:57:ARG:HG2	21:M:62:ARG:HD2	1.90	0.54
37:c:151:GLU:O	37:c:155:ASN:ND2	2.37	0.54
38:d:226:ASP:OD1	38:d:230:ARG:N	2.41	0.54
54:v:20:GLY:HA2	54:v:23:LEU:HD23	1.90	0.54
8:7:175:ILE:O	8:7:319:ARG:NH2	2.41	0.53
11:A:2069:U:H1'	11:A:2071:U:H1'	1.90	0.53
11:A:2143:G:OP1	27:S:173:ARG:NH2	2.41	0.53
8:7:275:CYS:HA	8:7:303:PRO:HA	1.90	0.53
14:E:275:ARG:NH2	14:E:331:ASP:OD2	2.42	0.53
18:J:66:LEU:HD13	18:J:85:PRO:HA	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:K:28:PRO:HG3	19:K:65:ILE:HD12	1.89	0.53
30:V:171:ILE:O	33:Y:80:LYS:NZ	2.41	0.53
35:a:45:CYS:HA	35:a:65:VAL:HG13	1.91	0.53
56:x:67:LEU:HD23	56:x:262:ARG:HH21	1.72	0.53
56:x:271:ASN:O	56:x:277:ARG:NH1	2.39	0.53
11:A:1868:G:H2'	21:M:40:PRO:HG3	1.89	0.53
43:i:87:GLU:HG2	43:i:117:LEU:HD11	1.91	0.53
52:s:117:GLY:N	52:s:395:GLY:O	2.37	0.53
7:6:240:ILE:HD12	7:6:245:VAL:HA	1.91	0.53
7:6:327:VAL:HA	7:6:330:ILE:HD12	1.89	0.53
8:7:165:ASN:OD1	8:7:165:ASN:N	2.40	0.53
18:J:64:ILE:HD11	18:J:90:PHE:HB2	1.89	0.53
20:L:46:LEU:HD12	20:L:78:LYS:HD2	1.90	0.53
24:P:109:GLU:HG3	24:P:111:ALA:H	1.73	0.53
11:A:2006:C:H2'	11:A:2007:U:C6	2.44	0.53
31:W:120:LEU:HD12	40:f:63:ILE:HD11	1.91	0.53
37:c:79:LEU:HD12	37:c:214:PHE:HE1	1.74	0.53
53:u:193:LEU:O	53:u:197:ARG:NH1	2.40	0.53
56:x:250:ASP:OD2	56:x:251:ARG:NH1	2.41	0.53
57:y:166:LEU:HD22	57:y:171:LEU:HD23	1.90	0.53
58:z:61:PRO:HB3	58:z:82:LEU:HD11	1.91	0.53
30:V:80:ILE:HB	30:V:85:TRP:HB2	1.90	0.53
33:Y:115:LEU:HD11	33:Y:127:PRO:HD2	1.91	0.53
55:w:93:ILE:HB	55:w:108:LEU:HD23	1.90	0.53
58:z:22:LEU:HD11	58:z:215:GLU:HG2	1.90	0.53
19:K:2:SAC:H2A2	37:c:309:GLU:HB3	1.89	0.53
20:L:94:PRO:O	20:L:97:THR:OG1	2.22	0.53
37:c:84:SER:OG	37:c:86:ASP:OD1	2.26	0.53
7:6:214:TRP:HB2	7:6:240:ILE:HB	1.91	0.53
7:6:311:MET:O	44:j:112:LYS:NZ	2.41	0.53
11:A:1747:G:N2	11:A:1750:G:O2'	2.41	0.53
11:A:5509:U:H2'	11:A:5510:A:C8	2.44	0.53
24:P:158:MET:O	24:P:162:GLN:HG2	2.09	0.53
32:X:78:GLY:HA2	32:X:125:VAL:HG23	1.91	0.53
15:F:226:MET:HG3	50:q:26:ARG:HH21	1.73	0.53
8:7:148:MET:HE1	8:7:255:HIS:HB2	1.91	0.53
15:F:123:GLY:HA3	15:F:142:ARG:HG2	1.90	0.53
15:F:291:SER:OG	41:g:52:LEU:O	2.27	0.53
21:M:154:ILE:HG23	21:M:174:VAL:HG23	1.92	0.53
11:A:2109:A:H62	22:N:62:VAL:HA	1.74	0.52
12:B:1622:A:H2'	12:B:1623:G:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:M:261:ASP:HB3	21:M:264:GLN:HB2	1.91	0.52
25:Q:120:THR:HB	25:Q:173:GLU:HG3	1.91	0.52
51:r:162:ILE:HD12	51:r:162:ILE:O	2.08	0.52
5:4:96:PRO:HB2	11:A:3014:G:H5''	1.90	0.52
7:6:142:THR:OG1	24:P:109:GLU:OE2	2.25	0.52
8:7:243:LYS:O	8:7:246:GLN:NE2	2.42	0.52
49:p:82:CYS:SG	49:p:98:LYS:NZ	2.65	0.52
50:q:159:GLU:OE1	50:q:159:GLU:N	2.41	0.52
11:A:2275:U:H2'	11:A:2276:C:H6	1.73	0.52
23:O:20:LEU:N	23:O:24:SER:OG	2.41	0.52
52:s:201:ASP:HB2	52:s:240:GLN:HG2	1.91	0.52
57:y:107:ALA:HA	57:y:110:ASN:HD21	1.74	0.52
11:A:2086:A:H2'	11:A:2087:U:C6	2.45	0.52
16:H:102:VAL:H	16:H:106:GLY:HA2	1.75	0.52
32:X:114:PHE:HB3	32:X:141:LEU:HD22	1.91	0.52
39:e:81:ARG:NH2	47:m:46:GLN:O	2.42	0.52
38:d:182:ARG:NH2	38:d:225:TYR:OH	2.42	0.52
39:e:52:CYS:SG	39:e:235:LYS:NZ	2.72	0.52
42:h:87:GLN:HB3	42:h:124:ARG:HB2	1.91	0.52
4:3:169:ARG:NE	11:A:1892:A:OP2	2.39	0.52
5:4:87:ARG:HD3	5:4:101:ARG:HG3	1.91	0.52
9:8:150:LEU:HD21	9:8:157:LEU:HD23	1.92	0.52
11:A:1857:U:H2'	11:A:1858:G:C8	2.45	0.52
11:A:2052:A:H5'	41:g:105:ARG:HG3	1.92	0.52
30:V:48:PRO:HD3	33:Y:234:LEU:HD21	1.91	0.52
29:U:151:PHE:O	38:d:273:LYS:NZ	2.34	0.52
30:V:47:GLU:OE1	33:Y:240:HIS:NE2	2.34	0.52
40:f:207:LEU:HD22	56:x:244:LEU:HD13	1.91	0.52
57:y:283:THR:OG1	58:z:195:ARG:NH2	2.43	0.52
11:A:1964:U:H2'	11:A:1965:A:H8	1.75	0.52
11:A:2747:U:H2'	11:A:2748:A:C8	2.45	0.52
11:A:5509:U:H2'	11:A:5510:A:H8	1.74	0.52
15:F:216:VAL:HG22	15:F:258:THR:HB	1.92	0.52
22:N:65:GLU:HB2	22:N:66:PRO:HD3	1.90	0.52
36:b:76:VAL:HG22	36:b:86:GLU:HG3	1.91	0.52
11:A:2286:A:H2'	11:A:2287:U:C6	2.45	0.52
11:A:2299:U:H5''	11:A:2300:G:H5''	1.91	0.52
11:A:2860:G:O2'	31:W:63:ALA:O	2.26	0.52
7:6:136:ARG:NH1	7:6:140:GLU:OE2	2.43	0.52
37:c:137:LEU:HG	37:c:215:ILE:HD11	1.92	0.52
49:p:173:VAL:HA	49:p:176:HIS:CD2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:90:VAL:HB	5:4:100:GLN:HB2	1.91	0.51
10:9:86:LEU:HB3	33:Y:148:GLU:HG2	1.92	0.51
11:A:2253:U:H5'	34:Z:93:LYS:HG3	1.91	0.51
7:6:175:VAL:HG11	7:6:270:PHE:HE2	1.75	0.51
8:7:213:ASP:OD2	8:7:271:ARG:NH2	2.43	0.51
11:A:2975:G:H2'	11:A:2976:G:C8	2.44	0.51
11:A:3044:A:H2'	11:A:3045:A:C8	2.46	0.51
49:p:172:ASP:HB3	49:p:175:LEU:HG	1.92	0.51
58:z:309:PHE:HB2	58:z:314:LEU:HD12	1.92	0.51
7:6:233:LEU:HB2	7:6:298:PHE:HB3	1.91	0.51
8:7:77:THR:HG23	38:d:283:PRO:HA	1.91	0.51
11:A:3151:A:N1	11:A:3163:G:O2'	2.38	0.51
12:B:1672:C:O2'	39:e:216:LYS:O	2.22	0.51
27:S:152:ASP:OD1	27:S:152:ASP:N	2.43	0.51
33:Y:150:GLU:OE1	33:Y:154:ARG:NH1	2.43	0.51
34:Z:68:ILE:HD11	34:Z:122:LEU:HD13	1.92	0.51
41:g:110:ILE:HD11	41:g:157:LEU:HD13	1.92	0.51
10:9:77:LEU:HG	30:V:170:TRP:HD1	1.75	0.51
13:D:196:VAL:HG22	13:D:206:TYR:HB2	1.92	0.51
15:F:49:ARG:NH2	15:F:52:GLU:OE1	2.43	0.51
11:A:2006:C:H2'	11:A:2007:U:H6	1.75	0.51
19:K:140:ASN:HB2	37:c:262:GLY:HA2	1.93	0.51
53:u:193:LEU:HD12	53:u:197:ARG:HH12	1.75	0.51
1:0:117:LYS:NZ	1:0:118:GLN:O	2.38	0.51
9:8:177:HIS:CG	47:m:62:SER:HB2	2.46	0.51
11:A:1952:U:H2'	11:A:1953:A:C8	2.46	0.51
25:Q:237:ASN:OD1	25:Q:237:ASN:N	2.44	0.51
28:T:94:ASP:OD1	28:T:94:ASP:N	2.44	0.51
35:a:73:LYS:NZ	36:b:141:ARG:O	2.40	0.51
41:g:89:SER:HA	41:g:112:LYS:HE2	1.93	0.51
4:3:94:LEU:N	11:A:1752:U:OP1	2.44	0.51
7:6:338:ARG:NE	24:P:42:GLU:OE2	2.33	0.51
11:A:1862:U:H2'	11:A:1863:A:C8	2.46	0.51
14:E:177:LYS:HB3	14:E:298:LYS:HD2	1.92	0.51
11:A:2198:A:H61	18:J:147:SER:HA	1.76	0.51
11:A:2930:U:H2'	11:A:2931:A:H8	1.75	0.51
17:I:44:ARG:NH2	22:N:234:ASP:OD2	2.36	0.51
22:N:197:LYS:NZ	22:N:201:ASP:OD2	2.37	0.51
32:X:79:LEU:HB2	32:X:127:VAL:HG12	1.91	0.51
52:s:212:ARG:HD2	52:s:379:LEU:HB3	1.93	0.51
11:A:2459:A:N6	11:A:2668:A:O2'	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Z:133:ASN:OD1	34:Z:133:ASN:N	2.43	0.51
15:F:72:PHE:HA	15:F:206:LEU:HD13	1.93	0.51
33:Y:170:ARG:HH21	33:Y:201:ALA:HB3	1.77	0.51
56:x:212:ARG:HA	56:x:215:LYS:HG3	1.92	0.51
11:A:6001:U:H2'	11:A:6002:A:C8	2.45	0.50
13:D:69:ARG:NH1	13:D:71:LYS:O	2.43	0.50
15:F:62:VAL:HG11	15:F:182:LEU:HD21	1.92	0.50
28:T:56:GLN:NE2	28:T:61:PRO:O	2.42	0.50
56:x:139:ILE:O	57:y:322:ARG:NH2	2.44	0.50
57:y:214:LYS:O	57:y:218:SER:OG	2.24	0.50
7:6:60:ARG:HD3	31:W:123:GLY:HA2	1.92	0.50
11:A:1732:C:O2	43:i:115:ARG:NH1	2.41	0.50
11:A:3171:C:H5''	11:A:3196:G:H21	1.76	0.50
16:H:53:THR:OG1	32:X:83:GLU:OE2	2.27	0.50
56:x:79:ASN:OD1	56:x:130:ARG:NH1	2.44	0.50
1:0:82:LYS:O	1:0:83:ASN:ND2	2.44	0.50
7:6:184:LEU:N	49:p:190:GLN:O	2.40	0.50
47:m:55:LEU:HD21	47:m:63:THR:HB	1.93	0.50
11:A:1964:U:H2'	11:A:1965:A:C8	2.47	0.50
21:M:223:LEU:O	49:p:49:TYR:OH	2.28	0.50
39:e:177:GLU:O	39:e:190:ARG:NH2	2.45	0.50
43:i:83:TRP:HZ3	43:i:90:ARG:HG2	1.77	0.50
7:6:35:MET:HB2	7:6:38:SER:HB3	1.93	0.50
7:6:63:GLN:O	7:6:66:GLN:NE2	2.38	0.50
11:A:2262:C:O5'	27:S:182:LYS:NZ	2.44	0.50
33:Y:233:ILE:HA	33:Y:236:LYS:HD2	1.93	0.50
39:e:201:GLU:OE2	39:e:240:THR:OG1	2.22	0.50
47:m:51:LEU:HB3	47:m:67:ARG:HB3	1.93	0.50
53:u:135:LEU:HA	53:u:138:MET:HE3	1.93	0.50
11:A:2740:A:H2'	11:A:2741:A:H8	1.74	0.50
14:E:345:ILE:HG12	25:Q:169:PRO:HB2	1.94	0.50
17:I:56:PRO:HG3	22:N:208:ASN:HB2	1.94	0.50
37:c:96:CYS:HB2	37:c:182:GLU:HG2	1.93	0.50
39:e:64:THR:HB	39:e:67:GLN:HG3	1.92	0.50
1:0:134:THR:HG23	23:O:130:LEU:HD22	1.93	0.50
6:5:280:GLN:NE2	52:s:155:PHE:O	2.45	0.50
6:5:297:ALA:HB3	6:5:303:ARG:HG3	1.92	0.50
9:8:173:LYS:NZ	39:e:237:LEU:HD11	2.27	0.50
11:A:2930:U:H2'	11:A:2931:A:C8	2.46	0.50
11:A:3115:U:H2'	11:A:3116:C:H6	1.77	0.50
24:P:133:ALA:HB1	24:P:168:GLY:HA3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:e:184:LEU:O	39:e:187:THR:OG1	2.22	0.50
39:e:273:ARG:HA	39:e:276:VAL:HG22	1.93	0.50
49:p:115:VAL:HG13	49:p:161:ALA:HB3	1.93	0.50
53:u:135:LEU:HD23	53:u:179:LEU:HB3	1.92	0.50
7:6:148:LYS:NZ	7:6:316:LEU:O	2.41	0.50
11:A:1786:C:OP1	38:d:49:LYS:NZ	2.45	0.50
11:A:3141:A:H2'	11:A:3142:A:C8	2.46	0.50
27:S:129:ARG:HH21	27:S:155:ARG:HB2	1.76	0.50
30:V:52:GLU:HA	30:V:143:ARG:HH12	1.77	0.50
54:v:14:ARG:NH1	55:w:132:ASP:OD2	2.45	0.50
2:1:35:ASN:HD22	2:1:38:ARG:HH21	1.60	0.50
6:5:274:LYS:NZ	6:5:275:ASN:O	2.44	0.50
11:A:1905:C:OP1	15:F:117:ARG:NH1	2.41	0.50
11:A:2795:U:H2'	11:A:2796:G:H8	1.76	0.50
14:E:131:LYS:H	14:E:146:SER:HG	1.58	0.50
22:N:90:LEU:HB2	22:N:190:VAL:HG11	1.94	0.50
5:4:71:VAL:HG22	11:A:2953:U:H5''	1.94	0.49
23:O:40:GLU:HG2	23:O:128:ASN:HB3	1.94	0.49
24:P:55:ASN:OD1	24:P:56:LEU:N	2.45	0.49
38:d:211:GLN:HE22	38:d:262:HIS:CD2	2.30	0.49
4:3:124:ARG:NH1	4:3:125:ARG:O	2.45	0.49
7:6:66:GLN:O	7:6:75:ARG:NH2	2.45	0.49
11:A:1749:C:OP2	11:A:2899:C:O2'	2.28	0.49
11:A:2187:C:H2'	11:A:2188:A:C8	2.46	0.49
30:V:51:ASP:OD1	30:V:52:GLU:N	2.45	0.49
31:W:47:SER:OG	31:W:50:ARG:NH2	2.45	0.49
32:X:222:ASP:OD1	32:X:222:ASP:N	2.45	0.49
38:d:235:GLN:NE2	38:d:237:ASP:H	2.10	0.49
53:u:213:GLU:N	53:u:213:GLU:OE1	2.44	0.49
56:x:307:TYR:OH	56:x:316:GLN:O	2.29	0.49
7:6:360:ARG:NH1	11:A:2869:A:N7	2.60	0.49
9:8:122:SER:OG	12:B:1641:G:N2	2.45	0.49
11:A:2896:G:C6	11:A:2915:C:H1'	2.47	0.49
21:M:26:ASN:N	21:M:26:ASN:OD1	2.45	0.49
22:N:64:ARG:NE	22:N:66:PRO:O	2.46	0.49
34:Z:117:ILE:O	48:o:45:ASN:ND2	2.46	0.49
45:k:16:VAL:HG12	45:k:66:VAL:HG22	1.94	0.49
56:x:65:VAL:HG12	56:x:368:LEU:HD21	1.94	0.49
57:y:153:LYS:H	57:y:153:LYS:HZ3	1.60	0.49
6:5:166:THR:O	52:s:287:LYS:NZ	2.35	0.49
15:F:217:LEU:HD11	15:F:243:ILE:HG12	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:x:328:LEU:HB3	56:x:334:ILE:HB	1.94	0.49
11:A:3081:A:OP1	57:y:280:LYS:NZ	2.42	0.49
37:c:245:LEU:HD12	37:c:253:PRO:HD3	1.94	0.49
58:z:32:PRO:HD2	58:z:35:MET:SD	2.52	0.49
58:z:240:LEU:HD12	58:z:305:PHE:CE2	2.47	0.49
7:6:252:CYS:SG	7:6:296:ARG:NH1	2.85	0.49
11:A:2234:C:HO2'	11:A:2688:C:HO2'	1.58	0.49
11:A:2410:U:H2'	11:A:2411:U:C6	2.47	0.49
11:A:5500:A:H2'	11:A:5501:U:H6	1.78	0.49
14:E:234:THR:HG22	14:E:235:LYS:HG3	1.95	0.49
15:F:87:PHE:HB3	15:F:182:LEU:HD22	1.94	0.49
21:M:295:THR:HG22	49:p:39:PHE:HE1	1.78	0.49
22:N:78:GLU:OE1	22:N:78:GLU:N	2.45	0.49
26:R:122:ARG:NH1	27:S:72:GLU:OE2	2.38	0.49
57:y:144:VAL:HG11	57:y:180:LEU:HG	1.95	0.49
9:8:168:LEU:C	9:8:170:PRO:HD3	2.38	0.49
11:A:5002:U:H2'	11:A:5003:A:C8	2.47	0.49
23:O:33:LEU:HD21	23:O:59:LEU:HD22	1.95	0.49
27:S:109:THR:OG1	27:S:110:SER:N	2.43	0.49
39:e:86:ASP:OD2	47:m:69:ARG:NH2	2.46	0.49
54:v:45:LEU:HD21	54:v:51:ARG:HB3	1.94	0.49
1:0:95:ARG:NH1	11:A:1821:A:OP2	2.42	0.49
4:3:96:TYR:OH	43:i:128:ARG:O	2.23	0.49
7:6:90:ILE:HG22	44:j:112:LYS:HG2	1.94	0.49
7:6:346:ARG:NH2	24:P:178:ILE:O	2.45	0.49
11:A:2099:U:H2'	11:A:2100:C:C6	2.47	0.49
11:A:2142:A:O2'	11:A:2262:C:OP1	2.28	0.49
24:P:156:ASP:OD1	24:P:156:ASP:N	2.45	0.49
42:h:135:GLN:OE1	42:h:137:ARG:N	2.46	0.49
52:s:90:LYS:NZ	52:s:278:TYR:O	2.45	0.49
53:u:169:CYS:SG	53:u:170:VAL:N	2.85	0.49
54:v:47:ASP:OD2	54:v:50:ALA:N	2.34	0.49
57:y:106:ASN:OD1	57:y:106:ASN:N	2.44	0.49
58:z:116:ASP:O	58:z:120:LYS:NZ	2.46	0.49
11:A:2240:C:H5'	19:K:29:GLY:HA3	1.95	0.49
11:A:2447:A:OP1	52:s:59:ARG:NH1	2.46	0.49
15:F:241:ASN:OD1	15:F:256:HIS:NE2	2.42	0.49
39:e:58:VAL:HG13	39:e:59:VAL:HG13	1.95	0.49
3:2:59:LYS:NZ	11:A:1981:G:OP2	2.37	0.49
3:2:79:ILE:O	3:2:83:MET:HG3	2.13	0.49
11:A:2275:U:H2'	11:A:2276:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:2277:U:H2'	11:A:2278:A:H8	1.77	0.49
11:A:2651:A:H4'	58:z:282:VAL:HG12	1.94	0.49
11:A:2994:U:C2	11:A:3068:G:O6	2.61	0.49
14:E:218:VAL:HG11	14:E:240:PRO:HB3	1.94	0.49
16:H:69:ARG:HG3	50:q:49:ARG:HH22	1.78	0.49
33:Y:95:ASN:OD1	33:Y:149:ARG:NH1	2.42	0.49
40:f:131:THR:HA	40:f:151:THR:HA	1.94	0.49
2:1:34:ARG:NH1	2:1:35:ASN:O	2.46	0.48
6:5:160:HIS:HA	6:5:164:TRP:HB2	1.95	0.48
7:6:339:GLU:N	31:W:148:LEU:OXT	2.45	0.48
7:6:342:PHE:CE1	24:P:48:PHE:HB2	2.48	0.48
9:8:99:ARG:NH2	39:e:83:LEU:HB2	2.28	0.48
11:A:2093:U:C2	11:A:2094:G:C8	3.01	0.48
11:A:2099:U:H2'	11:A:2100:C:H6	1.78	0.48
18:J:111:LEU:HG	18:J:154:ARG:HD2	1.94	0.48
23:O:80:LEU:HD12	23:O:86:ILE:HG12	1.94	0.48
52:s:103:ASP:N	52:s:103:ASP:OD1	2.46	0.48
3:2:88:LYS:HE3	11:A:1783:U:H5''	1.94	0.48
8:7:93:MET:O	28:T:132:SER:OG	2.25	0.48
11:A:2127:A:H4'	11:A:2251:A:C5	2.48	0.48
11:A:2532:U:H2'	11:A:2533:A:H8	1.78	0.48
15:F:49:ARG:NH1	15:F:81:ASP:O	2.46	0.48
16:H:56:VAL:HB	16:H:80:TYR:HB3	1.95	0.48
62:w:200:PM8:O40	62:w:200:PM8:N36	2.40	0.48
6:5:300:ARG:NH2	11:A:2395:A:OP2	2.46	0.48
14:E:82:ASP:O	14:E:188:LYS:NZ	2.47	0.48
27:S:114:ILE:HG22	36:b:119:PHE:HB3	1.95	0.48
34:Z:128:LEU:HG	44:j:78:VAL:HG22	1.95	0.48
8:7:180:CYS:SG	8:7:296:ARG:NH1	2.86	0.48
11:A:2511:C:H3'	11:A:2512:A:H8	1.77	0.48
11:A:6003:U:H2'	11:A:6004:A:C8	2.49	0.48
17:I:151:ASN:OD1	45:k:31:ARG:NH2	2.46	0.48
50:q:37:PRO:HG2	50:q:68:SER:HA	1.95	0.48
54:v:21:ARG:HH21	55:w:124:ASP:HB3	1.78	0.48
7:6:187:VAL:HA	7:6:191:ASN:HD21	1.79	0.48
11:A:2253:U:H2'	11:A:2254:C:C6	2.49	0.48
11:A:2653:C:OP1	58:z:283:LYS:NZ	2.41	0.48
30:V:198:VAL:HG13	30:V:202:MET:HE3	1.95	0.48
39:e:222:ARG:HG3	39:e:227:LEU:HD12	1.95	0.48
50:q:153:ARG:NH1	56:x:82:ALA:HA	2.28	0.48
53:u:191:GLU:OE1	53:u:191:GLU:N	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:162:THR:O	4:3:167:LYS:NZ	2.44	0.48
11:A:2049:U:H2'	11:A:2050:A:H8	1.79	0.48
11:A:3224:G:H2'	11:A:3225:G:H8	1.79	0.48
30:V:64:ILE:HD11	30:V:70:ALA:HA	1.94	0.48
34:Z:81:TRP:NE1	34:Z:82:GLU:OE2	2.47	0.48
49:p:78:THR:HB	49:p:102:ARG:HG3	1.95	0.48
51:r:70:CYS:O	51:r:74:ARG:HB2	2.13	0.48
51:r:158:SER:O	51:r:158:SER:OG	2.27	0.48
58:z:164:ARG:O	58:z:169:ARG:N	2.46	0.48
7:6:221:LEU:O	24:P:51:ARG:NH2	2.41	0.48
10:9:72:PRO:HG3	33:Y:104:VAL:HG22	1.95	0.48
11:A:2065:A:OP1	40:f:48:TYR:N	2.47	0.48
11:A:2147:G:OP1	27:S:104:ARG:NE	2.45	0.48
11:A:2661:U:H2'	11:A:2662:A:C8	2.49	0.48
11:A:3000:A:H2'	11:A:3001:G:H8	1.77	0.48
11:A:5507:U:H2'	11:A:5508:A:H8	1.78	0.48
22:N:97:LEU:HB3	22:N:102:PHE:HE1	1.78	0.48
38:d:88:TYR:HB2	38:d:198:ARG:HH22	1.79	0.48
49:p:94:LYS:HE2	49:p:96:ASN:HB2	1.95	0.48
57:y:129:SER:OG	57:y:130:GLU:OE2	2.31	0.48
11:A:2360:U:H3'	11:A:2361:G:H4'	1.96	0.48
11:A:3125:A:H62	11:A:3132:G:H21	1.62	0.48
20:L:71:ASP:O	20:L:86:ILE:HG12	2.13	0.48
24:P:111:ALA:O	24:P:114:LYS:NZ	2.46	0.48
54:v:13:TYR:HB2	54:v:39:PHE:HE2	1.78	0.48
56:x:259:THR:HA	56:x:272:ILE:HD13	1.96	0.48
11:A:2049:U:H2'	11:A:2050:A:C8	2.48	0.48
11:A:2924:U:H2'	11:A:2925:U:C6	2.48	0.48
17:I:164:MET:O	17:I:167:ILE:HG22	2.14	0.48
28:T:63:ARG:NH1	38:d:228:PHE:O	2.46	0.48
40:f:204:LEU:HD22	56:x:244:LEU:HD12	1.96	0.48
11:A:2041:U:H2'	11:A:2042:U:C6	2.49	0.48
11:A:2374:A:N1	52:s:97:THR:OG1	2.37	0.48
54:v:42:ASN:ND2	62:w:200:PM8:O1	2.46	0.48
5:4:68:ASN:HD21	5:4:101:ARG:HD2	1.79	0.47
5:4:83:LYS:HE2	11:A:3189:C:H5	1.79	0.47
6:5:139:LEU:HD13	6:5:423:ALA:HB3	1.96	0.47
10:9:24:LYS:HG2	11:A:2421:G:H5''	1.96	0.47
11:A:1952:U:H2'	11:A:1953:A:H8	1.77	0.47
14:E:135:LYS:NZ	14:E:136:GLU:OE2	2.45	0.47
17:I:51:THR:OG1	22:N:250:ARG:NH2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:J:66:LEU:HG	18:J:82:ILE:HD11	1.94	0.47
21:M:22:VAL:HA	21:M:26:ASN:HD21	1.79	0.47
25:Q:182:ARG:HD2	25:Q:218:ASN:HB3	1.96	0.47
34:Z:130:ALA:O	34:Z:134:MET:HG2	2.14	0.47
36:b:35:ARG:HG2	48:o:101:TRP:HB2	1.95	0.47
38:d:59:HIS:HA	38:d:61:ARG:HH21	1.78	0.47
40:f:149:VAL:N	47:m:68:TYR:OH	2.45	0.47
8:7:107:LEU:HB3	8:7:126:LYS:HB3	1.95	0.47
11:A:3143:U:H2'	11:A:3144:A:H8	1.79	0.47
12:B:1639:U:H2'	12:B:1640:A:C8	2.48	0.47
29:U:81:ASP:HB3	29:U:87:ILE:HD11	1.96	0.47
30:V:150:SER:HB2	30:V:152:ARG:HH21	1.80	0.47
40:f:122:GLU:HB2	40:f:158:GLN:HB3	1.96	0.47
48:o:13:PRO:HG2	48:o:21:HIS:HB2	1.96	0.47
11:A:1750:G:H5''	21:M:76:ILE:HD12	1.95	0.47
11:A:5511:U:H2'	11:A:5512:A:C8	2.48	0.47
38:d:235:GLN:CD	38:d:237:ASP:H	2.22	0.47
45:k:22:PRO:HA	45:k:27:VAL:HG21	1.95	0.47
54:v:50:ALA:HA	54:v:53:ARG:HG2	1.95	0.47
58:z:213:SER:OG	58:z:216:THR:OG1	2.30	0.47
29:U:11:ARG:NH1	30:V:212:LYS:O	2.47	0.47
50:q:145:LYS:O	50:q:145:LYS:NZ	2.35	0.47
55:w:115:GLN:HE22	55:w:139:MET:HE2	1.80	0.47
11:A:2262:C:OP2	27:S:173:ARG:NH1	2.48	0.47
15:F:67:GLU:HB2	15:F:190:MET:HE3	1.95	0.47
15:F:164:MET:HE2	43:i:69:HIS:CE1	2.49	0.47
46:l:114:SER:OG	46:l:115:ARG:N	2.48	0.47
58:z:194:GLU:HG2	58:z:195:ARG:HG3	1.96	0.47
7:6:88:ILE:HG23	44:j:111:PRO:HB3	1.96	0.47
11:A:2098:G:H2'	11:A:2099:U:H6	1.79	0.47
11:A:2689:C:O3'	48:o:9:ARG:N	2.48	0.47
11:A:3073:C:O2	38:d:37:THR:OG1	2.30	0.47
15:F:215:SER:N	15:F:257:GLN:OE1	2.39	0.47
27:S:71:GLU:N	27:S:71:GLU:OE1	2.48	0.47
35:a:72:THR:HG22	37:c:258:THR:HA	1.97	0.47
37:c:159:PHE:CE2	37:c:231:MET:HG2	2.49	0.47
9:8:150:LEU:HD11	9:8:157:LEU:HB3	1.97	0.47
10:9:137:ARG:NH2	33:Y:143:ASP:OD2	2.47	0.47
11:A:1951:C:H2'	11:A:1952:U:H6	1.80	0.47
11:A:2420:U:OP1	29:U:93:LYS:NZ	2.48	0.47
11:A:2841:U:H2'	11:A:2842:C:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:3078:C:N4	11:A:3079:G:O6	2.47	0.47
11:A:3088:C:O2'	11:A:3090:G:OP1	2.33	0.47
15:F:195:LEU:HB2	15:F:229:SER:HB2	1.97	0.47
17:I:115:GLN:OE1	17:I:167:ILE:HD11	2.14	0.47
18:J:101:ALA:HB3	18:J:104:THR:HG22	1.96	0.47
28:T:192:GLU:O	28:T:196:GLN:HG2	2.15	0.47
33:Y:90:LEU:HB2	33:Y:145:VAL:HG21	1.97	0.47
39:e:185:ARG:NH1	39:e:204:PHE:HB3	2.27	0.47
47:m:56:LEU:HD23	47:m:75:LEU:HB3	1.97	0.47
52:s:90:LYS:HZ3	52:s:278:TYR:H	1.62	0.47
53:u:104:GLU:O	53:u:134:HIS:NE2	2.41	0.47
57:y:237:ALA:HB2	57:y:253:TYR:CZ	2.50	0.47
8:7:209:LEU:HA	8:7:212:LYS:HZ2	1.79	0.47
11:A:2158:U:OP2	51:r:195:TYR:OH	2.21	0.47
11:A:2688:C:H2'	11:A:2689:C:C6	2.49	0.47
17:I:81:LEU:HD23	17:I:84:ARG:HE	1.79	0.47
20:L:127:LEU:HB3	20:L:134:TYR:HB3	1.96	0.47
24:P:86:THR:OG1	24:P:89:HIS:O	2.33	0.47
29:U:47:GLU:OE1	29:U:47:GLU:N	2.48	0.47
39:e:213:TYR:HE1	39:e:267:LYS:HG2	1.79	0.47
49:p:48:LEU:HD11	50:q:96:LEU:HD13	1.96	0.47
56:x:129:LEU:HD23	56:x:129:LEU:HA	1.77	0.47
2:1:55:LEU:HG	50:q:132:ILE:HG12	1.96	0.47
8:7:44:ARG:HB3	8:7:261:ILE:HD13	1.96	0.47
10:9:75:SER:HB3	30:V:170:TRP:HE1	1.79	0.47
11:A:3000:A:H2'	11:A:3001:G:C8	2.49	0.47
11:A:3034:U:H2'	11:A:3035:C:C6	2.49	0.47
35:a:51:LEU:HD22	35:a:55:GLY:HA2	1.97	0.47
56:x:296:LEU:HD23	56:x:305:VAL:HG21	1.96	0.47
56:x:312:LEU:HD23	56:x:363:LEU:HD11	1.97	0.47
57:y:116:ARG:HG3	57:y:119:ALA:HB3	1.97	0.47
9:8:107:THR:O	9:8:111:THR:HG23	2.14	0.47
9:8:130:LYS:HA	9:8:133:ARG:HG2	1.97	0.47
11:A:2847:C:H2'	11:A:2848:A:O4'	2.15	0.47
11:A:3123:G:OP1	53:u:144:LYS:NZ	2.47	0.47
32:X:19:GLY:O	32:X:22:SER:OG	2.33	0.47
49:p:171:GLU:HB3	49:p:176:HIS:HE1	1.78	0.47
52:s:119:PRO:HG3	52:s:394:TRP:CD2	2.49	0.47
56:x:34:THR:OG1	56:x:35:GLU:N	2.48	0.47
58:z:247:HIS:O	58:z:247:HIS:ND1	2.39	0.47
2:1:33:LYS:HE2	2:1:65:LEU:HD11	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:156:LYS:HB2	4:3:156:LYS:HE2	1.58	0.46
11:A:1711:C:H41	33:Y:195:ASN:HB3	1.80	0.46
11:A:5004:U:H2'	11:A:5005:A:H8	1.80	0.46
11:A:5500:A:H2'	11:A:5501:U:C6	2.51	0.46
11:A:5507:U:H4'	57:y:297:SER:HB3	1.97	0.46
12:B:1628:C:H42	12:B:1640:A:H61	1.63	0.46
28:T:85:ALA:O	28:T:139:SER:OG	2.32	0.46
50:q:118:GLU:HA	50:q:121:ILE:HD12	1.97	0.46
57:y:143:VAL:O	57:y:147:LYS:HG2	2.15	0.46
11:A:3158:A:H2'	11:A:3159:A:C8	2.50	0.46
22:N:51:ARG:O	22:N:106:ARG:NH2	2.37	0.46
58:z:192:VAL:HG21	58:z:200:LEU:HD13	1.97	0.46
5:4:87:ARG:HD2	5:4:89:TYR:CZ	2.50	0.46
11:A:1815:A:OP1	26:R:37:ARG:HB2	2.15	0.46
11:A:1951:C:H2'	11:A:1952:U:C6	2.49	0.46
11:A:1995:A:H4'	11:A:2499:U:H4'	1.98	0.46
11:A:2037:U:H4'	11:A:2040:G:N1	2.30	0.46
11:A:2180:A:H1'	11:A:2206:C:H4'	1.97	0.46
11:A:2302:U:H2'	11:A:2303:A:H8	1.80	0.46
22:N:127:PRO:HA	22:N:152:THR:HG22	1.97	0.46
24:P:167:GLU:O	49:p:187:ARG:NH1	2.47	0.46
39:e:203:LYS:N	39:e:237:LEU:O	2.39	0.46
54:v:25:TYR:HD2	54:v:70:ILE:HG22	1.80	0.46
56:x:328:LEU:O	56:x:333:SER:N	2.49	0.46
6:5:96:HIS:HD1	11:A:2410:U:HO2'	1.59	0.46
6:5:332:ASP:N	6:5:332:ASP:OD1	2.48	0.46
7:6:44:ASN:HB2	7:6:47:ARG:HB2	1.98	0.46
11:A:1857:U:H4'	11:A:2989:G:C8	2.51	0.46
11:A:2456:U:OP1	23:O:16:ARG:NH1	2.43	0.46
11:A:6003:U:H2'	11:A:6004:A:H8	1.80	0.46
20:L:71:ASP:HB2	20:L:86:ILE:HD11	1.97	0.46
50:q:159:GLU:H	50:q:159:GLU:CD	2.24	0.46
51:r:92:PHE:HA	51:r:100:LEU:HD22	1.96	0.46
51:r:120:LYS:HB2	51:r:124:ARG:HH21	1.81	0.46
57:y:91:GLU:HG3	57:y:94:ARG:HH22	1.79	0.46
9:8:135:THR:O	9:8:139:MET:HG3	2.15	0.46
10:9:24:LYS:NZ	11:A:2422:U:OP2	2.49	0.46
11:A:1883:G:OP2	21:M:100:ARG:NH2	2.49	0.46
11:A:1894:G:H2'	11:A:1895:C:C6	2.51	0.46
11:A:2085:A:H2'	11:A:2086:A:C8	2.50	0.46
11:A:2268:G:N7	21:M:44:ARG:NH2	2.55	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:B:1673:A:N1	39:e:172:ILE:HG21	2.31	0.46
19:K:139:LYS:HE2	19:K:139:LYS:HB2	1.84	0.46
22:N:50:LEU:O	22:N:106:ARG:NH1	2.49	0.46
36:b:44:ARG:O	36:b:48:GLU:HG2	2.16	0.46
49:p:182:ASN:HD22	49:p:185:ARG:HH21	1.64	0.46
56:x:308:SER:OG	56:x:375:MET:SD	2.73	0.46
58:z:80:LEU:HD12	58:z:108:VAL:HG13	1.97	0.46
11:A:1698:C:O2'	11:A:1702:A:N3	2.42	0.46
11:A:2529:U:H2'	13:D:208:ARG:HB2	1.98	0.46
11:A:2938:A:OP1	11:A:2984:A:N6	2.49	0.46
15:F:75:GLU:OE2	15:F:210:ARG:NE	2.48	0.46
20:L:100:PHE:HB3	25:Q:158:GLN:HE22	1.80	0.46
21:M:8:GLY:H	41:g:115:GLY:HA2	1.80	0.46
22:N:196:GLU:N	22:N:196:GLU:OE1	2.48	0.46
30:V:105:ARG:HG3	38:d:174:TRP:CE2	2.51	0.46
43:i:88:LEU:O	43:i:92:ILE:HD12	2.16	0.46
47:m:72:ARG:HD3	47:m:75:LEU:HD23	1.97	0.46
53:u:104:GLU:HB3	53:u:138:MET:HG2	1.98	0.46
53:u:165:ASP:OD1	53:u:166:ASP:N	2.49	0.46
56:x:191:LEU:O	56:x:194:THR:OG1	2.29	0.46
6:5:46:LEU:HD23	6:5:46:LEU:HA	1.81	0.46
11:A:1894:G:H2'	11:A:1895:C:H6	1.80	0.46
24:P:81:LEU:HB2	24:P:144:MET:HE3	1.97	0.46
56:x:315:LEU:HD13	56:x:319:TYR:HD2	1.80	0.46
7:6:239:ASN:H	7:6:275:GLN:NE2	2.10	0.46
11:A:1936:A:H1'	11:A:1938:A:C6	2.50	0.46
11:A:2408:U:H2'	11:A:2409:A:C8	2.48	0.46
13:D:143:ALA:HB2	13:D:148:LYS:HG2	1.97	0.46
18:J:45:SER:OG	18:J:47:ASN:OD1	2.34	0.46
23:O:40:GLU:OE2	23:O:96:ARG:NH1	2.43	0.46
55:w:91:ASP:OD1	55:w:91:ASP:N	2.38	0.46
58:z:130:ILE:O	58:z:133:SER:OG	2.30	0.46
3:2:78:VAL:HG21	11:A:1790:A:H4'	1.98	0.46
6:5:123:LEU:HD22	6:5:220:LEU:HD21	1.98	0.46
11:A:1924:U:H2'	11:A:1925:A:H8	1.81	0.46
11:A:2042:U:H2'	11:A:2043:C:C6	2.51	0.46
14:E:177:LYS:HG3	14:E:298:LYS:HB2	1.97	0.46
17:I:66:PRO:HG3	51:r:67:SER:O	2.16	0.46
30:V:100:LYS:NZ	30:V:101:THR:O	2.37	0.46
39:e:87:HIS:CE1	47:m:71:PRO:HG3	2.51	0.46
53:u:163:ASP:OD1	53:u:163:ASP:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:y:108:HIS:O	57:y:111:GLU:HG2	2.16	0.46
1:0:84:ARG:NH2	11:A:2306:A:O2'	2.48	0.46
7:6:175:VAL:HG11	7:6:270:PHE:CE2	2.51	0.46
11:A:1977:U:H2'	11:A:1978:A:H8	1.80	0.46
11:A:2100:C:H2'	11:A:2101:C:C6	2.51	0.46
11:A:2361:G:H5'	11:A:2362:A:H5''	1.98	0.46
15:F:62:VAL:HG21	15:F:88:ALA:HB2	1.98	0.46
17:I:81:LEU:HD11	46:l:114:SER:HA	1.98	0.46
25:Q:120:THR:HG22	25:Q:172:GLN:HB2	1.97	0.46
25:Q:278:ILE:O	25:Q:282:ILE:HG12	2.16	0.46
43:i:57:TYR:OH	50:q:28:ARG:O	2.32	0.46
1:0:93:ARG:HG3	11:A:2709:A:H5''	1.98	0.45
8:7:51:GLU:OE2	8:7:54:ARG:NH2	2.41	0.45
9:8:175:GLY:N	40:f:182:VAL:O	2.49	0.45
11:A:1852:C:P	27:S:177:ARG:HH22	2.38	0.45
22:N:113:MET:SD	22:N:118:MET:HB3	2.56	0.45
38:d:94:ASP:OD2	38:d:245:TYR:OH	2.34	0.45
38:d:208:VAL:HG12	38:d:252:LEU:HD12	1.97	0.45
53:u:111:VAL:H	54:v:26:THR:HG22	1.80	0.45
11:A:2410:U:H2'	11:A:2411:U:H6	1.82	0.45
19:K:119:ARG:HA	19:K:119:ARG:HD3	1.63	0.45
21:M:99:ASN:OD1	21:M:99:ASN:N	2.48	0.45
48:o:15:ARG:HD2	48:o:18:ILE:HD11	1.98	0.45
55:w:115:GLN:O	55:w:119:ILE:HG12	2.16	0.45
57:y:175:LYS:HD2	57:y:217:HIS:CD2	2.52	0.45
58:z:42:MET:HE1	58:z:203:THR:HG21	1.97	0.45
7:6:72:ARG:NH1	11:A:2062:A:O3'	2.49	0.45
11:A:1737:A:N6	11:A:1760:G:H1'	2.31	0.45
11:A:2236:C:O3'	51:r:171:ARG:NH2	2.49	0.45
22:N:98:HIS:HA	22:N:151:VAL:HG12	1.99	0.45
39:e:151:ARG:HH22	39:e:255:VAL:HA	1.81	0.45
40:f:178:LEU:HD13	40:f:184:LEU:HD23	1.99	0.45
47:m:54:VAL:HA	47:m:73:ARG:HA	1.98	0.45
49:p:156:ASP:HA	49:p:159:THR:HG22	1.99	0.45
58:z:82:LEU:HD23	58:z:82:LEU:HA	1.79	0.45
58:z:144:TYR:HB2	58:z:198:MET:HB2	1.98	0.45
1:0:82:LYS:HE2	11:A:2717:A:H2'	1.98	0.45
8:7:315:LYS:HZ2	14:E:64:LEU:HD21	1.80	0.45
11:A:2089:U:H2'	11:A:2090:A:H8	1.81	0.45
11:A:2387:U:O2'	11:A:2406:A:N7	2.46	0.45
30:V:105:ARG:HD2	38:d:170:PRO:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:e:156:ASN:OD1	39:e:157:LEU:N	2.49	0.45
40:f:127:MET:SD	40:f:127:MET:N	2.87	0.45
58:z:122:ILE:HG22	58:z:123:ILE:HD13	1.98	0.45
11:A:1883:G:H5'	41:g:91:MET:HG3	1.97	0.45
12:B:1639:U:H2'	12:B:1640:A:H8	1.82	0.45
22:N:114:ASP:OD1	22:N:114:ASP:N	2.50	0.45
25:Q:277:LYS:HB2	25:Q:277:LYS:HE2	1.75	0.45
54:v:10:LEU:HB3	55:w:116:VAL:HG21	1.98	0.45
5:4:97:ARG:NH1	11:A:2965:A:OP1	2.49	0.45
11:A:3115:U:H2'	11:A:3116:C:C6	2.52	0.45
14:E:252:TRP:O	14:E:255:THR:OG1	2.26	0.45
30:V:194:LEU:HD23	33:Y:95:ASN:HB3	1.99	0.45
33:Y:229:LYS:O	33:Y:233:ILE:HD12	2.17	0.45
37:c:79:LEU:HD12	37:c:214:PHE:CE1	2.52	0.45
40:f:174:ILE:HD12	40:f:175:GLN:N	2.32	0.45
41:g:85:PHE:HB3	41:g:114:GLU:OE2	2.17	0.45
42:h:112:VAL:HG22	42:h:129:PHE:CE2	2.52	0.45
50:q:34:ARG:HD3	50:q:38:ARG:HH12	1.82	0.45
57:y:274:TYR:HD1	57:y:288:PRO:HD2	1.81	0.45
11:A:2082:G:OP1	48:o:66:ARG:NH2	2.50	0.45
11:A:2361:G:H5''	11:A:2362:A:H8	1.81	0.45
11:A:3117:C:H2'	11:A:3118:U:H6	1.80	0.45
11:A:3144:A:H2'	11:A:3145:A:H8	1.80	0.45
12:B:1622:A:H2'	12:B:1623:G:H8	1.79	0.45
12:B:1628:C:C2	12:B:1629:A:C8	3.04	0.45
17:I:104:LEU:HG	17:I:108:ASP:HB2	1.98	0.45
19:K:76:VAL:HG12	19:K:91:THR:HG22	1.99	0.45
28:T:195:GLN:O	28:T:199:SER:OG	2.25	0.45
35:a:77:ARG:O	35:a:77:ARG:NE	2.50	0.45
39:e:128:PHE:HA	39:e:131:PHE:CE1	2.52	0.45
53:u:139:ALA:HB1	53:u:159:ILE:HD12	1.99	0.45
55:w:138:LEU:HB3	55:w:143:GLU:OE2	2.16	0.45
56:x:342:THR:O	56:x:346:ARG:HG2	2.17	0.45
1:0:142:GLY:HA3	11:A:2321:A:N7	2.31	0.45
11:A:2086:A:H2'	11:A:2087:U:H6	1.81	0.45
11:A:2339:G:N2	11:A:2426:C:O2'	2.49	0.45
11:A:2365:U:H2'	11:A:2366:G:H8	1.80	0.45
11:A:2503:A:H5'	11:A:3095:G:H4'	1.97	0.45
11:A:2530:A:H5''	13:D:212:THR:HG21	1.99	0.45
11:A:3038:U:O2'	58:z:32:PRO:HB3	2.16	0.45
17:I:176:LEU:HB3	17:I:188:ARG:HG3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:M:156:VAL:O	21:M:176:THR:HA	2.16	0.45
22:N:175:PHE:O	22:N:179:VAL:HG23	2.16	0.45
24:P:103:VAL:HG21	24:P:135:ARG:HB3	1.99	0.45
27:S:115:LEU:HD11	27:S:190:GLN:HB2	1.99	0.45
47:m:68:TYR:HD1	47:m:69:ARG:H	1.64	0.45
50:q:59:LYS:HE3	50:q:59:LYS:HB3	1.74	0.45
51:r:109:GLN:O	51:r:109:GLN:NE2	2.50	0.45
52:s:87:GLN:NE2	52:s:279:GLU:OE1	2.50	0.45
4:3:108:LYS:HA	4:3:108:LYS:HD3	1.81	0.45
11:A:2056:G:H2'	11:A:2057:C:C6	2.52	0.45
11:A:2333:G:HO2'	11:A:2447:A:HO2'	1.63	0.45
15:F:65:TRP:CD1	42:h:117:LEU:HD11	2.52	0.45
16:H:72:ARG:HA	16:H:72:ARG:HE	1.82	0.45
22:N:48:PRO:HG2	22:N:115:PRO:HB3	1.99	0.45
30:V:133:ILE:HA	30:V:147:SER:HA	1.99	0.45
34:Z:44:LYS:HE2	34:Z:44:LYS:HB2	1.74	0.45
36:b:149:GLN:OE1	36:b:149:GLN:N	2.48	0.45
53:u:95:ASP:OD1	54:v:25:TYR:OH	2.24	0.45
11:A:1861:U:H2'	11:A:1862:U:C6	2.52	0.45
11:A:2042:U:H2'	11:A:2043:C:H6	1.82	0.45
11:A:2748:A:H2'	11:A:2749:A:H8	1.81	0.45
11:A:3008:C:O2'	11:A:3051:A:N3	2.45	0.45
39:e:67:GLN:HA	39:e:70:MET:HG3	1.97	0.45
11:A:1979:U:H2'	11:A:1980:A:H8	1.82	0.44
11:A:2005:C:H2'	11:A:2006:C:H6	1.82	0.44
11:A:2134:A:N6	11:A:2135:A:H62	2.15	0.44
11:A:2135:A:N3	11:A:2135:A:H2'	2.32	0.44
13:D:138:ASP:OD1	13:D:249:ASN:ND2	2.50	0.44
23:O:46:TRP:CD1	23:O:121:ALA:HB2	2.52	0.44
23:O:83:LYS:HA	23:O:83:LYS:HD3	1.82	0.44
27:S:132:LYS:HE3	44:j:43:LEU:O	2.17	0.44
32:X:226:LEU:HD12	33:Y:155:LEU:HB3	2.00	0.44
37:c:86:ASP:OD1	37:c:87:LEU:N	2.48	0.44
38:d:235:GLN:OE1	38:d:238:VAL:HG22	2.18	0.44
45:k:25:LYS:HE3	45:k:25:LYS:HB3	1.65	0.44
9:8:147:LEU:HD23	9:8:147:LEU:HA	1.87	0.44
11:A:2693:A:OP1	48:o:15:ARG:NH1	2.50	0.44
11:A:3054:G:H2'	11:A:3055:U:H6	1.82	0.44
21:M:191:VAL:HG13	21:M:277:MET:HE1	1.98	0.44
28:T:134:LEU:HD23	28:T:174:GLU:HA	2.00	0.44
52:s:271:LEU:HD23	52:s:273:LEU:HD13	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:y:162:ARG:NH2	57:y:186:ILE:O	2.50	0.44
8:7:156:ARG:O	35:a:95:ARG:NH2	2.38	0.44
9:8:135:THR:HG23	9:8:136:ILE:HD12	1.98	0.44
11:A:2245:A:H2'	51:r:189:ARG:CZ	2.48	0.44
11:A:5004:U:H2'	11:A:5005:A:C8	2.53	0.44
11:A:5513:U:H2'	11:A:5514:A:C8	2.52	0.44
15:F:102:TRP:O	15:F:106:PHE:HB3	2.17	0.44
22:N:177:ASP:OD1	22:N:178:GLN:N	2.50	0.44
24:P:47:GLU:HG2	31:W:143:LYS:HG2	1.99	0.44
29:U:150:TRP:CD1	38:d:172:MET:HG2	2.52	0.44
40:f:144:MET:SD	40:f:144:MET:N	2.90	0.44
54:v:21:ARG:HA	54:v:28:ARG:HH21	1.81	0.44
58:z:110:PHE:O	58:z:118:ASN:ND2	2.44	0.44
7:6:227:GLU:HG3	7:6:230:ALA:H	1.82	0.44
11:A:1861:U:H2'	11:A:1862:U:H6	1.83	0.44
11:A:2005:C:H2'	11:A:2006:C:C6	2.51	0.44
11:A:2346:U:H2'	11:A:2347:C:H6	1.83	0.44
11:A:3141:A:H2'	11:A:3142:A:H8	1.81	0.44
14:E:216:GLN:HG3	14:E:261:MET:HE3	1.98	0.44
15:F:191:ASP:OD1	15:F:191:ASP:N	2.42	0.44
20:L:83:LYS:HB2	20:L:83:LYS:HE2	1.73	0.44
23:O:135:LEU:HD13	23:O:136:PRO:HD2	2.00	0.44
28:T:187:VAL:O	28:T:191:LYS:HG2	2.18	0.44
39:e:159:LEU:HG	39:e:254:TRP:CD1	2.52	0.44
44:j:45:GLU:CD	44:j:70:ARG:HH22	2.25	0.44
7:6:139:TRP:O	7:6:144:GLY:N	2.50	0.44
8:7:243:LYS:HE3	8:7:265:GLU:HB3	2.00	0.44
11:A:2533:A:H2'	11:A:2534:G:C8	2.53	0.44
12:B:1628:C:H2'	12:B:1629:A:H8	1.83	0.44
54:v:38:GLU:O	54:v:42:ASN:ND2	2.51	0.44
11:A:2346:U:H2'	11:A:2347:C:C6	2.53	0.44
14:E:99:LEU:HD21	14:E:193:LEU:HB3	1.98	0.44
15:F:292:ASP:OD1	41:g:55:THR:OG1	2.35	0.44
21:M:43:ARG:NH1	27:S:179:ASN:O	2.46	0.44
24:P:57:GLU:O	49:p:177:ARG:NH1	2.46	0.44
38:d:226:ASP:OD2	38:d:230:ARG:NE	2.43	0.44
39:e:152:LYS:HA	39:e:152:LYS:HD3	1.83	0.44
52:s:207:HIS:ND1	52:s:234:ASP:OD1	2.50	0.44
53:u:98:VAL:O	53:u:102:ARG:HG2	2.18	0.44
57:y:137:ASN:C	57:y:140:PRO:HD2	2.43	0.44
7:6:112:GLU:H	7:6:112:GLU:HG2	1.63	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:2093:U:H4'	43:i:126:LYS:HE2	1.99	0.44
11:A:2200:A:H5''	46:l:134:LYS:HE2	2.00	0.44
11:A:2246:A:H2'	11:A:2247:C:O4'	2.16	0.44
11:A:2691:U:OP2	48:o:11:ARG:NE	2.51	0.44
24:P:70:THR:HG21	31:W:76:HIS:HB3	2.00	0.44
26:R:89:ASN:OD1	26:R:124:ARG:HB2	2.18	0.44
30:V:124:ASP:HB2	30:V:131:THR:HG21	2.00	0.44
56:x:129:LEU:HD13	56:x:163:LEU:HD11	1.99	0.44
1:0:180:LYS:HD3	1:0:181:ARG:H	1.83	0.44
1:0:184:TRP:CD1	1:0:184:TRP:H	2.35	0.44
6:5:213:TRP:HB3	6:5:322:LEU:HD21	1.99	0.44
16:H:71:PRO:HG3	32:X:65:VAL:HG22	1.99	0.44
17:I:65:LEU:O	17:I:67:SER:N	2.50	0.44
19:K:144:GLU:HB2	36:b:145:PRO:HB3	2.00	0.44
47:m:53:PRO:HA	47:m:67:ARG:NE	2.33	0.44
56:x:181:CYS:HB3	63:x:401:SAM:O4'	2.17	0.44
7:6:96:LYS:HD2	7:6:96:LYS:HA	1.82	0.44
8:7:236:LYS:HA	8:7:236:LYS:HD3	1.82	0.44
9:8:164:ARG:HE	40:f:88:TYR:HD1	1.66	0.44
11:A:1737:A:O2'	43:i:93:ARG:NH2	2.45	0.44
11:A:1925:A:H2'	11:A:1926:A:C8	2.53	0.44
11:A:2098:G:H2'	11:A:2099:U:C6	2.53	0.44
11:A:2253:U:H2'	11:A:2254:C:H6	1.83	0.44
11:A:3009:C:H42	11:A:3028:A:H2	1.65	0.44
17:I:126:PHE:HB2	17:I:131:LEU:HD21	1.99	0.44
22:N:167:CYS:SG	22:N:168:GLU:N	2.91	0.44
22:N:202:GLN:NE2	22:N:206:GLU:OE2	2.50	0.44
34:Z:154:VAL:HG12	34:Z:156:GLN:H	1.83	0.44
36:b:54:PHE:HD1	36:b:57:ARG:HH21	1.66	0.44
40:f:120:LYS:HB2	40:f:120:LYS:HE2	1.73	0.44
50:q:78:SER:N	50:q:81:GLN:OE1	2.51	0.44
53:u:94:ILE:HA	53:u:97:MET:HB3	1.99	0.44
57:y:225:GLU:OE1	57:y:225:GLU:N	2.41	0.44
3:2:51:ASN:O	3:2:54:GLN:NE2	2.51	0.43
6:5:232:THR:HG22	6:5:289:HIS:HB2	2.00	0.43
7:6:126:ARG:HG2	24:P:122:VAL:HB	1.99	0.43
10:9:39:LYS:HD3	11:A:1705:A:C8	2.52	0.43
11:A:2037:U:H4'	11:A:2040:G:C6	2.53	0.43
11:A:2075:U:OP1	34:Z:38:ARG:NH1	2.43	0.43
11:A:2407:U:H2'	11:A:2408:U:C6	2.53	0.43
39:e:165:PHE:HE2	39:e:215:PHE:HE2	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:f:185:SER:OG	40:f:187:LYS:NZ	2.51	0.43
51:r:79:HIS:HB3	51:r:184:ASN:HA	1.99	0.43
57:y:127:ILE:HD11	57:y:159:MET:HE3	2.00	0.43
10:9:92:PHE:HB2	33:Y:156:LEU:HD11	2.00	0.43
10:9:137:ARG:NH1	29:U:23:ASN:HB3	2.33	0.43
11:A:1770:G:H4'	15:F:112:ALA:HB2	2.00	0.43
11:A:2048:U:H2'	11:A:2049:U:H6	1.82	0.43
11:A:2734:A:H2'	11:A:2735:G:H8	1.82	0.43
17:I:141:GLN:NE2	17:I:142:ASN:OD1	2.52	0.43
18:J:86:THR:O	18:J:90:PHE:HB3	2.17	0.43
22:N:104:MET:O	22:N:108:THR:HG22	2.18	0.43
29:U:133:GLU:OE1	30:V:104:TYR:OH	2.35	0.43
30:V:54:TRP:NE1	30:V:56:LEU:O	2.49	0.43
36:b:89:ILE:HA	36:b:92:LYS:NZ	2.33	0.43
40:f:137:LEU:HD11	40:f:142:SER:HA	1.98	0.43
40:f:173:ILE:O	40:f:177:SER:OG	2.33	0.43
44:j:34:ALA:HB2	44:j:40:TYR:CE2	2.53	0.43
53:u:144:LYS:HE2	53:u:144:LYS:HB2	1.76	0.43
54:v:54:GLN:HA	54:v:57:LYS:HG2	2.01	0.43
57:y:268:LEU:HB3	57:y:274:TYR:HB2	2.00	0.43
2:1:42:THR:O	2:1:42:THR:OG1	2.35	0.43
6:5:40:LYS:HD2	6:5:40:LYS:HA	1.83	0.43
11:A:2695:G:OP2	11:A:2942:C:H5'	2.17	0.43
17:I:65:LEU:O	17:I:66:PRO:C	2.60	0.43
37:c:240:LEU:O	37:c:243:GLU:HG3	2.18	0.43
57:y:104:PHE:HZ	57:y:128:ILE:HD11	1.83	0.43
1:0:179:ARG:HH21	1:0:182:PRO:HG3	1.84	0.43
7:6:193:VAL:HB	7:6:319:PHE:CD2	2.54	0.43
11:A:2795:U:H2'	11:A:2796:G:C8	2.53	0.43
11:A:3165:C:H2'	11:A:3166:U:C6	2.53	0.43
22:N:206:GLU:HG3	22:N:251:VAL:HG13	2.00	0.43
30:V:36:PRO:HD2	30:V:39:ILE:HB	2.00	0.43
35:a:41:ASP:OD1	35:a:41:ASP:N	2.51	0.43
37:c:159:PHE:HD2	37:c:160:LEU:HD12	1.82	0.43
39:e:161:VAL:HG21	39:e:174:PRO:HG3	2.01	0.43
39:e:198:ASN:HB2	39:e:200:MET:SD	2.58	0.43
43:i:96:LYS:HG3	43:i:97:MET:HG3	2.00	0.43
57:y:320:LEU:O	57:y:324:GLU:HG2	2.18	0.43
58:z:97:MET:HE2	58:z:97:MET:HB2	1.91	0.43
11:A:2494:C:H3'	11:A:2495:U:C6	2.53	0.43
15:F:278:SER:OG	41:g:56:ARG:NH1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:S:67:PRO:HG3	35:a:36:TYR:HB3	2.00	0.43
32:X:4:HIS:NE2	33:Y:214:GLU:OE2	2.51	0.43
34:Z:46:PHE:CZ	34:Z:111:LYS:HG2	2.54	0.43
39:e:163:GLU:HB2	39:e:172:ILE:HD11	2.00	0.43
41:g:84:TYR:CE2	41:g:120:LEU:HD23	2.54	0.43
52:s:174:LEU:HB3	52:s:175:PRO:HD3	1.99	0.43
4:3:94:LEU:HD13	4:3:107:VAL:HG23	2.00	0.43
6:5:78:TRP:NE1	30:V:214:TYR:OH	2.46	0.43
6:5:289:HIS:ND1	6:5:290:THR:OG1	2.45	0.43
11:A:2094:G:H2'	11:A:2095:U:C6	2.53	0.43
11:A:2104:A:O4'	34:Z:35:LYS:N	2.52	0.43
11:A:2302:U:H2'	11:A:2303:A:C8	2.54	0.43
11:A:2700:G:H2'	11:A:2701:G:C8	2.53	0.43
19:K:69:GLY:HA2	51:r:152:THR:HA	1.99	0.43
19:K:72:TRP:CD1	51:r:149:ARG:HG2	2.53	0.43
26:R:108:TYR:O	36:b:125:SER:OG	2.34	0.43
39:e:127:LYS:HB3	47:m:74:MET:SD	2.59	0.43
40:f:96:THR:HB	40:f:183:ARG:HH21	1.83	0.43
40:f:133:GLU:HA	40:f:149:VAL:HA	1.99	0.43
40:f:162:LEU:HD11	40:f:167:ALA:HA	2.00	0.43
11:A:1707:C:C4	33:Y:185:VAL:HG21	2.54	0.43
11:A:1805:A:OP2	30:V:94:HIS:NE2	2.48	0.43
11:A:1839:C:H2'	11:A:1840:C:C6	2.54	0.43
24:P:52:ASN:HB3	24:P:55:ASN:HB3	2.00	0.43
42:h:120:MET:HA	42:h:125:ASP:OD2	2.19	0.43
51:r:78:LYS:NZ	51:r:110:GLU:OE2	2.52	0.43
53:u:196:LEU:HB3	53:u:199:TYR:HB2	1.99	0.43
1:0:85:ARG:HH21	11:A:2308:A:H5'	1.83	0.43
1:0:121:VAL:HG22	23:O:109:GLN:HG2	2.00	0.43
4:3:140:ARG:HA	4:3:143:ARG:HE	1.82	0.43
10:9:28:ARG:HG2	10:9:31:ARG:NH2	2.33	0.43
10:9:114:LEU:HD11	32:X:231:VAL:HG11	2.00	0.43
11:A:1974:A:H5'	13:D:261:GLY:HA2	2.00	0.43
11:A:2247:C:OP1	44:j:24:GLY:N	2.49	0.43
11:A:2301:U:H2'	11:A:2302:U:C6	2.54	0.43
19:K:60:MET:HB3	19:K:133:ILE:HD11	2.01	0.43
21:M:281:LYS:HE2	21:M:281:LYS:HB2	1.75	0.43
24:P:94:VAL:HG23	24:P:132:LEU:HD11	2.01	0.43
27:S:100:HIS:HB2	27:S:134:LEU:HD11	2.00	0.43
29:U:8:PRO:HA	33:Y:183:GLN:HE22	1.84	0.43
36:b:45:GLU:HG3	36:b:94:VAL:HG21	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:x:187:LYS:HG3	56:x:253:LEU:HD21	2.01	0.43
56:x:252:VAL:HG13	56:x:305:VAL:HG13	2.00	0.43
58:z:80:LEU:HD12	58:z:108:VAL:HG22	2.01	0.43
2:1:63:ARG:HH12	2:1:65:LEU:HB3	1.84	0.43
7:6:372:SER:OG	49:p:141:ARG:HD3	2.19	0.43
10:9:74:VAL:O	33:Y:83:ALA:N	2.49	0.43
11:A:2310:G:O2'	11:A:2675:G:O6	2.33	0.43
11:A:2674:U:H2'	11:A:2675:G:O4'	2.18	0.43
11:A:5507:U:O2	57:y:295:ARG:NH2	2.39	0.43
12:B:1641:G:H2'	12:B:1642:G:C8	2.53	0.43
14:E:50:ASP:HA	14:E:53:LEU:HG	2.01	0.43
18:J:87:VAL:O	18:J:91:LEU:HB2	2.19	0.43
35:a:140:LYS:NZ	35:a:141:ASP:O	2.51	0.43
36:b:85:ARG:NH2	36:b:87:GLU:OE2	2.52	0.43
36:b:136:LYS:O	37:c:259:ARG:NH2	2.37	0.43
55:w:81:ASP:OD1	55:w:82:ARG:N	2.51	0.43
56:x:203:ASN:HA	56:x:234:THR:O	2.19	0.43
57:y:285:ILE:C	58:z:195:ARG:HE	2.26	0.43
58:z:56:HIS:NE2	58:z:60:ILE:O	2.51	0.43
6:5:44:PRO:HG2	6:5:72:ARG:HH12	1.83	0.43
6:5:167:THR:HG21	52:s:281:HIS:CD2	2.54	0.43
11:A:2286:A:H2'	11:A:2287:U:H6	1.83	0.43
11:A:2863:U:O3'	31:W:50:ARG:HG3	2.19	0.43
31:W:57:GLU:OE1	31:W:99:TYR:N	2.49	0.43
32:X:114:PHE:HZ	32:X:127:VAL:HG21	1.83	0.43
33:Y:156:LEU:HD23	33:Y:156:LEU:HA	1.91	0.43
58:z:58:ALA:HA	58:z:82:LEU:HD13	2.01	0.43
58:z:286:THR:OG1	58:z:289:GLY:O	2.33	0.43
7:6:191:ASN:OD1	7:6:191:ASN:N	2.43	0.42
9:8:108:PHE:O	9:8:111:THR:OG1	2.32	0.42
11:A:1795:A:N6	11:A:1796:A:N1	2.66	0.42
11:A:2186:C:H2'	11:A:2187:C:C6	2.54	0.42
11:A:2493:C:O2'	11:A:2641:A:N1	2.43	0.42
11:A:2531:U:H5''	11:A:2532:U:H5	1.84	0.42
13:D:211:GLY:H	13:D:247:VAL:HB	1.84	0.42
19:K:42:LEU:HD23	19:K:42:LEU:HA	1.89	0.42
25:Q:77:SER:HB3	25:Q:80:PHE:HD1	1.84	0.42
27:S:129:ARG:HE	27:S:155:ARG:HG3	1.84	0.42
38:d:96:ARG:NH1	38:d:96:ARG:HA	2.34	0.42
53:u:194:TRP:HA	53:u:197:ARG:HH11	1.83	0.42
57:y:302:LEU:O	57:y:307:CYS:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:z:41:LYS:HA	58:z:41:LYS:HD3	1.83	0.42
58:z:160:ILE:HG12	58:z:200:LEU:HD23	2.00	0.42
4:3:113:ARG:HG3	21:M:80:LYS:HG2	2.01	0.42
11:A:1728:U:H2'	11:A:1729:U:O4'	2.20	0.42
11:A:2087:U:H2'	11:A:2088:U:H6	1.84	0.42
11:A:2244:U:O3'	51:r:189:ARG:NH1	2.31	0.42
14:E:99:LEU:HD13	14:E:124:VAL:HG21	2.00	0.42
14:E:244:ALA:HB1	14:E:248:ILE:HD11	2.01	0.42
22:N:55:ARG:HG2	22:N:99:TRP:CE2	2.54	0.42
22:N:130:PRO:HA	22:N:150:TYR:HA	2.01	0.42
25:Q:284:LYS:HA	25:Q:284:LYS:HD3	1.80	0.42
32:X:40:PRO:HB3	32:X:43:TYR:CZ	2.54	0.42
39:e:86:ASP:O	39:e:90:ARG:HG2	2.19	0.42
54:v:36:ARG:HH22	55:w:117:GLU:HG3	1.84	0.42
3:2:56:SER:OG	11:A:1980:A:OP1	2.33	0.42
9:8:99:ARG:NH2	47:m:48:TYR:O	2.52	0.42
11:A:1884:G:O2'	11:A:1895:C:O2	2.33	0.42
11:A:2002:G:N3	11:A:2735:G:O2'	2.40	0.42
11:A:2515:U:H2'	11:A:2516:C:H6	1.85	0.42
11:A:3144:A:H2'	11:A:3145:A:C8	2.53	0.42
11:A:3213:A:H2'	11:A:3214:C:C6	2.55	0.42
22:N:83:THR:O	22:N:84:GLU:HG3	2.20	0.42
22:N:200:LYS:HA	22:N:200:LYS:HD3	1.74	0.42
23:O:38:ARG:NH2	23:O:84:ASP:OD2	2.51	0.42
23:O:149:LEU:HD23	23:O:149:LEU:HA	1.92	0.42
26:R:141:ILE:HD12	26:R:144:ARG:HH22	1.83	0.42
44:j:104:LYS:H	44:j:104:LYS:HG2	1.69	0.42
48:o:35:MET:HE2	48:o:35:MET:HB3	1.74	0.42
53:u:190:LEU:HA	53:u:193:LEU:HD23	2.00	0.42
54:v:37:ARG:O	54:v:41:LYS:HG2	2.19	0.42
1:0:81:PRO:O	11:A:2679:U:O2'	2.36	0.42
1:0:125:TYR:OH	38:d:287:LEU:O	2.37	0.42
8:7:323:MET:HE2	8:7:323:MET:HB3	1.97	0.42
9:8:169:PHE:HB3	40:f:186:VAL:HG12	2.00	0.42
11:A:2365:U:H2'	11:A:2366:G:C8	2.54	0.42
11:A:2532:U:H2'	11:A:2533:A:C8	2.53	0.42
11:A:3117:C:H2'	11:A:3118:U:C6	2.54	0.42
15:F:291:SER:HB2	41:g:54:ALA:HA	2.00	0.42
17:I:119:HIS:CE1	17:I:163:GLU:HG2	2.54	0.42
17:I:122:LEU:H	17:I:122:LEU:HD23	1.84	0.42
17:I:171:VAL:HG11	17:I:174:LEU:HD12	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:c:162:GLY:O	37:c:166:VAL:HG22	2.19	0.42
56:x:71:GLN:HA	56:x:371:ASN:CG	2.44	0.42
56:x:178:LEU:HB2	56:x:249:TYR:CD2	2.54	0.42
56:x:380:MET:SD	56:x:380:MET:N	2.92	0.42
57:y:194:ILE:HG23	57:y:223:LEU:HD11	2.00	0.42
5:4:83:LYS:HE2	11:A:3189:C:C5	2.53	0.42
11:A:1875:C:H2'	11:A:1876:U:H6	1.85	0.42
11:A:2039:A:N6	11:A:2729:U:O2	2.53	0.42
11:A:2139:U:O4	34:Z:77:ARG:NH1	2.52	0.42
11:A:2700:G:H2'	11:A:2701:G:H8	1.85	0.42
11:A:3116:C:H2'	11:A:3117:C:H6	1.84	0.42
11:A:3165:C:H2'	11:A:3166:U:H6	1.83	0.42
17:I:92:ASP:OD1	17:I:93:ASN:N	2.52	0.42
19:K:7:ALA:HB3	19:K:8:PRO:HD3	2.00	0.42
29:U:2:AYA:OT	29:U:22:THR:OG1	2.26	0.42
33:Y:69:ASP:HB2	33:Y:111:MET:HE2	2.02	0.42
45:k:18:VAL:HG21	45:k:34:LEU:HD21	2.00	0.42
52:s:385:GLN:HG2	52:s:386:ASN:CG	2.44	0.42
7:6:39:ASP:N	7:6:39:ASP:OD1	2.52	0.42
9:8:142:ALA:HA	9:8:145:GLU:HG2	2.00	0.42
11:A:2089:U:H2'	11:A:2090:A:C8	2.55	0.42
23:O:64:LYS:NZ	23:O:100:GLN:O	2.50	0.42
25:Q:188:LEU:HD22	25:Q:191:ARG:HH22	1.84	0.42
25:Q:194:LEU:HB2	25:Q:197:TYR:HD2	1.84	0.42
35:a:37:SER:OG	35:a:39:LEU:O	2.36	0.42
53:u:189:GLU:CD	53:u:192:LYS:HG3	2.45	0.42
56:x:274:LYS:HG3	56:x:276:SER:N	2.35	0.42
57:y:244:LYS:H	57:y:244:LYS:HG3	1.63	0.42
11:A:2318:A:H2'	11:A:2319:A:C8	2.55	0.42
11:A:2533:A:H2'	11:A:2534:G:H8	1.84	0.42
13:D:176:ALA:HB1	13:D:244:VAL:HG11	2.02	0.42
19:K:72:TRP:HD1	51:r:149:ARG:HG2	1.85	0.42
27:S:114:ILE:HD12	27:S:114:ILE:O	2.20	0.42
56:x:230:GLN:H	56:x:230:GLN:HG3	1.66	0.42
6:5:122:TRP:HE3	6:5:123:LEU:HD23	1.84	0.42
6:5:176:TYR:HA	6:5:179:VAL:HG12	2.01	0.42
7:6:64:GLU:OE1	31:W:127:TYR:OH	2.35	0.42
7:6:167:PHE:CE1	7:6:313:PRO:HB2	2.55	0.42
9:8:99:ARG:CZ	39:e:83:LEU:HB2	2.50	0.42
10:9:114:LEU:HA	10:9:117:TYR:HD2	1.85	0.42
11:A:2662:A:H2'	11:A:2663:C:H6	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:2662:A:H2'	11:A:2663:C:C6	2.54	0.42
11:A:5501:U:H2'	11:A:5502:A:H8	1.85	0.42
53:u:197:ARG:HB2	54:v:66:LEU:HD13	2.02	0.42
57:y:89:SER:O	57:y:93:GLU:HG2	2.19	0.42
3:2:60:ARG:NH1	3:2:92:HIS:O	2.53	0.42
11:A:2236:C:N4	11:A:2688:C:O2	2.52	0.42
11:A:3213:A:H2'	11:A:3214:C:H6	1.85	0.42
15:F:72:PHE:HE2	42:h:50:LEU:HB3	1.85	0.42
24:P:76:GLU:OE1	24:P:76:GLU:N	2.42	0.42
27:S:82:LYS:O	27:S:85:GLU:HG3	2.20	0.42
27:S:89:THR:O	27:S:89:THR:OG1	2.37	0.42
36:b:15:LEU:HD23	36:b:15:LEU:HA	1.87	0.42
37:c:227:GLU:HB2	37:c:230:GLU:HG3	2.02	0.42
38:d:90:PRO:HB3	38:d:245:TYR:CE2	2.55	0.42
39:e:43:SER:O	39:e:46:ARG:NH1	2.53	0.42
47:m:57:VAL:HG22	47:m:63:THR:HG22	2.01	0.42
51:r:65:ASN:O	51:r:74:ARG:HG3	2.20	0.42
57:y:124:LEU:HD13	57:y:152:LEU:HD21	2.02	0.42
2:1:47:ASP:HB3	2:1:50:VAL:HG22	2.02	0.42
7:6:132:LEU:HD23	7:6:132:LEU:HA	1.82	0.42
8:7:66:GLU:HG3	8:7:80:VAL:HG22	2.01	0.42
11:A:1924:U:H2'	11:A:1925:A:C8	2.55	0.42
11:A:2042:U:OP2	21:M:57:ARG:NH1	2.53	0.42
11:A:2082:G:P	48:o:66:ARG:HH22	2.43	0.42
11:A:2374:A:OP1	52:s:305:LYS:NZ	2.53	0.42
11:A:3224:G:H2'	11:A:3225:G:C8	2.55	0.42
12:B:1607:U:H2'	12:B:1608:G:H8	1.81	0.42
26:R:148:TYR:CE2	34:Z:153:PRO:HG3	2.55	0.42
49:p:110:TRP:CD1	49:p:110:TRP:H	2.38	0.42
49:p:178:ILE:HA	49:p:181:GLU:OE2	2.19	0.42
57:y:291:LYS:O	57:y:295:ARG:HB3	2.20	0.42
7:6:218:LEU:HG	7:6:234:HIS:HB2	2.02	0.41
8:7:97:GLU:HB3	28:T:94:ASP:OD2	2.20	0.41
8:7:219:LEU:HD23	8:7:219:LEU:HA	1.87	0.41
11:A:2044:A:H5'	11:A:2866:A:O2'	2.20	0.41
11:A:2180:A:H4'	11:A:2181:A:C8	2.55	0.41
11:A:2298:A:N6	15:F:145:LEU:HD22	2.35	0.41
11:A:2343:G:H3'	11:A:2343:G:N3	2.35	0.41
11:A:2752:C:C2	11:A:2753:A:C8	3.08	0.41
15:F:63:GLN:NE2	15:F:79:LEU:HD13	2.34	0.41
15:F:94:ASP:OD1	15:F:94:ASP:N	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:N:214:THR:OG1	22:N:216:GLU:OE2	2.35	0.41
39:e:61:LYS:HE3	39:e:61:LYS:HB3	1.88	0.41
40:f:117:LEU:HD13	40:f:117:LEU:HA	1.90	0.41
42:h:77:VAL:HG23	42:h:78:PHE:CD1	2.55	0.41
48:o:17:TRP:HH2	48:o:25:ARG:HH21	1.67	0.41
51:r:59:GLU:OE1	51:r:60:SER:N	2.53	0.41
58:z:86:ASP:OD1	58:z:86:ASP:N	2.51	0.41
6:5:343:GLN:OE1	6:5:420:HIS:ND1	2.52	0.41
7:6:176:ALA:HA	7:6:186:PRO:HA	2.01	0.41
7:6:184:LEU:HD11	49:p:192:ARG:HG2	2.02	0.41
7:6:185:MET:HE1	49:p:189:ARG:NE	2.34	0.41
8:7:315:LYS:NZ	14:E:64:LEU:HD21	2.35	0.41
11:A:2016:C:H2'	11:A:2017:U:H6	1.86	0.41
11:A:2310:G:N2	11:A:2676:A:OP2	2.44	0.41
11:A:2688:C:H2'	11:A:2689:C:H6	1.85	0.41
11:A:2826:G:H2'	11:A:2827:A:C8	2.55	0.41
11:A:3038:U:H4'	58:z:30:TRP:HH2	1.84	0.41
25:Q:205:LYS:HD3	25:Q:206:PRO:HD2	2.02	0.41
39:e:79:ILE:HD12	39:e:80:GLU:N	2.34	0.41
40:f:93:ILE:O	40:f:93:ILE:HD12	2.20	0.41
48:o:25:ARG:NH1	48:o:25:ARG:HA	2.35	0.41
57:y:202:LYS:HG3	57:y:212:VAL:HG21	2.01	0.41
7:6:58:ARG:HH12	24:P:73:PRO:HD3	1.84	0.41
8:7:222:GLU:HB3	8:7:225:VAL:HG23	2.02	0.41
9:8:157:LEU:HD12	9:8:157:LEU:HA	1.90	0.41
11:A:1802:A:H4'	30:V:114:PRO:HG2	2.02	0.41
11:A:2091:A:H2'	11:A:2092:C:O4'	2.21	0.41
11:A:5508:A:H2'	11:A:5509:U:C6	2.54	0.41
13:D:185:GLY:HA3	13:D:238:GLU:HB3	2.02	0.41
38:d:55:GLU:OE1	38:d:55:GLU:N	2.53	0.41
42:h:49:ILE:HD12	42:h:49:ILE:HA	1.85	0.41
56:x:170:GLY:O	56:x:251:ARG:NH2	2.50	0.41
7:6:130:VAL:H	24:P:130:ARG:HH22	1.67	0.41
7:6:139:TRP:CZ2	7:6:144:GLY:HA2	2.56	0.41
8:7:146:CYS:O	8:7:278:TYR:OH	2.38	0.41
9:8:133:ARG:NH2	12:B:1626:C:O2'	2.54	0.41
11:A:1857:U:H2'	11:A:1858:G:H8	1.83	0.41
11:A:3048:A:H5'	20:L:81:LYS:NZ	2.35	0.41
18:J:35:LEU:HD23	18:J:35:LEU:HA	1.87	0.41
18:J:48:GLN:NE2	18:J:52:GLU:HG2	2.32	0.41
18:J:92:LYS:HG2	18:J:97:ILE:HB	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:U:153:LEU:HD11	38:d:222:LEU:HB2	2.02	0.41
35:a:42:ASP:OD1	35:a:42:ASP:N	2.53	0.41
37:c:148:MET:HE3	37:c:149:PRO:HD2	2.02	0.41
39:e:152:LYS:HG3	39:e:155:ARG:HB2	2.02	0.41
40:f:131:THR:OG1	40:f:150:LEU:O	2.32	0.41
40:f:174:ILE:H	40:f:174:ILE:HG13	1.68	0.41
45:k:25:LYS:O	45:k:27:VAL:HG13	2.20	0.41
51:r:114:LYS:HB3	51:r:114:LYS:HE2	1.82	0.41
53:u:187:ILE:HD13	53:u:187:ILE:HA	1.86	0.41
5:4:83:LYS:HB2	5:4:88:TRP:CZ3	2.55	0.41
7:6:58:ARG:O	7:6:62:GLU:HG3	2.21	0.41
7:6:233:LEU:HD12	7:6:298:PHE:CD2	2.56	0.41
7:6:263:SER:HB3	7:6:342:PHE:CD2	2.56	0.41
11:A:1782:G:O2'	11:A:1793:G:O6	2.37	0.41
18:J:30:MET:HE3	18:J:32:GLY:HA2	2.02	0.41
18:J:157:LYS:HE2	18:J:157:LYS:HB2	1.85	0.41
23:O:67:ASP:N	23:O:67:ASP:OD1	2.53	0.41
27:S:156:VAL:HG23	27:S:198:ILE:HG12	2.01	0.41
31:W:117:ILE:H	31:W:117:ILE:HG13	1.64	0.41
37:c:238:MET:HE2	37:c:238:MET:HB2	1.81	0.41
38:d:186:VAL:HG13	38:d:219:ARG:HB3	2.02	0.41
45:k:33:PHE:O	45:k:37:VAL:HG12	2.21	0.41
52:s:91:TYR:HE2	52:s:229:LEU:HD22	1.83	0.41
53:u:131:SER:O	53:u:135:LEU:HD12	2.20	0.41
1:0:126:CYS:HA	1:0:129:LYS:HD3	2.03	0.41
6:5:53:PRO:HG2	32:X:119:LEU:HD22	2.01	0.41
6:5:313:MET:H	6:5:313:MET:HG3	1.72	0.41
7:6:99:ARG:NH2	12:B:1621:A:O5'	2.52	0.41
8:7:203:THR:HG22	8:7:279:GLU:HA	2.02	0.41
11:A:2400:C:O2'	11:A:2401:A:H5''	2.20	0.41
11:A:2524:A:N3	13:D:92:ARG:HG2	2.36	0.41
11:A:2805:A:H2'	11:A:2806:U:C6	2.56	0.41
11:A:3024:U:C2	11:A:3025:A:C8	3.09	0.41
11:A:3097:U:H2'	11:A:3098:U:C6	2.55	0.41
11:A:5508:A:H2'	11:A:5509:U:H6	1.85	0.41
14:E:179:PHE:CE2	14:E:298:LYS:HE3	2.56	0.41
15:F:166:PRO:HB2	15:F:169:VAL:HG23	2.03	0.41
19:K:25:MET:HE2	19:K:25:MET:HB2	1.84	0.41
22:N:72:ILE:HD11	22:N:96:TYR:CE1	2.55	0.41
34:Z:75:THR:HG22	34:Z:83:LYS:HG2	2.02	0.41
35:a:41:ASP:HB2	35:a:46:ASN:HA	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:d:85:PHE:CZ	38:d:200:SER:HB3	2.55	0.41
51:r:168:ARG:HA	51:r:171:ARG:HH12	1.85	0.41
52:s:403:GLU:OE1	52:s:403:GLU:N	2.51	0.41
57:y:289:LEU:O	57:y:293:ILE:HG12	2.21	0.41
3:2:64:HIS:HB2	3:2:92:HIS:HB3	2.02	0.41
8:7:159:LYS:HD3	35:a:93:LYS:HG2	2.02	0.41
10:9:79:PRO:HD2	30:V:183:LEU:HD21	2.01	0.41
11:A:2407:U:H2'	11:A:2408:U:H6	1.86	0.41
11:A:3218:A:H2'	11:A:3219:G:C8	2.56	0.41
13:D:289:LEU:HB3	13:D:291:PRO:HD2	2.02	0.41
14:E:239:ARG:HE	14:E:239:ARG:HB3	1.81	0.41
32:X:11:TRP:O	32:X:15:GLN:HG2	2.19	0.41
50:q:153:ARG:HG2	56:x:83:TRP:HE1	1.85	0.41
52:s:109:PHE:O	52:s:212:ARG:HD3	2.21	0.41
56:x:52:TYR:CZ	56:x:312:LEU:HB2	2.55	0.41
4:3:172:TYR:HB2	4:3:175:ASP:HB2	2.02	0.41
11:A:1934:U:H2'	11:A:1935:A:O4'	2.20	0.41
11:A:2036:C:H1'	11:A:2810:G:O2'	2.21	0.41
11:A:2283:C:O2	37:c:43:LYS:NZ	2.42	0.41
11:A:2392:U:H2'	11:A:2394:A:H62	1.85	0.41
11:A:3143:U:H2'	11:A:3144:A:C8	2.55	0.41
12:B:1611:G:H2'	12:B:1612:C:C6	2.55	0.41
14:E:206:VAL:HG12	14:E:299:VAL:HG22	2.02	0.41
22:N:159:LEU:HD13	22:N:159:LEU:HA	1.97	0.41
30:V:39:ILE:HD12	30:V:39:ILE:HA	1.82	0.41
38:d:177:LYS:HB2	38:d:177:LYS:HE2	1.75	0.41
39:e:123:MET:H	39:e:123:MET:HG2	1.65	0.41
7:6:94:PRO:HA	7:6:95:PRO:HD3	1.98	0.41
7:6:99:ARG:NH1	7:6:102:GLN:OE1	2.54	0.41
7:6:104:LEU:HD22	7:6:107:LYS:HD3	2.03	0.41
8:7:167:VAL:HG12	8:7:168:ARG:HG2	2.02	0.41
11:A:1709:G:H4'	33:Y:192:LYS:HD3	2.03	0.41
11:A:1760:G:OP2	50:q:55:ARG:NH2	2.54	0.41
11:A:1800:G:N1	11:A:1803:A:OP2	2.54	0.41
11:A:2067:C:OP1	40:f:58:LYS:HG3	2.21	0.41
11:A:2081:U:H2'	11:A:2082:G:H8	1.82	0.41
11:A:2119:U:H1'	34:Z:35:LYS:HG2	2.03	0.41
11:A:2170:G:C5	11:A:2171:U:H5	2.39	0.41
11:A:2293:A:C6	21:M:39:ARG:HD2	2.55	0.41
11:A:2324:U:H2'	11:A:2325:U:C6	2.56	0.41
11:A:2748:A:H2'	11:A:2749:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:2804:A:H2'	11:A:2805:A:H8	1.86	0.41
11:A:3114:U:H2'	11:A:3115:U:C6	2.56	0.41
13:D:66:TRP:CE2	13:D:79:MET:HB2	2.55	0.41
15:F:294:PRO:HB3	43:i:65:ASN:ND2	2.34	0.41
17:I:101:ASN:OD1	17:I:150:HIS:HB3	2.21	0.41
18:J:56:ARG:H	18:J:56:ARG:HG2	1.64	0.41
19:K:27:PRO:HA	19:K:28:PRO:HD3	1.98	0.41
20:L:98:PRO:HA	25:Q:162:ILE:HG12	2.02	0.41
20:L:125:THR:HG22	20:L:144:PHE:HD1	1.85	0.41
21:M:68:GLU:OE1	21:M:73:PRO:HA	2.20	0.41
30:V:69:ASP:OD1	30:V:69:ASP:N	2.54	0.41
30:V:206:GLU:OE2	30:V:208:ARG:NE	2.49	0.41
33:Y:226:LEU:HD11	33:Y:230:LYS:HE3	2.03	0.41
38:d:86:ASP:HB3	38:d:198:ARG:HD2	2.02	0.41
39:e:55:ARG:HD3	39:e:157:LEU:HD12	2.03	0.41
39:e:59:VAL:HG22	39:e:153:LEU:HB3	2.02	0.41
39:e:253:VAL:HG21	39:e:263:TYR:HE2	1.85	0.41
52:s:152:GLN:HA	52:s:156:TYR:HB2	2.03	0.41
53:u:180:MET:HE1	53:u:190:LEU:HD22	2.03	0.41
54:v:18:ARG:HH22	55:w:120:MET:HG3	1.85	0.41
55:w:100:VAL:HB	55:w:142:GLN:HB2	2.02	0.41
58:z:16:TRP:CD1	58:z:245:ASN:HB3	2.56	0.41
58:z:119:VAL:HA	58:z:122:ILE:HD13	2.03	0.41
58:z:184:ARG:HD3	58:z:184:ARG:HA	1.92	0.41
3:2:60:ARG:HH11	3:2:92:HIS:CD2	2.39	0.41
6:5:63:LYS:H	6:5:63:LYS:HG2	1.58	0.41
6:5:236:LEU:HD21	6:5:289:HIS:CD2	2.55	0.41
6:5:310:ARG:HA	6:5:313:MET:SD	2.61	0.41
7:6:101:GLN:O	7:6:105:GLU:HG2	2.21	0.41
8:7:81:MET:HE3	8:7:81:MET:HB3	1.89	0.41
9:8:174:GLU:HA	40:f:183:ARG:HA	2.03	0.41
11:A:1765:C:O2'	43:i:75:ARG:NH1	2.30	0.41
11:A:2153:A:OP1	17:I:46:LYS:NZ	2.44	0.41
11:A:2382:A:H2'	11:A:2383:U:C6	2.56	0.41
11:A:2746:U:H2'	11:A:2747:U:H6	1.86	0.41
11:A:3139:G:H2'	11:A:3140:A:C8	2.55	0.41
14:E:329:PRO:HD2	14:E:332:LEU:HD21	2.02	0.41
17:I:65:LEU:HD22	17:I:65:LEU:HA	1.75	0.41
17:I:79:ILE:HG22	17:I:83:ARG:HH11	1.85	0.41
19:K:175:ASP:OD1	19:K:175:ASP:N	2.45	0.41
22:N:53:ILE:HG21	22:N:102:PHE:CD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:P:165:MET:HG3	24:P:172:LEU:HD21	2.03	0.41
27:S:163:LYS:HB3	27:S:163:LYS:HE3	1.87	0.41
39:e:203:LYS:CB	39:e:237:LEU:HB3	2.48	0.41
52:s:119:PRO:HG3	52:s:394:TRP:CE3	2.56	0.41
52:s:239:ASN:HB2	52:s:299:PHE:HB2	2.03	0.41
52:s:385:GLN:OE1	52:s:385:GLN:N	2.52	0.41
55:w:129:GLU:HG3	55:w:151:LYS:HG2	2.03	0.41
56:x:296:LEU:HD23	56:x:296:LEU:HA	1.84	0.41
1:0:145:GLU:OE1	1:0:150:LYS:HB2	2.21	0.40
7:6:139:TRP:CG	24:P:135:ARG:HH22	2.39	0.40
7:6:218:LEU:HD22	7:6:270:PHE:HE1	1.85	0.40
8:7:247:ASN:ND2	8:7:251:ILE:O	2.45	0.40
9:8:99:ARG:O	39:e:83:LEU:HB3	2.21	0.40
9:8:161:ALA:O	39:e:207:ASN:HB3	2.21	0.40
11:A:1710:A:H4'	11:A:1711:C:C2	2.55	0.40
11:A:2347:C:H2'	11:A:2348:A:H8	1.86	0.40
11:A:2494:C:H3'	11:A:2495:U:H5	1.81	0.40
11:A:2747:U:C2	11:A:2748:A:C8	3.09	0.40
22:N:171:GLU:O	46:l:135:ASN:ND2	2.50	0.40
33:Y:73:ASN:HA	33:Y:76:GLN:NE2	2.36	0.40
35:a:46:ASN:O	35:a:62:HIS:HA	2.22	0.40
38:d:201:SER:OG	38:d:204:ASN:HB3	2.21	0.40
42:h:62:PRO:HA	42:h:63:PRO:HD3	1.96	0.40
49:p:178:ILE:O	49:p:181:GLU:HG2	2.21	0.40
57:y:127:ILE:HD12	57:y:159:MET:HG2	2.02	0.40
8:7:238:ASP:O	8:7:241:GLU:HG3	2.21	0.40
10:9:126:LYS:HB3	10:9:126:LYS:HE2	1.88	0.40
11:A:1940:A:H2'	11:A:1941:G:H8	1.87	0.40
11:A:1979:U:H2'	11:A:1980:A:C8	2.57	0.40
11:A:1991:A:H1'	11:A:2509:A:H1'	2.02	0.40
11:A:2048:U:H2'	11:A:2049:U:C6	2.56	0.40
11:A:3174:U:H2'	11:A:3175:A:H8	1.86	0.40
12:B:1602:C:H2'	12:B:1603:A:H8	1.85	0.40
19:K:109:TYR:HB2	19:K:122:MET:HE2	2.02	0.40
34:Z:80:TYR:HA	34:Z:83:LYS:HG3	2.03	0.40
56:x:96:LYS:HA	56:x:96:LYS:HD3	1.86	0.40
56:x:223:GLU:O	56:x:227:ASP:N	2.54	0.40
58:z:232:GLY:O	58:z:235:THR:HG22	2.21	0.40
2:1:43:LEU:HA	2:1:43:LEU:HD23	1.80	0.40
7:6:276:ASP:OD1	7:6:276:ASP:N	2.53	0.40
11:A:1942:C:H2'	11:A:1943:A:O4'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:2301:U:H2'	11:A:2302:U:H6	1.86	0.40
11:A:2954:C:O2'	22:N:182:LYS:NZ	2.33	0.40
12:B:1616:A:HO2'	12:B:1618:A:H62	1.61	0.40
13:D:79:MET:HE2	13:D:102:GLN:HB2	2.02	0.40
15:F:62:VAL:HA	42:h:118:HIS:HB3	2.03	0.40
15:F:220:ASP:O	15:F:245:ALA:N	2.55	0.40
15:F:292:ASP:OD1	15:F:292:ASP:N	2.54	0.40
18:J:19:VAL:HG13	18:J:21:ARG:HG2	2.02	0.40
25:Q:194:LEU:HB2	25:Q:197:TYR:CD2	2.57	0.40
27:S:119:GLU:HG2	27:S:189:PRO:HB2	2.02	0.40
36:b:144:ARG:O	36:b:147:GLU:HG2	2.21	0.40
56:x:89:LYS:O	56:x:93:LEU:HD12	2.20	0.40
58:z:147:MET:HE3	58:z:147:MET:HB2	1.81	0.40
6:5:121:LEU:HD21	6:5:128:LEU:HD13	2.04	0.40
6:5:263:ILE:HG13	13:D:146:SER:HA	2.03	0.40
7:6:360:ARG:NE	11:A:2869:A:H62	2.19	0.40
10:9:31:ARG:HD2	11:A:2421:G:H4'	2.02	0.40
11:A:1744:A:OP1	21:M:87:HIS:NE2	2.40	0.40
11:A:1829:A:H5''	26:R:31:PHE:CE1	2.57	0.40
11:A:2838:A:H1'	11:A:2839:C:C5	2.56	0.40
11:A:5001:A:H2'	11:A:5002:U:H6	1.87	0.40
11:A:5512:A:H2'	11:A:5513:U:C6	2.56	0.40
14:E:225:LYS:HE2	14:E:225:LYS:HB2	1.94	0.40
27:S:111:GLU:HG2	36:b:19:LEU:HD11	2.03	0.40
31:W:144:LEU:HD23	31:W:144:LEU:HA	1.88	0.40
38:d:133:LYS:HD3	38:d:135:LYS:NZ	2.36	0.40
41:g:85:PHE:HA	41:g:166:PHE:CE1	2.56	0.40
41:g:94:ILE:HG22	41:g:96:VAL:HG23	2.04	0.40
42:h:78:PHE:CE1	42:h:96:LEU:HB3	2.56	0.40
52:s:318:ASP:OD1	52:s:318:ASP:N	2.54	0.40
57:y:90:LEU:H	57:y:90:LEU:HD23	1.86	0.40
57:y:274:TYR:CD1	57:y:288:PRO:HD2	2.57	0.40
58:z:262:CYS:SG	58:z:263:ASP:N	2.94	0.40
6:5:189:LYS:O	6:5:192:ILE:HG13	2.22	0.40
7:6:280:ASP:OD1	7:6:280:ASP:N	2.43	0.40
8:7:94:HIS:HB3	38:d:281:MET:SD	2.61	0.40
11:A:2138:U:O2'	11:A:2151:A:N3	2.52	0.40
11:A:2439:U:H2'	11:A:2440:G:C8	2.57	0.40
11:A:2493:C:H2'	11:A:2494:C:O4'	2.22	0.40
11:A:2530:A:H4'	11:A:2531:U:O5'	2.21	0.40
11:A:3113:A:O2'	11:A:3114:U:H5''	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:I:61:HIS:CE1	51:r:78:LYS:HE3	2.57	0.40
19:K:133:ILE:HB	19:K:138:LEU:HD13	2.03	0.40
24:P:40:GLU:OE1	24:P:40:GLU:N	2.53	0.40
24:P:54:ARG:NH2	24:P:58:LEU:HD21	2.37	0.40
30:V:97:TYR:C	30:V:98:ILE:HD13	2.46	0.40
31:W:101:LYS:HG2	40:f:56:ILE:HG21	2.02	0.40
35:a:71:HIS:CD2	36:b:140:PHE:HA	2.56	0.40
35:a:141:ASP:HB2	36:b:10:PHE:CD2	2.57	0.40
36:b:75:VAL:HG12	36:b:89:ILE:HD11	2.02	0.40
38:d:146:ILE:HG22	38:d:150:LEU:HD23	2.03	0.40
38:d:245:TYR:HB2	38:d:265:ILE:HB	2.03	0.40
42:h:147:ASN:OD1	42:h:147:ASN:N	2.55	0.40
47:m:57:VAL:HB	47:m:76:ALA:HA	2.03	0.40
52:s:237:PRO:HB3	52:s:300:HIS:CE1	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	108/188 (57%)	108 (100%)	0	0	100	100
2	1	53/65 (82%)	52 (98%)	1 (2%)	0	100	100
3	2	44/92 (48%)	44 (100%)	0	0	100	100
4	3	93/188 (50%)	92 (99%)	1 (1%)	0	100	100
5	4	35/103 (34%)	35 (100%)	0	0	100	100
6	5	392/423 (93%)	383 (98%)	9 (2%)	0	100	100
7	6	352/380 (93%)	342 (97%)	10 (3%)	0	100	100
8	7	292/338 (86%)	283 (97%)	9 (3%)	0	100	100
9	8	100/206 (48%)	96 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	9	122/137 (89%)	119 (98%)	3 (2%)	0	100	100
13	D	238/305 (78%)	235 (99%)	3 (1%)	0	100	100
14	E	303/348 (87%)	298 (98%)	5 (2%)	0	100	100
15	F	250/311 (80%)	246 (98%)	4 (2%)	0	100	100
16	H	95/267 (36%)	95 (100%)	0	0	100	100
17	I	163/261 (62%)	151 (93%)	11 (7%)	1 (1%)	21	56
18	J	133/192 (69%)	120 (90%)	13 (10%)	0	100	100
19	K	175/178 (98%)	173 (99%)	2 (1%)	0	100	100
20	L	113/145 (78%)	111 (98%)	2 (2%)	0	100	100
21	M	289/296 (98%)	288 (100%)	1 (0%)	0	100	100
22	N	190/251 (76%)	181 (95%)	8 (4%)	1 (0%)	24	60
23	O	152/175 (87%)	150 (99%)	2 (1%)	0	100	100
24	P	142/180 (79%)	142 (100%)	0	0	100	100
25	Q	219/292 (75%)	216 (99%)	3 (1%)	0	100	100
26	R	138/149 (93%)	137 (99%)	1 (1%)	0	100	100
27	S	159/205 (78%)	158 (99%)	1 (1%)	0	100	100
28	T	164/206 (80%)	162 (99%)	2 (1%)	0	100	100
29	U	150/153 (98%)	148 (99%)	2 (1%)	0	100	100
30	V	202/216 (94%)	200 (99%)	2 (1%)	0	100	100
31	W	104/148 (70%)	102 (98%)	2 (2%)	0	100	100
32	X	242/256 (94%)	239 (99%)	3 (1%)	0	100	100
33	Y	179/250 (72%)	178 (99%)	1 (1%)	0	100	100
34	Z	120/161 (74%)	118 (98%)	2 (2%)	0	100	100
35	a	96/142 (68%)	95 (99%)	1 (1%)	0	100	100
36	b	148/215 (69%)	145 (98%)	3 (2%)	0	100	100
37	c	282/332 (85%)	278 (99%)	4 (1%)	0	100	100
38	d	245/306 (80%)	239 (98%)	6 (2%)	0	100	100
39	e	224/279 (80%)	217 (97%)	7 (3%)	0	100	100
40	f	146/212 (69%)	139 (95%)	7 (5%)	0	100	100
41	g	132/166 (80%)	131 (99%)	1 (1%)	0	100	100
42	h	108/158 (68%)	106 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	i	95/128 (74%)	95 (100%)	0	0	100	100
44	j	88/123 (72%)	87 (99%)	1 (1%)	0	100	100
45	k	76/112 (68%)	74 (97%)	2 (3%)	0	100	100
46	l	21/138 (15%)	21 (100%)	0	0	100	100
47	m	33/128 (26%)	32 (97%)	1 (3%)	0	100	100
48	o	92/102 (90%)	92 (100%)	0	0	100	100
49	p	141/206 (68%)	137 (97%)	4 (3%)	0	100	100
50	q	139/222 (63%)	139 (100%)	0	0	100	100
51	r	140/196 (71%)	132 (94%)	8 (6%)	0	100	100
52	s	382/439 (87%)	377 (99%)	5 (1%)	0	100	100
53	u	124/234 (53%)	121 (98%)	3 (2%)	0	100	100
54	v	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
55	w	77/156 (49%)	73 (95%)	4 (5%)	0	100	100
56	x	334/384 (87%)	323 (97%)	11 (3%)	0	100	100
57	y	242/381 (64%)	240 (99%)	2 (1%)	0	100	100
58	z	309/334 (92%)	301 (97%)	8 (3%)	0	100	100
All	All	9252/12228 (76%)	9061 (98%)	189 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
22	N	66	PRO
17	I	66	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	99/164 (60%)	99 (100%)	0	100	100
2	1	52/60 (87%)	52 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	2	40/72 (56%)	40 (100%)	0	100	100
4	3	88/166 (53%)	88 (100%)	0	100	100
5	4	36/89 (40%)	36 (100%)	0	100	100
6	5	353/368 (96%)	348 (99%)	5 (1%)	59	80
7	6	313/332 (94%)	312 (100%)	1 (0%)	86	91
8	7	270/303 (89%)	266 (98%)	4 (2%)	57	80
9	8	93/190 (49%)	92 (99%)	1 (1%)	65	83
10	9	104/112 (93%)	104 (100%)	0	100	100
13	D	194/245 (79%)	193 (100%)	1 (0%)	81	89
14	E	260/290 (90%)	259 (100%)	1 (0%)	84	90
15	F	219/262 (84%)	218 (100%)	1 (0%)	81	89
16	H	88/228 (39%)	88 (100%)	0	100	100
17	I	153/232 (66%)	148 (97%)	5 (3%)	33	67
18	J	112/150 (75%)	111 (99%)	1 (1%)	70	85
19	K	154/155 (99%)	154 (100%)	0	100	100
20	L	98/124 (79%)	96 (98%)	2 (2%)	48	76
21	M	246/249 (99%)	244 (99%)	2 (1%)	73	86
22	N	167/211 (79%)	163 (98%)	4 (2%)	43	73
23	O	134/150 (89%)	130 (97%)	4 (3%)	36	69
24	P	126/155 (81%)	124 (98%)	2 (2%)	55	79
25	Q	203/256 (79%)	202 (100%)	1 (0%)	81	89
26	R	118/126 (94%)	118 (100%)	0	100	100
27	S	146/180 (81%)	144 (99%)	2 (1%)	59	80
28	T	146/176 (83%)	145 (99%)	1 (1%)	76	86
29	U	134/135 (99%)	134 (100%)	0	100	100
30	V	182/191 (95%)	179 (98%)	3 (2%)	55	79
31	W	86/119 (72%)	84 (98%)	2 (2%)	44	74
32	X	220/229 (96%)	219 (100%)	1 (0%)	81	89
33	Y	163/223 (73%)	163 (100%)	0	100	100
34	Z	113/147 (77%)	113 (100%)	0	100	100
35	a	96/133 (72%)	95 (99%)	1 (1%)	68	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	b	131/185 (71%)	128 (98%)	3 (2%)	44	74
37	c	251/288 (87%)	250 (100%)	1 (0%)	84	90
38	d	228/274 (83%)	227 (100%)	1 (0%)	84	90
39	e	198/236 (84%)	195 (98%)	3 (2%)	57	80
40	f	133/188 (71%)	125 (94%)	8 (6%)	17	50
41	g	124/148 (84%)	121 (98%)	3 (2%)	43	73
42	h	104/148 (70%)	104 (100%)	0	100	100
43	i	86/110 (78%)	86 (100%)	0	100	100
44	j	72/97 (74%)	72 (100%)	0	100	100
45	k	71/90 (79%)	70 (99%)	1 (1%)	59	80
46	l	23/116 (20%)	23 (100%)	0	100	100
47	m	31/113 (27%)	30 (97%)	1 (3%)	34	67
48	o	80/87 (92%)	80 (100%)	0	100	100
49	p	135/181 (75%)	134 (99%)	1 (1%)	76	86
50	q	119/178 (67%)	119 (100%)	0	100	100
51	r	133/169 (79%)	131 (98%)	2 (2%)	57	80
52	s	340/381 (89%)	333 (98%)	7 (2%)	47	75
53	u	118/200 (59%)	115 (98%)	3 (2%)	42	72
54	v	59/60 (98%)	59 (100%)	0	100	100
55	w	73/136 (54%)	71 (97%)	2 (3%)	39	71
56	x	293/328 (89%)	289 (99%)	4 (1%)	59	80
57	y	226/350 (65%)	224 (99%)	2 (1%)	70	85
58	z	270/287 (94%)	267 (99%)	3 (1%)	65	83
All	All	8304/10572 (78%)	8214 (99%)	90 (1%)	63	83

All (90) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	5	63	LYS
6	5	203	CYS
6	5	262	ILE
6	5	361	THR
6	5	401	VAL
7	6	90	ILE

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Mol	Chain	Res	Type
8	7	150	MET
8	7	165	ASN
8	7	221	VAL
8	7	233	SER
9	8	107	THR
13	D	196	VAL
14	E	207	THR
15	F	246	VAL
17	I	39	VAL
17	I	61	HIS
17	I	63	SER
17	I	65	LEU
17	I	91	GLN
18	J	153	ILE
20	L	77	ILE
20	L	108	ILE
21	M	99	ASN
21	M	147	THR
22	N	90	LEU
22	N	160	VAL
22	N	235	LEU
22	N	247	MET
23	O	81	THR
23	O	101	THR
23	O	114	SER
23	O	122	VAL
24	P	83	VAL
24	P	137	LEU
25	Q	95	GLU
27	S	66	LEU
27	S	89	THR
28	T	203	VAL
30	V	53	ASP
30	V	76	VAL
30	V	131	THR
31	W	118	THR
31	W	120	LEU
32	X	125	VAL
35	a	39	LEU
36	b	36	ASP
36	b	47	VAL
36	b	148	VAL

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Mol	Chain	Res	Type
37	c	219	LEU
38	d	77	HIS
39	e	79	ILE
39	e	158	VAL
39	e	240	THR
40	f	84	THR
40	f	90	VAL
40	f	93	ILE
40	f	117	LEU
40	f	124	SER
40	f	132	ILE
40	f	134	VAL
40	f	162	LEU
41	g	70	SER
41	g	109	VAL
41	g	137	VAL
45	k	44	SER
47	m	79	ILE
49	p	122	THR
51	r	39	VAL
51	r	148	ASN
52	s	41	VAL
52	s	77	ASP
52	s	142	LEU
52	s	163	VAL
52	s	215	GLU
52	s	243	ILE
52	s	405	ILE
53	u	170	VAL
53	u	174	SER
53	u	193	LEU
55	w	80	GLN
55	w	112	SER
56	x	140	SER
56	x	231	VAL
56	x	263	HIS
56	x	272	ILE
57	y	102	MET
57	y	213	THR
58	z	45	SER
58	z	227	LEU
58	z	228	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (70) such sidechains are listed below:

Mol	Chain	Res	Type
3	2	54	GLN
5	4	68	ASN
6	5	360	ASN
6	5	384	GLN
7	6	63	GLN
7	6	69	HIS
7	6	239	ASN
7	6	275	GLN
7	6	354	GLN
8	7	255	HIS
13	D	156	ASN
13	D	205	GLN
13	D	233	GLN
15	F	103	GLN
15	F	223	HIS
17	I	91	GLN
17	I	141	GLN
18	J	48	GLN
18	J	84	GLN
20	L	52	HIS
20	L	142	GLN
21	M	53	HIS
21	M	123	ASN
21	M	130	GLN
22	N	98	HIS
23	O	39	HIS
23	O	147	GLN
24	P	41	ASN
24	P	97	GLN
24	P	121	ASN
24	P	162	GLN
25	Q	139	GLN
26	R	77	GLN
26	R	89	ASN
27	S	100	HIS
28	T	189	HIS
29	U	55	ASN
29	U	103	GLN
32	X	76	GLN
32	X	177	HIS
33	Y	76	GLN

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Mol	Chain	Res	Type
36	b	25	GLN
36	b	135	ASN
37	c	69	HIS
37	c	168	HIS
38	d	47	GLN
38	d	211	GLN
39	e	168	GLN
40	f	189	HIS
41	g	121	GLN
46	l	124	GLN
47	m	59	GLN
48	o	58	GLN
49	p	176	HIS
49	p	194	HIS
50	q	142	ASN
52	s	87	GLN
52	s	179	GLN
52	s	238	ASN
52	s	423	HIS
53	u	148	HIS
54	v	42	ASN
55	w	103	HIS
55	w	142	GLN
56	x	47	ASN
56	x	78	ASN
56	x	193	GLN
56	x	314	HIS
57	y	108	HIS
57	y	110	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A	1401/1603 (87%)	260 (18%)	5 (0%)
12	B	71/72 (98%)	11 (15%)	0
All	All	1472/1675 (87%)	271 (18%)	5 (0%)

All (271) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	A	1672	C

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Mol	Chain	Res	Type
11	A	1681	G
11	A	1689	C
11	A	1694	U
11	A	1700	U
11	A	1704	U
11	A	1707	C
11	A	1708	A
11	A	1711	C
11	A	1713	A
11	A	1715	C
11	A	1724	A
11	A	1727	A
11	A	1731	A
11	A	1748	G
11	A	1750	G
11	A	1751	A
11	A	1761	A
11	A	1762	A
11	A	1764	C
11	A	1765	C
11	A	1766	U
11	A	1767	G
11	A	1770	G
11	A	1777	A
11	A	1780	U
11	A	1791	G
11	A	1804	A
11	A	1805	A
11	A	1827	C
11	A	1828	A
11	A	1829	A
11	A	1832	A
11	A	1836	A
11	A	1844	A
11	A	1853	A
11	A	1854	U
11	A	1855	A
11	A	1869	A
11	A	1871	A
11	A	1882	A
11	A	1883	G
11	A	1887	A

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Mol	Chain	Res	Type
11	A	1892	A
11	A	1893	A
11	A	1901	C
11	A	1903	C
11	A	1918	G
11	A	1937	A
11	A	1940	A
11	A	1974	A
11	A	1984	A
11	A	1985	G
11	A	1986	A
11	A	1987	G
11	A	1992	C
11	A	1994	A
11	A	2000	C
11	A	2002	G
11	A	2015	G
11	A	2021	U
11	A	2022	G
11	A	2029	A
11	A	2030	U
11	A	2031	A
11	A	2036	C
11	A	2037	U
11	A	2039	A
11	A	2060	A
11	A	2065	A
11	A	2068	C
11	A	2069	U
11	A	2071	U
11	A	2074	A
11	A	2079	C
11	A	2083	U
11	A	2098	G
11	A	2105	G
11	A	2109	A
11	A	2110	A
11	A	2111	C
11	A	2125	C
11	A	2126	U
11	A	2147	G
11	A	2154	A

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Mol	Chain	Res	Type
11	A	2158	U
11	A	2163	A
11	A	2168	U
11	A	2171	U
11	A	2172	A
11	A	2173	G
11	A	2174	G
11	A	2181	A
11	A	2182	G
11	A	2183	C
11	A	2184	A
11	A	2187	C
11	A	2197	G
11	A	2198	A
11	A	2200	A
11	A	2202	C
11	A	2210	C
11	A	2211	U
11	A	2216	A
11	A	2233	U
11	A	2237	A
11	A	2239	A
11	A	2241	A
11	A	2245	A
11	A	2246	A
11	A	2260	A
11	A	2262	C
11	A	2263	C
11	A	2269	G
11	A	2283	C
11	A	2284	C
11	A	2285	U
11	A	2293	A
11	A	2297	A
11	A	2299	U
11	A	2300	G
11	A	2316	U
11	A	2322	C
11	A	2332	C
11	A	2345	G
11	A	2359	C
11	A	2360	U

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Mol	Chain	Res	Type
11	A	2361	G
11	A	2362	A
11	A	2363	A
11	A	2374	A
11	A	2381	A
11	A	2390	A
11	A	2393	C
11	A	2396	C
11	A	2401	A
11	A	2405	C
11	A	2406	A
11	A	2407	U
11	A	2415	C
11	A	2416	U
11	A	2432	A
11	A	2444	A
11	A	2446	A
11	A	2449	G
11	A	2451	A
11	A	2452	A
11	A	2478	G
11	A	2480	A
11	A	2485	U
11	A	2493	C
11	A	2500	A
11	A	2502	C
11	A	2507	A
11	A	2511	C
11	A	2520	C
11	A	2521	A
11	A	2523	C
11	A	2527	A
11	A	2531	U
11	A	2540	C
11	A	2640	C
11	A	2645	G
11	A	2654	U
11	A	2656	U
11	A	2660	U
11	A	2683	C
11	A	2686	G
11	A	2693	A

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Mol	Chain	Res	Type
11	A	2694	A
11	A	2695	G
11	A	2696	A
11	A	2706	A
11	A	2718	C
11	A	2719	G
11	A	2722	A
11	A	2724	G
11	A	2727	C
11	A	2732	G
11	A	2745	A
11	A	2750	U
11	A	2801	A
11	A	2810	G
11	A	2811	G
11	A	2814	G
11	A	2830	A
11	A	2832	A
11	A	2833	A
11	A	2839	C
11	A	2840	C
11	A	2841	U
11	A	2842	C
11	A	2844	G
11	A	2847	C
11	A	2854	U
11	A	2864	U
11	A	2865	C
11	A	2895	U
11	A	2906	C
11	A	2910	A
11	A	2913	A
11	A	2916	G
11	A	2917	G
11	A	2922	A
11	A	2926	A
11	A	2928	C
11	A	2935	A
11	A	2936	U
11	A	2939	C
11	A	2947	U
11	A	2948	C

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Mol	Chain	Res	Type
11	A	2949	C
11	A	2950	U
11	A	2956	A
11	A	2963	A
11	A	2977	G
11	A	2985	C
11	A	2989	G
11	A	2990	A
11	A	3000	A
11	A	3005	A
11	A	3016	G
11	A	3021	C
11	A	3047	G
11	A	3053	A
11	A	3054	G
11	A	3056	C
11	A	3059	A
11	A	3060	C
11	A	3061	G
11	A	3069	A
11	A	3072	U
11	A	3073	C
11	A	3086	U
11	A	3090	G
11	A	3097	U
11	A	3100	U
11	A	3101	A
11	A	3102	U
11	A	3108	U
11	A	3112	A
11	A	3113	A
11	A	3129	A
11	A	3131	G
11	A	3155	C
11	A	3157	C
11	A	3158	A
11	A	3162	C
11	A	3169	C
11	A	3172	C
11	A	3180	A
11	A	3189	C
11	A	3190	A

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Mol	Chain	Res	Type
11	A	3197	U
11	A	3207	A
11	A	3208	C
11	A	3212	C
11	A	3217	A
11	A	3218	A
11	A	3228	U
12	B	1611	G
12	B	1617	C
12	B	1621	A
12	B	1646	U
12	B	1647	U
12	B	1649	C
12	B	1650	A
12	B	1652	C
12	B	1653	U
12	B	1654	U
12	B	1656	A

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	A	2030	U
11	A	2186	C
11	A	2245	A
11	A	2530	A
11	A	2905	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
29	AYA	U	2	29	6,7,8	1.27	1 (16%)	6,8,10	1.06	1 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
19	SAC	K	2	19	7,8,9	1.03	0	7,9,11	0.97	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
29	AYA	U	2	29	-	0/5/6/8	-
19	SAC	K	2	19	-	3/7/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	U	2	AYA	CA-N	-2.37	1.44	1.46

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	U	2	AYA	CB-CA-N	2.32	112.30	109.68

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	K	2	SAC	O-C-CA-CB
19	K	2	SAC	N-CA-CB-OG
19	K	2	SAC	C-CA-CB-OG

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
29	U	2	AYA	1	0
19	K	2	SAC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 44 ligands modelled in this entry, 40 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
62	PM8	w	200	55	26,31,31	1.79	6 (23%)	30,38,38	1.75	7 (23%)
61	FES	r	201	51	0,4,4	-	-	-		
63	SAM	x	401	-	27,29,29	1.11	5 (18%)	34,42,42	2.00	9 (26%)
64	GNP	z	401	60	34,34,34	1.29	5 (14%)	47,54,54	0.63	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
62	PM8	w	200	55	-	14/36/38/38	-
61	FES	r	201	51	-	-	0/1/1/1
63	SAM	x	401	-	-	7/17/33/33	0/3/3/3
64	GNP	z	401	60	-	4/18/38/38	0/3/3/3

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	w	200	PM8	C34-N36	5.37	1.46	1.33
62	w	200	PM8	C39-N41	5.10	1.45	1.33
64	z	401	GNP	PB-O3A	4.34	1.64	1.59
64	z	401	GNP	PB-O1B	3.16	1.51	1.46
64	z	401	GNP	PG-N3B	3.03	1.71	1.63
64	z	401	GNP	PG-O1G	2.81	1.50	1.46
63	x	401	SAM	C2-N3	2.61	1.38	1.33
63	x	401	SAM	C2-N1	2.48	1.38	1.33
62	w	200	PM8	C1-S1	2.45	1.82	1.76
64	z	401	GNP	PB-O2B	-2.32	1.50	1.56
62	w	200	PM8	C2-C1	2.28	1.53	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	w	200	PM8	O40-C39	-2.28	1.18	1.23
62	w	200	PM8	O35-C34	-2.25	1.19	1.23
63	x	401	SAM	OXT-C	-2.25	1.23	1.30
63	x	401	SAM	C8-N7	2.02	1.35	1.31
63	x	401	SAM	C5-N7	-2.02	1.35	1.39

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	w	200	PM8	C2-C1-S1	5.84	120.36	113.40
63	x	401	SAM	N3-C2-N1	-5.42	120.38	128.58
63	x	401	SAM	C5-C4-N3	-4.77	120.15	126.72
63	x	401	SAM	N9-C8-N7	-3.73	108.64	113.94
62	w	200	PM8	O1-C1-C2	-3.47	119.97	123.98
63	x	401	SAM	C2-N3-C4	3.46	120.28	111.83
63	x	401	SAM	C5-N7-C8	3.33	108.68	103.45
63	x	401	SAM	N3-C4-N9	3.22	132.65	127.17
62	w	200	PM8	C37-C38-C39	2.88	117.19	112.39
63	x	401	SAM	OXT-C-O	-2.66	118.05	124.08
62	w	200	PM8	C38-C39-N41	2.54	120.96	116.34
62	w	200	PM8	C43-S1-C1	2.42	108.98	101.84
62	w	200	PM8	O1-C1-S1	-2.37	119.67	122.68
63	x	401	SAM	C3'-C2'-C1'	2.25	105.72	101.46
63	x	401	SAM	C4-C5-N7	-2.25	108.01	110.58
62	w	200	PM8	C32-C34-N36	2.03	120.33	116.48

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
62	w	200	PM8	O27-C28-C29-C30
62	w	200	PM8	O27-C28-C29-C31
62	w	200	PM8	O27-C28-C29-C32
62	w	200	PM8	C32-C34-N36-C37
62	w	200	PM8	N36-C37-C38-C39
62	w	200	PM8	N41-C42-C43-S1
62	w	200	PM8	C42-C43-S1-C1
63	x	401	SAM	CB-CG-SD-C5'
63	x	401	SAM	C4'-C5'-SD-CE
64	z	401	GNP	PG-N3B-PB-O1B
64	z	401	GNP	PG-N3B-PB-O3A
64	z	401	GNP	PA-O3A-PB-O2B

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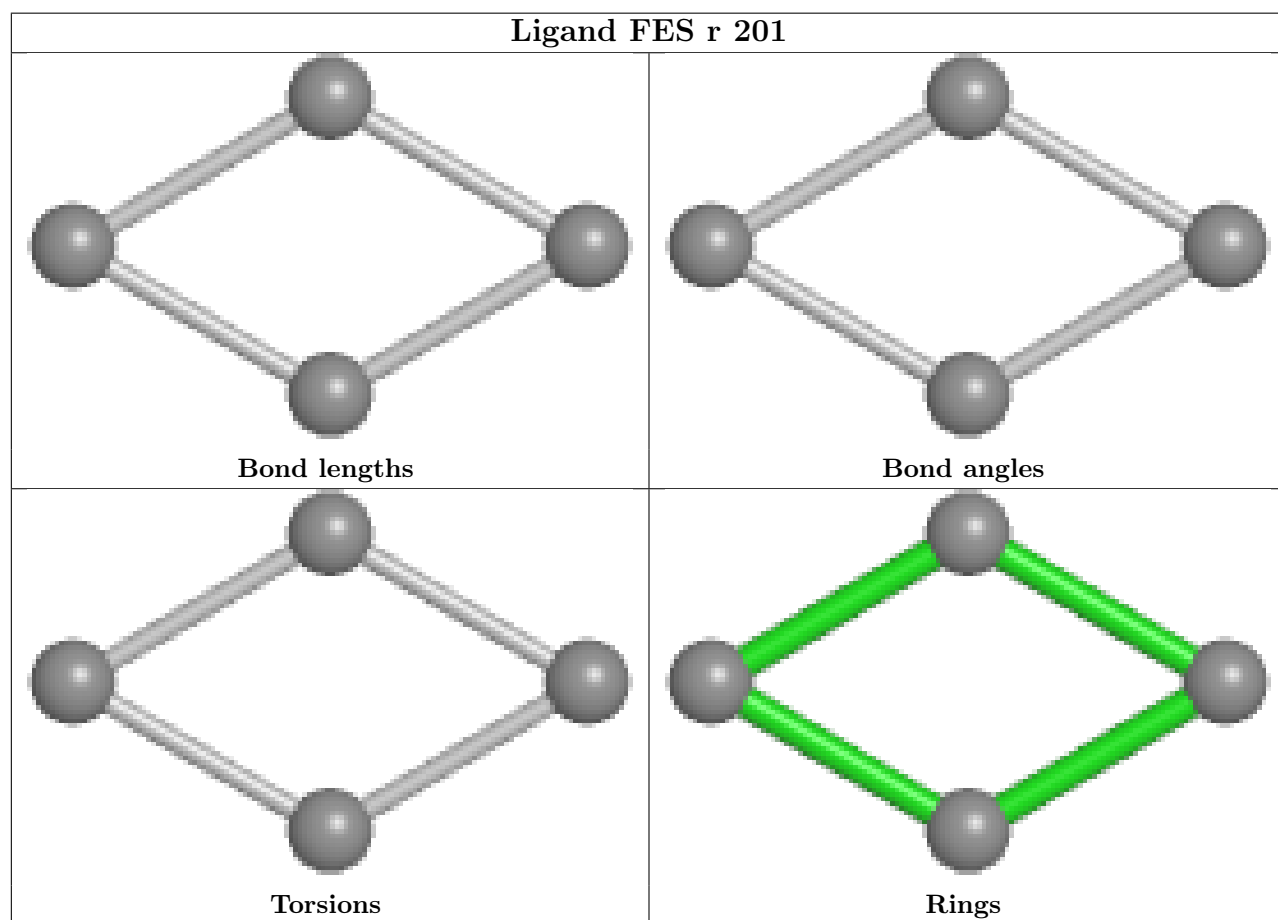
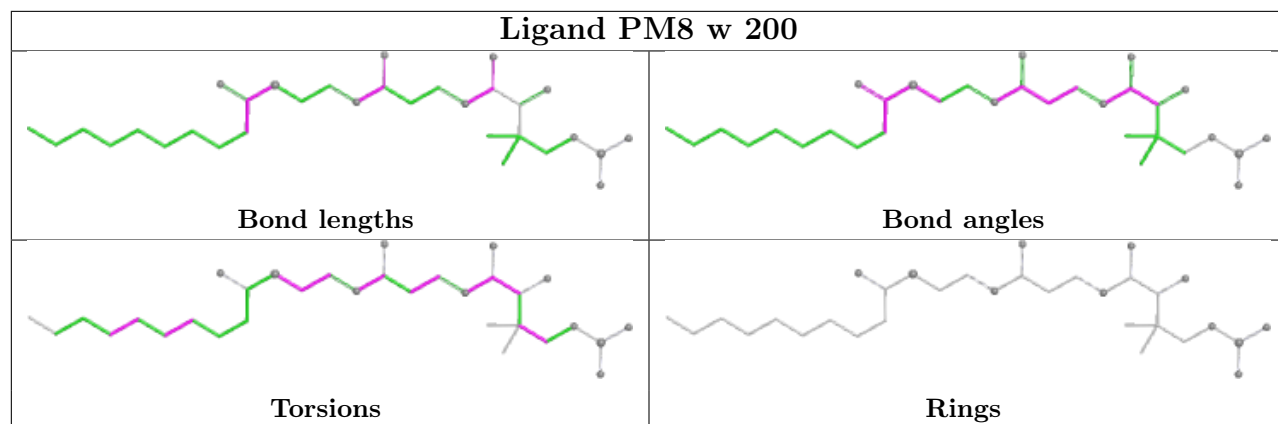
Mol	Chain	Res	Type	Atoms
62	w	200	PM8	C38-C39-N41-C42
62	w	200	PM8	O35-C34-N36-C37
62	w	200	PM8	O40-C39-N41-C42
63	x	401	SAM	CB-CG-SD-CE
62	w	200	PM8	C3-C4-C5-C6
63	x	401	SAM	C2'-C1'-N9-C8
63	x	401	SAM	C-CA-CB-CG
63	x	401	SAM	C2'-C1'-N9-C4
62	w	200	PM8	O33-C32-C34-O35
63	x	401	SAM	O4'-C1'-N9-C8
62	w	200	PM8	C5-C6-C7-C8
64	z	401	GNP	PA-O3A-PB-O1B
62	w	200	PM8	O33-C32-C34-N36

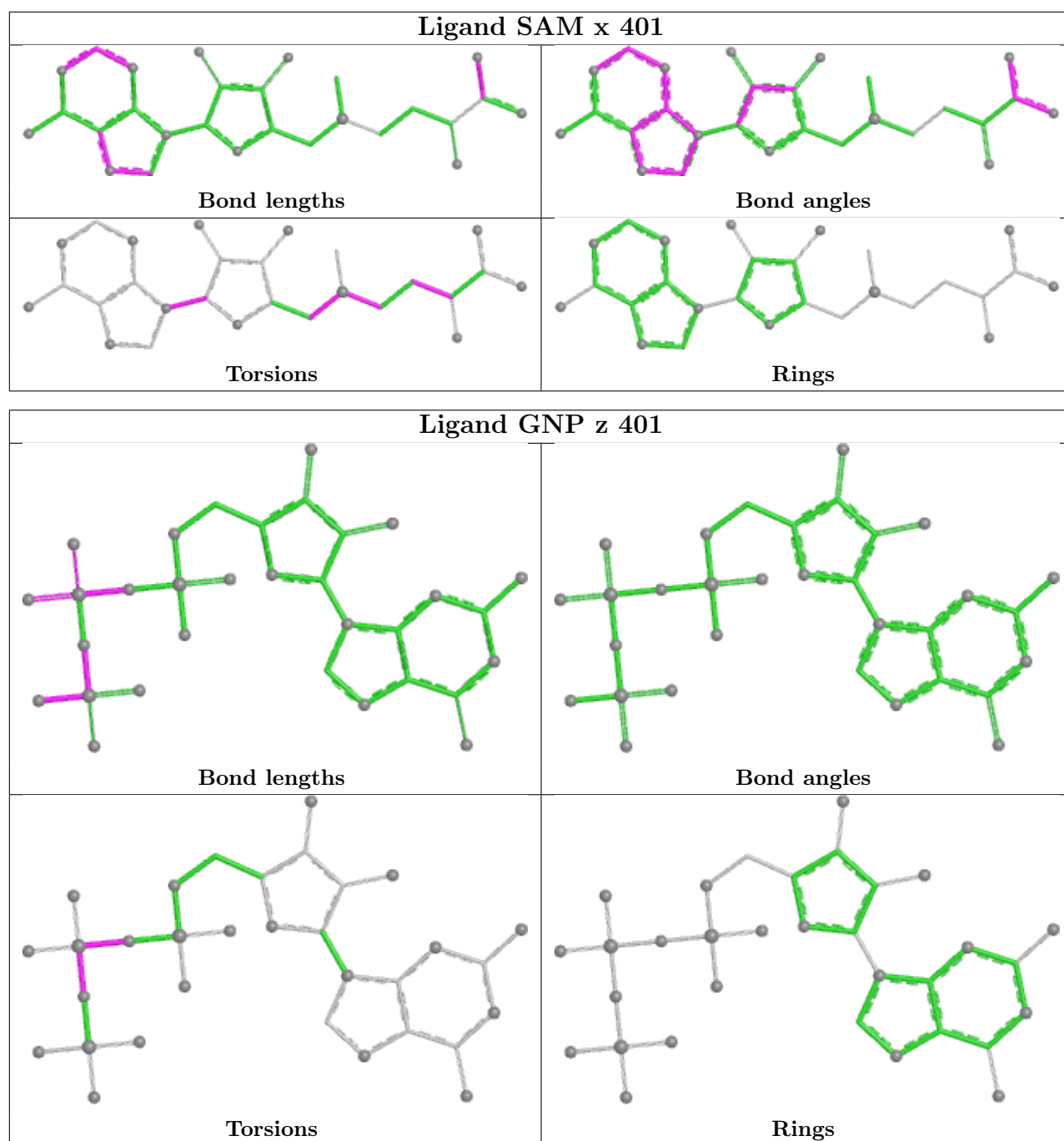
There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
62	w	200	PM8	2	0
61	r	201	FES	1	0
63	x	401	SAM	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

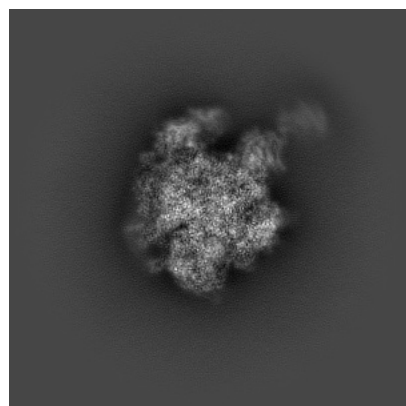
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17720. These allow visual inspection of the internal detail of the map and identification of artifacts.

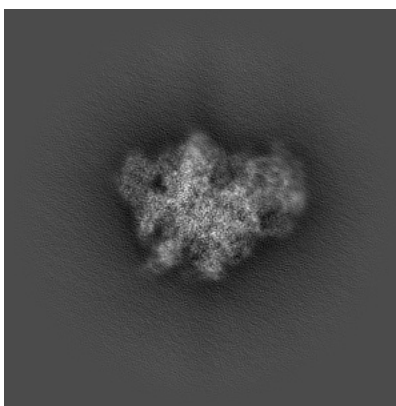
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

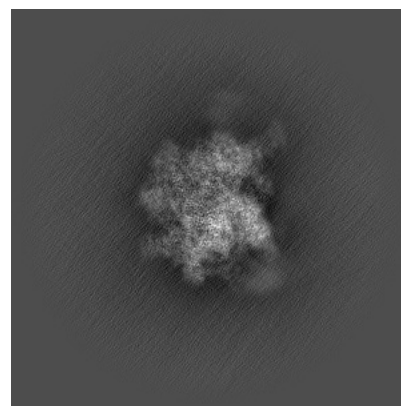
6.1.1 Primary map



X

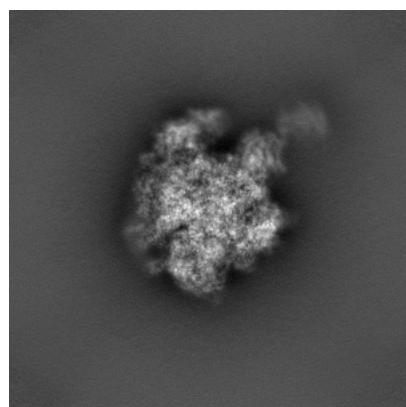


Y

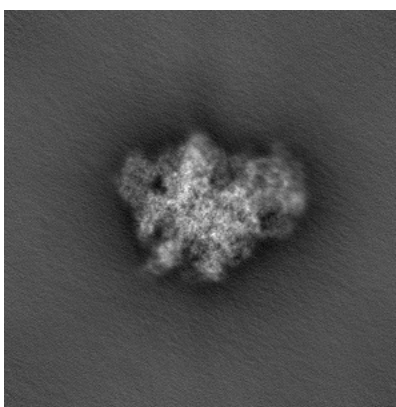


Z

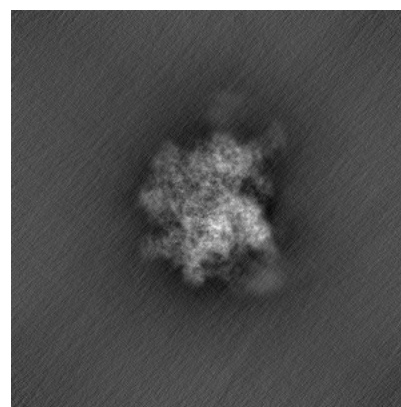
6.1.2 Raw map



X



Y

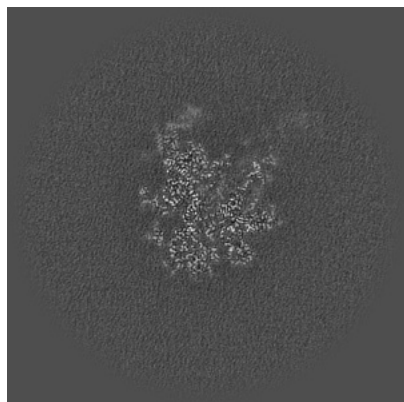


Z

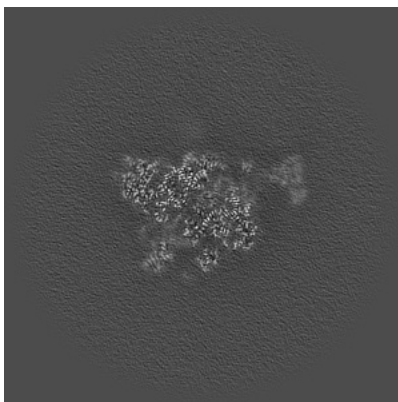
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

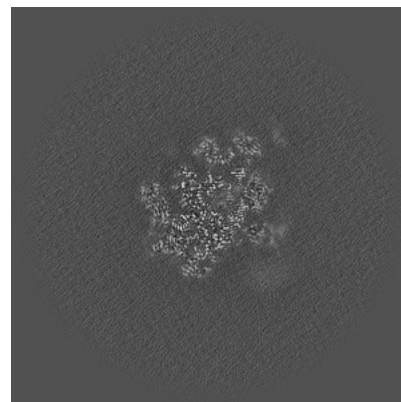
6.2.1 Primary map



X Index: 240

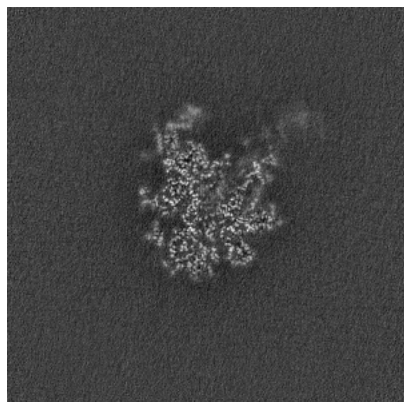


Y Index: 240

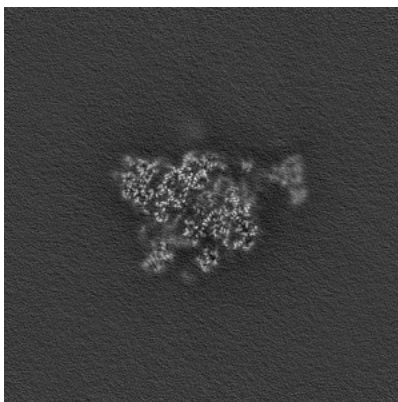


Z Index: 240

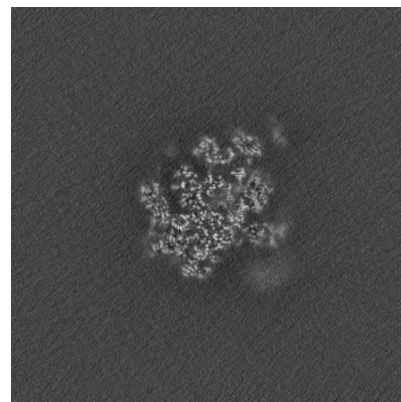
6.2.2 Raw map



X Index: 240



Y Index: 240

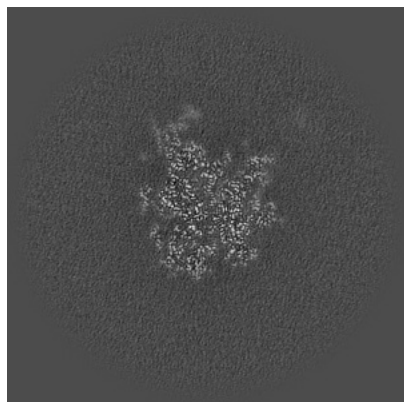


Z Index: 240

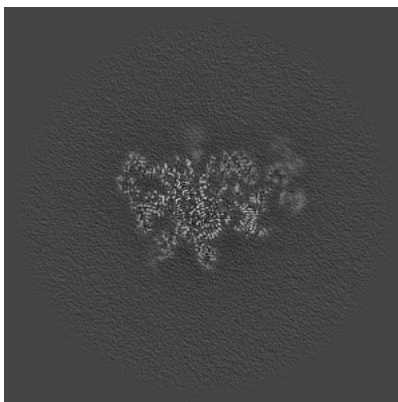
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

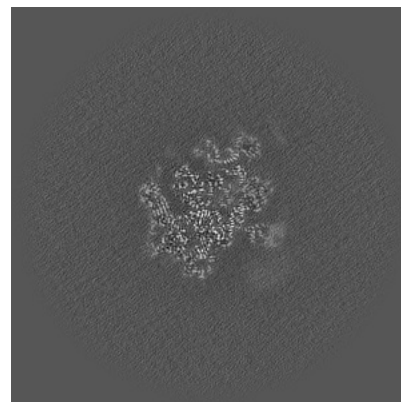
6.3.1 Primary map



X Index: 237

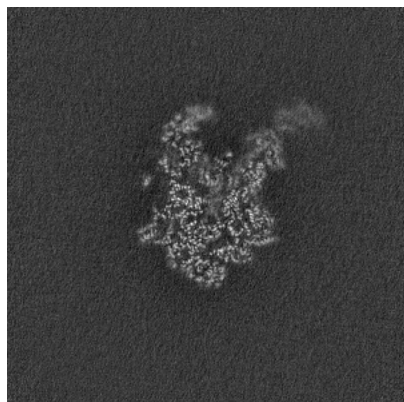


Y Index: 226

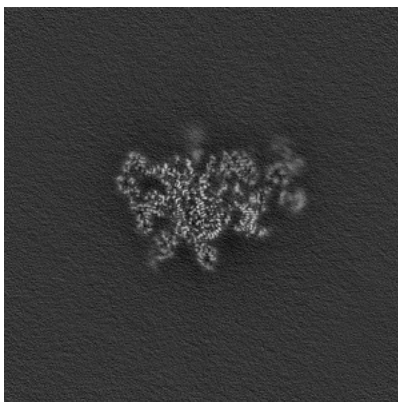


Z Index: 242

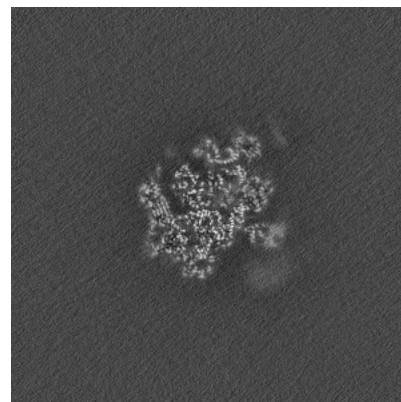
6.3.2 Raw map



X Index: 250



Y Index: 226

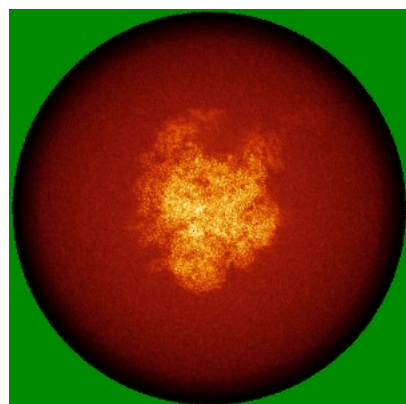


Z Index: 242

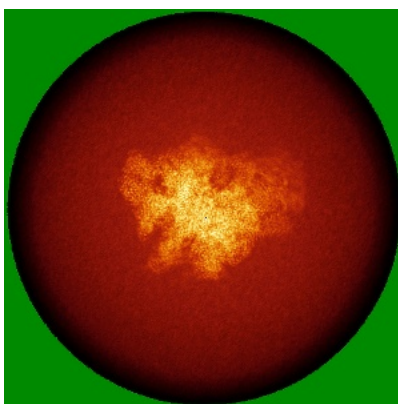
The images above show the largest variance slices of the map in three orthogonal directions.

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

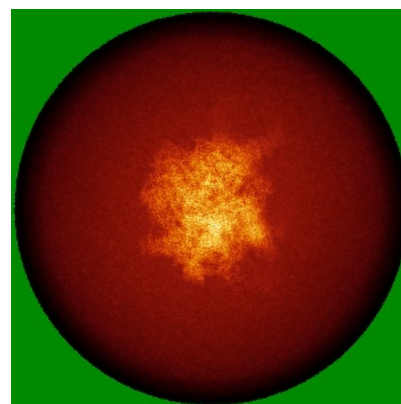
6.4.1 Primary map



X

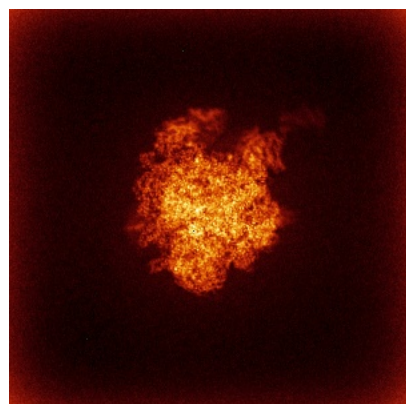


Y

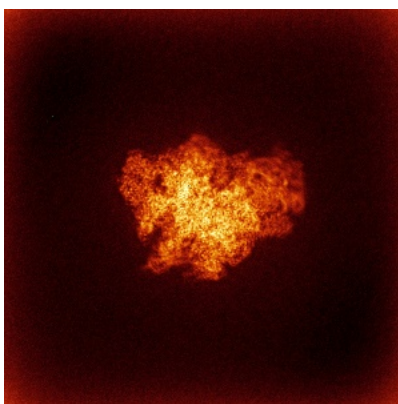


Z

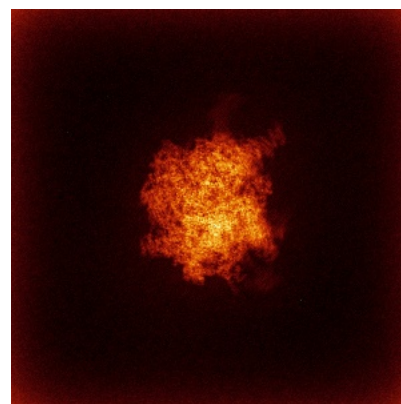
6.4.2 Raw map



X



Y

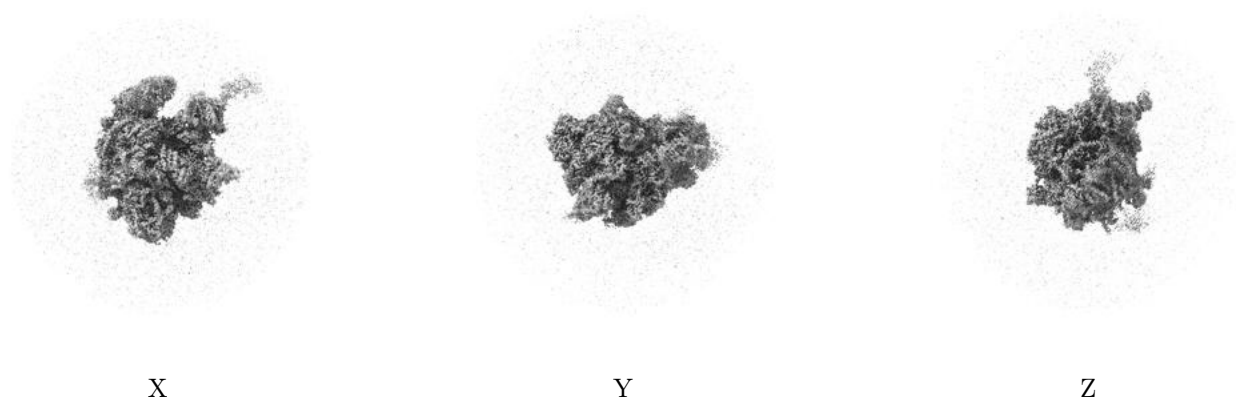


Z

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.

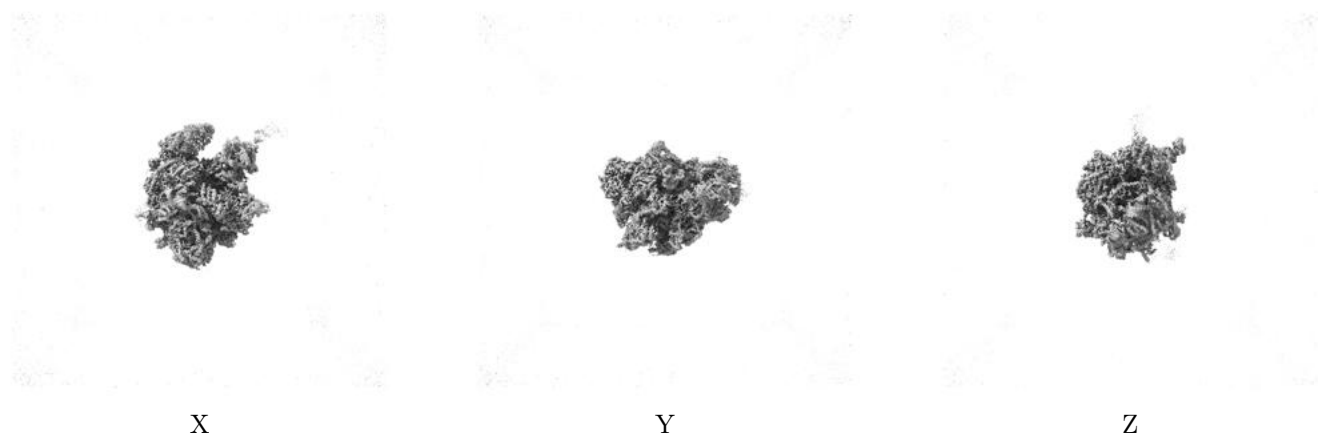
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.814. 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.

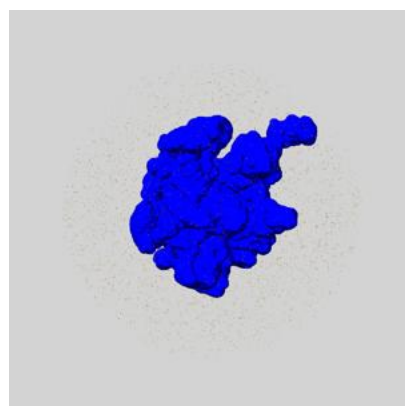
6.6 Mask visualisation [i](#)

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

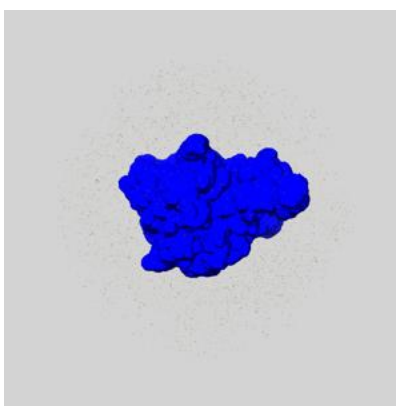
A mask typically either:

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

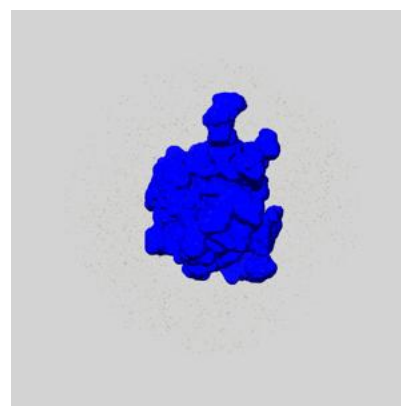
6.6.1 emd_17720_msk_1.map [i](#)



X



Y

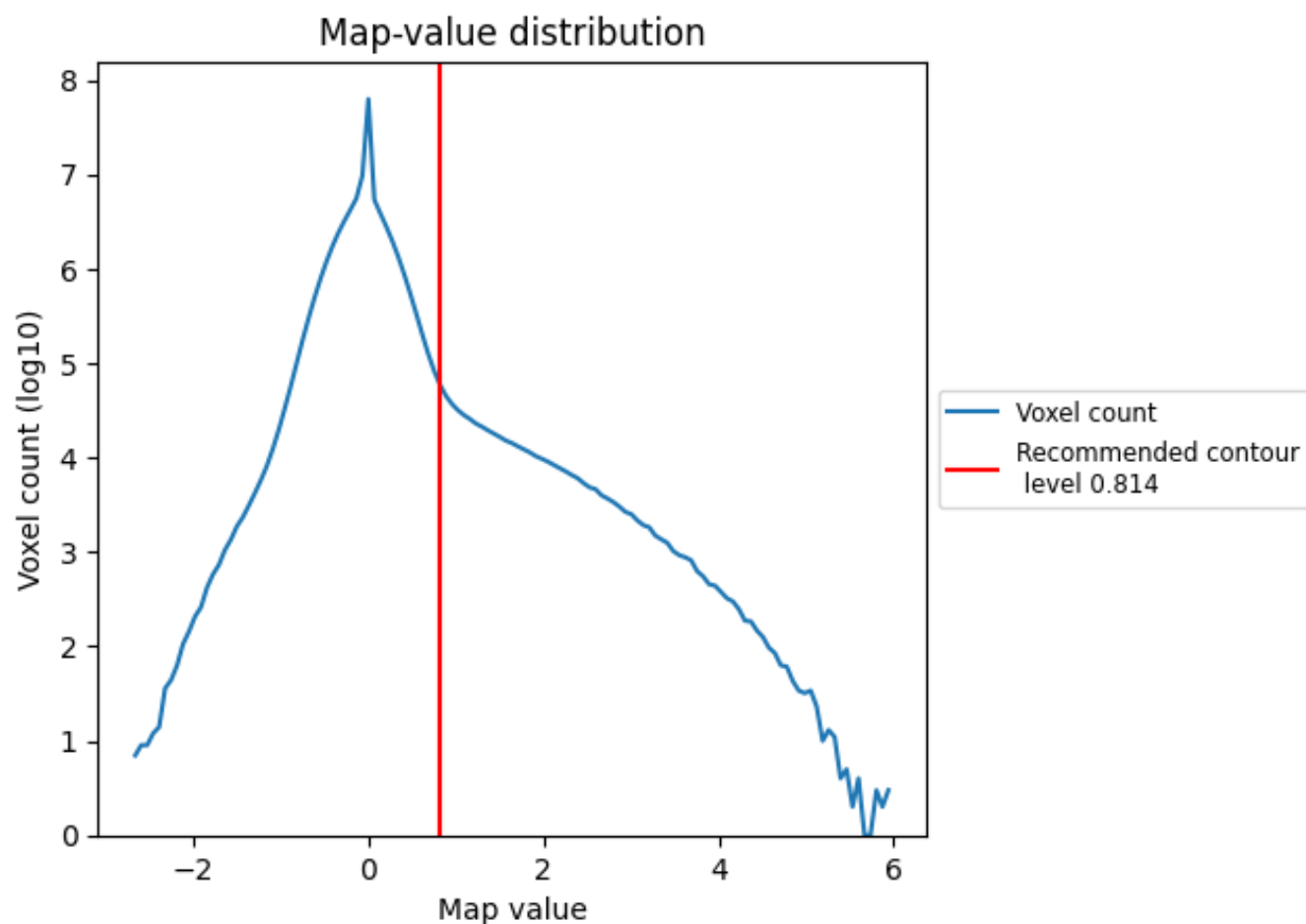


Z

7 Map analysis [i](#)

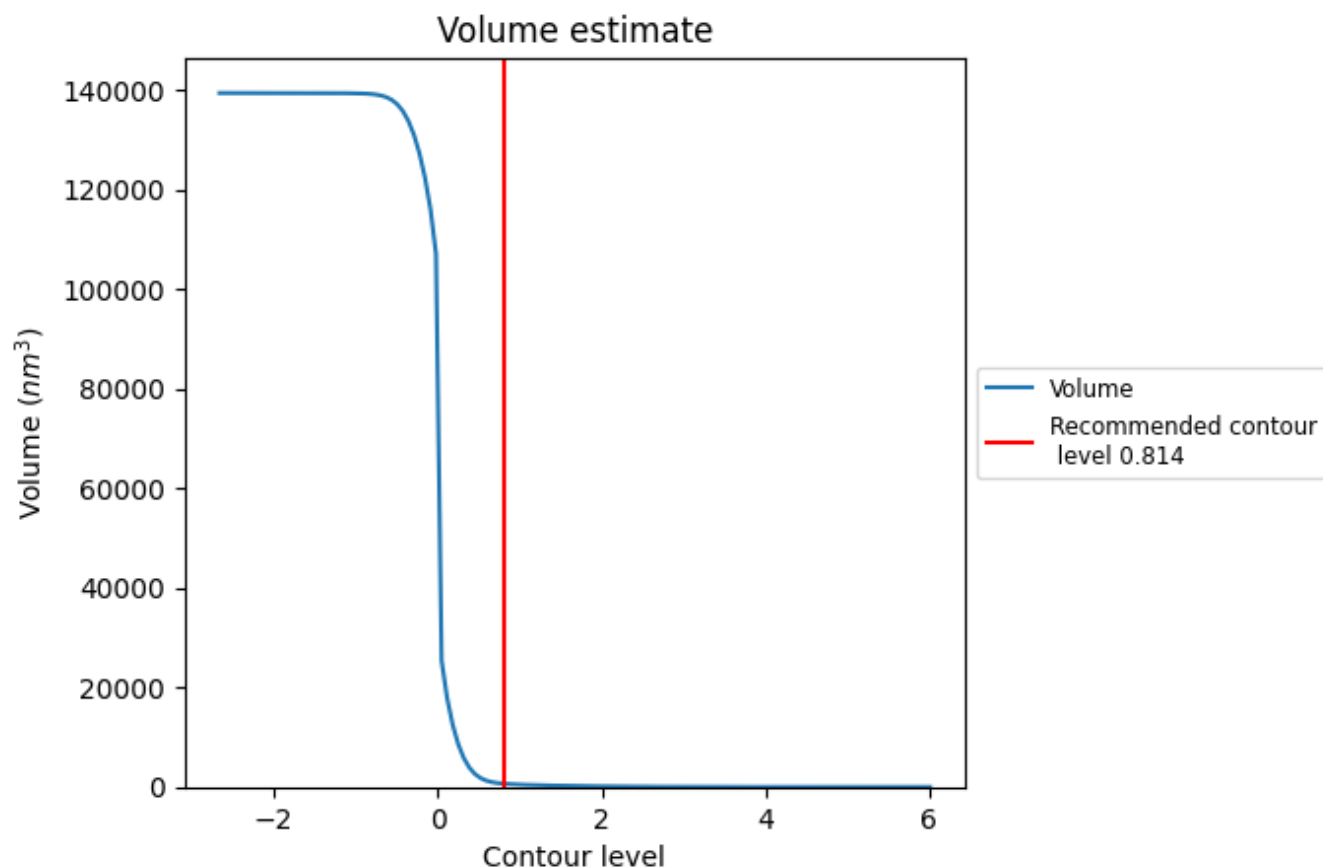
This section contains the results of statistical analysis of the map.

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.

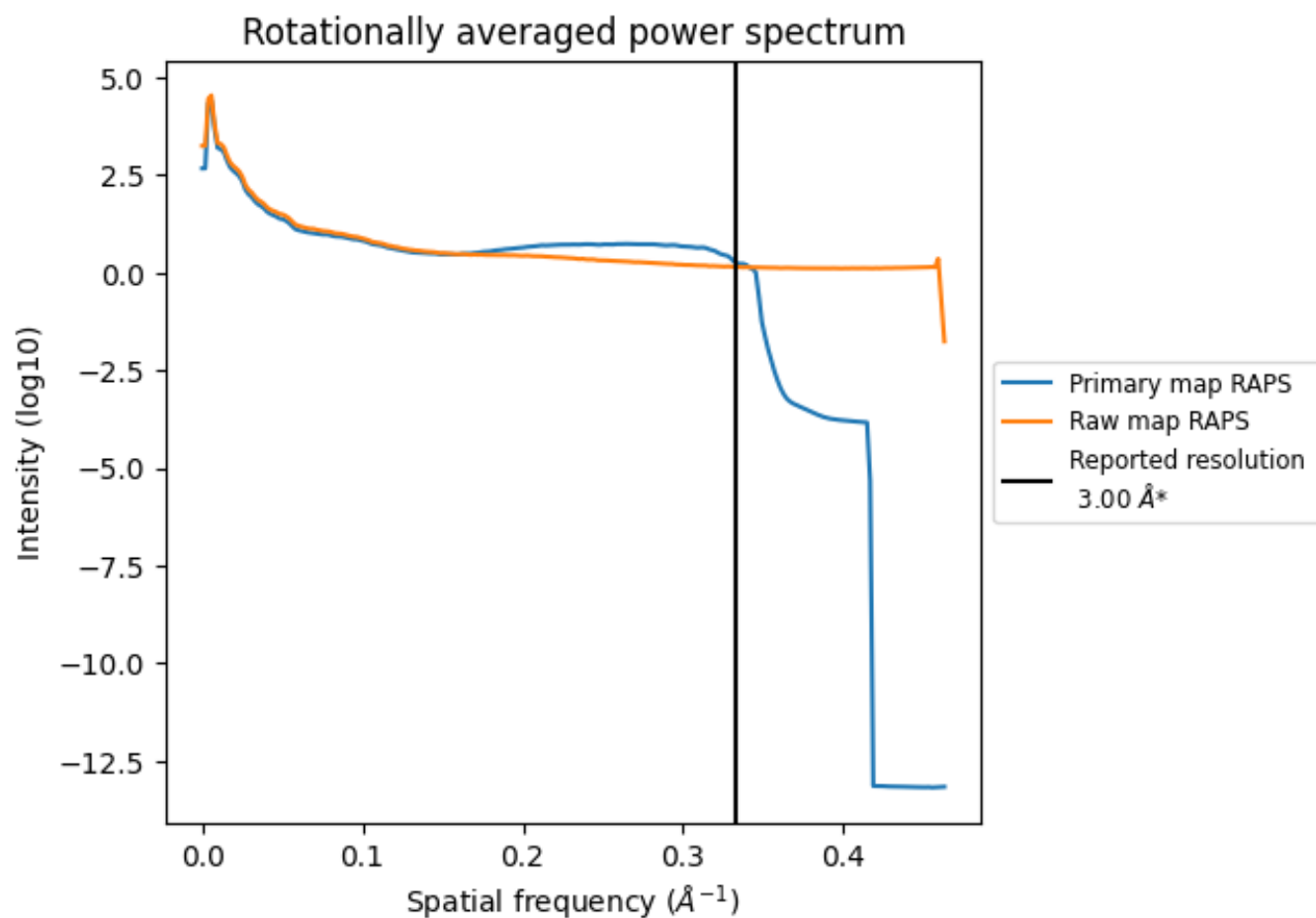
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 647 nm^3 ; this corresponds to an approximate mass of 584 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 ⓘ

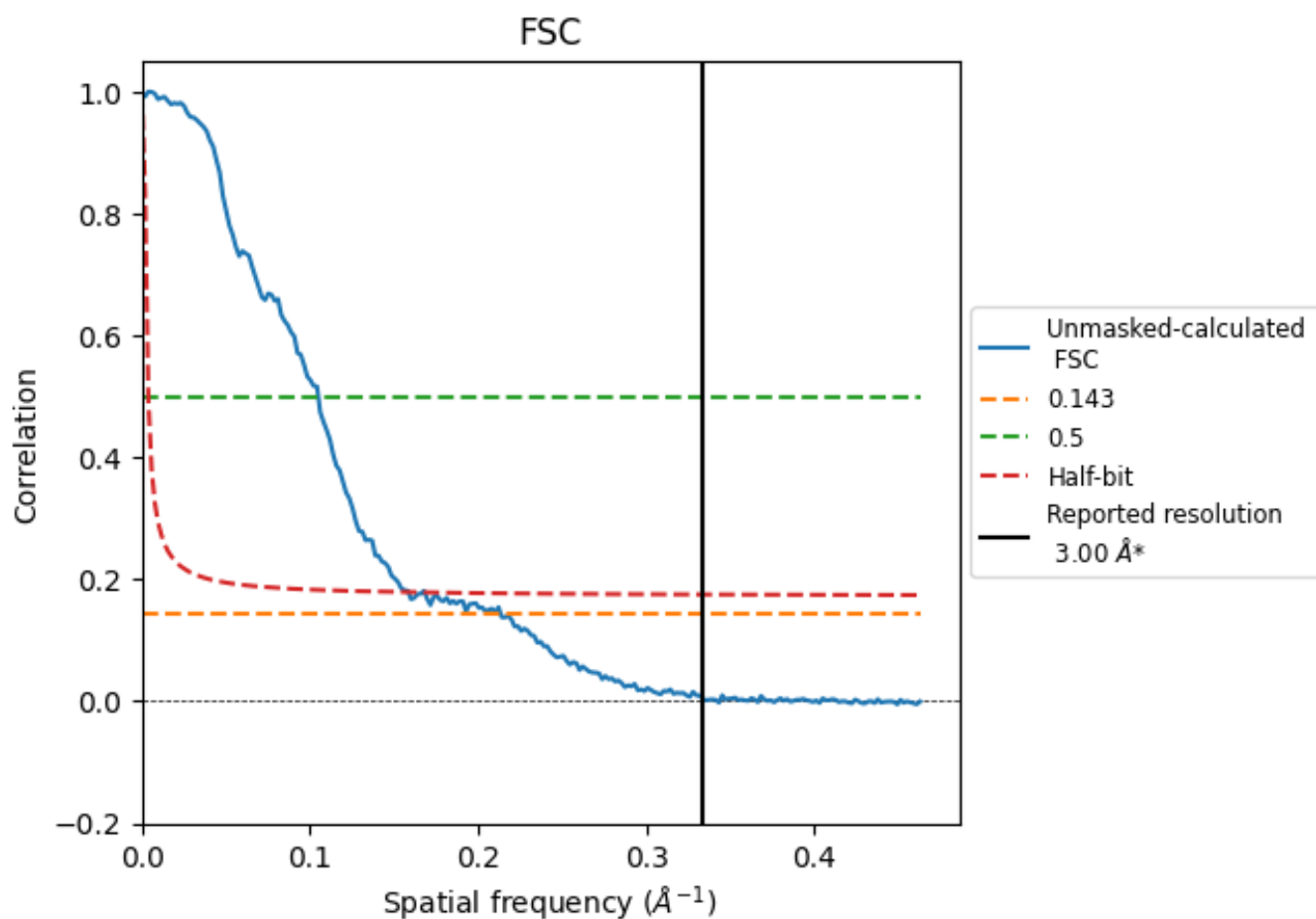


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

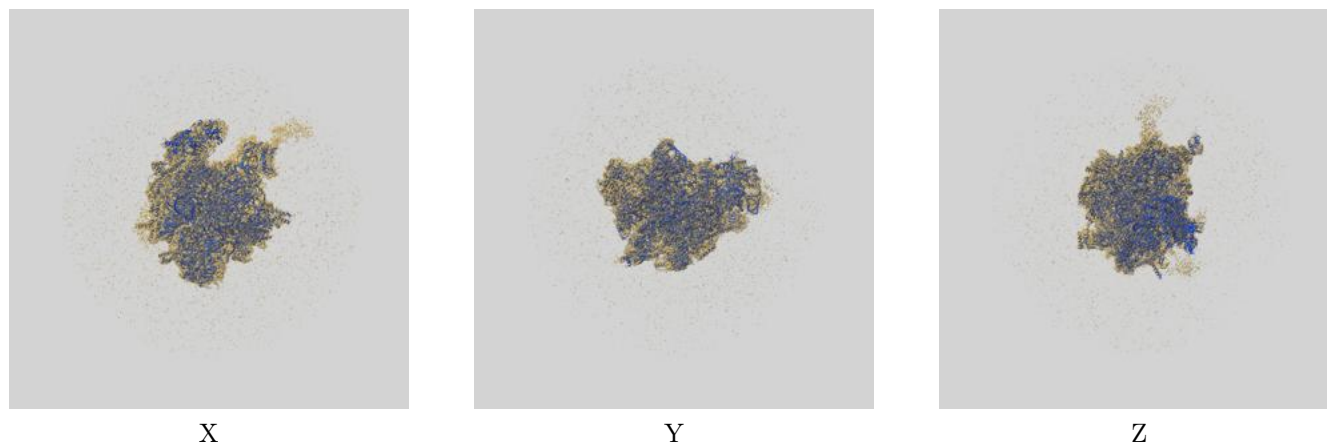
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.68	9.53	6.31

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.68 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

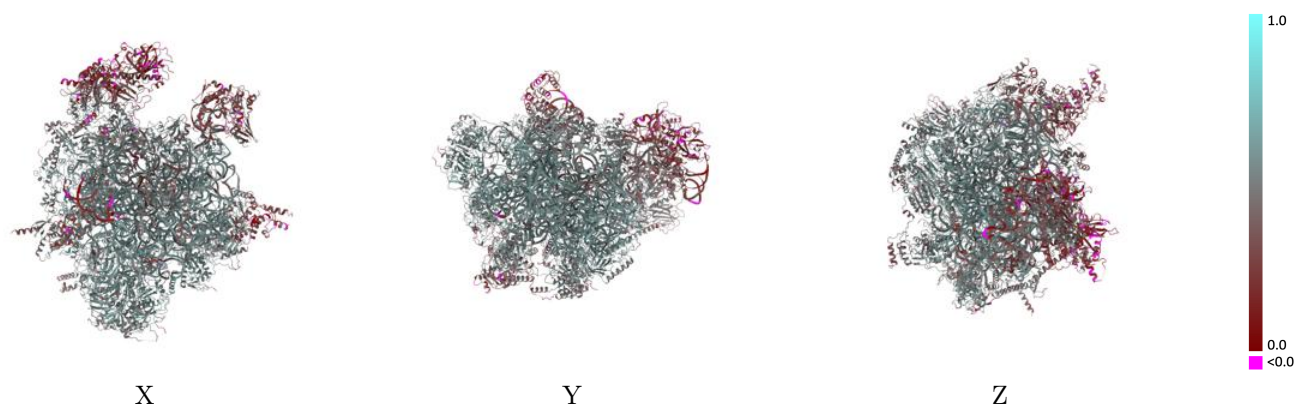
This section contains information regarding the fit between EMDB map EMD-17720 and PDB model 8QSJ. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



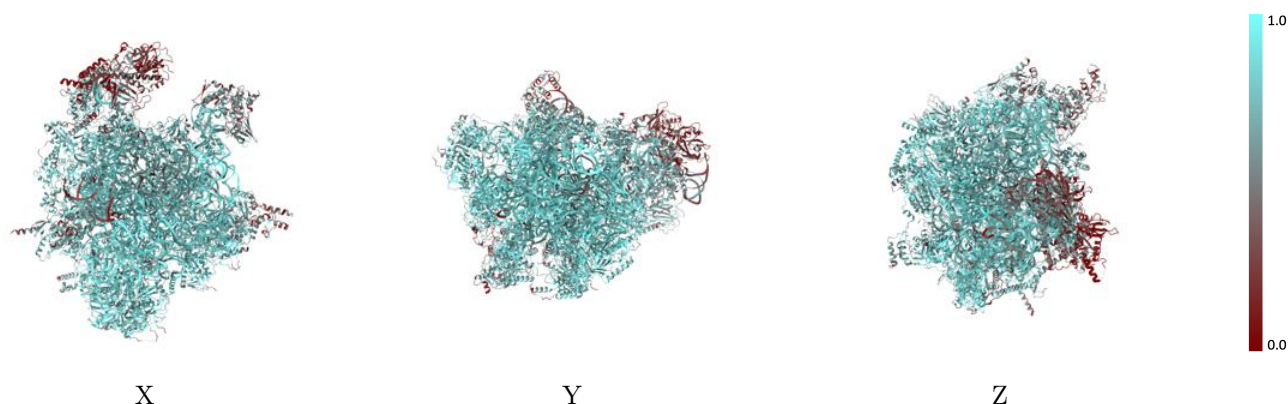
The images above show the 3D surface view of the map at the recommended contour level 0.814 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



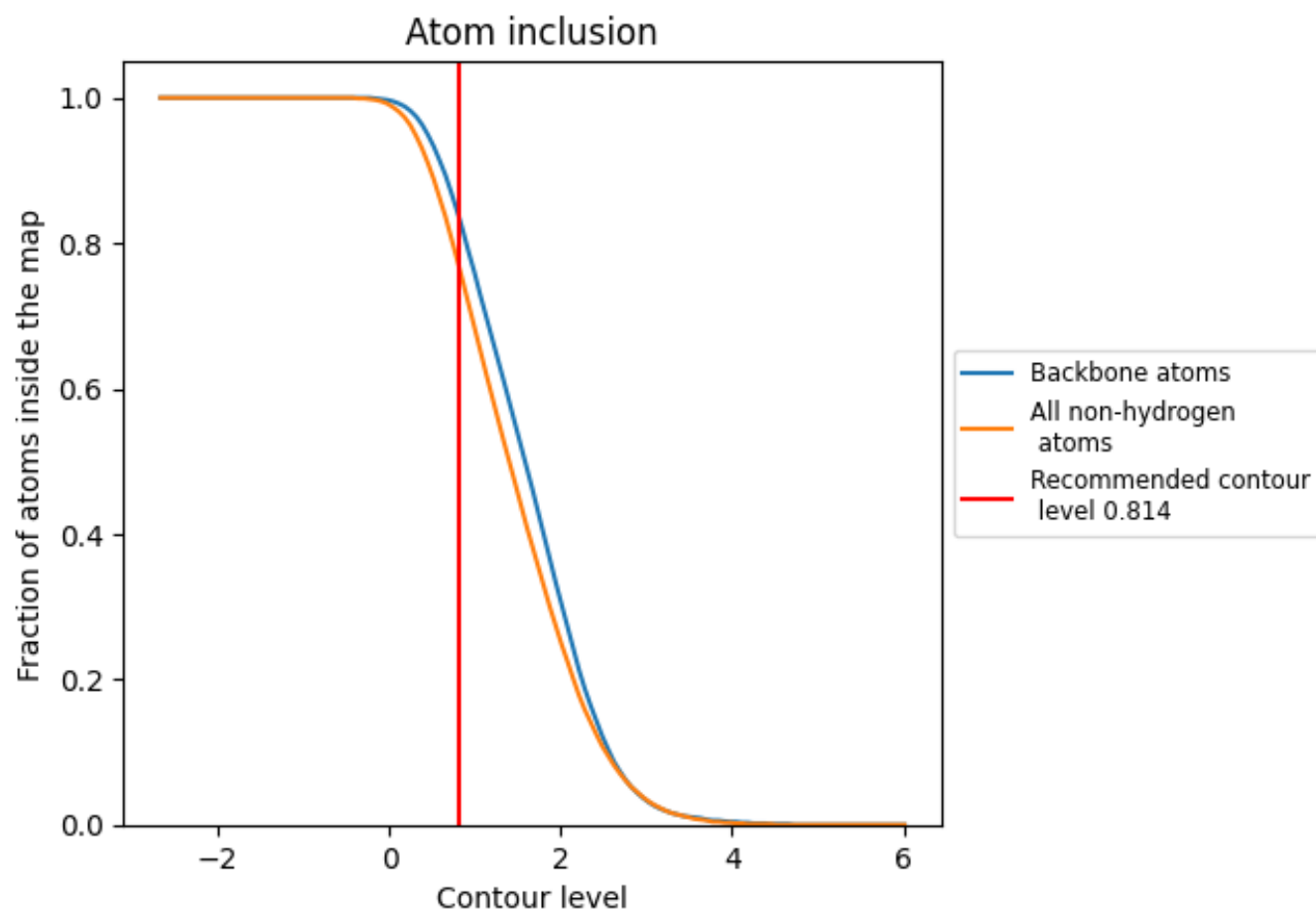
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.814).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 77% 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 (0.814) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7680	 0.4930
0	 0.8060	 0.5420
1	 0.7600	 0.5180
2	 0.8970	 0.5980
3	 0.9240	 0.6070
4	 0.8650	 0.5570
5	 0.8100	 0.5290
6	 0.7070	 0.4530
7	 0.7230	 0.4500
8	 0.2770	 0.2360
9	 0.8000	 0.5130
A	 0.8780	 0.5350
B	 0.6300	 0.3020
D	 0.7990	 0.5340
E	 0.8500	 0.5550
F	 0.8420	 0.5390
H	 0.6910	 0.4750
I	 0.5260	 0.3510
J	 0.3570	 0.1980
K	 0.8710	 0.5760
L	 0.8170	 0.5460
M	 0.8470	 0.5590
N	 0.7100	 0.4730
O	 0.8620	 0.5680
P	 0.7210	 0.4550
Q	 0.8000	 0.5360
R	 0.8750	 0.5790
S	 0.8330	 0.5400
T	 0.8370	 0.5590
U	 0.7380	 0.5100
V	 0.6800	 0.4460
W	 0.8480	 0.5750
X	 0.7950	 0.5340
Y	 0.8210	 0.5340
Z	 0.8470	 0.5610



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Chain	Atom inclusion	Q-score
a	 0.7220	 0.4820
b	 0.8510	 0.5410
c	 0.7640	 0.4860
d	 0.5670	 0.3940
e	 0.1930	 0.1730
f	 0.3710	 0.2980
g	 0.8400	 0.5350
h	 0.6950	 0.4210
i	 0.8770	 0.5830
j	 0.7950	 0.5090
k	 0.6480	 0.3900
l	 0.6800	 0.3900
m	 0.1150	 0.1670
o	 0.7520	 0.5350
p	 0.6320	 0.4340
q	 0.6860	 0.4490
r	 0.8400	 0.5160
s	 0.8310	 0.5490
u	 0.6710	 0.4510
v	 0.5750	 0.3340
w	 0.3040	 0.2010
x	 0.6750	 0.4630
y	 0.6250	 0.4220
z	 0.7060	 0.4640