



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 07:58 PM UTC

PDB ID : 8AGU / pdb_00008agu
EMDB ID : EMD-15424
Title : Yeast RQC complex in state E
Authors : Tesina, P.; Buschauer, R.; Beckmann, R.
Deposited on : 2022-07-20
Resolution : 2.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

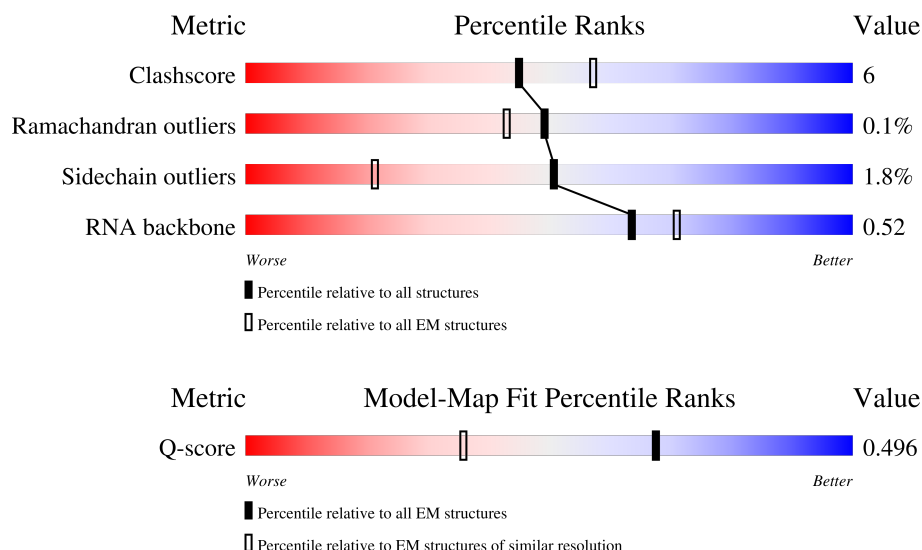
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.70 Å.

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



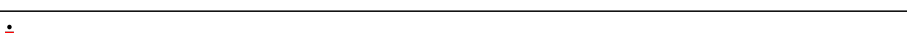
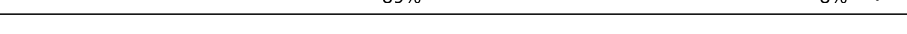
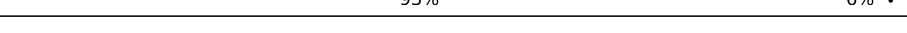
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10327 (2.20 - 3.20)

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

Mol	Chain	Length	Quality of chain
1	A	204	
2	B	199	
3	C	184	

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Mol	Chain	Length	Quality of chain
4	D	186	
5	E	189	
6	F	172	
7	G	160	
8	H	121	
9	I	137	
10	J	155	
11	K	142	
12	L	127	
13	M	136	
14	N	149	
15	O	59	
16	P	105	
17	Q	113	
18	R	130	
19	S	107	
20	T	121	
21	U	120	
22	V	100	
23	W	88	
24	X	78	
25	Y	51	
26	Z	128	
27	b	106	
28	c	92	

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Mol	Chain	Length	Quality of chain
29	d	25	
30	f	3395	
31	h	121	
32	i	158	
33	j	254	
34	k	387	
35	l	362	
36	m	297	
37	n	176	
38	o	244	
39	p	256	
40	q	191	
41	r	221	
42	s	174	
43	t	199	
44	u	138	
45	a	1038	
46	e	1562	
47	g	245	
48	v	157	
49	w	217	
50	y	76	
51	z	165	
52	0	312	
53	1	18	

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 149748 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 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 2 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	197	Total	C	N	O	S	197	0
			1555	1003	289	262	1		

- Molecule 3 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	183	Total	C	N	O		0	0
			1416	879	284	253			

- Molecule 4 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 5 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	156	Total	C	N	O		0	0
			1258	781	265	212			

- Molecule 6 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 7 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	159	Total	C	N	O	S	0	0
			1272	802	245	221	4		

- Molecule 8 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	100	Total	C	N	O		0	0
			796	516	131	149			

- Molecule 9 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 10 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	63	Total	C	N	O	S	0	0
			518	333	102	82	1		

- Molecule 11 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 12 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	125	Total	C	N	O		0	0
			984	620	191	173			

- Molecule 13 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	135	Total	C	N	O		0	0
			1080	701	199	180			

- Molecule 14 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	148	Total	C	N	O	S	0	0
			1169	747	231	188	3		

- Molecule 15 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	58	Total	C	N	O	S	0	0
			462	289	100	73			

- Molecule 16 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 17 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 18 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	127	Total	C	N	O	S	0	0
			1013	642	205	165	1		

- Molecule 19 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 20 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 21 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 22 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 23 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	81	Total	C	N	O	S	0	0
			645	393	141	106	5		

- Molecule 24 is a protein called BJ4_G0032190.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	77	Total	C	N	O		0	0
			612	391	115	106			

- Molecule 25 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 26 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	52	Total	C	N	O	S	0	0
			410	254	86	65	5		

- Molecule 27 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 28 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 29 is a protein called RPL41A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	22	Total	C	N	O	S	0	0
			207	127	56	23	1		

- Molecule 30 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	3216	Total	C	N	O	P	0	0
			68782	30723	12389	22454	3216		

- Molecule 31 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	h	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 32 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	i	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 33 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	j	246	Total	C	N	O	S	0	0
			1874	1168	380	325	1		

- Molecule 34 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	k	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 35 is a protein called BJ4_G0008850.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	l	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 36 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 37 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	n	167	Total	C	N	O	0	0
			1307	843	234	230		

- Molecule 38 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	o	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 39 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	p	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 40 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	q	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 41 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	r	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 42 is a protein called BJ4_G0027750.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	s	169	Total	C	N	O	S	0	0
			1346	843	252	247	4		

- Molecule 43 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	t	193	Total	C	N	O	S	0	0
			1543	962	315	266			

- Molecule 44 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 45 is a protein called RQC2 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	a	848	Total	C	N	O	S	0	0
			6569	4188	1138	1226	17		

- Molecule 46 is a protein called E3 ubiquitin-protein ligase listerin.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	e	1527	Total	C	N	O	S	0	0
			11509	7353	1937	2181	38		

- Molecule 47 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	g	225	Total	C	N	O	S	0	0
			1651	1030	282	332	7		

- Molecule 48 is a protein called Eukaryotic translation initiation factor 5A-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	v	142	Total	C	N	O	S	0	0
			1085	676	183	217	9		

- Molecule 49 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	w	216	Total	C	N	O	S	0	0
			1709	1092	298	310	9		

- Molecule 50 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	y	73	Total	C	N	O	P	0	0
			1556	692	273	518	73		

- Molecule 51 is a protein called 60S ribosomal protein L12-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	z	148	Total	C	N	O	0	0
			728	432	148	148		

- Molecule 52 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	0	121	Total	C	N	O	S	0	0
			961	618	167	173	3		

- Molecule 53 is a protein called CAT-tailed nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	1	17	Total	C	N	O	0	0
			85	51	17	17		

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	A	1	Total	Mg	0
			1	1	
54	C	1	Total	Mg	0
			1	1	
54	E	1	Total	Mg	0
			1	1	
54	I	1	Total	Mg	0
			1	1	
54	R	1	Total	Mg	0
			1	1	
54	T	1	Total	Mg	0
			1	1	

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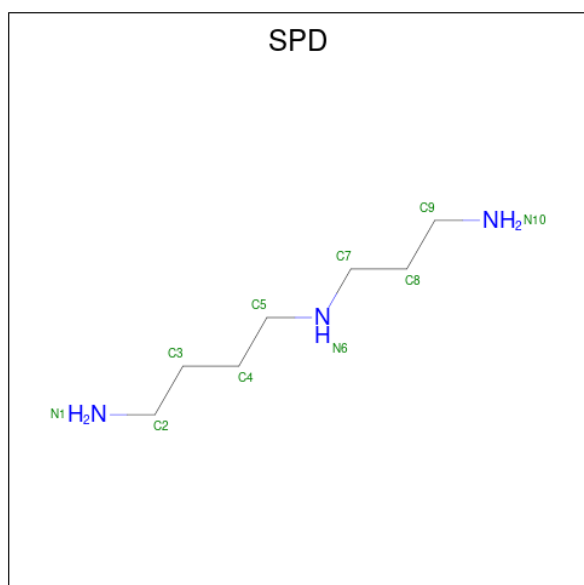
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Mol	Chain	Residues	Atoms		AltConf
54	f	3	Total 3	Mg 3	0
54	h	1	Total 1	Mg 1	0
54	j	2	Total 2	Mg 2	0
54	k	1	Total 1	Mg 1	0

- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
55	T	1	Total 1	Zn 1	0
55	W	1	Total 1	Zn 1	0
55	Z	1	Total 1	Zn 1	0
55	b	1	Total 1	Zn 1	0
55	c	1	Total 1	Zn 1	0
55	e	2	Total 2	Zn 2	0

- Molecule 56 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).

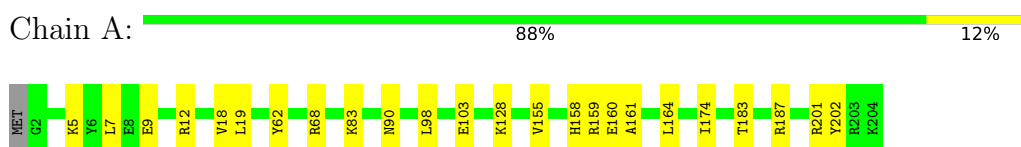


Mol	Chain	Residues	Atoms			AltConf
56	f	1	Total	C	N	0
			10	7	3	

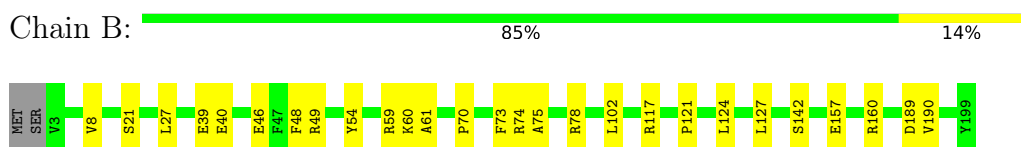
3 Residue-property plots [i](#)

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

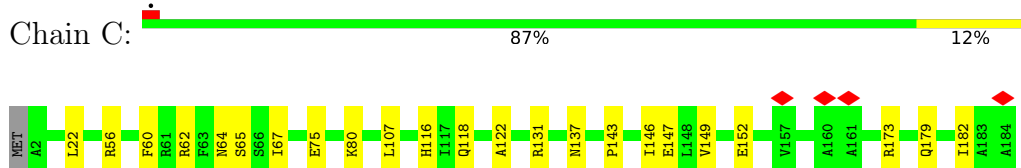
- Molecule 1: 60S ribosomal protein L15-A



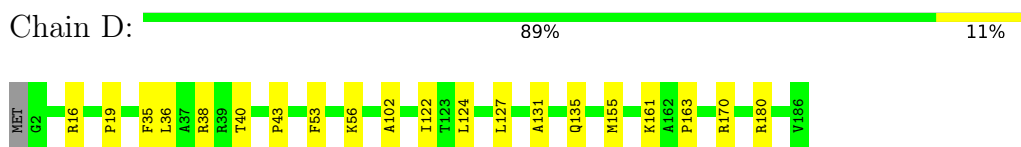
- Molecule 2: 60S ribosomal protein L16-A



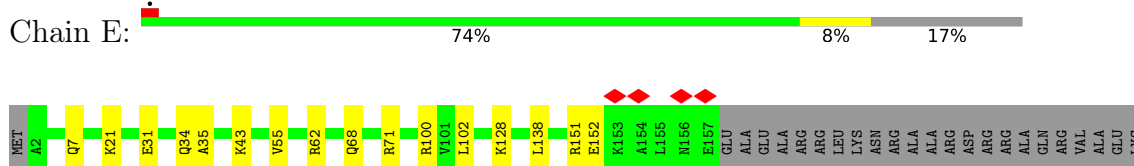
- Molecule 3: 60S ribosomal protein L17-A



- Molecule 4: 60S ribosomal protein L18-A



- Molecule 5: 60S ribosomal protein L19-A



ARG
ASP
ALA
LEU
LYS
GLU
ASP
ALA

- Molecule 6: 60S ribosomal protein L20-A

Chain F:  84% 15%

MET A2 Q8 P22 S32 I36 R40 Y43 I64 T70 V77 R80 T87 H90 E93 I94 R95 D96 V97 L106 M110 H122 I123 L124 K125 V126 R137 V140 R155 V156 Y172

- Molecule 7: 60S ribosomal protein L21-A

Chain G:  88% 11%

MET G2 R17 H22 G73 Y84 R88 L89 S99 K100 C101 R102 R108 M112 R116 A133 R136 R139 M146 P155 T158 F159 I160

- Molecule 8: 60S ribosomal protein L22-A

Chain H:  73% 10% 17%

MET ALA PRO ASN THR SER ARG LYS D9 S20 T23 V27 I41 E44 M49 L50 G51 V54 T55 V56 V65 R90 D91 W92 Y108 G1N VAL THR PRO GLU GLU ASP GLU GLU ASP GLU

- Molecule 9: 60S ribosomal protein L23-A

Chain I:  88% 11%

MET S2 G3 N4 R12 I13 S14 P18 A38 A51 M59 R80 Q81 Y94 A99 P117 R128 V129 S133 G134 V135 V136 V137

- Molecule 10: 60S ribosomal protein L24-A

Chain J:  35% 5% 59%

M1 D6 G16 Q32 R33 S34 K41 K44 R47 H58 I63 THR GLU GLU VAL ALA LYS LYS ARG SER THR VAL LYS VAL LYS ALA GLN ARG PRO ILE THR GLY ALA SER LEU ASP LEU ILE LYS ALA GLU ARG SER LEU LYS PRO VAL ARG LYS ALA ASN

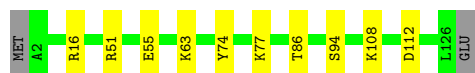
- Molecule 11: 60S ribosomal protein L25

Chain K:  85% 15%

MET ALA PRO SER LYS LYS ALA ALA THR ALA LYS LYS VAL VAL VAL THR ASN LYS K22 A50 I142

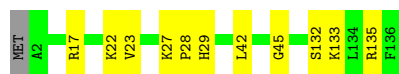
- Molecule 12: 60S ribosomal protein L26-A

Chain L:  91% 8% .



- Molecule 13: 60S ribosomal protein L27-A

Chain M:  91% 8% .



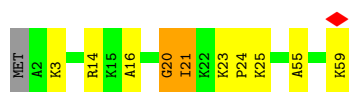
- Molecule 14: 60S ribosomal protein L28

Chain N:  87% 13% .



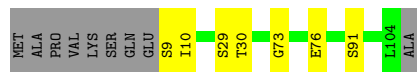
- Molecule 15: 60S ribosomal protein L29

Chain O:  81% 14% . .



- Molecule 16: 60S ribosomal protein L30

Chain P:  85% 7% 9%



- Molecule 17: 60S ribosomal protein L31-A

Chain Q:  79% 18% .

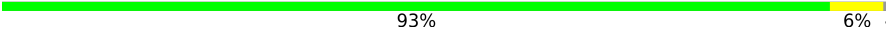


- Molecule 18: 60S ribosomal protein L32

Chain R:  89% 8% .



- Molecule 19: 60S ribosomal protein L33-A

Chain S:  93% 6%

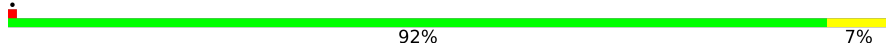


- Molecule 20: 60S ribosomal protein L34-A

Chain T:  85% 7% 7%



- Molecule 21: 60S ribosomal protein L35-A

Chain U:  92% 7%



- Molecule 22: 60S ribosomal protein L36-A

Chain V:  90% 9%



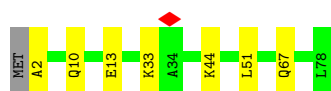
- Molecule 23: 60S ribosomal protein L37-A

Chain W:  76% 16% 8%

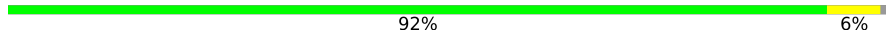


- Molecule 24: BJ4_G0032190.mRNA.1.CDS.1

Chain X:  90% 9%



- Molecule 25: 60S ribosomal protein L39

Chain Y:  92% 6%



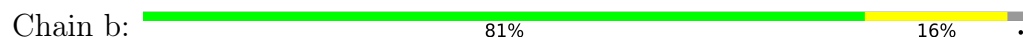
- Molecule 26: Ubiquitin-60S ribosomal protein L40



MET GLN ILE PHE VAL THR LEU THR THR LYS THR THR LEU VAL SER ASP THR ILE ASP ASN VAL LYS SER LYS ILE GLN ASP LYS GLY ILE PRO PRO ASP GLN GLN ARG ARG LEU ILE PHE ALA GLY LYS GLN LEU GLU ASP ARG THR LEU SER ASP TYR ASN

ILE GLN LYS SER THR LEU HIS VAL LEU LEU ARG ARG ARG GLY I77 Y100 R113 K124 K125 K128

- Molecule 27: 60S ribosomal protein L42-A



MET V2 T7 T10 H20 Q22 Y28 K29 A30 R41 R45 K61 A62 K63 V69 L72 V75 K76 H90 K100 L104 GLN PHE

- Molecule 28: 60S ribosomal protein L43-A



MET A2 K3 R4 R17 Y18 R44 R49 G66 R87 A92

- Molecule 29: RPL41A isoform 1



M4 R20 R21 K22 V23 R24 A25 ARG SER LYS

- Molecule 30: 25S rRNA



G U U3 A6 A13 U14 U19 A20 G21 A26 C36 A40 A43 A49 A58 G59 A60 A63 A65 A66 A67 C68 G76 A77 U78 G86 G92 G93 G94 A95 G98 A99 A109 G110 C111 A116 G120 A121 A122 A123 U129

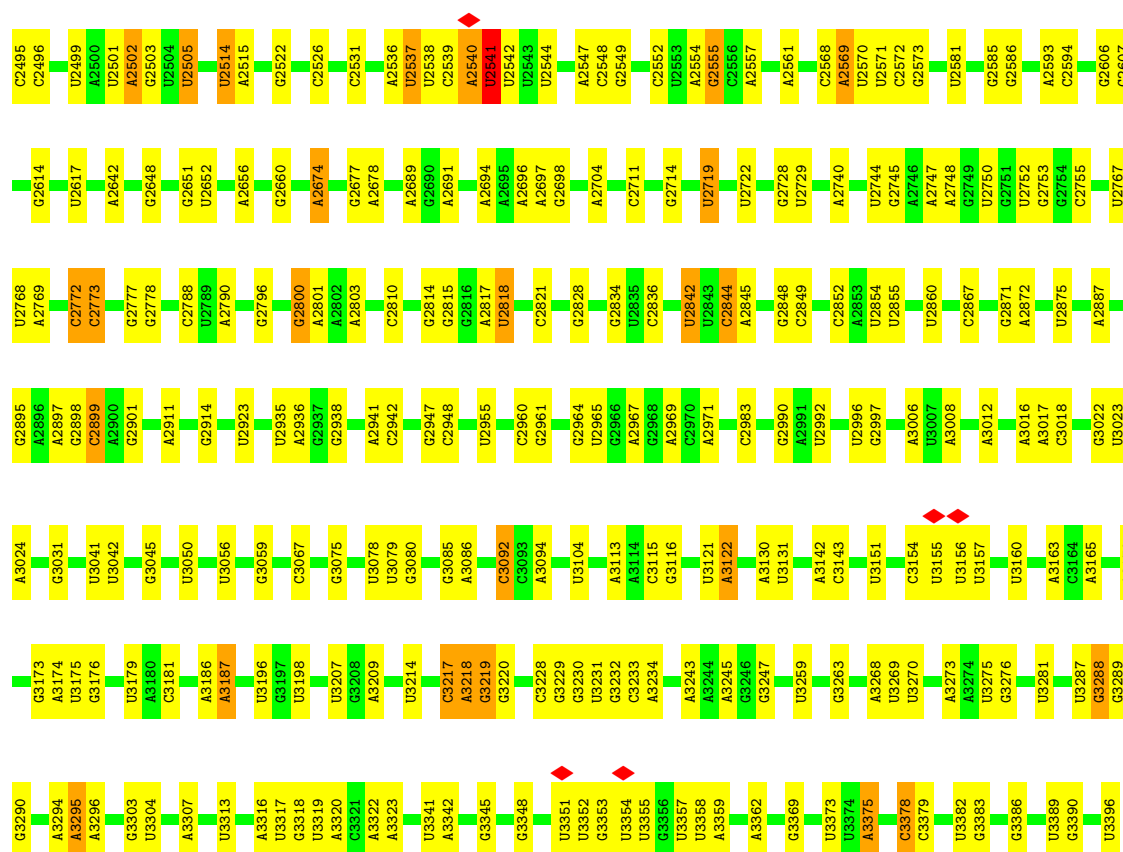
A130 U133 U134 A295 A296 G297 G298 G299 G301 U305 A306 A307 A308 A323 U329 C339 A348 A349 C350 A351 A352 G358 A361 A365 A374 A375 G376 G394 A397 A398 A399 G400 U401 A402 C403 G409 U411 G412 A417 A418 G421 A422 C439 A440 A284

A485 U286 A295 A296 G297 G298 G299 G301 U305 A306 A307 A308 A323 U329 C339 A348 A349 C350 A351 A352 G358 A361 A365 A374 A375 G376 G394 A397 A398 A399 G400 U401 A402 C403 G409 U411 G412 A417 A418 G421 A422 C439 A440 A284

G442 G443 U444 G445 U446 U447 U448 U449 G450 U451 G C C C U U G C U C C U U A A A C C U U U A486 U487 U488 U489 C490 G494 G495 G505 G518 A519 U520 A521 A522 A523

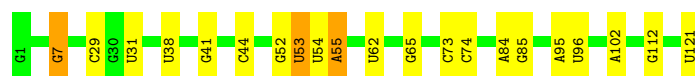
U528 A529 G530 G531 A532 G535 U536 G542 C543 C544 U545 C546 C547 G548 U549 A550 A551 G552 U555 U556 A557 U558 A559 U571 A572 A578 G579 A585 A589 G590 G591 G595 C596 G597 G604 A608 G609 G610 A611 G617 C618 A619 U620 A621 A622 U627 A628





• Molecule 31: 5S rRNA

Chain h: 83% 15% .



• Molecule 32: 5.8S rRNA

Chain i: 73% 23% .



• Molecule 33: 60S ribosomal protein L2-A

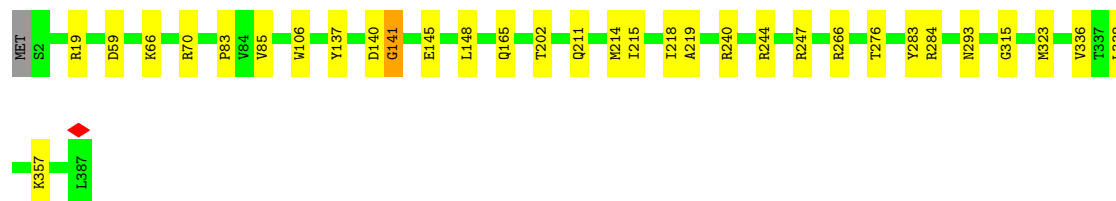
Chain j: 83% 13% .





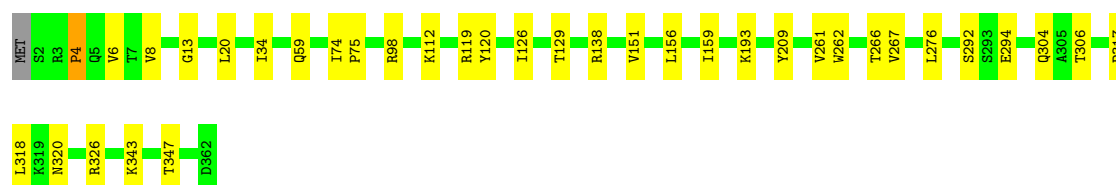
- Molecule 34: 60S ribosomal protein L3

Chain k: 91% 8%



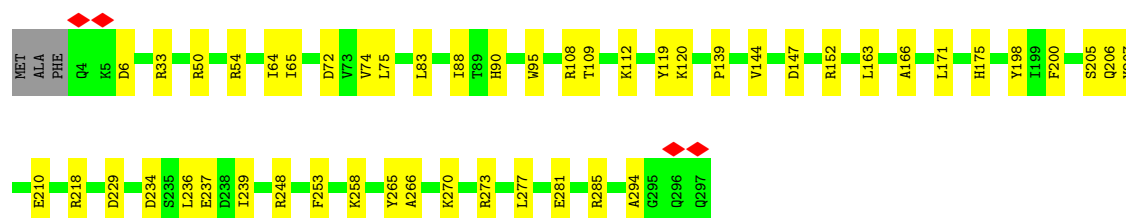
- Molecule 35: BJ4_G0008850.mRNA.1.CDS.1

Chain l: 90% 10%



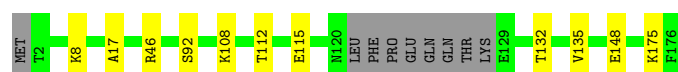
- Molecule 36: 60S ribosomal protein L5

Chain m: 82% 16%



- Molecule 37: 60S ribosomal protein L6-B

Chain n: 89% 6% 5%



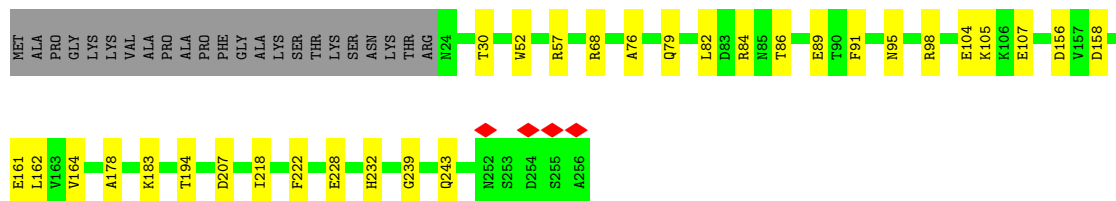
- Molecule 38: 60S ribosomal protein L7-A

Chain o: 85% 6% 9%



- Molecule 39: 60S ribosomal protein L8-A

Chain p:  79% 12% 9%



- Molecule 40: 60S ribosomal protein L9-A

Chain q:  87% 12% .



- Molecule 41: 60S ribosomal protein L10

Chain r:  87% 11% .



- Molecule 42: BJ4_G0027750.mRNA.1.CDS.1

Chain s:  87% 10% . .



- Molecule 43: 60S ribosomal protein L13-A

Chain t:  88% 9% .



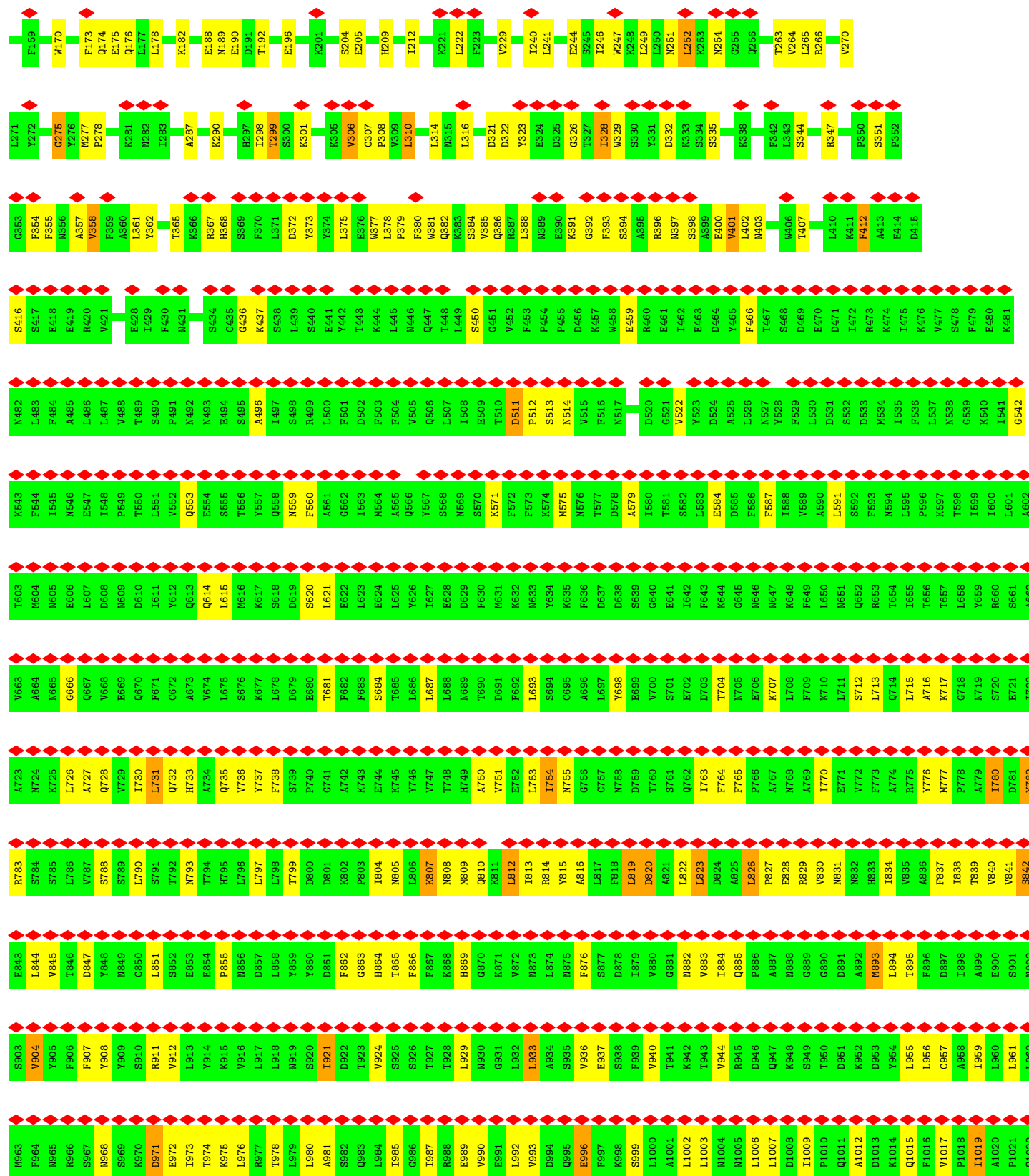
- Molecule 44: 60S ribosomal protein L14-A

Chain u:  88% 11% .



- Molecule 45: RQC2 isoform 1

Chain a:  14% 59% 20% 18%



PRO GLU SER ILE SER GLY ASN LEU ARG ASP THR LEU ILE GLU THR TYR SER

- Molecule 48: Eukaryotic translation initiation factor 5A-1

Chain v:



MET SER ASP GLU HIS THR PHE GLU THR ALA ASP ALA GLY SER S16 A17 T18 G30 T41 V42 D43 T46 S47 K48 T49 G50 K51 H52 G53 H54 A55 K56 V57 H58 L59 V60 E71 D72 L73 M80 P83 D86 N104 M105 D106 E117 E130 A154

R155 T156 D157

- Molecule 49: 60S ribosomal protein L1-A

Chain w:



MET S2 E22 N27 G37 P43 R48 F49 S50 P59 R60 I65 N96 L99 A109 R122 V138 L144 K147 V151 E152 S153 T154 F157 Q158 L159 L163 G202 S203 L204 K207 M210 R215 L216 Y217

- Molecule 50: P-site tRNA

Chain y:



G1 G2 G3 C4 G5 U6 G7 U8 G9 G10 U13 U14 A14 G15 U16 C17 G A21 G22 C23 C31 U32 U33 A34 G35 C36 A37 U38 G39 A42 G43 A44 G45 G46 U47 C48 G53 U54 U55 C56 G57 A58 U59 U60 C61 C62 G63 C68 C71 C74 C75 A76

- Molecule 51: 60S ribosomal protein L12-B

Chain z:



MET PRO LYS ASP PRO ASN V10 V18 G19 G20 E21 VAL GLY ALA SER ALA L28 A29 K51 E52 F53 K54 E57 P58 P59 R90 D91 K94 N97 M103 T104 Q105 R117 T124 V128 T135 A136 Q137 S138 V139 V143 D144 F145 K146 N147

T162 P163 ASN

- Molecule 52: 60S acidic ribosomal protein P0

Chain 0:



MET GLY G3 I4 F12 A13 K14 L15 L19 F26 V30 D31 N32 V33 S34 S35 Q36 R42 R43 F44 L45 R46 A49 V50 V51 L52 M53 T57 L67 L70 F73 G74 K75 L76 L77 P78 F79 V80 V87 F88 T89 L93 T94 E95 R104 V105 A106

A107 PRO ALA ARG ALA GLY VAL PRO PRO ASP ILE TRP VAL ARG ALA VAL ASN THR MET GLU PRO PRO GLY LYS THR SER PHE PHE GLN ALA LEU GLY VAL PRO THR LYS ILE ALA ARG GLY THR ILE GLU ILE VAL SER ASP VAL LYS VAL VAL VAL ASP ALA GLY ASN LYS VAL GLY

GLN	SER	GLU	ALA	SER	LEU	LEU	ASN	LEU	ASN	ILE	SER	PRO	PHE	THR	PHE	G184	Q189	D192	F197	P198	S199	SER	ILE	LEU	ASP	ILE	THR	ASP	GLU	GLU	LEU	VAL	SER	HIS	PHE	VAL	SER	ALA	ALA	VAL	SER	THR	ILE	ALA	SER	ILE	ALA	GLY	TYR	PRO	THR	LEU	PRO
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SER	VAL	GLY	HIS	THR	LEU	ILE	ASN	TYR	LYS	ASP	LEU	LEU	ALA	VAL	ALA	ILE	ALA	ALA	SER	TYR	HIS	TYR	PRO	GLU	ILE	GLU	ASP	LEU	VAL	ASP	ARG	ILE	GLU	ASN	PRO	GLU	LYS	TYR	ALA	ALA	ALA	PRO	ALA	ALA	THR	SER	ALA	ALA	SER	GLY	ASP	ALA	ALA	PRO	ALA	GLU
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ALA	ALA	ALA	GLU	GLU	GLU	GLU	GLU	SER	ASP	ASP	MET	GLY	PHE	GLY	PHE	ASP
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 53: CAT-tailed nascent peptide

Chain 1:

94%

6%

X41	X57	UNK
-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	44241	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	46	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.554	Depositor
Minimum map value	-0.671	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.128	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	476.55002, 476.55002, 476.55002	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SPD, MG, ZN, 5CT

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	A	0.31	0/1757	0.54	0/2354
2	B	0.31	0/1585	0.54	0/2128
3	C	0.33	0/1439	0.62	0/1938
4	D	0.28	0/1465	0.57	0/1965
5	E	0.29	0/1275	0.56	0/1702
6	F	0.31	0/1473	0.56	0/1980
7	G	0.27	0/1296	0.56	0/1739
8	H	0.29	0/812	0.75	2/1099 (0.2%)
9	I	0.27	0/1018	0.50	0/1369
10	J	0.27	0/530	0.52	0/703
11	K	0.31	0/979	0.57	0/1321
12	L	0.27	0/995	0.53	0/1329
13	M	0.27	0/1106	0.57	0/1485
14	N	0.32	0/1200	0.56	1/1607 (0.1%)
15	O	0.25	0/473	0.62	0/629
16	P	0.26	0/745	0.59	0/1001
17	Q	0.31	0/890	0.68	2/1196 (0.2%)
18	R	0.25	0/1034	0.47	0/1385
19	S	0.30	0/868	0.47	0/1168
20	T	0.29	0/890	0.58	2/1189 (0.2%)
21	U	0.27	0/978	0.53	0/1301
22	V	0.28	0/772	0.57	0/1026
23	W	0.32	0/660	0.60	0/875
24	X	0.28	0/618	0.65	1/826 (0.1%)
25	Y	0.29	0/443	0.46	0/588
26	Z	0.28	0/416	0.60	0/553
27	b	0.28	0/836	0.53	0/1104
28	c	0.27	0/701	0.56	0/934
29	d	0.22	0/208	0.81	2/267 (0.7%)
30	f	0.30	0/76989	0.39	5/120031 (0.0%)
31	h	0.26	0/2883	0.32	0/4491
32	i	0.30	0/3746	0.36	0/5832

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	j	0.36	0/1908	0.55	0/2564
34	k	0.29	0/3146	0.53	0/4228
35	l	0.29	0/2800	0.57	4/3790 (0.1%)
36	m	0.27	0/2400	0.57	0/3239
37	n	0.28	0/1329	0.60	0/1794
38	o	0.31	0/1821	0.58	0/2451
39	p	0.27	0/1836	0.58	1/2481 (0.0%)
40	q	0.30	0/1529	0.64	2/2060 (0.1%)
41	r	0.25	0/1801	0.49	0/2416
42	s	0.26	0/1367	0.69	4/1834 (0.2%)
43	t	0.29	0/1568	0.62	1/2106 (0.0%)
44	u	0.30	0/1068	0.53	0/1438
45	a	0.42	0/6679	0.83	16/9012 (0.2%)
46	e	0.42	0/11708	0.80	26/15899 (0.2%)
47	g	0.24	0/1672	0.58	1/2281 (0.0%)
48	v	0.31	0/1084	0.63	1/1456 (0.1%)
49	w	0.27	0/1736	0.61	0/2332
50	y	0.36	0/1735	0.65	0/2701
51	z	0.66	0/726	1.27	14/1006 (1.4%)
52	0	0.49	0/976	0.95	3/1313 (0.2%)
All	All	0.32	0/159969	0.52	88/233516 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
15	O	0	1
21	U	0	1
34	k	0	1
35	l	0	2
39	p	0	3
40	q	0	1
44	u	0	1
46	e	0	1
47	g	0	1
All	All	0	12

There are no bond length outliers.

All (88) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	51	GLY	CA-C-N	7.90	136.62	121.54
8	H	51	GLY	C-N-CA	7.90	136.62	121.54
48	v	53	GLY	N-CA-C	7.66	124.23	112.51
46	e	884	ILE	N-CA-C	-7.62	102.85	110.62
46	e	1298	GLY	N-CA-C	-7.43	104.97	115.30
51	z	87	GLU	CA-C-N	-7.37	112.79	120.38
51	z	87	GLU	C-N-CA	-7.37	112.79	120.38
45	a	603	LYS	N-CA-C	7.32	119.34	111.36
51	z	138	SER	N-CA-C	-7.29	103.27	111.14
46	e	132	PHE	N-CA-C	7.28	119.30	111.36
51	z	52	GLU	N-CA-C	-7.12	103.59	111.36
51	z	94	LYS	N-CA-C	-6.80	103.95	111.36
35	l	4	PRO	CA-C-N	6.72	134.38	121.54
35	l	4	PRO	C-N-CA	6.72	134.38	121.54
46	e	275	GLY	N-CA-C	-6.67	106.03	115.43
46	e	148	SER	N-CA-C	6.62	118.57	111.36
46	e	666	GLY	N-CA-C	-6.55	106.19	115.43
46	e	57	ARG	N-CA-C	6.53	118.39	111.28
45	a	583	SER	N-CA-C	-6.48	104.22	111.28
46	e	793	ASN	N-CA-C	-6.42	105.45	113.28
14	N	66	ALA	N-CA-C	-6.41	106.42	114.56
40	q	138	THR	CA-C-N	6.26	133.49	121.54
40	q	138	THR	C-N-CA	6.26	133.49	121.54
29	d	4	MET	CA-C-N	6.21	133.41	121.54
29	d	4	MET	C-N-CA	6.21	133.41	121.54
46	e	996	GLU	N-CA-C	6.21	118.05	111.28
46	e	1545	SER	N-CA-C	6.20	118.04	111.28
46	e	1391	ILE	N-CA-C	6.20	116.94	110.62
45	a	45	LYS	N-CA-C	-6.07	98.52	109.09
45	a	539	VAL	N-CA-C	6.05	116.79	110.62
51	z	124	THR	N-CA-C	5.90	117.71	111.28
45	a	45	LYS	CA-C-N	-5.89	113.47	119.83
45	a	45	LYS	C-N-CA	-5.89	113.47	119.83
45	a	648	ALA	N-CA-C	-5.89	104.86	111.28
46	e	553	GLN	N-CA-C	-5.85	100.05	108.60
45	a	59	ARG	N-CA-C	5.80	118.22	109.23
46	e	971	ASP	N-CA-C	5.74	117.53	111.28
46	e	204	SER	N-CA-C	-5.74	105.11	111.36
46	e	1364	GLY	N-CA-C	5.72	120.09	112.77
30	f	2541	U	P-O3'-C3'	5.71	128.76	120.20
47	g	171	GLU	N-CA-CB	5.68	119.09	110.28
46	e	306	VAL	N-CA-C	5.66	116.39	110.62
42	s	114	ILE	CA-C-N	5.60	132.23	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	s	114	ILE	C-N-CA	5.60	132.23	121.54
45	a	669	ASP	N-CA-C	5.56	117.47	108.41
46	e	1283	SER	N-CA-C	-5.56	101.07	109.85
46	e	436	GLY	N-CA-C	-5.54	104.75	112.18
46	e	1480	ILE	N-CA-C	5.52	116.29	110.72
42	s	7	ASN	N-CA-C	5.52	117.52	109.30
46	e	1516	HIS	N-CA-C	-5.48	102.17	110.28
46	e	1531	LYS	N-CA-C	5.47	117.24	111.28
43	t	136	GLU	CA-CB-CG	5.46	125.03	114.10
45	a	32	ILE	N-CA-C	5.45	115.74	108.11
20	T	94	LEU	CA-C-N	-5.43	112.77	121.35
20	T	94	LEU	C-N-CA	-5.43	112.77	121.35
42	s	108	GLU	CA-CB-CG	5.41	124.92	114.10
46	e	737	TYR	N-CA-C	5.41	120.57	112.94
45	a	334	ASN	N-CA-C	-5.41	105.47	111.36
30	f	2502	A	P-O3'-C3'	5.39	128.28	120.20
51	z	19	GLY	N-CA-C	5.35	119.39	112.54
45	a	96	ASP	CB-CA-C	-5.34	110.40	116.54
45	a	688	ASP	N-CA-C	5.33	117.09	111.28
30	f	282	G	C2'-C3'-O3'	5.33	121.69	113.70
52	0	94	THR	N-CA-C	5.32	117.08	111.28
45	a	127	GLU	N-CA-C	-5.32	105.48	111.28
51	z	29	ALA	N-CA-C	-5.31	105.62	113.16
30	f	1307	G	P-O3'-C3'	5.30	128.16	120.20
30	f	1815	U	P-O3'-C3'	5.30	128.15	120.20
17	Q	83	GLU	CA-C-N	5.29	131.65	121.54
17	Q	83	GLU	C-N-CA	5.29	131.65	121.54
51	z	117	ARG	N-CA-C	-5.22	105.59	111.28
39	p	79	GLN	CA-CB-CG	5.17	124.45	114.10
51	z	18	VAL	N-CA-C	-5.17	102.91	109.58
51	z	103	ASN	N-CA-C	5.16	117.03	109.24
35	l	317	PRO	CA-C-N	5.15	131.38	121.54
35	l	317	PRO	C-N-CA	5.15	131.38	121.54
52	0	89	THR	N-CA-C	5.12	117.76	109.06
46	e	511	ASP	CA-C-N	-5.10	113.46	119.84
46	e	511	ASP	C-N-CA	-5.10	113.46	119.84
51	z	139	VAL	N-CA-C	5.10	115.33	110.53
51	z	147	ASN	CA-C-N	-5.09	114.33	119.83
51	z	147	ASN	C-N-CA	-5.09	114.33	119.83
52	0	104	ARG	N-CA-C	5.09	118.46	111.54
24	X	67	GLN	N-CA-CB	5.08	118.67	110.40
45	a	439	LEU	CA-C-N	-5.05	114.60	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	a	439	LEU	C-N-CA	-5.05	114.60	119.90
46	e	736	VAL	N-CA-C	5.04	115.81	110.72
46	e	1365	CYS	N-CA-C	5.03	120.06	113.88

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	O	20	GLY	Peptide
21	U	83	LYS	Peptide
46	e	392	GLY	Peptide
47	g	8	GLU	Peptide
34	k	141	GLY	Peptide
35	l	13	GLY	Peptide
35	l	318	LEU	Peptide
39	p	158	ASP	Peptide
39	p	30	THR	Peptide
39	p	76	ALA	Peptide
40	q	21	LYS	Peptide
44	u	12	TRP	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1720	0	1779	18	0
2	B	1555	0	1659	17	0
3	C	1416	0	1433	14	0
4	D	1441	0	1543	15	0
5	E	1258	0	1342	11	0
6	F	1437	0	1475	20	0
7	G	1272	0	1312	13	0
8	H	796	0	812	14	0
9	I	1003	0	1048	10	0
10	J	518	0	542	6	0
11	K	964	0	1025	1	0
12	L	984	0	1075	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	M	1080	0	1122	7	0
14	N	1169	0	1211	14	0
15	O	462	0	491	9	0
16	P	737	0	792	4	0
17	Q	876	0	912	20	0
18	R	1013	0	1077	8	0
19	S	850	0	880	4	0
20	T	880	0	942	8	0
21	U	969	0	1078	5	0
22	V	766	0	844	7	0
23	W	645	0	645	12	0
24	X	612	0	682	6	0
25	Y	436	0	475	2	0
26	Z	410	0	442	5	0
27	b	824	0	888	11	0
28	c	694	0	734	8	0
29	d	207	0	250	3	0
30	f	68782	0	34563	332	0
31	h	2579	0	1304	9	0
32	i	3353	0	1695	13	0
33	j	1874	0	1943	25	0
34	k	3075	0	3142	20	0
35	l	2748	0	2859	23	0
36	m	2351	0	2294	31	0
37	n	1307	0	1377	8	0
38	o	1784	0	1862	10	0
39	p	1804	0	1877	17	0
40	q	1508	0	1572	16	0
41	r	1764	0	1804	17	0
42	s	1346	0	1370	9	0
43	t	1543	0	1608	14	0
44	u	1053	0	1149	11	0
45	a	6569	0	6459	291	0
46	e	11509	0	10765	598	0
47	g	1651	0	1613	22	0
48	v	1085	0	1087	16	0
49	w	1709	0	1799	17	0
50	y	1556	0	788	37	0
51	z	728	0	337	13	0
52	0	961	0	979	45	0
53	1	85	0	19	0	0
54	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	C	1	0	0	0	0
54	E	1	0	0	0	0
54	I	1	0	0	0	0
54	R	1	0	0	0	0
54	T	1	0	0	0	0
54	f	3	0	0	0	0
54	h	1	0	0	0	0
54	j	2	0	0	0	0
54	k	1	0	0	0	0
55	T	1	0	0	0	0
55	W	1	0	0	0	0
55	Z	1	0	0	0	0
55	b	1	0	0	0	0
55	c	1	0	0	0	0
55	e	2	0	0	0	0
56	f	10	0	19	1	0
All	All	149748	0	112794	1624	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (1624) 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)
46:e:684:SER:CB	46:e:715:LEU:HD13	1.16	1.63
45:a:705:TRP:CZ3	45:a:993:GLU:HG2	1.11	1.62
46:e:816:ALA:CA	46:e:819:LEU:HD21	1.13	1.61
46:e:992:LEU:HD12	46:e:996:GLU:CB	1.30	1.59
46:e:684:SER:CB	46:e:715:LEU:CD1	1.85	1.55
45:a:706:LYS:N	45:a:934:VAL:CG2	1.71	1.53
45:a:705:TRP:CZ3	45:a:993:GLU:CG	1.91	1.50
46:e:816:ALA:C	46:e:819:LEU:HD21	1.40	1.47
30:f:1259:A:C8	52:0:53:MET:HB2	1.51	1.46
45:a:705:TRP:CH2	45:a:993:GLU:CD	1.95	1.43
46:e:838:ILE:HG23	46:e:862:PHE:CD2	1.53	1.41
46:e:804:ILE:HD12	46:e:809:MET:SD	1.59	1.41
30:f:1258:U:H4'	52:0:42:ARG:NH1	1.26	1.40
46:e:804:ILE:HD12	46:e:809:MET:CE	1.50	1.40
45:a:185:ILE:CD1	45:a:254:LEU:O	1.72	1.36
46:e:750:ALA:O	46:e:754:ILE:HG23	1.21	1.36
30:f:1258:U:C4'	52:0:42:ARG:HH12	1.36	1.35

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:27:VAL:HA	46:e:1478:HIS:NE2	1.35	1.35
45:a:89:LEU:CD2	45:a:103:LEU:HD12	1.55	1.34
46:e:816:ALA:CA	46:e:819:LEU:CD2	2.07	1.33
45:a:188:VAL:CG1	45:a:251:CYS:HB3	1.58	1.33
46:e:815:TYR:O	46:e:819:LEU:CD2	1.75	1.32
46:e:819:LEU:O	46:e:823:LEU:CD2	1.77	1.32
45:a:706:LYS:O	45:a:934:VAL:CA	1.79	1.31
17:Q:110:GLU:CB	46:e:1424:ILE:HD12	1.61	1.31
45:a:89:LEU:HD21	45:a:103:LEU:CD1	1.61	1.30
45:a:706:LYS:CA	45:a:934:VAL:HG23	1.61	1.29
46:e:402:LEU:CD2	46:e:437:LYS:CB	2.10	1.29
45:a:185:ILE:HD13	45:a:254:LEU:C	1.58	1.27
45:a:664:ASN:O	45:a:684:LYS:HG3	1.16	1.27
46:e:765:PHE:CZ	46:e:822:LEU:CD1	2.04	1.27
46:e:838:ILE:HG21	46:e:863:GLY:O	1.32	1.27
46:e:816:ALA:HA	46:e:819:LEU:CD2	1.62	1.27
46:e:1081:ALA:HA	46:e:1084:LEU:CD1	1.64	1.27
46:e:1283:SER:OG	46:e:1286:MET:HG2	1.22	1.27
46:e:278:PRO:HG3	46:e:323:TYR:CE2	1.71	1.26
46:e:782:TYR:OH	46:e:1096:LEU:CG	1.82	1.26
46:e:823:LEU:CB	46:e:830:VAL:HG22	1.65	1.26
46:e:826:LEU:CD2	46:e:827:PRO:HD2	1.66	1.25
50:y:59:U:C2'	50:y:60:U:H5'	1.67	1.25
45:a:706:LYS:N	45:a:934:VAL:HG23	1.29	1.24
45:a:6:SER:HB3	45:a:9:ASP:CG	1.63	1.24
46:e:816:ALA:C	46:e:819:LEU:CD2	2.10	1.23
46:e:750:ALA:O	46:e:754:ILE:CG2	1.85	1.23
46:e:992:LEU:CD1	46:e:996:GLU:CB	2.20	1.19
46:e:251:ASN:OD1	46:e:254:ASN:CG	1.86	1.19
46:e:815:TYR:O	46:e:819:LEU:HD22	1.28	1.18
46:e:804:ILE:CD1	46:e:809:MET:SD	2.31	1.18
30:f:1257:C:H5'	51:z:124:THR:CB	1.74	1.18
46:e:1081:ALA:HA	46:e:1084:LEU:HD12	1.24	1.17
46:e:765:PHE:CZ	46:e:822:LEU:HD13	1.59	1.17
46:e:278:PRO:HG3	46:e:323:TYR:CZ	1.79	1.17
46:e:992:LEU:CD1	46:e:996:GLU:HB2	1.72	1.17
46:e:1283:SER:OG	46:e:1286:MET:CG	1.93	1.16
46:e:819:LEU:H	46:e:819:LEU:HD23	1.03	1.16
46:e:754:ILE:HG13	46:e:829:ARG:NH1	1.57	1.16
46:e:1307:ILE:HG21	46:e:1356:LEU:HD22	1.23	1.16
46:e:1184:ILE:HG23	46:e:1191:SER:HB2	1.26	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:a:185:ILE:HD13	45:a:254:LEU:O	1.00	1.15
46:e:782:TYR:CE1	46:e:1141:GLN:NE2	2.14	1.15
46:e:882:ASN:O	46:e:885:GLN:O	1.62	1.15
45:a:188:VAL:HG12	45:a:251:CYS:CB	1.75	1.15
45:a:246:ASP:HB2	45:a:249:GLU:HB2	1.17	1.15
46:e:782:TYR:OH	46:e:1096:LEU:HG	1.00	1.15
46:e:838:ILE:CG2	46:e:862:PHE:HD2	1.60	1.15
17:Q:110:GLU:HB2	46:e:1424:ILE:HD12	1.26	1.14
45:a:706:LYS:O	45:a:934:VAL:HA	1.00	1.14
46:e:278:PRO:CB	46:e:323:TYR:OH	1.95	1.14
46:e:278:PRO:CG	46:e:323:TYR:CZ	2.31	1.14
46:e:782:TYR:HE1	46:e:1141:GLN:NE2	1.44	1.14
45:a:706:LYS:N	45:a:934:VAL:HG21	1.54	1.13
46:e:1081:ALA:CA	46:e:1084:LEU:HD12	1.77	1.13
46:e:809:MET:HE2	46:e:844:LEU:HD11	1.27	1.13
46:e:819:LEU:O	46:e:823:LEU:HD23	1.40	1.13
50:y:22:G:OP2	50:y:46:G:O6	1.67	1.12
30:f:1259:A:C8	52:0:53:MET:CB	2.32	1.12
46:e:1087:CYS:SG	46:e:1099:ARG:HA	1.90	1.12
46:e:278:PRO:CG	46:e:323:TYR:OH	1.98	1.11
46:e:354:PHE:O	46:e:358:VAL:HG23	1.49	1.11
46:e:804:ILE:CD1	46:e:809:MET:CE	2.29	1.10
46:e:251:ASN:OD1	46:e:254:ASN:OD1	1.70	1.09
45:a:1:MET:O	45:a:309:PHE:CE2	2.04	1.09
46:e:1184:ILE:HG23	46:e:1191:SER:CB	1.82	1.09
30:f:1221:A:C2	52:0:12:PHE:HE2	1.69	1.08
45:a:660:CYS:SG	45:a:688:ASP:OD1	2.11	1.08
45:a:644:SER:OG	45:a:699:MET:CE	2.01	1.08
46:e:278:PRO:HB3	46:e:323:TYR:OH	1.52	1.08
45:a:188:VAL:CG1	45:a:251:CYS:CB	2.29	1.08
50:y:21:A:H3'	50:y:46:G:O6	1.55	1.07
46:e:591:LEU:CB	46:e:621:LEU:HA	1.85	1.07
46:e:826:LEU:HD23	46:e:827:PRO:CD	1.84	1.07
46:e:1080:LEU:O	46:e:1084:LEU:CD1	2.03	1.06
46:e:823:LEU:HB3	46:e:830:VAL:HG22	1.31	1.06
17:Q:110:GLU:HB3	46:e:1424:ILE:HD12	1.38	1.06
45:a:26:LEU:HD12	45:a:42:LYS:O	1.54	1.06
46:e:735:GLN:HG2	46:e:815:TYR:HB2	1.28	1.06
45:a:284:TYR:CE1	45:a:313:LYS:HB2	1.92	1.05
45:a:705:TRP:HZ3	45:a:993:GLU:CG	1.45	1.05
46:e:819:LEU:O	46:e:823:LEU:HD21	1.52	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:e:1290:PHE:O	46:e:1294:LEU:HD13	1.54	1.05
45:a:705:TRP:CH2	45:a:993:GLU:OE2	2.07	1.05
46:e:882:ASN:O	46:e:885:GLN:C	1.98	1.05
45:a:284:TYR:CB	45:a:314:PRO:HD3	1.85	1.04
45:a:649:TRP:HD1	45:a:650:SER:N	1.54	1.04
46:e:1516:HIS:HB3	46:e:1519:ASP:HB2	1.40	1.04
45:a:928:LEU:HD11	45:a:932:ASP:O	1.58	1.03
17:Q:110:GLU:CB	46:e:1424:ILE:CD1	2.34	1.03
46:e:402:LEU:HD23	46:e:437:LYS:CB	1.82	1.02
46:e:731:LEU:HD12	46:e:732:GLN:N	1.74	1.02
46:e:816:ALA:O	46:e:819:LEU:CD2	2.08	1.02
46:e:882:ASN:HA	46:e:885:GLN:O	1.59	1.02
45:a:664:ASN:O	45:a:684:LYS:CG	2.07	1.01
45:a:284:TYR:CD1	45:a:313:LYS:HB2	1.95	1.01
45:a:4:ARG:O	45:a:309:PHE:CZ	2.12	1.01
45:a:6:SER:HB3	45:a:9:ASP:OD2	1.58	1.01
50:y:59:U:O2'	50:y:60:U:H5'	1.58	1.01
45:a:644:SER:OG	45:a:699:MET:HE2	1.57	1.01
46:e:1090:ASP:HA	46:e:1095:LEU:HD13	1.42	1.01
45:a:142:GLU:CD	45:a:150:GLU:OE2	2.04	1.01
45:a:392:ILE:HD11	45:a:521:TYR:HE2	1.25	1.00
46:e:981:ALA:HB3	46:e:1023:ARG:HD3	1.37	1.00
45:a:705:TRP:CH2	45:a:993:GLU:CG	2.35	1.00
46:e:382:GLN:O	46:e:385:VAL:HG12	1.61	1.00
46:e:1087:CYS:SG	46:e:1099:ARG:CA	2.49	1.00
46:e:1303:MET:HG2	46:e:1359:LEU:CD2	1.91	1.00
8:H:27:VAL:CA	46:e:1478:HIS:NE2	2.26	0.99
46:e:992:LEU:HD12	46:e:996:GLU:HB3	1.44	0.99
30:f:1259:A:N7	52:0:53:MET:CB	2.25	0.99
45:a:284:TYR:HB3	45:a:314:PRO:HD3	1.45	0.98
46:e:882:ASN:C	46:e:885:GLN:O	2.06	0.98
45:a:625:PRO:HG2	45:a:921:LYS:HZ3	1.24	0.98
45:a:188:VAL:HG13	45:a:251:CYS:SG	2.03	0.98
45:a:930:LYS:O	45:a:930:LYS:HG2	1.62	0.98
45:a:705:TRP:CE3	45:a:937:ILE:HD13	1.99	0.97
45:a:625:PRO:HG2	45:a:921:LYS:NZ	1.77	0.97
46:e:782:TYR:HH	46:e:1096:LEU:HG	1.17	0.97
30:f:1259:A:H8	52:0:53:MET:HB2	1.29	0.97
46:e:819:LEU:CD2	46:e:819:LEU:H	1.78	0.97
46:e:812:LEU:O	46:e:812:LEU:HD23	1.64	0.96
46:e:684:SER:CB	46:e:715:LEU:HD11	1.93	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:e:1080:LEU:O	46:e:1084:LEU:HD12	1.63	0.96
46:e:1178:VAL:HA	46:e:1184:ILE:HD11	1.48	0.95
30:f:1258:U:P	52:0:46:ARG:HH22	1.89	0.95
45:a:1:MET:O	45:a:309:PHE:CD2	2.18	0.95
46:e:1279:PHE:CZ	46:e:1294:LEU:HD21	2.01	0.95
45:a:220:ILE:CB	45:a:249:GLU:HB3	1.97	0.94
46:e:402:LEU:HD21	46:e:437:LYS:CB	1.97	0.94
45:a:649:TRP:CD1	45:a:650:SER:N	2.35	0.94
46:e:812:LEU:HD23	46:e:812:LEU:C	1.91	0.94
45:a:705:TRP:CZ3	45:a:993:GLU:CD	2.34	0.94
46:e:823:LEU:HB2	46:e:830:VAL:HG22	1.48	0.94
46:e:804:ILE:CD1	46:e:809:MET:HE1	1.98	0.94
46:e:882:ASN:CA	46:e:885:GLN:O	2.16	0.94
46:e:826:LEU:CD2	46:e:827:PRO:CD	2.45	0.93
30:f:1257:C:O3'	52:0:46:ARG:NH2	2.02	0.93
46:e:1178:VAL:HA	46:e:1184:ILE:CD1	1.97	0.93
46:e:816:ALA:HA	46:e:819:LEU:HD21	0.94	0.93
46:e:819:LEU:HD23	46:e:819:LEU:N	1.81	0.93
50:y:59:U:H2'	50:y:60:U:O4'	1.67	0.93
46:e:354:PHE:O	46:e:358:VAL:CG2	2.16	0.92
45:a:705:TRP:HB2	45:a:928:LEU:HD23	1.49	0.92
45:a:4:ARG:O	45:a:309:PHE:HZ	1.47	0.92
50:y:59:U:H2'	50:y:60:U:H5'	1.51	0.92
46:e:936:VAL:O	46:e:940:VAL:HG23	1.70	0.91
46:e:838:ILE:HG23	46:e:862:PHE:HD2	0.75	0.91
45:a:375:ILE:HG23	45:a:532:GLN:HE21	1.33	0.91
46:e:1279:PHE:HZ	46:e:1294:LEU:HD21	1.35	0.91
46:e:1178:VAL:HG22	46:e:1184:ILE:HD11	1.52	0.91
17:Q:110:GLU:HB2	46:e:1424:ILE:CD1	1.97	0.91
46:e:1340:TYR:O	46:e:1344:ILE:HG12	1.70	0.91
45:a:284:TYR:CG	45:a:313:LYS:HA	2.07	0.90
15:O:16:ALA:O	15:O:20:GLY:HA3	1.69	0.90
46:e:937:GLU:HG3	46:e:972:GLU:HB3	1.53	0.90
45:a:142:GLU:CG	45:a:150:GLU:OE2	2.20	0.90
45:a:284:TYR:HB2	45:a:314:PRO:HD3	1.54	0.90
30:f:1222:G:OP2	52:0:57:THR:OG1	1.90	0.89
46:e:826:LEU:HD23	46:e:827:PRO:HD2	0.92	0.89
30:f:1258:U:O5'	52:0:42:ARG:NH1	2.04	0.89
45:a:1003:GLN:HE21	45:a:1003:GLN:N	1.71	0.89
46:e:809:MET:CE	46:e:844:LEU:HD11	2.02	0.89
45:a:284:TYR:HB2	45:a:313:LYS:HA	1.55	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:a:951:LYS:NZ	45:a:990:TRP:CZ2	2.41	0.89
46:e:1087:CYS:SG	46:e:1099:ARG:HB2	2.14	0.88
46:e:815:TYR:O	46:e:819:LEU:HD23	1.70	0.88
46:e:1087:CYS:SG	46:e:1099:ARG:CB	2.62	0.88
46:e:944:VAL:HG21	46:e:980:LEU:HD21	1.54	0.88
45:a:884:MET:SD	45:a:884:MET:C	2.57	0.88
46:e:819:LEU:C	46:e:823:LEU:HD21	1.98	0.88
46:e:1307:ILE:CG2	46:e:1356:LEU:HD22	2.02	0.87
30:f:1258:U:C5'	52:0:42:ARG:HH12	1.86	0.87
45:a:188:VAL:CG1	45:a:251:CYS:SG	2.61	0.87
45:a:705:TRP:HH2	45:a:993:GLU:CD	1.81	0.87
45:a:284:TYR:CB	45:a:313:LYS:HA	2.04	0.87
46:e:971:ASP:O	46:e:975:LYS:HG3	1.73	0.87
45:a:284:TYR:HB3	45:a:314:PRO:CD	2.05	0.87
50:y:59:U:C2'	50:y:60:U:C5'	2.53	0.87
46:e:782:TYR:HE2	46:e:1096:LEU:HB2	1.40	0.86
46:e:815:TYR:C	46:e:819:LEU:CD2	2.47	0.86
45:a:309:PHE:CD1	45:a:309:PHE:O	2.28	0.86
46:e:809:MET:HE2	46:e:844:LEU:CD1	2.04	0.86
46:e:251:ASN:OD1	46:e:254:ASN:ND2	2.08	0.86
45:a:392:ILE:HD11	45:a:521:TYR:CE2	2.11	0.85
45:a:928:LEU:CD1	45:a:932:ASP:O	2.24	0.85
46:e:754:ILE:CG1	46:e:829:ARG:NH1	2.37	0.85
46:e:981:ALA:CB	46:e:1023:ARG:HD3	2.05	0.85
45:a:246:ASP:HB2	45:a:249:GLU:CB	2.06	0.85
45:a:649:TRP:CD1	45:a:649:TRP:C	2.53	0.85
46:e:782:TYR:CE2	46:e:1096:LEU:HB2	2.12	0.85
45:a:685:ASN:HB2	45:a:688:ASP:OD2	1.77	0.85
30:f:1221:A:C2	52:0:12:PHE:CE2	2.62	0.84
45:a:706:LYS:O	45:a:934:VAL:CB	2.24	0.84
50:y:59:U:H2'	50:y:60:U:C4'	2.08	0.84
45:a:705:TRP:CZ3	45:a:937:ILE:HD13	2.13	0.84
46:e:266:ARG:O	46:e:270:VAL:HG23	1.76	0.84
46:e:384:SER:O	46:e:388:LEU:HG	1.75	0.84
46:e:1184:ILE:CG2	46:e:1191:SER:HB2	2.05	0.84
50:y:59:U:H2'	50:y:60:U:C5'	2.06	0.84
45:a:644:SER:OG	45:a:699:MET:HE3	1.76	0.84
45:a:415:ASP:HB3	45:a:418:THR:HG23	1.60	0.84
46:e:731:LEU:HD12	46:e:731:LEU:C	2.03	0.84
46:e:750:ALA:C	46:e:754:ILE:HG23	2.02	0.83
30:f:1259:A:N7	52:0:53:MET:HG3	1.92	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:a:89:LEU:HD13	45:a:89:LEU:C	2.03	0.83
46:e:944:VAL:HG11	46:e:980:LEU:HD23	1.60	0.83
46:e:1080:LEU:HD21	46:e:1106:TYR:HB2	1.59	0.83
46:e:992:LEU:CD1	46:e:996:GLU:HB3	1.99	0.83
46:e:1066:ARG:NE	46:e:1111:GLN:NE2	2.27	0.83
30:f:1258:U:H4'	52:0:42:ARG:HH12	0.66	0.83
46:e:820:ASP:HB2	46:e:838:ILE:HD11	1.60	0.83
46:e:1316:THR:O	46:e:1390:PHE:HZ	1.60	0.83
46:e:1327:ILE:HD13	46:e:1390:PHE:HB3	1.59	0.83
46:e:388:LEU:O	46:e:391:LYS:O	1.97	0.82
46:e:1081:ALA:HA	46:e:1084:LEU:HD13	1.60	0.82
45:a:706:LYS:CB	45:a:934:VAL:HG23	2.09	0.82
46:e:321:ASP:CG	46:e:329:TRP:HE1	1.87	0.82
46:e:804:ILE:HD12	46:e:809:MET:HE3	1.62	0.82
45:a:350:ALA:O	45:a:354:GLN:HG3	1.79	0.82
45:a:188:VAL:HG12	45:a:251:CYS:HB3	0.82	0.81
46:e:820:ASP:O	46:e:823:LEU:HG	1.79	0.81
46:e:1081:ALA:CA	46:e:1084:LEU:CD1	2.45	0.81
46:e:1303:MET:HG2	46:e:1359:LEU:HD22	1.60	0.81
30:f:1229:G:H4'	52:0:32:ASN:OD1	1.79	0.81
45:a:930:LYS:O	45:a:930:LYS:CG	2.29	0.81
45:a:928:LEU:HD11	45:a:932:ASP:C	2.06	0.81
46:e:815:TYR:C	46:e:819:LEU:HD22	2.06	0.81
46:e:1335:ASN:OD1	46:e:1338:SER:HB2	1.81	0.81
30:f:1222:G:N7	52:0:57:THR:HB	1.96	0.81
46:e:275:GLY:C	46:e:278:PRO:HD2	2.05	0.81
46:e:1444:LYS:HD2	46:e:1455:GLN:HE21	1.46	0.80
45:a:6:SER:CB	45:a:9:ASP:OD2	2.29	0.80
46:e:684:SER:CA	46:e:715:LEU:HD13	2.11	0.80
46:e:992:LEU:HD12	46:e:996:GLU:HB2	0.80	0.80
46:e:1279:PHE:HE1	46:e:1290:PHE:HB3	1.45	0.80
46:e:838:ILE:CG2	46:e:862:PHE:CD2	2.46	0.80
46:e:782:TYR:CZ	46:e:1141:GLN:NE2	2.50	0.79
46:e:838:ILE:CD1	46:e:864:HIS:HB2	2.11	0.79
46:e:1283:SER:HG	46:e:1286:MET:HG2	1.45	0.79
8:H:27:VAL:HG12	46:e:1478:HIS:CD2	2.17	0.79
45:a:412:GLN:O	45:a:413:GLN:HB2	1.80	0.79
45:a:595:ALA:O	45:a:599:GLN:HG3	1.83	0.79
46:e:1279:PHE:CE1	46:e:1290:PHE:HB3	2.17	0.79
45:a:705:TRP:CZ2	45:a:993:GLU:OE2	2.37	0.78
46:e:1066:ARG:CZ	46:e:1111:GLN:NE2	2.46	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:e:765:PHE:CE2	46:e:822:LEU:HD13	2.19	0.78
46:e:805:ASN:O	46:e:809:MET:HG3	1.83	0.78
45:a:26:LEU:CD1	45:a:42:LYS:O	2.30	0.78
46:e:816:ALA:O	46:e:819:LEU:HD21	1.79	0.78
45:a:706:LYS:C	45:a:934:VAL:HG23	2.09	0.77
46:e:809:MET:CE	46:e:844:LEU:CD1	2.62	0.77
30:f:1259:A:N7	52:0:53:MET:CG	2.47	0.77
46:e:750:ALA:O	46:e:754:ILE:HG22	1.83	0.77
30:f:1258:U:C5'	52:0:42:ARG:NH1	2.46	0.77
46:e:1432:TYR:OH	46:e:1441:ILE:CG2	2.32	0.77
45:a:644:SER:CB	45:a:699:MET:HE3	2.14	0.77
46:e:944:VAL:CG2	46:e:980:LEU:HD21	2.15	0.77
46:e:1178:VAL:CG2	46:e:1184:ILE:HD11	2.15	0.77
45:a:89:LEU:HD21	45:a:103:LEU:HD12	0.78	0.76
46:e:1090:ASP:HA	46:e:1095:LEU:CD1	2.15	0.76
45:a:1003:GLN:HE21	45:a:1003:GLN:H	1.33	0.76
46:e:681:THR:HA	46:e:715:LEU:HD21	1.68	0.76
45:a:284:TYR:CD1	45:a:313:LYS:CB	2.69	0.76
46:e:1080:LEU:C	46:e:1084:LEU:CD1	2.59	0.75
46:e:992:LEU:HD12	46:e:996:GLU:CG	2.13	0.75
45:a:928:LEU:CD1	45:a:932:ASP:HB2	2.16	0.75
46:e:820:ASP:HB2	46:e:838:ILE:CD1	2.15	0.75
46:e:1291:ILE:HD13	46:e:1484:ASN:HD22	1.51	0.75
46:e:1316:THR:O	46:e:1390:PHE:CZ	2.39	0.75
46:e:278:PRO:HG2	46:e:323:TYR:CZ	2.22	0.75
45:a:389:GLY:O	45:a:393:ILE:HG13	1.87	0.74
46:e:251:ASN:HB3	46:e:254:ASN:HB2	1.69	0.74
45:a:928:LEU:HD13	45:a:932:ASP:HB2	1.69	0.74
46:e:205:GLU:O	46:e:209:HIS:ND1	2.20	0.74
46:e:812:LEU:C	46:e:812:LEU:CD2	2.59	0.74
45:a:408:GLY:O	45:a:412:GLN:HG3	1.87	0.74
45:a:951:LYS:NZ	45:a:990:TRP:CE2	2.55	0.74
46:e:866:PHE:HD1	46:e:893:MET:HB3	1.52	0.74
45:a:90:THR:HB	45:a:104:GLN:CB	2.17	0.74
45:a:881:GLU:OE2	45:a:881:GLU:CA	2.36	0.74
46:e:782:TYR:OH	46:e:1141:GLN:NE2	2.21	0.74
46:e:1287:ARG:HA	46:e:1290:PHE:HD2	1.52	0.74
46:e:816:ALA:O	46:e:819:LEU:HG	1.88	0.74
46:e:513:SER:N	46:e:559:ASN:CB	2.51	0.73
46:e:788:SER:HB2	46:e:911:ARG:HD3	1.69	0.73
50:y:53:G:C6	50:y:54:U:C4	2.75	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:f:1258:U:C4'	52:0:42:ARG:NH1	2.13	0.73
46:e:804:ILE:CG1	46:e:809:MET:SD	2.76	0.73
15:O:16:ALA:O	15:O:20:GLY:CA	2.36	0.73
45:a:1002:GLU:N	45:a:1002:GLU:OE1	2.19	0.73
46:e:1279:PHE:HZ	46:e:1294:LEU:CD2	2.01	0.73
46:e:684:SER:CA	46:e:715:LEU:CD1	2.66	0.73
46:e:1191:SER:O	46:e:1195:THR:OG1	2.06	0.73
46:e:981:ALA:HB1	46:e:1023:ARG:HG2	1.71	0.72
51:z:105:GLN:HA	51:z:143:VAL:HA	1.71	0.72
46:e:1307:ILE:HG21	46:e:1356:LEU:CD2	2.12	0.72
45:a:589:MET:HE2	45:a:589:MET:HA	1.70	0.72
46:e:981:ALA:HB1	46:e:1023:ARG:CG	2.20	0.72
45:a:544:LYS:O	45:a:548:VAL:HG23	1.90	0.72
46:e:816:ALA:O	46:e:819:LEU:CG	2.37	0.72
46:e:838:ILE:HD12	46:e:864:HIS:HB2	1.72	0.72
46:e:278:PRO:HG2	46:e:323:TYR:OH	1.87	0.72
46:e:1080:LEU:C	46:e:1084:LEU:HD12	2.15	0.72
45:a:589:MET:HA	45:a:589:MET:CE	2.20	0.71
46:e:816:ALA:C	46:e:819:LEU:HD23	2.11	0.71
17:Q:110:GLU:HB3	46:e:1424:ILE:CD1	2.12	0.71
46:e:27:LEU:HB2	46:e:188:GLU:OE2	1.91	0.71
46:e:820:ASP:HA	46:e:823:LEU:CG	2.21	0.71
46:e:713:LEU:O	46:e:717:LYS:HG3	1.91	0.71
40:q:92:TYR:HB2	40:q:142:ASP:HB3	1.73	0.71
46:e:466:PHE:HA	46:e:522:VAL:CB	2.21	0.71
46:e:1144:ASN:HA	46:e:1339:PRO:HG2	1.71	0.71
45:a:705:TRP:CB	45:a:928:LEU:HD23	2.20	0.70
46:e:1303:MET:HA	46:e:1303:MET:HE3	1.72	0.70
46:e:1184:ILE:HG23	46:e:1191:SER:HB3	1.71	0.70
45:a:220:ILE:CB	45:a:249:GLU:O	2.40	0.70
8:H:27:VAL:HG12	46:e:1478:HIS:CG	2.27	0.70
45:a:414:MET:HG2	45:a:418:THR:OG1	1.91	0.70
46:e:838:ILE:CG2	46:e:863:GLY:O	2.27	0.70
46:e:1427:GLU:CD	46:e:1442:SER:HB2	2.16	0.70
30:f:1219:C:OP1	52:0:4:ILE:HG21	1.92	0.69
30:f:1018:G:H1	30:f:1034:U:H3	1.38	0.69
45:a:387:ARG:HG2	45:a:391:LEU:HD11	1.75	0.69
46:e:1015:GLN:HG2	46:e:1063:GLU:HB2	1.73	0.69
46:e:823:LEU:HD12	46:e:864:HIS:ND1	2.07	0.69
46:e:1335:ASN:OD1	46:e:1335:ASN:O	2.10	0.69
45:a:625:PRO:CG	45:a:921:LYS:NZ	2.55	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:a:664:ASN:HA	45:a:684:LYS:HD2	1.72	0.69
45:a:881:GLU:OE2	45:a:881:GLU:N	2.25	0.69
46:e:684:SER:CB	46:e:715:LEU:CG	2.71	0.69
23:W:21:ARG:HE	23:W:39:TYR:HB2	1.58	0.69
45:a:644:SER:HG	45:a:699:MET:HE2	1.57	0.69
46:e:838:ILE:HD12	46:e:864:HIS:CB	2.23	0.69
46:e:1432:TYR:OH	46:e:1441:ILE:HG22	1.91	0.69
46:e:1506:GLU:OE1	46:e:1532:ASN:HA	1.92	0.69
30:f:2193:U:H5'	30:f:2194:G:H5'	1.75	0.69
46:e:816:ALA:N	46:e:819:LEU:HD21	2.03	0.69
46:e:118:VAL:O	46:e:122:ARG:HB3	1.93	0.68
2:B:46[A]:GLU:HB3	2:B:49[A]:ARG:HG3	1.75	0.68
8:H:27:VAL:HA	46:e:1478:HIS:CE1	2.22	0.68
45:a:89:LEU:C	45:a:89:LEU:CD1	2.67	0.68
52:0:26:PHE:HB2	52:0:87:VAL:HB	1.73	0.68
50:y:59:U:C3'	50:y:60:U:H5'	2.23	0.68
46:e:251:ASN:CG	46:e:254:ASN:CG	2.60	0.68
30:f:1242:G:H22	45:a:519:THR:HG22	1.59	0.68
46:e:937:GLU:CG	46:e:972:GLU:HB3	2.22	0.68
46:e:104:LYS:H	47:g:1:MET:HE3	1.59	0.68
46:e:838:ILE:O	46:e:842:SER:OG	2.11	0.68
45:a:392:ILE:CD1	45:a:521:TYR:CE2	2.77	0.68
30:f:1222:G:C8	52:0:57:THR:HB	2.29	0.68
46:e:372:ASP:HB3	46:e:375:LEU:HB2	1.76	0.68
46:e:1178:VAL:HG22	46:e:1184:ILE:CD1	2.23	0.68
46:e:1476:THR:HG23	46:e:1490:SER:HB3	1.73	0.67
46:e:1427:GLU:OE1	46:e:1442:SER:CB	2.41	0.67
45:a:943:PRO:HB2	45:a:945:PRO:HD2	1.75	0.67
46:e:820:ASP:HA	46:e:823:LEU:HD11	1.76	0.67
46:e:1303:MET:HA	46:e:1303:MET:CE	2.25	0.67
49:w:138:VAL:HG23	49:w:147:LYS:HD2	1.75	0.67
46:e:838:ILE:HD13	46:e:863:GLY:O	1.93	0.67
50:y:22:G:OP2	50:y:46:G:C6	2.47	0.67
45:a:705:TRP:CZ3	45:a:993:GLU:OE2	2.44	0.67
46:e:1279:PHE:HE1	46:e:1290:PHE:CB	2.06	0.67
46:e:1404:ASN:HA	46:e:1407:MET:HE3	1.76	0.67
46:e:591:LEU:CB	46:e:620:SER:O	2.43	0.67
50:y:1:G:H2'	50:y:2:G:C8	2.29	0.67
46:e:1009:ILE:HB	46:e:1012:ALA:HB2	1.77	0.67
46:e:1192:ARG:HG2	46:e:1270:TRP:CH2	2.29	0.67
46:e:1427:GLU:OE2	46:e:1444:LYS:CE	2.42	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:y:53:G:C5	50:y:54:U:C5	2.82	0.67
45:a:928:LEU:HD12	45:a:990:TRP:CZ3	2.24	0.66
46:e:170:TRP:HE3	46:e:222:LEU:HD13	1.60	0.66
46:e:684:SER:CB	46:e:715:LEU:CD2	2.73	0.66
30:f:1222:G:C8	52:0:57:THR:CB	2.79	0.66
45:a:309:PHE:O	45:a:309:PHE:HD1	1.78	0.66
46:e:816:ALA:HB2	46:e:837:PHE:HE2	1.58	0.66
46:e:1474:MET:O	46:e:1478:HIS:N	2.27	0.66
30:f:1240:A:OP1	51:z:97:ASN:O	2.14	0.66
30:f:1254:C:O2	51:z:135:THR:CB	2.43	0.66
45:a:506:VAL:HG13	45:a:521:TYR:OH	1.95	0.66
46:e:1081:ALA:C	46:e:1084:LEU:HD12	2.20	0.66
45:a:6:SER:HB3	45:a:9:ASP:OD1	1.95	0.66
46:e:1427:GLU:OE1	46:e:1442:SER:HB2	1.95	0.66
30:f:1222:G:C8	52:0:57:THR:HG21	2.31	0.66
30:f:1258:U:P	52:0:46:ARG:NH2	2.64	0.66
45:a:426:GLU:HB3	45:a:434:ALA:HB2	1.77	0.66
46:e:205:GLU:C	46:e:209:HIS:HD1	2.03	0.66
45:a:848:GLN:O	45:a:852:ALA:HB2	1.96	0.66
30:f:1940:G:H21	30:f:3362:A:H8	1.44	0.66
45:a:426:GLU:CB	45:a:434:ALA:HB2	2.26	0.66
45:a:284:TYR:CD1	45:a:313:LYS:HA	2.30	0.66
45:a:284:TYR:CD1	45:a:313:LYS:CA	2.78	0.66
46:e:1279:PHE:CZ	46:e:1294:LEU:CD2	2.78	0.66
30:f:1221:A:N3	52:0:12:PHE:HE2	1.93	0.65
46:e:839:THR:HB	46:e:866:PHE:H	1.60	0.65
30:f:2969:A:N7	33:j:215:ASN:ND2	2.42	0.65
46:e:1066:ARG:CZ	46:e:1111:GLN:HE21	2.06	0.65
30:f:1238:C:H4'	51:z:139:VAL:CB	2.27	0.65
45:a:426:GLU:CB	45:a:434:ALA:CB	2.74	0.65
46:e:754:ILE:CD1	46:e:829:ARG:HH11	2.09	0.65
46:e:1410:LEU:HD23	46:e:1419:ILE:HD11	1.76	0.65
30:f:3018:C:OP1	47:g:9:ASN:ND2	2.29	0.65
46:e:1050:LEU:HD11	46:e:1097:GLU:HB3	1.77	0.65
46:e:981:ALA:HB3	46:e:1023:ARG:CD	2.20	0.65
30:f:687:U:OP2	43:t:36:ARG:NH2	2.30	0.65
46:e:750:ALA:C	46:e:754:ILE:CG2	2.67	0.65
45:a:660:CYS:SG	45:a:688:ASP:CG	2.79	0.65
7:G:84:TYR:HB2	15:O:24:PRO:HD3	1.78	0.64
46:e:1283:SER:OG	46:e:1286:MET:HG3	1.94	0.64
45:a:1003:GLN:N	45:a:1003:GLN:NE2	2.43	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:e:1441:ILE:CD1	46:e:1443:PHE:CE1	2.81	0.64
45:a:705:TRP:C	45:a:934:VAL:HG21	2.22	0.64
46:e:1080:LEU:O	46:e:1084:LEU:CG	2.46	0.64
46:e:402:LEU:HD22	46:e:437:LYS:CB	2.23	0.64
45:a:246:ASP:CB	45:a:249:GLU:HB2	2.11	0.64
45:a:426:GLU:HB2	45:a:434:ALA:CB	2.27	0.64
45:a:863:LEU:HB3	45:a:869:LEU:HG	1.80	0.64
46:e:764:PHE:HB3	46:e:822:LEU:CD1	2.28	0.64
46:e:820:ASP:HA	46:e:823:LEU:CD1	2.28	0.64
46:e:1080:LEU:HD21	46:e:1106:TYR:CB	2.26	0.64
46:e:60:THR:O	46:e:64:LYS:HG3	1.98	0.64
46:e:1303:MET:HG2	46:e:1359:LEU:HD21	1.79	0.64
50:y:62:C:H2'	50:y:63:G:H8	1.63	0.64
46:e:542:GLY:HA2	46:e:579:ALA:HB2	1.80	0.63
2:B:27[A]:LEU:HD21	2:B:102[A]:LEU:HB2	1.80	0.63
45:a:185:ILE:HD11	45:a:254:LEU:O	1.88	0.63
46:e:816:ALA:N	46:e:819:LEU:CD2	2.62	0.63
50:y:22:G:P	50:y:46:G:O6	2.56	0.63
46:e:820:ASP:HA	46:e:823:LEU:HG	1.80	0.63
46:e:797:LEU:HD13	46:e:907:PHE:HD1	1.63	0.63
9:I:12:ARG:NH1	30:f:3041:U:OP1	2.32	0.63
47:g:111:ASN:ND2	47:g:114:VAL:O	2.32	0.63
45:a:884:MET:HE1	45:a:885:LYS:CG	2.29	0.63
46:e:944:VAL:CG1	46:e:980:LEU:HD23	2.28	0.63
46:e:1327:ILE:CD1	46:e:1390:PHE:HB3	2.28	0.63
17:Q:110:GLU:CG	46:e:1424:ILE:CD1	2.77	0.63
46:e:118:VAL:O	46:e:122:ARG:N	2.31	0.63
46:e:831:ASN:HB2	46:e:834:ILE:HG13	1.79	0.63
46:e:1017:VAL:HG13	46:e:1065:VAL:HG22	1.81	0.63
46:e:1282:THR:OG1	46:e:1287:ARG:HB2	1.99	0.63
46:e:1444:LYS:HD2	46:e:1455:GLN:NE2	2.13	0.63
45:a:928:LEU:CD1	45:a:932:ASP:N	2.62	0.62
46:e:1178:VAL:CA	46:e:1184:ILE:HD11	2.28	0.62
45:a:529:ALA:O	45:a:533:LYS:HG2	1.98	0.62
28:c:87:ARG:NH1	33:j:97:ASN:OD1	2.33	0.62
45:a:375:ILE:HG23	45:a:532:GLN:NE2	2.12	0.62
29:d:4:MET:N	30:f:1802:C:OP1	2.32	0.62
30:f:2442:G:H1	30:f:2505:U:H3	1.46	0.62
13:M:27:LYS:HB3	13:M:42:LEU:HB2	1.81	0.62
30:f:1232:C:O2'	52:0:36:GLN:NE2	2.31	0.62
46:e:1187:ASN:HB3	46:e:1190:GLN:HB3	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:e:820:ASP:C	46:e:823:LEU:HG	2.24	0.62
45:a:188:VAL:O	45:a:191:LYS:HG2	1.99	0.62
5:E:43:LYS:NZ	30:f:1764:U:OP1	2.31	0.62
45:a:431:ASN:O	45:a:435:GLN:HG3	1.99	0.62
46:e:1168:GLU:O	46:e:1171:TYR:HB3	1.99	0.62
9:I:14:SER:O	9:I:81:GLN:NE2	2.33	0.62
46:e:782:TYR:HE1	46:e:1141:GLN:HE22	0.68	0.61
45:a:58:LEU:HD13	45:a:59:ARG:NH2	2.15	0.61
46:e:826:LEU:HD22	46:e:827:PRO:CD	2.30	0.61
46:e:102:ASP:OD1	46:e:102:ASP:N	2.30	0.61
46:e:1035:LEU:HD13	46:e:1078:ARG:HD2	1.82	0.61
46:e:1495:THR:O	46:e:1499:HIS:CD2	2.52	0.61
23:W:21:ARG:HG2	32:i:103:G:H4'	1.82	0.61
30:f:1221:A:N3	52:0:12:PHE:CE2	2.67	0.61
46:e:105:VAL:HG22	47:g:1:MET:HE1	1.81	0.61
46:e:805:ASN:HB3	46:e:807:LYS:HE3	1.81	0.61
45:a:928:LEU:HD11	45:a:932:ASP:CA	2.31	0.61
30:f:3348:G:H1	30:f:3357:U:H3	1.48	0.61
46:e:1184:ILE:CG2	46:e:1191:SER:CB	2.67	0.61
46:e:1192:ARG:HG2	46:e:1270:TRP:CZ2	2.36	0.61
46:e:1441:ILE:HD13	46:e:1443:PHE:CE1	2.34	0.61
46:e:321:ASP:OD1	46:e:321:ASP:C	2.43	0.61
46:e:731:LEU:C	46:e:731:LEU:CD1	2.72	0.61
30:f:1348:U:O2	30:f:1349:G:N2	2.34	0.61
45:a:25:ARG:HA	45:a:88:ARG:HA	1.80	0.61
46:e:782:TYR:OH	46:e:1096:LEU:CD1	2.48	0.61
30:f:1235:U:O4	51:z:136:ALA:HA	2.00	0.61
36:m:50:ARG:NH1	36:m:147:ASP:OD2	2.34	0.61
46:e:816:ALA:HB2	46:e:837:PHE:CE2	2.36	0.61
38:o:87:VAL:HG11	38:o:243:MET:HE1	1.83	0.61
46:e:823:LEU:HD23	46:e:823:LEU:H	1.66	0.61
46:e:844:LEU:HD12	46:e:844:LEU:O	2.01	0.60
46:e:1432:TYR:OH	46:e:1441:ILE:HG21	2.00	0.60
5:E:128:LYS:NZ	30:f:1724:U:OP2	2.31	0.60
46:e:358:VAL:HG11	46:e:380:PHE:HE2	1.66	0.60
46:e:1080:LEU:O	46:e:1084:LEU:HD11	2.01	0.60
36:m:294:ALA:HB1	41:r:217:PHE:HB3	1.83	0.60
45:a:28:ASN:HB3	45:a:30:TYR:CE2	2.35	0.60
46:e:1080:LEU:C	46:e:1084:LEU:HD11	2.24	0.60
20:T:74:ARG:NH2	30:f:1639:C:OP2	2.30	0.60
46:e:170:TRP:O	46:e:174:GLN:HB3	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:e:937:GLU:HG3	46:e:972:GLU:CB	2.27	0.60
45:a:185:ILE:CD1	45:a:254:LEU:C	2.49	0.60
46:e:807:LYS:HD2	46:e:808:ASN:OD1	2.01	0.60
4:D:38:ARG:NH2	30:f:1348:U:OP2	2.34	0.60
23:W:2:GLY:N	30:f:2138:A:HO2'	1.99	0.60
45:a:705:TRP:HA	45:a:934:VAL:HG21	1.83	0.60
45:a:928:LEU:HD12	45:a:932:ASP:N	2.16	0.60
50:y:21:A:C3'	50:y:46:G:O6	2.40	0.60
14:N:21:ARG:NH2	30:f:640:U:OP1	2.32	0.60
30:f:1253:U:H5''	30:f:1254:C:H5'	1.83	0.60
40:q:89:LYS:HG2	40:q:145:VAL:HG22	1.84	0.60
45:a:578:SER:HB3	45:a:590:MET:HB3	1.83	0.60
45:a:644:SER:CB	45:a:699:MET:CE	2.78	0.60
45:a:928:LEU:HD11	45:a:932:ASP:CB	2.32	0.60
46:e:981:ALA:CB	46:e:1023:ARG:CD	2.78	0.60
46:e:1179:LEU:HA	46:e:1247:LYS:HZ3	1.66	0.60
1:A:201:ARG:NH2	30:f:692:A:OP1	2.35	0.60
3:C:173:ARG:NH2	30:f:618:C:OP1	2.35	0.60
6:F:80:ARG:HH21	6:F:87:THR:HG21	1.66	0.60
45:a:57:GLY:HA2	45:a:117:PHE:O	2.02	0.60
45:a:625:PRO:CG	45:a:921:LYS:HZ1	2.15	0.60
46:e:712:SER:O	46:e:716:ALA:N	2.35	0.60
23:W:55:ARG:NH2	35:l:59:GLN:OE1	2.34	0.59
46:e:511:ASP:CB	46:e:514:ASN:CB	2.80	0.59
31:h:31:U:O2'	36:m:218:ARG:NH1	2.35	0.59
43:t:27:ASP:O	43:t:31:LYS:HB2	2.01	0.59
45:a:881:GLU:OE2	45:a:881:GLU:HA	2.00	0.59
36:m:277:LEU:HG	36:m:281:GLU:HG3	1.82	0.59
48:v:43:ASP:HB3	48:v:60:VAL:HB	1.83	0.59
52:0:192:ASP:HB2	52:0:197:PHE:HE2	1.67	0.59
6:F:8:GLN:HB3	6:F:64:ILE:HD11	1.85	0.59
45:a:368:ARG:HD2	45:a:543:MET:HE2	1.84	0.59
1:A:183:THR:HG22	1:A:187:ARG:HB2	1.85	0.59
45:a:220:ILE:CB	45:a:249:GLU:CB	2.79	0.59
45:a:287:ALA:HB1	45:a:304:PHE:HB3	1.83	0.59
45:a:506:VAL:CG1	45:a:521:TYR:OH	2.51	0.59
46:e:980:LEU:HD22	46:e:999:SER:HB3	1.85	0.59
46:e:1335:ASN:OD1	46:e:1338:SER:CB	2.51	0.59
46:e:361:LEU:O	46:e:365:THR:HG23	2.03	0.59
46:e:1053:LEU:HG	46:e:1079:LEU:HD12	1.84	0.59
31:h:52:G:H21	42:s:9:MET:HE1	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:j:27:ALA:O	33:j:128:ARG:NH2	2.36	0.59
45:a:299:THR:OG1	45:a:302:LEU:HG	2.02	0.59
50:y:6:U:H2'	50:y:7:G:C8	2.38	0.59
30:f:439:C:O2'	30:f:494:G:N2	2.34	0.59
30:f:1268:G:O2'	30:f:1273:A:N6	2.36	0.59
46:e:378:LEU:HB3	46:e:379:PRO:HD3	1.85	0.59
30:f:804:C:OP1	35:l:98:ARG:NH2	2.35	0.58
45:a:705:TRP:CA	45:a:934:VAL:HG21	2.33	0.58
45:a:884:MET:CE	45:a:885:LYS:HG3	2.32	0.58
46:e:1178:VAL:HA	46:e:1184:ILE:HD12	1.82	0.58
21:U:5:LYS:HB2	21:U:8:GLU:HG2	1.84	0.58
46:e:754:ILE:HD12	46:e:829:ARG:HD3	1.83	0.58
5:E:100:ARG:NH1	30:f:1722:U:OP1	2.36	0.58
14:N:21:ARG:NH1	30:f:1369:A:OP1	2.36	0.58
28:c:4:ARG:NH1	30:f:837:A:OP2	2.36	0.58
30:f:1354:G:N3	37:n:8:LYS:NZ	2.51	0.58
45:a:706:LYS:HB3	45:a:934:VAL:HG23	1.84	0.58
49:w:65:ILE:HG12	49:w:109:ALA:HB3	1.84	0.58
17:Q:110:GLU:CG	46:e:1424:ILE:HD11	2.33	0.58
30:f:2854:U:OP2	41:r:3:ARG:NH2	2.37	0.58
6:F:77:VAL:HG22	6:F:126:VAL:HG23	1.85	0.58
45:a:142:GLU:HB2	45:a:150:GLU:OE2	2.04	0.58
46:e:1307:ILE:O	46:e:1311:ILE:HG12	2.04	0.58
46:e:1532:ASN:HD22	46:e:1532:ASN:N	2.00	0.58
28:c:17:ARG:NH1	30:f:860:G:OP1	2.36	0.58
45:a:625:PRO:HG2	45:a:921:LYS:HZ1	1.68	0.58
46:e:804:ILE:HD11	46:e:809:MET:HE1	1.83	0.58
46:e:1132:ILE:HD11	46:e:1162:MET:HE1	1.86	0.58
14:N:42:ARG:NH2	30:f:2800:G:O6	2.37	0.58
46:e:591:LEU:CB	46:e:621:LEU:CA	2.73	0.58
30:f:1259:A:N7	52:0:53:MET:HB3	2.15	0.58
46:e:263:THR:HA	46:e:266:ARG:HD3	1.85	0.58
46:e:838:ILE:HG23	46:e:862:PHE:CE2	2.30	0.58
46:e:1080:LEU:O	46:e:1084:LEU:HG	2.04	0.58
8:H:27:VAL:CA	46:e:1478:HIS:CE1	2.84	0.58
41:r:205:SER:OG	41:r:208:ASN:OD1	2.21	0.58
45:a:111:TYR:HB2	45:a:125:LEU:HB2	1.86	0.58
45:a:142:GLU:OE1	45:a:150:GLU:OE2	2.22	0.58
46:e:104:LYS:N	47:g:1:MET:HE3	2.18	0.58
32:i:21:C:OP1	35:l:193:LYS:NZ	2.36	0.58
45:a:928:LEU:CD1	45:a:990:TRP:CZ3	2.70	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:f:3187:A:OP1	40:q:23:ARG:NH1	2.37	0.57
45:a:22:GLU:HA	45:a:89:LEU:HD12	1.86	0.57
46:e:1066:ARG:NE	46:e:1111:GLN:HE22	2.02	0.57
45:a:284:TYR:CB	45:a:314:PRO:CD	2.67	0.57
45:a:959:GLY:HA3	45:a:1015:LYS:HB2	1.85	0.57
46:e:1080:LEU:CD1	46:e:1102:CYS:O	2.51	0.57
46:e:1474:MET:O	46:e:1478:HIS:HB2	2.03	0.57
52:0:43:LYS:HA	52:0:46:ARG:HG2	1.87	0.57
11:K:50:ALA:HB1	21:U:66:VAL:HG11	1.86	0.57
46:e:823:LEU:HB3	46:e:830:VAL:CG2	2.20	0.57
46:e:840:VAL:HG13	46:e:908:TYR:HB2	1.86	0.57
46:e:1149:THR:HG22	46:e:1339:PRO:HD3	1.86	0.57
50:y:62:C:H2'	50:y:63:G:C8	2.38	0.57
2:B:60[A]:LYS:HE3	30:f:1307:G:H5'	1.86	0.57
26:Z:125:LYS:O	40:q:173:ARG:NH1	2.35	0.57
45:a:142:GLU:CB	45:a:150:GLU:OE2	2.51	0.57
46:e:251:ASN:CB	46:e:254:ASN:ND2	2.68	0.57
46:e:816:ALA:HA	46:e:819:LEU:CD1	2.35	0.57
46:e:684:SER:CB	46:e:715:LEU:HD22	2.34	0.57
36:m:64:ILE:HG13	36:m:109:THR:HG21	1.87	0.57
36:m:166:ALA:HB1	36:m:171:LEU:HD12	1.86	0.57
46:e:937:GLU:CB	46:e:972:GLU:HB3	2.34	0.57
46:e:1523:PRO:HA	46:e:1535:HIS:HA	1.85	0.57
50:y:53:G:O2'	50:y:54:U:H5'	2.04	0.57
46:e:104:LYS:HG3	46:e:147:VAL:HG22	1.86	0.57
8:H:27:VAL:HA	46:e:1478:HIS:CD2	2.30	0.57
28:c:4:ARG:NH2	30:f:838:G:O6	2.38	0.57
46:e:738:PHE:HB3	46:e:814:ARG:HB3	1.86	0.57
30:f:2842:U:OP1	30:f:2844:C:N4	2.37	0.57
45:a:414:MET:CG	45:a:418:THR:OG1	2.52	0.57
46:e:252:LEU:HD13	46:e:298:ILE:HG12	1.86	0.57
46:e:968:ASN:HA	46:e:973:ILE:HG13	1.87	0.57
45:a:426:GLU:HB3	45:a:434:ALA:CB	2.34	0.57
45:a:705:TRP:CE3	45:a:937:ILE:CD1	2.83	0.57
46:e:816:ALA:O	46:e:819:LEU:HD23	2.01	0.56
46:e:1510:ILE:HD12	46:e:1538:CYS:HB3	1.87	0.56
30:f:1390:A:N6	30:f:1418:A:O2'	2.38	0.56
34:k:59:ASP:HB2	34:k:357:LYS:HE3	1.87	0.56
37:n:132:THR:HA	37:n:135:VAL:HG12	1.87	0.56
46:e:1059:LEU:HG	46:e:1065:VAL:HG11	1.86	0.56
4:D:43:PRO:HB2	30:f:728:G:H5''	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:a:928:LEU:CD1	45:a:932:ASP:CA	2.84	0.56
46:e:275:GLY:CA	46:e:278:PRO:HD2	2.36	0.56
46:e:726:LEU:HG	46:e:753:LEU:CD2	2.35	0.56
48:v:49:THR:HG22	48:v:56:LYS:HE3	1.87	0.56
13:M:17:ARG:NH1	30:f:1634:G:N7	2.53	0.56
17:Q:4:LEU:O	17:Q:79:ARG:NH2	2.38	0.56
28:c:49:ARG:NH2	30:f:1793:C:OP2	2.38	0.56
30:f:1231:A:H5''	30:f:1232:C:H5'	1.86	0.56
46:e:804:ILE:HG13	46:e:809:MET:SD	2.45	0.56
22:V:68:ARG:NH2	30:f:2219:A:OP2	2.38	0.56
26:Z:100:TYR:O	30:f:2895:G:O2'	2.24	0.56
46:e:826:LEU:HD22	46:e:828:GLU:H	1.70	0.56
46:e:1279:PHE:CE2	46:e:1294:LEU:HD21	2.41	0.56
47:g:118:HIS:HD1	47:g:120:ASP:H	1.52	0.56
17:Q:55:LEU:HB2	17:Q:95:PRO:HD3	1.86	0.56
45:a:5:ILE:O	45:a:99:ARG:NH2	2.38	0.56
25:Y:5:LYS:HE2	25:Y:13:MET:HE1	1.87	0.56
30:f:542:G:H1	30:f:549:U:H3	1.52	0.56
46:e:1287:ARG:HA	46:e:1290:PHE:CD2	2.38	0.56
46:e:1501:GLN:HG3	46:e:1522:LEU:HD11	1.87	0.56
34:k:66:LYS:O	34:k:70:ARG:NH2	2.39	0.56
45:a:928:LEU:CD1	45:a:932:ASP:CB	2.83	0.56
46:e:512:PRO:CB	46:e:560:PHE:N	2.69	0.56
50:y:53:G:C4	50:y:54:U:C5	2.94	0.56
45:a:706:LYS:O	45:a:934:VAL:CG2	2.53	0.56
46:e:321:ASP:OD1	46:e:368:HIS:NE2	2.34	0.56
46:e:1066:ARG:NE	46:e:1111:GLN:HE21	2.00	0.55
20:T:87:GLU:OE2	20:T:91:ARG:NH1	2.39	0.55
36:m:75:LEU:O	36:m:112:LYS:NZ	2.40	0.55
41:r:143:SER:C	41:r:144:ASN:HD22	2.14	0.55
30:f:2493:U:OP1	49:w:215:ARG:NH2	2.39	0.55
46:e:278:PRO:CG	46:e:323:TYR:CE2	2.61	0.55
33:j:111:THR:HB	33:j:136:ILE:HD13	1.87	0.55
52:0:42:ARG:HG2	52:0:51:VAL:HG11	1.88	0.55
18:R:19:ARG:HD3	18:R:33:ARG:HB2	1.89	0.55
45:a:426:GLU:HB2	45:a:434:ALA:HB1	1.87	0.55
46:e:1081:ALA:N	46:e:1084:LEU:HD12	2.22	0.55
14:N:44:ASN:ND2	43:t:4:SER:O	2.40	0.55
30:f:394:G:N1	30:f:397:A:OP2	2.39	0.55
46:e:731:LEU:HD12	46:e:732:GLN:CA	2.37	0.55
30:f:3042:U:OP2	30:f:3092:C:N4	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:f:3045:G:OP1	34:k:19:ARG:NH2	2.39	0.55
33:j:70:ARG:HD2	33:j:72:ARG:HE	1.72	0.55
46:e:321:ASP:CB	46:e:329:TRP:HE1	2.19	0.55
46:e:810:GLN:HG3	46:e:814:ARG:HE	1.71	0.55
34:k:106:TRP:O	34:k:137:TYR:OH	2.24	0.55
46:e:321:ASP:O	46:e:326:GLY:N	2.40	0.55
46:e:820:ASP:CA	46:e:823:LEU:HG	2.37	0.55
49:w:48:ARG:HG2	49:w:159:LEU:HD23	1.88	0.55
2:B:157[A]:GLU:OE2	2:B:160[A]:ARG:NH2	2.40	0.54
45:a:392:ILE:CG2	45:a:518:ALA:HB2	2.37	0.54
46:e:816:ALA:HA	46:e:819:LEU:CG	2.33	0.54
45:a:185:ILE:HD13	45:a:255:LEU:N	2.16	0.54
30:f:1222:G:C8	52:0:57:THR:CG2	2.91	0.54
30:f:1352:A:H4'	30:f:1353:U:H5'	1.88	0.54
30:f:3231:U:H2'	30:f:3232:G:H8	1.73	0.54
41:r:61:SER:OG	41:r:63:GLU:OE1	2.25	0.54
45:a:83:HIS:HB3	45:a:110:PHE:CE2	2.42	0.54
45:a:142:GLU:HG3	45:a:150:GLU:OE2	2.06	0.54
46:e:726:LEU:HG	46:e:753:LEU:HD21	1.89	0.54
40:q:57:VAL:HG12	40:q:68:LEU:HD22	1.88	0.54
46:e:933:LEU:O	46:e:937:GLU:N	2.34	0.54
46:e:1175:PHE:HD1	46:e:1198:LEU:HD21	1.72	0.54
17:Q:9:THR:HG23	17:Q:109:VAL:HG23	1.88	0.54
30:f:1256:G:O2'	51:z:124:THR:CB	2.55	0.54
40:q:23:ARG:HE	40:q:39:LYS:HA	1.71	0.54
45:a:903:GLN:HA	45:a:906:LYS:HE2	1.89	0.54
46:e:838:ILE:HD13	46:e:864:HIS:HB2	1.86	0.54
8:H:90:ARG:NH1	30:f:1682:U:O4	2.40	0.54
46:e:1406:LYS:HD2	46:e:1488:LEU:HD13	1.89	0.54
30:f:2674:A:H5''	42:s:105:GLY:HA3	1.89	0.54
36:m:236:LEU:HA	36:m:239:ILE:HG12	1.90	0.54
14:N:95:SER:OG	14:N:98:THR:OG1	2.25	0.54
30:f:68:C:OP2	30:f:301:G:N2	2.40	0.54
30:f:2162:U:OP1	33:j:234:LYS:NZ	2.39	0.54
36:m:270:LYS:HG2	36:m:273:ARG:HE	1.73	0.54
45:a:884:MET:HE1	45:a:885:LYS:HG3	1.90	0.54
46:e:377:TRP:HB3	46:e:412:PHE:CZ	2.42	0.54
46:e:782:TYR:OH	46:e:1096:LEU:CB	2.54	0.54
5:E:128:LYS:NZ	30:f:1721:U:O4	2.39	0.54
30:f:76:G:O2'	43:t:100:ARG:NH1	2.37	0.54
30:f:1221:A:C4	52:0:12:PHE:CE2	2.96	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:f:1221:A:C4	52:0:12:PHE:CZ	2.95	0.54
45:a:387:ARG:HG2	45:a:391:LEU:CD1	2.36	0.54
45:a:706:LYS:O	45:a:934:VAL:HG23	2.06	0.54
46:e:104:LYS:HA	46:e:107:ARG:HE	1.73	0.54
30:f:3268:A:OP1	37:n:46:ARG:NH2	2.35	0.53
45:a:392:ILE:HD12	45:a:521:TYR:CD2	2.43	0.53
7:G:17:ARG:HG2	7:G:22:HIS:HA	1.90	0.53
46:e:921:ILE:HG12	46:e:929:LEU:HD11	1.91	0.53
8:H:56:VAL:HG12	8:H:65:VAL:HG22	1.88	0.53
30:f:1256:G:H4'	51:z:128:VAL:CB	2.39	0.53
30:f:3115:C:OP1	40:q:62:ARG:NH2	2.41	0.53
34:k:140:ASP:OD1	34:k:141:GLY:N	2.36	0.53
46:e:251:ASN:HB3	46:e:254:ASN:CB	2.36	0.53
46:e:466:PHE:CB	46:e:522:VAL:CB	2.86	0.53
46:e:1516:HIS:HB3	46:e:1519:ASP:CB	2.28	0.53
10:J:44:LYS:HD2	30:f:2111:G:H1'	1.90	0.53
30:f:1156:C:OP2	38:o:94:LYS:NZ	2.40	0.53
46:e:314:LEU:CB	46:e:357:ALA:HB1	2.39	0.53
46:e:1080:LEU:CD2	46:e:1106:TYR:HA	2.38	0.53
30:f:3375:A:O2'	30:f:3378:C:OP2	2.26	0.53
42:s:32:ARG:HD2	42:s:120:ILE:HA	1.91	0.53
46:e:754:ILE:HD11	46:e:829:ARG:HH11	1.74	0.53
46:e:1080:LEU:HD22	46:e:1106:TYR:HA	1.90	0.53
34:k:284:ARG:NH1	34:k:293:ASN:O	2.42	0.53
48:v:46:THR:HG22	48:v:57:VAL:HG22	1.90	0.53
2:B:75[A]:ALA:HB3	2:B:78[A]:ARG:HG2	1.90	0.53
10:J:6:ASP:OD1	10:J:32:GLN:N	2.40	0.53
23:W:52:LYS:NZ	35:l:59:GLN:O	2.39	0.53
30:f:2266:U:H2'	30:f:2267:C:C6	2.44	0.53
2:B:21[A]:SER:OG	30:f:1181:U:O4	2.27	0.53
46:e:1294:LEU:N	46:e:1294:LEU:CD1	2.72	0.53
20:T:31:ARG:NH2	30:f:1598:G:OP2	2.42	0.53
36:m:120:LYS:O	36:m:248:ARG:NH2	2.42	0.53
8:H:44:GLU:OE2	8:H:49:ASN:ND2	2.41	0.52
46:e:53:SER:HB3	46:e:65:ALA:HB2	1.90	0.52
10:J:47:ARG:HH21	10:J:58:HIS:HB2	1.73	0.52
30:f:1257:C:C5'	51:z:124:THR:CB	2.68	0.52
45:a:58:LEU:HD13	45:a:59:ARG:HH22	1.74	0.52
45:a:415:ASP:HB3	45:a:418:THR:CG2	2.36	0.52
2:B:61[A]:ALA:HA	2:B:70[A]:PRO:HD2	1.90	0.52
6:F:96:ASP:OD1	6:F:97:VAL:N	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:f:2406:C:OP1	48:v:51:5CT:H12	2.09	0.52
30:f:3230:G:H4'	44:u:132:LYS:HD3	1.92	0.52
46:e:321:ASP:OD2	46:e:365:THR:HG22	2.10	0.52
45:a:884:MET:HE1	45:a:885:LYS:HG2	1.90	0.52
30:f:2264:U:H2'	30:f:2265:C:C6	2.45	0.52
45:a:606:GLU:HG3	45:a:609:ASP:H	1.75	0.52
6:F:77:VAL:HG11	6:F:106:LEU:HD22	1.92	0.52
7:G:158:THR:OG1	41:r:169:LYS:NZ	2.42	0.52
45:a:309:PHE:CD1	45:a:309:PHE:C	2.87	0.52
46:e:1132:ILE:HD13	46:e:1170:GLN:HG3	1.90	0.52
46:e:1403:ILE:HA	46:e:1488:LEU:HD11	1.91	0.52
46:e:1439:LEU:HB3	46:e:1462:VAL:HB	1.92	0.52
50:y:74:C:O2'	50:y:75:C:H5'	2.09	0.52
17:Q:102:LYS:NZ	30:f:3373:U:OP2	2.38	0.52
24:X:44:LYS:NZ	30:f:1750:A:OP1	2.37	0.52
27:b:2:VAL:N	27:b:90:HIS:O	2.42	0.52
30:f:1288:U:H2'	30:f:1289:G:H8	1.74	0.52
46:e:355:PHE:HE2	46:e:401:VAL:HG13	1.74	0.52
46:e:1206:GLN:HB3	46:e:1281:ASP:HB2	1.92	0.52
3:C:118:GLN:NE2	3:C:147:GLU:OE2	2.39	0.52
30:f:2177:G:OP2	33:j:128:ARG:NH1	2.43	0.52
46:e:584:GLU:CB	46:e:614:GLN:CB	2.88	0.52
46:e:777:MET:HE1	46:e:809:MET:HE3	1.92	0.52
2:B:74[A]:ARG:O	2:B:142[A]:SER:OG	2.23	0.52
6:F:80:ARG:HB2	6:F:122:HIS:HB2	1.91	0.52
7:G:136:ARG:HD2	7:G:139:ARG:HH12	1.74	0.52
46:e:373:TYR:CZ	46:e:416:SER:HB3	2.45	0.52
46:e:865:THR:O	46:e:869:HIS:N	2.31	0.52
46:e:1210:ILE:HD11	46:e:1281:ASP:HB3	1.92	0.52
9:I:94:TYR:OH	10:J:41:LYS:NZ	2.39	0.52
45:a:185:ILE:HD13	45:a:255:LEU:CA	2.38	0.52
46:e:275:GLY:HA2	46:e:278:PRO:HD2	1.91	0.52
46:e:1303:MET:O	46:e:1307:ILE:HG13	2.10	0.52
10:J:16:GLY:O	30:f:3050:U:O2'	2.27	0.51
30:f:2245:C:O2'	33:j:220:GLY:O	2.26	0.51
30:f:2557:A:OP1	33:j:69:TYR:OH	2.24	0.51
46:e:1286:MET:O	46:e:1290:PHE:CD2	2.63	0.51
46:e:1410:LEU:HG	46:e:1417:LEU:HD11	1.91	0.51
14:N:100:PRO:HG2	14:N:123:VAL:HG23	1.93	0.51
45:a:973:TYR:HB2	45:a:1018:ILE:HG23	1.91	0.51
46:e:754:ILE:CG1	46:e:829:ARG:HH11	2.14	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:e:1206:GLN:HE21	46:e:1278:TYR:HD1	1.58	0.51
51:z:51:LYS:HA	51:z:54:LYS:CB	2.40	0.51
30:f:123:A:OP1	39:p:105:LYS:NZ	2.37	0.51
30:f:3160:U:H3	30:f:3290:G:H1	1.59	0.51
36:m:54:ARG:NH1	36:m:147:ASP:O	2.42	0.51
42:s:49:LYS:HG3	42:s:64:LYS:HD3	1.92	0.51
45:a:356:GLN:OE1	45:a:557:LYS:HB3	2.09	0.51
46:e:328:ILE:HG13	46:e:329:TRP:N	2.24	0.51
50:y:1:G:H2'	50:y:2:G:H8	1.76	0.51
27:b:41:ARG:NH1	30:f:284:A:OP2	2.40	0.51
30:f:1234:G:N2	51:z:135:THR:CB	2.73	0.51
30:f:1778:G:O2'	30:f:1780:G:OP2	2.28	0.51
35:l:266:THR:HG23	35:l:267:VAL:HG13	1.92	0.51
36:m:50:ARG:NH2	36:m:72:ASP:OD2	2.43	0.51
46:e:130:LYS:HA	46:e:173:PHE:HE2	1.75	0.51
46:e:209:HIS:HA	46:e:212:ILE:HG22	1.93	0.51
27:b:75:VAL:HG23	27:b:76:LYS:HD2	1.92	0.51
46:e:53:SER:CB	46:e:65:ALA:HB2	2.41	0.51
30:f:2540:A:N3	30:f:2541:U:N3	2.59	0.51
45:a:426:GLU:HA	45:a:429:LYS:HD2	1.93	0.51
45:a:572:TYR:HB2	45:a:575:GLU:HG3	1.93	0.51
45:a:884:MET:SD	45:a:884:MET:O	2.69	0.51
46:e:385:VAL:HG13	46:e:386:GLN:N	2.26	0.51
46:e:823:LEU:HD12	46:e:864:HIS:CE1	2.46	0.51
47:g:68:ARG:NH2	47:g:112:ASP:O	2.44	0.51
20:T:96:GLU:OE2	30:f:2555:G:N1	2.42	0.51
21:U:67:ARG:NH2	32:i:97:A:OP1	2.44	0.51
29:d:20:ARG:HA	29:d:23:VAL:HG12	1.92	0.51
40:q:22:SER:OG	40:q:39:LYS:NZ	2.44	0.51
46:e:373:TYR:HA	46:e:377:TRP:HD1	1.76	0.51
46:e:1192:ARG:CG	46:e:1270:TRP:CH2	2.94	0.51
30:f:591:G:O2'	37:n:17:ALA:O	2.28	0.51
39:p:207:ASP:OD1	39:p:207:ASP:N	2.44	0.51
8:H:92:TRP:CZ2	46:e:1471:GLN:HA	2.45	0.51
19:S:70:LYS:HD2	30:f:585:A:H5''	1.92	0.51
30:f:1661:G:H2'	30:f:1662:G:C8	2.46	0.51
30:f:2489:C:O2'	49:w:210:MET:SD	2.69	0.51
46:e:118:VAL:O	46:e:122:ARG:CA	2.59	0.51
46:e:252:LEU:HD22	46:e:306:VAL:HG22	1.93	0.51
1:A:103:GLU:HG3	1:A:160:GLU:HB2	1.93	0.51
30:f:544:C:H2'	30:f:547:G:H1	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:f:1256:G:O3'	51:z:124:THR:CB	2.59	0.51
35:l:156:LEU:HD12	35:l:159:ILE:HD12	1.94	0.51
45:a:705:TRP:CZ3	45:a:937:ILE:CD1	2.90	0.51
45:a:881:GLU:O	45:a:884:MET:HE3	2.10	0.51
46:e:816:ALA:HA	46:e:819:LEU:HD11	1.93	0.51
15:O:23:LYS:HG3	15:O:24:PRO:HD2	1.93	0.50
21:U:118:ILE:HD11	43:t:145:PHE:HE2	1.76	0.50
32:i:29:U:H5''	43:t:27:ASP:HB3	1.92	0.50
45:a:944:TRP:N	45:a:945:PRO:CD	2.74	0.50
30:f:110:G:OP2	43:t:73:ARG:NH2	2.42	0.50
30:f:2828:G:OP2	41:r:7:ARG:NH2	2.44	0.50
36:m:206:GLN:NE2	36:m:210:GLU:OE2	2.44	0.50
46:e:989:GLU:O	46:e:993:VAL:HG23	2.11	0.50
46:e:1015:GLN:HA	46:e:1064:GLY:H	1.76	0.50
46:e:1303:MET:CE	46:e:1303:MET:CA	2.88	0.50
48:v:18:THR:HG22	48:v:83:PRO:HA	1.93	0.50
30:f:655:C:H2'	30:f:656:A:H8	1.75	0.50
35:l:126:ILE:O	35:l:129:THR:OG1	2.30	0.50
39:p:52:TRP:O	39:p:57:ARG:NH1	2.44	0.50
45:a:701:PHE:HB2	45:a:956:ILE:HD11	1.94	0.50
45:a:954:VAL:HG21	45:a:970:ILE:HG23	1.94	0.50
46:e:981:ALA:CB	46:e:1023:ARG:HG2	2.39	0.50
46:e:1128:GLN:HA	46:e:1131:LEU:HD12	1.93	0.50
50:y:59:U:O2'	50:y:60:U:C5'	2.45	0.50
3:C:65:SER:OG	30:f:1447:G:OP1	2.28	0.50
3:C:107:LEU:HD12	3:C:152:GLU:HG3	1.92	0.50
14:N:26:ARG:NH1	30:f:938:C:OP2	2.44	0.50
30:f:2307:G:O2'	30:f:2310:U:OP2	2.28	0.50
39:p:161:GLU:HA	39:p:164:VAL:HG22	1.93	0.50
45:a:83:HIS:HB3	45:a:110:PHE:CZ	2.46	0.50
46:e:754:ILE:HG13	46:e:829:ARG:CZ	2.34	0.50
30:f:2137:U:OP2	30:f:2142:A:N6	2.40	0.50
30:f:2965:U:H6	30:f:2965:U:O5'	1.93	0.50
45:a:340:PHE:CE2	45:a:341:PHE:CE1	2.99	0.50
46:e:797:LEU:HD13	46:e:907:PHE:CD1	2.44	0.50
46:e:981:ALA:CB	46:e:1023:ARG:CG	2.89	0.50
46:e:1077:GLU:HG3	46:e:1109:LEU:HD13	1.94	0.50
49:w:50:SER:HA	49:w:157:PHE:O	2.11	0.50
5:E:62:ARG:HH22	30:f:3067:C:H3'	1.77	0.50
30:f:3214:U:OP2	44:u:128:ARG:NH1	2.34	0.50
46:e:713:LEU:HA	46:e:716:ALA:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:e:1472:TRP:CH2	46:e:1501:GLN:HB2	2.46	0.50
28:c:18:TYR:HB3	33:j:180:LEU:HD22	1.93	0.50
30:f:664:U:H2'	30:f:665:A:C8	2.47	0.50
46:e:314:LEU:HB2	46:e:357:ALA:HB1	1.94	0.50
46:e:989:GLU:O	46:e:992:LEU:HB3	2.11	0.50
46:e:1307:ILE:HG22	46:e:1311:ILE:HD13	1.93	0.50
30:f:2948:C:OP1	34:k:244:ARG:NH2	2.36	0.50
45:a:284:TYR:HB3	45:a:314:PRO:HD2	1.90	0.50
46:e:1104:ASN:O	46:e:1108:THR:HG23	2.12	0.50
30:f:2897:A:H2'	30:f:2899:C:H5''	1.93	0.50
31:h:44:C:H4'	36:m:152:ARG:HG3	1.93	0.50
46:e:1210:ILE:HG23	46:e:1283:SER:HB3	1.93	0.50
49:w:59:PRO:HD2	49:w:153:SER:HA	1.93	0.50
45:a:294:ILE:HB	45:a:297:LYS:HG2	1.94	0.49
46:e:826:LEU:HD22	46:e:827:PRO:N	2.26	0.49
46:e:1427:GLU:OE2	46:e:1444:LYS:HE2	2.12	0.49
46:e:1472:TRP:HH2	46:e:1501:GLN:HB2	1.76	0.49
3:C:60:PHE:HB3	3:C:64:ASN:HB3	1.93	0.49
45:a:284:TYR:CZ	45:a:313:LYS:HB2	2.45	0.49
46:e:816:ALA:CB	46:e:837:PHE:HE2	2.25	0.49
46:e:823:LEU:CA	46:e:830:VAL:HG22	2.35	0.49
50:y:38:U:H2'	50:y:39:G:C8	2.48	0.49
32:i:156:U:OP2	39:p:84:ARG:NH2	2.45	0.49
46:e:866:PHE:CD1	46:e:893:MET:HB3	2.41	0.49
1:A:83:LYS:NZ	30:f:36:C:OP2	2.42	0.49
17:Q:77:ARG:HD2	17:Q:89:LEU:HD13	1.94	0.49
45:a:290:ASN:HB3	45:a:293:TYR:HB3	1.94	0.49
46:e:937:GLU:HB2	46:e:972:GLU:HB3	1.94	0.49
46:e:955:LEU:O	46:e:959:ILE:HG13	2.12	0.49
46:e:976:LEU:O	46:e:980:LEU:HG	2.13	0.49
3:C:62:ARG:NH1	30:f:412:G:OP1	2.45	0.49
24:X:2:ALA:N	30:f:1613:A:OP1	2.46	0.49
45:a:340:PHE:HE2	45:a:341:PHE:CE1	2.31	0.49
45:a:379:LEU:HG	45:a:532:GLN:HE22	1.76	0.49
46:e:1031:ILE:HA	46:e:1034:TRP:CE3	2.47	0.49
47:g:116:LEU:HG	47:g:177:LEU:HD21	1.94	0.49
2:B:46[A]:GLU:HG3	2:B:48[A]:PHE:H	1.77	0.49
16:P:30:THR:HG23	16:P:91:SER:HB2	1.95	0.49
30:f:1569:U:H5'	30:f:1570:U:H5''	1.94	0.49
35:l:292:SER:OG	35:l:294:GLU:OE1	2.31	0.49
46:e:27:LEU:HD12	46:e:188:GLU:HG3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:f:348:A:N3	30:f:352:A:O2'	2.46	0.49
45:a:934:VAL:CG2	45:a:936:ASP:O	2.61	0.49
46:e:251:ASN:CG	46:e:254:ASN:ND2	2.69	0.49
16:P:9:SER:OG	16:P:10:ILE:N	2.39	0.49
30:f:505:G:OP1	35:l:320:ASN:ND2	2.43	0.49
30:f:1019:G:H1	30:f:1033:U:H3	1.59	0.49
36:m:90:HIS:NE2	36:m:229:ASP:OD2	2.41	0.49
42:s:90:GLN:NE2	42:s:170:ASP:OD1	2.45	0.49
46:e:973:ILE:HG23	46:e:1006:LEU:HD22	1.95	0.49
46:e:1080:LEU:HD13	46:e:1105:LEU:HB3	1.95	0.49
46:e:1269:LEU:HD21	46:e:1352:LEU:HG	1.95	0.49
49:w:138:VAL:HG21	49:w:144:LEU:HD23	1.94	0.49
6:F:155:ARG:HB2	6:F:172:TYR:HD1	1.77	0.49
7:G:108:ARG:O	7:G:112:ASN:HB2	2.12	0.49
27:b:30:ALA:O	30:f:2767:U:O2'	2.29	0.49
45:a:54:VAL:HG13	45:a:116:PHE:HE1	1.78	0.49
4:D:56:LYS:NZ	30:f:674:G:O6	2.46	0.49
27:b:7:THR:OG1	27:b:22:GLN:NE2	2.36	0.49
30:f:1264:G:N2	30:f:1265:U:O4	2.40	0.49
30:f:2185:G:O2'	30:f:2314:U:OP2	2.28	0.49
45:a:601:TYR:O	45:a:605:ILE:HB	2.13	0.49
45:a:649:TRP:HD1	45:a:650:SER:CA	2.23	0.49
30:f:2901:G:O2'	30:f:3024:A:N1	2.44	0.48
46:e:322:ASP:HA	46:e:367:ARG:HH22	1.78	0.48
46:e:385:VAL:CG1	46:e:386:GLN:N	2.76	0.48
47:g:197:MET:HE3	47:g:218:ILE:HD12	1.95	0.48
14:N:94:ALA:HA	14:N:121:VAL:HG23	1.95	0.48
18:R:104:ASN:ND2	30:f:1389:G:OP1	2.42	0.48
46:e:823:LEU:HD23	46:e:823:LEU:N	2.27	0.48
4:D:131:ALA:HB1	4:D:135:GLN:H	1.79	0.48
17:Q:80:ASN:OD1	17:Q:81:GLU:N	2.45	0.48
37:n:92:SER:OG	37:n:148:GLU:OE2	2.30	0.48
39:p:91:PHE:O	39:p:95:ASN:ND2	2.46	0.48
15:O:3:LYS:HD3	30:f:2617:U:H3'	1.95	0.48
19:S:49:ILE:HD11	19:S:71:VAL:HG22	1.96	0.48
46:e:823:LEU:CB	46:e:830:VAL:CG2	2.61	0.48
46:e:838:ILE:HD12	46:e:864:HIS:HB3	1.94	0.48
46:e:1090:ASP:CA	46:e:1095:LEU:HD13	2.30	0.48
46:e:1427:GLU:OE2	46:e:1444:LYS:HE3	2.13	0.48
7:G:99:SER:HG	7:G:101:CYS:HG	1.61	0.48
34:k:145:GLU:HA	34:k:148:LEU:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:a:392:ILE:HD12	45:a:521:TYR:HD2	1.79	0.48
45:a:1003:GLN:HE21	45:a:1003:GLN:CA	2.23	0.48
46:e:355:PHE:HA	46:e:358:VAL:HG23	1.96	0.48
30:f:1814:A:H4'	30:f:1815:U:H5'	1.95	0.48
46:e:1363:VAL:HG11	46:e:1366:LEU:HB2	1.94	0.48
46:e:1440:GLU:H	46:e:1460:SER:HB2	1.78	0.48
4:D:102:ALA:HA	4:D:122:ILE:O	2.14	0.48
13:M:133:LYS:HE3	13:M:135:ARG:HD3	1.95	0.48
30:f:520:U:OP2	38:o:70:LYS:NZ	2.45	0.48
30:f:1477:A:OP1	30:f:3075:G:O2'	2.31	0.48
30:f:2568:C:O2'	30:f:2569:A:O4'	2.27	0.48
32:i:9:A:H2'	32:i:10:A:C8	2.49	0.48
35:l:304:GLN:NE2	35:l:306:THR:O	2.42	0.48
42:s:38:GLU:HB2	42:s:45:PRO:HD3	1.95	0.48
46:e:377:TRP:HB3	46:e:412:PHE:HZ	1.79	0.48
46:e:466:PHE:CA	46:e:522:VAL:CB	2.92	0.48
48:v:59:LEU:HB2	48:v:72:ASP:OD1	2.13	0.48
6:F:93:GLU:HG3	6:F:140:VAL:HG11	1.95	0.48
30:f:2270:A:H2'	30:f:2271:A:C8	2.47	0.48
40:q:18:VAL:HG12	40:q:27:VAL:HG22	1.94	0.48
45:a:196:ILE:HG22	45:a:200:LYS:HE3	1.96	0.48
30:f:1383:G:O3'	35:l:138:ARG:NH2	2.47	0.48
30:f:3198:U:O2	40:q:21:LYS:N	2.44	0.48
45:a:89:LEU:HD23	45:a:103:LEU:HD12	1.76	0.48
45:a:1003:GLN:NE2	45:a:1003:GLN:CA	2.76	0.48
30:f:1230:G:H4'	52:0:34:SER:HA	1.96	0.48
30:f:1805:C:H2'	30:f:1806:A:H8	1.79	0.48
30:f:2155:G:OP1	33:j:241:ARG:NH1	2.46	0.48
47:g:146:ILE:HG13	47:g:147:LEU:HD12	1.96	0.48
4:D:16:ARG:HB2	30:f:974:G:H5'	1.95	0.47
27:b:45:ARG:NH1	30:f:283:G:OP1	2.46	0.47
33:j:117:GLU:HG2	33:j:124:GLY:H	1.79	0.47
34:k:85:VAL:HG22	34:k:202:THR:HG22	1.95	0.47
40:q:47:LYS:H	44:u:7:VAL:HG21	1.78	0.47
46:e:380:PHE:HD2	46:e:381:TRP:CD1	2.32	0.47
46:e:751:VAL:HA	46:e:754:ILE:HG23	1.96	0.47
4:D:19:PRO:HB3	4:D:53:PHE:HA	1.96	0.47
13:M:23:VAL:HG12	13:M:45:GLY:HA3	1.94	0.47
17:Q:75:ILE:HG12	17:Q:93:VAL:HG22	1.96	0.47
43:t:76:THR:HG22	43:t:78:ALA:H	1.80	0.47
45:a:942:ALA:HB3	45:a:947:LEU:HD23	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:e:1443:PHE:HB3	46:e:1454:ILE:HD11	1.94	0.47
47:g:14:GLY:HA2	47:g:198:VAL:HG13	1.96	0.47
3:C:22:LEU:HD12	3:C:146:ILE:HD12	1.97	0.47
19:S:99:ARG:NH1	30:f:3275:U:O2'	2.48	0.47
26:Z:124:LYS:NZ	30:f:2897:A:OP2	2.47	0.47
30:f:655:C:H2'	30:f:656:A:C8	2.49	0.47
30:f:831:G:O2'	30:f:1864:A:N3	2.39	0.47
34:k:219:ALA:HB2	34:k:336:VAL:HG23	1.96	0.47
45:a:705:TRP:CD1	45:a:705:TRP:H	2.32	0.47
45:a:884:MET:HE3	45:a:885:LYS:HG3	1.96	0.47
48:v:48:LYS:HA	48:v:55:ALA:HA	1.96	0.47
30:f:829:U:H3	30:f:895:A:H62	1.63	0.47
52:0:26:PHE:HZ	52:0:93:LEU:HA	1.80	0.47
30:f:411:U:H2'	30:f:412:G:H8	1.79	0.47
32:i:103:G:OP2	32:i:105:A:O2'	2.33	0.47
45:a:25:ARG:HG3	50:y:33:U:H3	1.80	0.47
45:a:250:SER:O	45:a:254:LEU:HG	2.15	0.47
46:e:118:VAL:O	46:e:122:ARG:CB	2.62	0.47
46:e:332:ASP:HB3	46:e:335:SER:HB3	1.96	0.47
46:e:513:SER:CA	46:e:559:ASN:CB	2.92	0.47
47:g:88:LEU:HD12	47:g:92:VAL:HG21	1.96	0.47
5:E:151:ARG:NH2	5:E:152:GLU:OE2	2.45	0.47
7:G:116:ARG:NH2	30:f:1096:U:OP2	2.48	0.47
23:W:81:GLY:O	32:i:95:G:O2'	2.32	0.47
30:f:358:G:N2	30:f:361:A:OP2	2.42	0.47
33:j:32:LEU:HD13	33:j:163:ARG:HD3	1.96	0.47
45:a:287:ALA:HB2	45:a:327:ILE:CD1	2.44	0.47
45:a:287:ALA:HB2	45:a:327:ILE:HD13	1.96	0.47
45:a:287:ALA:CB	45:a:327:ILE:CD1	2.92	0.47
45:a:884:MET:SD	45:a:885:LYS:N	2.87	0.47
46:e:373:TYR:HA	46:e:377:TRP:CD1	2.50	0.47
46:e:1294:LEU:N	46:e:1294:LEU:HD12	2.29	0.47
4:D:170:ARG:HD2	14:N:57:GLY:HA3	1.97	0.47
5:E:21:LYS:HE3	5:E:55:VAL:HA	1.97	0.47
9:I:18:PRO:HA	9:I:51:ALA:HA	1.97	0.47
30:f:712:G:OP1	43:t:174:ARG:NH1	2.47	0.47
39:p:228:GLU:O	39:p:232:HIS:ND1	2.43	0.47
41:r:54:SER:HB3	41:r:135:ILE:HD11	1.97	0.47
41:r:66:GLU:OE1	41:r:69:ARG:NH2	2.48	0.47
46:e:134:PRO:HG3	46:e:176:GLN:HB3	1.96	0.47
46:e:937:GLU:HG3	46:e:972:GLU:CA	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:e:1087:CYS:HG	46:e:1099:ARG:HA	1.76	0.47
50:y:53:G:C4	50:y:54:U:C6	3.02	0.47
32:i:126:A:O2'	32:i:129:C:N4	2.48	0.47
45:a:185:ILE:HG22	45:a:255:LEU:CD1	2.45	0.47
45:a:928:LEU:HD11	45:a:932:ASP:HB2	1.90	0.47
1:A:5:LYS:HE2	22:V:40:VAL:HG21	1.97	0.47
14:N:115:LYS:HA	30:f:715:A:H5''	1.97	0.47
30:f:627:U:H2'	30:f:628:A:C8	2.50	0.47
34:k:211:GLN:NE2	34:k:283:TYR:O	2.45	0.47
36:m:163:LEU:HD11	36:m:175:HIS:HB3	1.97	0.47
44:u:38:ILE:HA	44:u:44:VAL:HG12	1.96	0.47
44:u:55:ARG:NH2	44:u:76:ALA:O	2.48	0.47
4:D:180:ARG:NH2	30:f:2790:A:OP1	2.42	0.47
30:f:912:G:OP2	33:j:9:ARG:NH2	2.45	0.47
30:f:1907:C:O2	34:k:240:ARG:NH2	2.45	0.47
46:e:240:ILE:HG22	46:e:246:ILE:HD11	1.97	0.47
30:f:835:G:O2'	30:f:857:G:N2	2.38	0.46
30:f:2491:A:H1'	49:w:207:LYS:HE2	1.97	0.46
46:e:754:ILE:HG12	46:e:755:ASN:N	2.29	0.46
46:e:1066:ARG:HE	46:e:1111:GLN:HE22	1.63	0.46
46:e:1081:ALA:N	46:e:1084:LEU:CD1	2.77	0.46
30:f:2815:G:N2	30:f:2818:U:O2	2.45	0.46
36:m:234:ASP:OD1	36:m:234:ASP:N	2.47	0.46
45:a:284:TYR:CG	45:a:313:LYS:CA	2.86	0.46
46:e:362:TYR:HA	46:e:377:TRP:CZ2	2.50	0.46
47:g:219:GLU:HA	47:g:224:LEU:HD12	1.96	0.46
5:E:68:GLN:OE1	5:E:71:ARG:NH2	2.43	0.46
30:f:2466:G:H5''	49:w:60:ARG:HH12	1.80	0.46
46:e:307:CYS:HA	46:e:310:LEU:HB2	1.96	0.46
3:C:67:ILE:HD11	3:C:80:LYS:HB3	1.98	0.46
15:O:55:ALA:O	15:O:59:LYS:HB3	2.16	0.46
30:f:297:G:OP2	30:f:297:G:N2	2.41	0.46
30:f:617:G:OP1	37:n:108:LYS:NZ	2.41	0.46
35:l:326:ARG:O	38:o:41:ARG:NH2	2.48	0.46
41:r:54:SER:OG	41:r:130:ASP:O	2.33	0.46
45:a:28:ASN:HB3	45:a:30:TYR:HE2	1.80	0.46
45:a:623:LYS:HZ3	45:a:917:TYR:HE2	1.64	0.46
46:e:397:ASN:HB2	46:e:400:GLU:HG3	1.97	0.46
2:B:59[A]:ARG:NH1	30:f:1307:G:OP1	2.48	0.46
8:H:27:VAL:CB	46:e:1478:HIS:CE1	2.99	0.46
12:L:55:GLU:HB2	12:L:108:LYS:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:74:TYR:HB3	12:L:77:LYS:HB2	1.98	0.46
13:M:28:PRO:O	13:M:29:HIS:ND1	2.48	0.46
18:R:9:ILE:HG12	18:R:63:THR:HG23	1.97	0.46
30:f:86:G:O2'	30:f:98:G:O6	2.32	0.46
36:m:119:TYR:OH	36:m:139:PRO:O	2.33	0.46
44:u:48:GLY:HA3	44:u:53:VAL:HB	1.98	0.46
46:e:251:ASN:CB	46:e:254:ASN:CG	2.89	0.46
46:e:1053:LEU:HD11	46:e:1083:SER:HB3	1.98	0.46
2:B:39[A]:GLU:HG2	2:B:40[A]:GLU:HG2	1.97	0.46
30:f:1152:G:OP2	30:f:1152:G:N2	2.44	0.46
45:a:81:ARG:O	45:a:85:LYS:HB3	2.15	0.46
46:e:1427:GLU:CD	46:e:1442:SER:CB	2.87	0.46
4:D:35:PHE:HE1	30:f:1348:U:H5'	1.80	0.46
20:T:95:ILE:HD11	30:f:2555:G:N7	2.30	0.46
45:a:697:LEU:H	45:a:697:LEU:HG	1.51	0.46
46:e:53:SER:OG	46:e:65:ALA:HB2	2.15	0.46
46:e:1003:LEU:O	46:e:1007:LEU:HG	2.15	0.46
46:e:1403:ILE:HG21	46:e:1428:VAL:HG11	1.96	0.46
46:e:1429:LYS:HE3	46:e:1442:SER:HB3	1.97	0.46
46:e:1474:MET:HG2	46:e:1477:GLN:OE1	2.16	0.46
47:g:11:ASN:ND2	47:g:209:ASP:OD2	2.49	0.46
14:N:96:LYS:HB2	14:N:96:LYS:HE2	1.70	0.46
18:R:60:ASN:HB3	18:R:63:THR:HB	1.97	0.46
30:f:40:A:OP1	56:f:3401:SPD:N10	2.48	0.46
30:f:696:C:OP2	35:l:119:ARG:NH2	2.49	0.46
30:f:1717:U:H2'	30:f:1718:G:C8	2.50	0.46
30:f:1949:G:H1	30:f:2097:U:H3	1.63	0.46
36:m:207:TYR:HA	36:m:210:GLU:HG2	1.97	0.46
39:p:156:ASP:OD1	39:p:156:ASP:N	2.47	0.46
42:s:131:MET:HE3	42:s:131:MET:HB3	1.81	0.46
45:a:431:ASN:HD21	46:e:12:TYR:HB2	1.81	0.46
15:O:25:LYS:NZ	30:f:1106:G:O3'	2.44	0.46
38:o:86:VAL:O	38:o:114:GLY:HA2	2.16	0.46
45:a:89:LEU:CD1	45:a:89:LEU:O	2.64	0.46
46:e:212:ILE:HG23	46:e:249:LEU:HD22	1.97	0.46
46:e:876:PHE:HB3	46:e:924:VAL:HG21	1.98	0.46
48:v:104:ASN:OD1	48:v:105:MET:N	2.49	0.46
13:M:22:LYS:NZ	13:M:132:SER:O	2.47	0.45
13:M:133:LYS:NZ	30:f:1808:G:OP2	2.44	0.45
45:a:392:ILE:HG21	45:a:518:ALA:HB2	1.97	0.45
46:e:726:LEU:O	46:e:730:ILE:HG12	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:e:765:PHE:HZ	46:e:822:LEU:HD22	1.80	0.45
1:A:159:ARG:HB3	1:A:164:LEU:HB2	1.98	0.45
1:A:202:TYR:HB3	35:l:112:LYS:HG3	1.97	0.45
17:Q:110:GLU:HG3	46:e:1424:ILE:CD1	2.47	0.45
19:S:14:LEU:HD11	19:S:31:LYS:HB2	1.98	0.45
30:f:2392:C:O2'	34:k:266:ARG:NH2	2.48	0.45
33:j:68:LYS:HE2	33:j:70:ARG:HH21	1.80	0.45
36:m:65:ILE:HG12	36:m:74:VAL:HG22	1.99	0.45
46:e:587:PHE:CB	46:e:615:LEU:CB	2.93	0.45
46:e:883:VAL:HG13	46:e:956:LEU:HB3	1.98	0.45
12:L:16:ARG:NH1	30:f:216:G:OP1	2.45	0.45
30:f:3022:G:O2'	30:f:3031:G:O6	2.32	0.45
45:a:412:GLN:O	45:a:413:GLN:CB	2.57	0.45
46:e:571:LYS:O	46:e:575:MET:N	2.39	0.45
46:e:1060:MET:HE1	46:e:1072:ALA:HB1	1.98	0.45
1:A:62:TYR:OH	32:i:141:C:O3'	2.34	0.45
17:Q:44:MET:O	17:Q:77:ARG:NH1	2.49	0.45
30:f:494:G:H2'	30:f:495:G:H8	1.82	0.45
30:f:1134:G:O2'	30:f:2642:A:N3	2.44	0.45
30:f:1497:C:H2'	30:f:1498:A:H8	1.81	0.45
30:f:3116:G:OP1	30:f:3116:G:N2	2.43	0.45
31:h:7:G:OP1	36:m:33:ARG:NH1	2.48	0.45
45:a:89:LEU:HD13	45:a:91:ALA:N	2.31	0.45
46:e:944:VAL:HG11	46:e:980:LEU:CD2	2.40	0.45
6:F:22:PRO:O	7:G:146:ASN:ND2	2.38	0.45
30:f:307:A:H2'	30:f:308:A:C8	2.51	0.45
30:f:1119:C:H2'	30:f:1120:A:H8	1.81	0.45
30:f:2218:G:H2'	30:f:2219:A:H8	1.80	0.45
36:m:83:LEU:HB3	36:m:88:ILE:HB	1.98	0.45
37:n:175:LYS:O	44:u:117:ARG:NH2	2.50	0.45
46:e:277:MET:HE3	46:e:287:ALA:HB3	1.99	0.45
46:e:1030:SER:O	46:e:1033:LYS:HG2	2.16	0.45
23:W:30:GLN:NE2	30:f:904:A:OP2	2.50	0.45
30:f:2697:A:H2'	30:f:2698:G:C8	2.52	0.45
31:h:62:U:O2'	36:m:285:ARG:NH2	2.50	0.45
45:a:29:ILE:HG21	45:a:80:LEU:HD12	1.98	0.45
45:a:421:LYS:HD2	45:a:424:LYS:HD2	1.99	0.45
45:a:700:GLY:HA3	45:a:947:LEU:HG	1.99	0.45
45:a:706:LYS:HB3	45:a:936:ASP:H	1.82	0.45
46:e:764:PHE:HB3	46:e:822:LEU:HD12	1.99	0.45
33:j:14:SER:OG	33:j:15:ILE:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:j:140:ASN:O	33:j:144:ASN:HA	2.16	0.45
46:e:290:LYS:HD2	46:e:290:LYS:HA	1.76	0.45
46:e:777:MET:CE	46:e:809:MET:HE3	2.47	0.45
46:e:1279:PHE:CE1	46:e:1290:PHE:CB	2.91	0.45
46:e:1403:ILE:HD12	46:e:1428:VAL:HG21	1.98	0.45
4:D:180:ARG:HH22	30:f:2719:U:H5''	1.82	0.45
30:f:571:U:H2'	30:f:572:A:H8	1.81	0.45
33:j:104:LEU:HD12	33:j:158:ILE:HD11	1.98	0.45
45:a:928:LEU:HG	45:a:990:TRP:HZ3	1.13	0.45
46:e:823:LEU:HB2	46:e:830:VAL:CG2	2.33	0.45
22:V:53:TYR:HA	22:V:56:ARG:HG2	1.99	0.45
30:f:2416:U:H2'	30:f:2417:U:C6	2.52	0.45
35:l:8:VAL:HG23	35:l:151:VAL:HG12	1.98	0.45
38:o:83:LEU:HD11	38:o:116:PHE:HB3	1.99	0.45
46:e:797:LEU:HD21	46:e:955:LEU:HD22	1.97	0.45
47:g:106:ASN:OD1	47:g:150:SER:OG	2.34	0.45
29:d:21:ARG:HA	29:d:21:ARG:HD2	1.80	0.45
30:f:528:U:H2'	30:f:529:A:C8	2.51	0.45
30:f:2094:C:H2'	30:f:2095:G:H8	1.81	0.45
38:o:232:ARG:O	38:o:235:PHE:N	2.48	0.45
45:a:170:LYS:HB3	45:a:170:LYS:HE3	1.69	0.45
45:a:575:GLU:HA	45:a:579:TRP:CD1	2.51	0.45
45:a:612:MET:HB3	45:a:612:MET:HE3	1.69	0.45
46:e:727:ALA:HB3	46:e:763:ILE:HD11	1.99	0.45
46:e:807:LYS:H	46:e:807:LYS:HG3	1.52	0.45
46:e:841:VAL:O	46:e:845:VAL:HG23	2.17	0.45
46:e:974:THR:O	46:e:978:THR:HG23	2.17	0.45
46:e:1080:LEU:HD23	46:e:1127:ILE:HD13	1.99	0.45
50:y:14:A:H2'	50:y:15:G:C8	2.52	0.45
1:A:7:LEU:HD11	39:p:162:LEU:HA	1.99	0.44
25:Y:37:TYR:O	30:f:351:A:N6	2.48	0.44
40:q:41:ILE:HD13	40:q:71:VAL:HB	1.99	0.44
45:a:706:LYS:N	45:a:934:VAL:CB	2.69	0.44
45:a:707:VAL:HA	45:a:933:VAL:O	2.16	0.44
45:a:937:ILE:H	45:a:996:MET:HE2	1.82	0.44
45:a:964:THR:O	45:a:968:THR:HG23	2.16	0.44
46:e:687:LEU:HA	46:e:693:LEU:CB	2.47	0.44
46:e:865:THR:HG22	46:e:866:PHE:N	2.32	0.44
46:e:1066:ARG:NH2	46:e:1111:GLN:NE2	2.65	0.44
46:e:1388:SER:HA	46:e:1392:SER:HB3	1.99	0.44
30:f:1899:G:O2'	30:f:2334:U:O4	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:k:215:ILE:HD12	34:k:338:LEU:HD12	1.98	0.44
46:e:1196:THR:CG2	46:e:1197:LEU:N	2.81	0.44
48:v:80:MET:HE3	48:v:80:MET:HB3	1.75	0.44
30:f:2660:G:OP1	30:f:2750:U:O2'	2.35	0.44
45:a:25:ARG:HE	45:a:88:ARG:HB3	1.82	0.44
30:f:2205:U:C5	45:a:859:ARG:HG3	2.53	0.44
30:f:2964:G:N2	30:f:2967:A:OP2	2.41	0.44
39:p:95:ASN:OD1	39:p:98:ARG:NH2	2.51	0.44
45:a:4:ARG:O	45:a:309:PHE:CE1	2.66	0.44
45:a:664:ASN:ND2	45:a:688:ASP:OD2	2.51	0.44
45:a:936:ASP:OD1	45:a:996:MET:CE	2.66	0.44
46:e:1192:ARG:CG	46:e:1270:TRP:HH2	2.30	0.44
46:e:1395:LEU:HG	46:e:1450:PRO:HG3	1.99	0.44
9:I:38:ALA:HB3	9:I:59:MET:HB2	1.99	0.44
9:I:128:ARG:NE	47:g:12:GLU:OE2	2.50	0.44
30:f:1203:A:N3	30:f:2855:U:O2'	2.46	0.44
30:f:2960:C:H2'	30:f:2961:G:C8	2.53	0.44
33:j:135:ILE:HD12	33:j:149:ARG:HE	1.82	0.44
45:a:928:LEU:CD1	45:a:932:ASP:H	2.31	0.44
46:e:751:VAL:CA	46:e:754:ILE:HG23	2.47	0.44
46:e:968:ASN:HB2	46:e:1009:ILE:HG23	1.99	0.44
46:e:1239:LYS:HD3	46:e:1293:GLN:HE22	1.82	0.44
30:f:19:U:H2'	30:f:20:A:C8	2.52	0.44
30:f:799:G:O2'	43:t:18:TRP:NE1	2.47	0.44
30:f:1786:G:H2'	30:f:1787:A:C8	2.52	0.44
30:f:1888:U:H5''	34:k:247:ARG:HB2	2.00	0.44
40:q:120:ASP:OD1	40:q:120:ASP:N	2.44	0.44
46:e:244:GLU:HA	46:e:247:TRP:HD1	1.83	0.44
46:e:776:TYR:HB2	46:e:812:LEU:HB2	1.98	0.44
46:e:992:LEU:HD11	46:e:996:GLU:HB3	1.95	0.44
46:e:1025:ASN:O	46:e:1029:ARG:HG2	2.18	0.44
2:B:74[A]:ARG:NH1	30:f:3008:A:OP2	2.51	0.44
6:F:80:ARG:HG3	6:F:124:LEU:HD21	1.99	0.44
15:O:21:ILE:HD12	15:O:21:ILE:HG23	1.83	0.44
24:X:10:GLN:HA	24:X:13:GLU:HG2	1.99	0.44
30:f:520:U:O4	35:l:347:THR:OG1	2.35	0.44
33:j:101:VAL:HG22	33:j:165:VAL:HG22	2.00	0.44
45:a:78:VAL:HG12	45:a:82:LYS:HE3	1.99	0.44
45:a:884:MET:SD	45:a:888:VAL:HG23	2.58	0.44
46:e:841:VAL:O	46:e:844:LEU:HB3	2.18	0.44
47:g:2:ALA:HA	47:g:204:ALA:O	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:v:30:GLY:H	48:v:41:ILE:HG22	1.82	0.44
2:B:127[A]:LEU:HD22	6:F:156:VAL:HG13	2.00	0.44
12:L:112:ASP:OD2	32:i:85:G:N1	2.49	0.44
17:Q:46:THR:HG22	17:Q:48:ASP:H	1.82	0.44
30:f:2284:C:N4	30:f:2308:C:OP2	2.50	0.44
31:h:38:U:N3	31:h:41:G:OP2	2.41	0.44
36:m:205:SER:HB3	36:m:236:LEU:HD21	2.00	0.44
45:a:284:TYR:CG	45:a:313:LYS:CB	3.00	0.44
46:e:275:GLY:O	46:e:278:PRO:HD2	2.18	0.44
46:e:378:LEU:O	46:e:382:GLN:HG3	2.18	0.44
46:e:780:ILE:HB	46:e:799:THR:H	1.82	0.44
46:e:820:ASP:HB2	46:e:838:ILE:HD13	1.98	0.44
46:e:1458:GLY:HA3	46:e:1469:TRP:HE1	1.82	0.44
9:I:129:VAL:O	9:I:133:SER:HB3	2.17	0.44
14:N:36:GLY:HA3	14:N:40:HIS:CE1	2.53	0.44
30:f:1259:A:N3	30:f:1280:C:O2'	2.50	0.44
30:f:1813:A:O2'	30:f:1816:A:N3	2.46	0.44
30:f:3379:C:H4'	34:k:315:GLY:HA2	1.98	0.44
35:l:74:ILE:HD12	35:l:75:PRO:HD2	2.00	0.44
39:p:104:GLU:HA	39:p:107:GLU:HG3	2.00	0.44
46:e:241:LEU:HD23	46:e:246:ILE:HD12	1.99	0.44
46:e:306:VAL:HG12	46:e:310:LEU:HG	1.99	0.44
46:e:1307:ILE:CG2	46:e:1356:LEU:CD2	2.84	0.44
4:D:161:LYS:HD3	4:D:161:LYS:HA	1.82	0.43
6:F:80:ARG:HD2	7:G:155:PRO:HA	2.00	0.43
15:O:14:ARG:NH2	30:f:1139:G:OP2	2.51	0.43
22:V:9:ILE:HD12	43:t:174:ARG:HB2	1.99	0.43
30:f:1657:C:O2'	30:f:1797:A:OP2	2.30	0.43
30:f:2116:G:OP1	30:f:2118:C:N4	2.51	0.43
30:f:2357:A:H2'	30:f:2358:A:C8	2.53	0.43
30:f:3322:A:H2'	30:f:3323:A:C8	2.53	0.43
45:a:928:LEU:HD22	45:a:928:LEU:HA	1.83	0.43
46:e:196:GLU:H	46:e:196:GLU:HG2	1.65	0.43
46:e:981:ALA:HB2	46:e:1019:ILE:HG21	1.99	0.43
30:f:710:A:H2'	30:f:711:A:C8	2.54	0.43
30:f:911:C:OP1	33:j:14:SER:OG	2.32	0.43
30:f:2768:U:H2'	30:f:2769:A:H8	1.83	0.43
36:m:258:LYS:O	36:m:265:TYR:OH	2.31	0.43
39:p:82:LEU:HD13	39:p:222:PHE:HE2	1.84	0.43
46:e:251:ASN:HB3	46:e:254:ASN:CG	2.43	0.43
49:w:37:GLY:O	49:w:202:GLY:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:0:45:LEU:HB3	52:0:49:ALA:HB3	1.99	0.43
7:G:133:ALA:HB3	38:o:121:LYS:HB2	2.00	0.43
30:f:595:G:OP2	38:o:30:ARG:NH1	2.51	0.43
30:f:1222:G:N2	30:f:1285:G:O2'	2.51	0.43
30:f:3016:A:H2'	30:f:3017:A:H8	1.83	0.43
41:r:184:LYS:HB2	41:r:184:LYS:HE2	1.86	0.43
45:a:955:LYS:HG2	45:a:957:GLN:HE22	1.82	0.43
46:e:307:CYS:SG	46:e:308:PRO:HD3	2.58	0.43
46:e:1395:LEU:HB3	46:e:1449:TYR:HD2	1.83	0.43
49:w:96:ASN:HD21	49:w:99:LEU:HD12	1.84	0.43
8:H:20:SER:HA	8:H:23:THR:HG22	2.00	0.43
9:I:117:PRO:HA	9:I:135:VAL:HG13	2.00	0.43
23:W:63:ARG:NH1	32:i:58:G:O6	2.50	0.43
30:f:3295:A:H2'	30:f:3296:A:C8	2.53	0.43
39:p:86:THR:HA	39:p:89:GLU:HG2	2.00	0.43
45:a:884:MET:SD	45:a:888:VAL:CG2	3.07	0.43
23:W:58:THR:OG1	23:W:59:THR:N	2.51	0.43
30:f:1237:G:H22	30:f:1251:A:H2	1.66	0.43
30:f:1666:G:H2'	30:f:1667:A:H8	1.83	0.43
39:p:239:GLY:O	39:p:243:GLN:HB2	2.19	0.43
46:e:43:TYR:CD2	46:e:82:PHE:HA	2.54	0.43
46:e:961:LEU:HD22	46:e:1006:LEU:HD21	2.01	0.43
46:e:1209:ILE:HG23	46:e:1238:PHE:HD1	1.82	0.43
1:A:12:ARG:NH1	30:f:297:G:O6	2.46	0.43
23:W:27:PHE:HA	23:W:34:CYS:HA	2.01	0.43
46:e:122:ARG:HA	46:e:125:ILE:HD11	2.01	0.43
46:e:1474:MET:O	46:e:1478:HIS:CB	2.66	0.43
47:g:119:PRO:O	47:g:139:ARG:NH1	2.50	0.43
52:0:15:LEU:O	52:0:19:LEU:HG	2.18	0.43
4:D:124:LEU:HD13	4:D:127:LEU:HD23	2.01	0.43
30:f:716:A:OP1	30:f:752:C:O2'	2.37	0.43
30:f:1288:U:H2'	30:f:1289:G:C8	2.54	0.43
30:f:2745:G:N2	30:f:2748:A:OP2	2.47	0.43
30:f:2836:C:H5	30:f:2852:C:H42	1.67	0.43
46:e:777:MET:HG3	46:e:904:VAL:HG11	2.00	0.43
48:v:72:ASP:OD1	48:v:72:ASP:N	2.50	0.43
52:0:75:LYS:O	52:0:78:PRO:HD2	2.19	0.43
1:A:158:HIS:HB3	1:A:161:ALA:HB3	2.00	0.43
3:C:56:ARG:NH2	3:C:75:GLU:OE2	2.51	0.43
5:E:102:LEU:HD22	5:E:138:LEU:HD22	2.01	0.43
6:F:70:THR:OG1	44:u:55:ARG:NH1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:34:SER:OG	30:f:3085:G:OP1	2.33	0.43
24:X:2:ALA:N	24:X:51:LEU:O	2.52	0.43
28:c:66:GLY:HA2	33:j:80:GLU:HG3	2.01	0.43
30:f:2129:U:H2'	30:f:2130:G:C8	2.54	0.43
30:f:2514:U:H5'	39:p:68:ARG:HG3	2.00	0.43
44:u:93:LYS:HE3	44:u:93:LYS:HB2	1.87	0.43
45:a:636:MET:HE2	45:a:636:MET:HB2	1.95	0.43
46:e:728:GLN:HA	46:e:731:LEU:HG	2.01	0.43
46:e:1532:ASN:N	46:e:1532:ASN:ND2	2.63	0.43
47:g:38:PHE:O	47:g:42:LEU:HB2	2.19	0.43
1:A:68:ARG:HA	1:A:98:LEU:HD21	2.01	0.43
30:f:2218:G:H2'	30:f:2219:A:C8	2.54	0.43
30:f:3121:U:H1'	30:f:3122:A:H5''	2.01	0.43
30:f:3358:U:H2'	30:f:3359:A:H8	1.84	0.43
46:e:1192:ARG:HA	46:e:1332:ILE:HD11	2.00	0.43
46:e:1409:ARG:H	46:e:1409:ARG:HE	1.67	0.43
2:B:54[A]:TYR:OH	2:B:73[A]:PHE:O	2.37	0.43
18:R:3:SER:OG	18:R:4:LEU:N	2.51	0.43
30:f:1675:G:H2'	30:f:1676:A:H8	1.83	0.43
30:f:2514:U:OP2	30:f:2586:G:N2	2.50	0.43
46:e:1330:TYR:HE1	46:e:1347:GLU:HB3	1.83	0.43
12:L:86:THR:OG1	12:L:94:SER:OG	2.36	0.42
23:W:45:ARG:NH2	30:f:361:A:O3'	2.52	0.42
30:f:2160:G:H2'	30:f:2161:G:H8	1.84	0.42
30:f:2747:A:H2'	30:f:2748:A:C8	2.54	0.42
45:a:332:PRO:O	45:a:333:TYR:HB3	2.19	0.42
45:a:934:VAL:HG22	45:a:936:ASP:O	2.19	0.42
46:e:189:ASN:HB2	46:e:192:THR:HG23	2.00	0.42
46:e:321:ASP:OD1	46:e:321:ASP:O	2.36	0.42
46:e:397:ASN:O	46:e:398:SER:C	2.60	0.42
49:w:43:PRO:HD3	49:w:163:LEU:HD21	2.01	0.42
50:y:53:G:C6	50:y:54:U:C5	3.06	0.42
3:C:179:GLN:HA	3:C:182:ILE:HG22	2.00	0.42
9:I:80:ARG:HB2	9:I:99:ALA:HB3	2.00	0.42
30:f:2213:A:H2'	30:f:2214:A:C8	2.54	0.42
30:f:3233:C:H2'	30:f:3234:A:C8	2.55	0.42
41:r:72:ALA:HB2	41:r:155:ALA:HB2	2.01	0.42
45:a:309:PHE:HD2	45:a:340:PHE:CE2	2.37	0.42
46:e:1206:GLN:HG3	46:e:1278:TYR:HA	2.01	0.42
27:b:28:TYR:HB3	27:b:69:VAL:HB	2.01	0.42
30:f:417:A:H2'	30:f:418:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:f:2442:G:H2'	30:f:2443:A:H8	1.83	0.42
44:u:47:ASP:HB2	44:u:55:ARG:HG3	2.02	0.42
45:a:349:TYR:HE2	45:a:565:LEU:HD13	1.85	0.42
45:a:515:TYR:O	45:a:519:THR:HG23	2.18	0.42
6:F:95:ARG:HB2	6:F:140:VAL:HG23	2.00	0.42
18:R:45:ARG:O	30:f:1145:G:O2'	2.36	0.42
30:f:63:A:N3	30:f:78:U:O2'	2.43	0.42
45:a:971:LEU:HD22	45:a:997:ILE:HG23	2.01	0.42
46:e:321:ASP:HB2	46:e:329:TRP:NE1	2.34	0.42
46:e:397:ASN:ND2	46:e:401:VAL:HG23	2.35	0.42
50:y:56:C:H2'	50:y:57:G:C8	2.55	0.42
21:U:78:LYS:HA	21:U:81:ARG:HG2	2.00	0.42
22:V:18:THR:HG23	43:t:106:GLN:HB3	2.01	0.42
28:c:44:LYS:NZ	30:f:1727:G:OP1	2.51	0.42
30:f:673:U:H2'	30:f:674:G:C8	2.55	0.42
30:f:1203:A:H2'	30:f:1204:A:C8	2.55	0.42
30:f:1666:G:H2'	30:f:1667:A:C8	2.54	0.42
36:m:6:ASP:OD1	36:m:6:ASP:N	2.48	0.42
39:p:183:LYS:HB2	39:p:194:THR:HG23	2.01	0.42
42:s:96:PHE:HB2	42:s:156:LYS:HE3	2.01	0.42
46:e:16:LEU:HB3	46:e:19:GLY:O	2.19	0.42
46:e:783:ARG:HB3	46:e:851:LEU:HD22	2.01	0.42
52:0:14:LYS:HE3	52:0:52:LEU:HD11	2.00	0.42
52:0:70:LEU:HB3	52:0:73:PHE:CD1	2.55	0.42
6:F:32:SER:HB2	6:F:36:ILE:HD12	2.01	0.42
8:H:41:ILE:HG21	8:H:54:VAL:HG21	2.02	0.42
30:f:158:G:H2'	30:f:159:A:H8	1.85	0.42
30:f:3023:U:H2'	30:f:3024:A:H8	1.84	0.42
33:j:46:LYS:HD2	33:j:46:LYS:HA	1.81	0.42
34:k:83:PRO:O	34:k:165:GLN:NE2	2.47	0.42
36:m:200:PHE:HB3	36:m:237:GLU:HG2	2.02	0.42
46:e:358:VAL:HG11	46:e:380:PHE:CE2	2.49	0.42
46:e:1196:THR:HG23	46:e:1197:LEU:N	2.34	0.42
46:e:1308:THR:HG21	46:e:1370:TRP:HH2	1.84	0.42
46:e:1407:MET:HB2	46:e:1419:ILE:HB	2.02	0.42
50:y:32:U:H2'	50:y:33:U:C6	2.54	0.42
4:D:36:LEU:O	4:D:40:THR:OG1	2.27	0.42
6:F:137:ARG:HH21	30:f:1213:G:H5'	1.85	0.42
24:X:33:LYS:HA	24:X:33:LYS:HD3	1.84	0.42
30:f:760:G:O2'	30:f:770:G:N2	2.43	0.42
30:f:1579:C:H2'	30:f:1580:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:f:3016:A:H2'	30:f:3017:A:C8	2.55	0.42
46:e:351:SER:O	46:e:354:PHE:HB2	2.19	0.42
46:e:354:PHE:O	46:e:358:VAL:HG22	2.15	0.42
3:C:182:ILE:HD12	3:C:182:ILE:HA	1.85	0.42
16:P:73:GLY:N	16:P:76:GLU:OE1	2.42	0.42
27:b:10:THR:HG21	27:b:72:LEU:HD13	2.01	0.42
35:l:261:VAL:HG23	35:l:262:TRP:CD1	2.55	0.42
45:a:3:GLN:HE21	45:a:3:GLN:HB2	1.50	0.42
45:a:181:VAL:HG21	45:a:262:ALA:HA	2.02	0.42
45:a:641:LEU:HA	45:a:699:MET:HE1	2.02	0.42
46:e:1194:LEU:HD23	46:e:1194:LEU:HA	1.87	0.42
47:g:199:VAL:HG23	47:g:204:ALA:HB2	2.02	0.42
52:0:67:LEU:HD22	52:0:67:LEU:HA	1.85	0.42
1:A:90:ASN:ND2	30:f:2424:A:OP1	2.50	0.42
20:T:95:ILE:HD13	20:T:95:ILE:HG21	1.81	0.42
30:f:1194:G:H2'	30:f:1195:A:C8	2.55	0.42
30:f:1660:C:H2'	30:f:1661:G:H8	1.85	0.42
30:f:2852:C:N3	41:r:158:LYS:NZ	2.68	0.42
35:l:6:VAL:N	35:l:20:LEU:O	2.48	0.42
45:a:426:GLU:HB2	45:a:434:ALA:HB2	1.95	0.42
46:e:344:SER:O	46:e:347:ARG:HG2	2.19	0.42
46:e:1330:TYR:CD2	46:e:1351:LEU:HD13	2.55	0.42
48:v:51:5CT:H5	48:v:52:HIS:CE1	2.55	0.42
50:y:17:C:H4'	50:y:60:U:N3	2.34	0.42
16:P:29:SER:OG	30:f:1730:G:O6	2.37	0.42
30:f:2413:A:H2'	30:f:2414:G:H8	1.85	0.42
30:f:2711:C:O2'	30:f:2744:U:OP1	2.38	0.42
30:f:3163:A:N6	30:f:3288:G:O6	2.53	0.42
36:m:95:TRP:CE3	36:m:198:TYR:HB3	2.54	0.42
46:e:265:LEU:HD22	46:e:316:LEU:HD22	2.01	0.42
46:e:321:ASP:HB2	46:e:329:TRP:HE1	1.85	0.42
46:e:813:ILE:HG12	46:e:845:VAL:HG22	2.02	0.42
46:e:985:ILE:HD11	46:e:1023:ARG:HG3	2.01	0.42
46:e:1080:LEU:HD11	46:e:1102:CYS:O	2.19	0.42
46:e:1429:LYS:HE2	46:e:1429:LYS:HB3	1.93	0.42
27:b:10:THR:HA	27:b:20:HIS:HD2	1.84	0.41
30:f:129:U:H2'	30:f:130:A:C8	2.54	0.41
30:f:296:A:N3	30:f:299:G:O2'	2.53	0.41
30:f:443:G:O6	30:f:490:C:N4	2.53	0.41
30:f:531:G:H2'	30:f:532:A:C8	2.55	0.41
30:f:2772:C:H4'	30:f:2773:C:H5'	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:k:214:MET:HE3	34:k:214:MET:HB3	1.94	0.41
35:l:276:LEU:HD23	35:l:276:LEU:HA	1.91	0.41
36:m:144:VAL:HG11	36:m:171:LEU:HD13	2.02	0.41
36:m:266:ALA:O	36:m:270:LYS:HB2	2.20	0.41
37:n:112:THR:HG23	37:n:115:GLU:H	1.85	0.41
45:a:284:TYR:CD2	45:a:313:LYS:HG3	2.55	0.41
46:e:1316:THR:HG22	46:e:1386:PHE:HA	2.01	0.41
1:A:98:LEU:HD22	1:A:128:LYS:HD2	2.02	0.41
3:C:116:HIS:HB3	3:C:149:VAL:HB	2.02	0.41
45:a:840:LYS:HD3	45:a:840:LYS:HA	1.70	0.41
46:e:1473:ILE:HA	46:e:1494:PHE:HE2	1.84	0.41
50:y:53:G:H2'	50:y:54:U:H6	1.85	0.41
7:G:88:ARG:O	30:f:2722:U:O2'	2.35	0.41
20:T:60:ARG:NH1	30:f:1593:A:OP1	2.53	0.41
27:b:61:LYS:NZ	27:b:63:LYS:O	2.53	0.41
30:f:2451:G:H2'	30:f:2452:G:C8	2.55	0.41
30:f:3218:A:H5''	30:f:3219:G:C5	2.55	0.41
45:a:21:LEU:HB3	45:a:89:LEU:HG	2.02	0.41
45:a:696:GLN:HE21	45:a:696:GLN:HB2	1.62	0.41
46:e:765:PHE:HD1	46:e:819:LEU:HA	1.86	0.41
46:e:1007:LEU:HD11	46:e:1055:PHE:CD1	2.55	0.41
30:f:675:C:O2'	30:f:679:U:OP1	2.34	0.41
46:e:1068:MET:HE3	46:e:1068:MET:HB3	1.91	0.41
30:f:20:A:H2'	30:f:21:G:C8	2.56	0.41
30:f:745:C:H2'	30:f:746:A:H8	1.85	0.41
30:f:1221:A:C4	52:0:12:PHE:HZ	2.38	0.41
30:f:1497:C:H2'	30:f:1498:A:C8	2.56	0.41
30:f:1577:G:H2'	30:f:1578:C:H6	1.86	0.41
31:h:53:U:O2'	31:h:55:A:N7	2.53	0.41
34:k:284:ARG:HB3	34:k:323:MET:HB3	2.01	0.41
45:a:24:TYR:HB3	45:a:43:PHE:HB3	2.02	0.41
46:e:1128:GLN:HB3	46:e:1162:MET:HE3	2.03	0.41
46:e:1184:ILE:CG2	46:e:1191:SER:HB3	2.43	0.41
46:e:1342:GLU:H	46:e:1342:GLU:HG3	1.64	0.41
6:F:110:MET:HE3	6:F:110:MET:HB3	1.95	0.41
30:f:1421:G:H2'	30:f:1422:G:H8	1.85	0.41
30:f:2418:G:N3	30:f:2418:G:H5'	2.35	0.41
30:f:3198:U:H1'	40:q:21:LYS:HB2	2.01	0.41
35:l:343:LYS:HE2	35:l:343:LYS:HB2	1.92	0.41
41:r:52:LEU:HB3	41:r:136:PHE:HB2	2.02	0.41
46:e:347:ARG:HB3	46:e:380:PHE:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:e:813:ILE:HG23	46:e:862:PHE:HE1	1.86	0.41
2:B:8[A]:VAL:HG12	2:B:117[A]:ARG:HG3	2.03	0.41
9:I:135:VAL:HG23	47:g:102:SER:HB3	2.03	0.41
12:L:63:LYS:HA	12:L:63:LYS:HD3	1.92	0.41
22:V:5:THR:HG23	22:V:12:ASN:HB2	2.03	0.41
30:f:352:A:H61	30:f:365:A:H5''	1.86	0.41
30:f:689:U:O4	35:l:209:TYR:OH	2.35	0.41
43:t:57:VAL:HG23	43:t:147:ILE:HD12	2.02	0.41
45:a:520:GLU:O	45:a:524:ILE:HG13	2.20	0.41
45:a:588:VAL:HG13	45:a:622:ILE:HG22	2.03	0.41
46:e:27:LEU:HB2	46:e:188:GLU:CD	2.45	0.41
46:e:684:SER:CA	46:e:715:LEU:HD11	2.43	0.41
46:e:957:CYS:O	46:e:961:LEU:HG	2.21	0.41
3:C:122:ALA:HB3	3:C:143:PRO:HB2	2.02	0.41
26:Z:100:TYR:OH	30:f:2848:G:OP1	2.29	0.41
30:f:1083:G:H2'	30:f:1084:A:C8	2.56	0.41
30:f:1764:U:H3'	30:f:1765:U:H4'	2.03	0.41
40:q:9:GLN:HB3	40:q:52:LEU:HD11	2.01	0.41
44:u:113:THR:OG1	44:u:114:ASP:N	2.52	0.41
45:a:896:ARG:HH12	48:v:130:GLU:HA	1.86	0.41
46:e:754:ILE:CG1	46:e:755:ASN:N	2.83	0.41
46:e:944:VAL:CG1	46:e:980:LEU:CD2	2.97	0.41
46:e:1421:LEU:HD23	46:e:1428:VAL:HG13	2.02	0.41
49:w:122:ARG:HA	49:w:122:ARG:HD2	1.65	0.41
1:A:155:VAL:HG12	30:f:58:G:H4'	2.03	0.41
3:C:131:ARG:HG3	3:C:137:ASN:ND2	2.36	0.41
5:E:7:GLN:NE2	5:E:35:ALA:O	2.53	0.41
7:G:102:ARG:HD2	7:G:102:ARG:HA	1.77	0.41
14:N:114:GLY:O	14:N:137:LYS:NZ	2.54	0.41
18:R:99:ASN:O	30:f:1388:U:O2'	2.36	0.41
23:W:31:LYS:NZ	30:f:815:G:OP2	2.52	0.41
27:b:100:LYS:HE3	27:b:100:LYS:HB3	1.90	0.41
30:f:946:U:H2'	30:f:947:G:H8	1.86	0.41
30:f:2470:C:OP1	49:w:27:ASN:N	2.47	0.41
30:f:3217:C:C5	30:f:3220:G:H1'	2.56	0.41
35:l:34:ILE:HG21	35:l:120:TYR:HD2	1.85	0.41
41:r:44:ASP:OD1	41:r:44:ASP:N	2.48	0.41
42:s:75:LYS:O	42:s:79:ILE:HG13	2.21	0.41
45:a:375:ILE:CG2	45:a:532:GLN:HE21	2.18	0.41
45:a:869:LEU:HD23	45:a:872:ILE:HD12	2.02	0.41
46:e:397:ASN:HB2	46:e:400:GLU:CG	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:e:591:LEU:CB	46:e:620:SER:C	2.94	0.41
46:e:894:LEU:HD21	46:e:912:VAL:HG11	2.02	0.41
46:e:1237:LYS:HE3	46:e:1237:LYS:HB2	1.87	0.41
46:e:1316:THR:O	46:e:1320:LYS:HG3	2.20	0.41
46:e:1335:ASN:HB2	46:e:1347:GLU:CD	2.46	0.41
48:v:96:ASP:OD1	48:v:96:ASP:N	2.54	0.41
49:w:151:VAL:O	49:w:154:THR:OG1	2.33	0.41
49:w:204:LEU:HB2	49:w:216:LEU:O	2.21	0.41
50:y:4:C:H2'	50:y:5:G:C8	2.55	0.41
50:y:21:A:O5'	50:y:21:A:C8	2.73	0.41
1:A:9:GLU:HG3	22:V:44:VAL:HG21	2.03	0.41
6:F:90:MET:HE3	30:f:1213:G:H4'	2.03	0.41
14:N:75:LEU:HD23	14:N:75:LEU:HA	1.92	0.41
18:R:4:LEU:HD12	18:R:5:PRO:HD2	2.01	0.41
30:f:1660:C:H2'	30:f:1661:G:C8	2.56	0.41
34:k:218:ILE:HG12	34:k:276:THR:HG23	2.03	0.41
45:a:597:THR:HG22	45:a:621:TRP:HE1	1.86	0.41
46:e:351:SER:O	46:e:354:PHE:CB	2.69	0.41
46:e:1444:LYS:HE3	46:e:1444:LYS:HB2	1.81	0.41
48:v:48:LYS:HD2	48:v:55:ALA:HB2	2.03	0.41
1:A:18:VAL:HG13	1:A:19:LEU:HD12	2.02	0.40
2:B:189[A]:ASP:OD1	2:B:190[A]:VAL:N	2.53	0.40
4:D:155:MET:HE2	4:D:163:PRO:HB3	2.03	0.40
6:F:43:TYR:OH	31:h:96:U:OP1	2.35	0.40
30:f:129:U:H3	30:f:139:G:H1	1.69	0.40
41:r:144:ASN:HD22	41:r:144:ASN:N	2.18	0.40
41:r:181:TYR:CE2	41:r:185:ARG:HD2	2.56	0.40
46:e:894:LEU:HD23	46:e:894:LEU:HA	1.83	0.40
48:v:60:VAL:HG13	48:v:71:GLU:OE2	2.21	0.40
1:A:174:ILE:HG21	30:f:63:A:H5''	2.04	0.40
2:B:121[A]:PRO:HA	2:B:124[A]:LEU:HD12	2.03	0.40
12:L:51:ARG:NH2	32:i:83:C:O2	2.54	0.40
17:Q:20:LEU:HD11	17:Q:32:ALA:HB2	2.03	0.40
17:Q:110:GLU:HG3	46:e:1424:ILE:HD11	2.01	0.40
20:T:93:PHE:HD2	20:T:94:LEU:HD22	1.86	0.40
24:X:2:ALA:HB1	30:f:1747:G:H21	1.86	0.40
30:f:1249:G:H2'	30:f:1250:G:H8	1.86	0.40
30:f:2357:A:H2'	30:f:2358:A:H8	1.85	0.40
30:f:2965:U:O2'	33:j:221:LYS:HD3	2.20	0.40
31:h:84:A:H2'	31:h:85:G:C8	2.56	0.40
40:q:90:MET:HE3	40:q:179:ILE:HG22	2.01	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:a:102:VAL:HA	45:a:112:LEU:O	2.20	0.40
45:a:106:ALA:HB3	45:a:109:HIS:HB2	2.03	0.40
45:a:220:ILE:CB	45:a:249:GLU:CA	2.99	0.40
45:a:577:TYR:CG	45:a:600:ILE:HD11	2.56	0.40
46:e:130:LYS:HA	46:e:173:PHE:CE2	2.55	0.40
46:e:299:THR:HG21	46:e:301:LYS:NZ	2.36	0.40
46:e:314:LEU:CD1	46:e:357:ALA:HB3	2.51	0.40
46:e:735:GLN:O	46:e:814:ARG:HD2	2.21	0.40
46:e:1392:SER:HB2	46:e:1448:ASN:HA	2.03	0.40
50:y:43:G:H3'	50:y:44:A:H8	1.87	0.40
5:E:31:GLU:HA	5:E:34:GLN:HB2	2.03	0.40
26:Z:113:ARG:NH2	30:f:1190:A:H4'	2.36	0.40
30:f:182:U:H2'	30:f:183:G:H8	1.85	0.40
30:f:1108:U:H2'	30:f:1109:U:C6	2.56	0.40
30:f:1238:C:C4'	51:z:139:VAL:CB	2.98	0.40
30:f:3092:C:O2'	30:f:3094:A:OP2	2.28	0.40
36:m:108:ARG:CZ	36:m:253:PHE:HB2	2.51	0.40
38:o:129:LEU:HD23	38:o:129:LEU:HA	1.89	0.40
43:t:189:GLU:HA	43:t:192:GLU:HG3	2.03	0.40
45:a:340:PHE:HE2	45:a:341:PHE:CZ	2.39	0.40
45:a:392:ILE:CD1	45:a:521:TYR:CD2	3.03	0.40
46:e:84:ASN:H	46:e:87:PHE:HB3	1.86	0.40
46:e:182:LYS:HE2	46:e:182:LYS:HB3	1.79	0.40
50:y:61:C:H2'	50:y:62:C:C6	2.57	0.40
6:F:40:ARG:HA	6:F:40:ARG:HD2	1.84	0.40
7:G:73:GLY:HA2	7:G:89:LEU:O	2.21	0.40
30:f:1553:U:H4'	30:f:1554:U:H5'	2.04	0.40
30:f:1596:C:H2'	30:f:1597:C:C6	2.56	0.40
30:f:1799:A:H2'	30:f:1800:A:C8	2.56	0.40
33:j:52:SER:HB3	33:j:191:LEU:HD23	2.03	0.40
39:p:178:ALA:HB2	39:p:218:ILE:HG23	2.02	0.40
45:a:284:TYR:CG	45:a:313:LYS:HB2	2.51	0.40
46:e:96:ALA:O	46:e:99:ILE:HG12	2.22	0.40
46:e:222:LEU:HG	46:e:229:VAL:HG11	2.02	0.40
46:e:314:LEU:HB3	46:e:357:ALA:HB1	2.03	0.40
46:e:407:THR:HG23	46:e:450:SER:CB	2.52	0.40
46:e:1274:LEU:HD13	46:e:1274:LEU:HA	1.76	0.40
46:e:1358:GLN:O	46:e:1362:ASN:CG	2.64	0.40
30:f:94:G:H2'	30:f:95:A:C8	2.57	0.40
30:f:240:U:H4'	30:f:241:G:H5'	2.02	0.40
30:f:2536:A:H2'	30:f:2537:U:C4	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:a:506:VAL:HG13	45:a:521:TYR:CZ	2.56	0.40
45:a:532:GLN:O	45:a:536:GLU:HG2	2.21	0.40
46:e:459:GLU:CB	46:e:496:ALA:HB1	2.52	0.40
46:e:847:ASP:O	46:e:851:LEU:HG	2.21	0.40
46:e:944:VAL:HG22	46:e:1002:LEU:HD12	2.03	0.40
46:e:1303:MET:O	46:e:1303:MET:HE2	2.21	0.40
46:e:1553:LEU:HD23	46:e:1553:LEU:HA	1.88	0.40
47:g:4:ARG:HD2	47:g:208:LEU:HA	2.04	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	A	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
2	B	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
3	C	181/184 (98%)	172 (95%)	9 (5%)	0	100	100
4	D	183/186 (98%)	176 (96%)	7 (4%)	0	100	100
5	E	154/189 (82%)	151 (98%)	3 (2%)	0	100	100
6	F	169/172 (98%)	163 (96%)	6 (4%)	0	100	100
7	G	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
8	H	98/121 (81%)	93 (95%)	5 (5%)	0	100	100
9	I	134/137 (98%)	132 (98%)	2 (2%)	0	100	100
10	J	61/155 (39%)	61 (100%)	0	0	100	100
11	K	119/142 (84%)	118 (99%)	1 (1%)	0	100	100
12	L	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
13	M	133/136 (98%)	126 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	N	146/149 (98%)	136 (93%)	10 (7%)	0	100	100
15	O	56/59 (95%)	52 (93%)	3 (5%)	1 (2%)	6	18
16	P	94/105 (90%)	93 (99%)	1 (1%)	0	100	100
17	Q	107/113 (95%)	98 (92%)	9 (8%)	0	100	100
18	R	125/130 (96%)	123 (98%)	2 (2%)	0	100	100
19	S	104/107 (97%)	101 (97%)	3 (3%)	0	100	100
20	T	110/121 (91%)	108 (98%)	2 (2%)	0	100	100
21	U	117/120 (98%)	112 (96%)	5 (4%)	0	100	100
22	V	97/100 (97%)	93 (96%)	4 (4%)	0	100	100
23	W	79/88 (90%)	75 (95%)	4 (5%)	0	100	100
24	X	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
25	Y	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
26	Z	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
27	b	101/106 (95%)	95 (94%)	6 (6%)	0	100	100
28	c	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
29	d	20/25 (80%)	19 (95%)	1 (5%)	0	100	100
33	j	244/254 (96%)	225 (92%)	19 (8%)	0	100	100
34	k	384/387 (99%)	364 (95%)	20 (5%)	0	100	100
35	l	359/362 (99%)	329 (92%)	29 (8%)	1 (0%)	36	60
36	m	292/297 (98%)	278 (95%)	14 (5%)	0	100	100
37	n	163/176 (93%)	154 (94%)	9 (6%)	0	100	100
38	o	220/244 (90%)	207 (94%)	13 (6%)	0	100	100
39	p	231/256 (90%)	220 (95%)	11 (5%)	0	100	100
40	q	189/191 (99%)	174 (92%)	14 (7%)	1 (0%)	24	48
41	r	216/221 (98%)	206 (95%)	10 (5%)	0	100	100
42	s	167/174 (96%)	161 (96%)	5 (3%)	1 (1%)	21	44
43	t	191/199 (96%)	174 (91%)	16 (8%)	1 (0%)	24	48
44	u	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
45	a	842/1038 (81%)	831 (99%)	11 (1%)	0	100	100
46	e	1519/1562 (97%)	1505 (99%)	11 (1%)	3 (0%)	43	68
47	g	223/245 (91%)	215 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	v	139/157 (88%)	139 (100%)	0	0	100	100
49	w	214/217 (99%)	211 (99%)	3 (1%)	0	100	100
51	z	144/165 (87%)	137 (95%)	6 (4%)	1 (1%)	18	41
52	0	117/312 (38%)	116 (99%)	0	1 (1%)	14	35
All	All	9314/10279 (91%)	8970 (96%)	334 (4%)	10 (0%)	49	73

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
46	e	393	PHE
51	z	88	PRO
46	e	396	ARG
35	l	4	PRO
40	q	107	ASP
42	s	108	GLU
52	0	93	LEU
46	e	855	PRO
15	O	21	ILE
43	t	47	ALA

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	A	175/176 (99%)	175 (100%)	0	100	100
2	B	160/162 (99%)	160 (100%)	0	100	100
3	C	138/146 (94%)	138 (100%)	0	100	100
4	D	150/151 (99%)	150 (100%)	0	100	100
5	E	129/154 (84%)	129 (100%)	0	100	100
6	F	155/156 (99%)	155 (100%)	0	100	100
7	G	135/137 (98%)	135 (100%)	0	100	100
8	H	87/107 (81%)	87 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	I	104/105 (99%)	104 (100%)	0	100	100
10	J	54/129 (42%)	54 (100%)	0	100	100
11	K	104/118 (88%)	104 (100%)	0	100	100
12	L	108/110 (98%)	108 (100%)	0	100	100
13	M	112/116 (97%)	112 (100%)	0	100	100
14	N	117/119 (98%)	117 (100%)	0	100	100
15	O	46/47 (98%)	46 (100%)	0	100	100
16	P	81/88 (92%)	81 (100%)	0	100	100
17	Q	92/97 (95%)	92 (100%)	0	100	100
18	R	107/111 (96%)	107 (100%)	0	100	100
19	S	90/91 (99%)	90 (100%)	0	100	100
20	T	95/103 (92%)	95 (100%)	0	100	100
21	U	104/105 (99%)	104 (100%)	0	100	100
22	V	80/82 (98%)	80 (100%)	0	100	100
23	W	67/71 (94%)	67 (100%)	0	100	100
24	X	68/69 (99%)	68 (100%)	0	100	100
25	Y	45/46 (98%)	45 (100%)	0	100	100
26	Z	45/116 (39%)	45 (100%)	0	100	100
27	b	87/91 (96%)	87 (100%)	0	100	100
28	c	71/72 (99%)	71 (100%)	0	100	100
29	d	20/23 (87%)	20 (100%)	0	100	100
33	j	189/196 (96%)	188 (100%)	1 (0%)	81	92
34	k	320/323 (99%)	320 (100%)	0	100	100
35	l	288/289 (100%)	288 (100%)	0	100	100
36	m	241/245 (98%)	241 (100%)	0	100	100
37	n	139/155 (90%)	139 (100%)	0	100	100
38	o	186/205 (91%)	186 (100%)	0	100	100
39	p	187/208 (90%)	187 (100%)	0	100	100
40	q	168/171 (98%)	168 (100%)	0	100	100
41	r	185/187 (99%)	184 (100%)	1 (0%)	81	92
42	s	145/150 (97%)	145 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	t	154/159 (97%)	154 (100%)	0	100	100
44	u	107/109 (98%)	107 (100%)	0	100	100
45	a	676/949 (71%)	637 (94%)	39 (6%)	18	42
46	e	1150/1451 (79%)	1067 (93%)	83 (7%)	13	32
47	g	180/211 (85%)	180 (100%)	0	100	100
48	v	119/132 (90%)	116 (98%)	3 (2%)	42	71
49	w	197/198 (100%)	197 (100%)	0	100	100
52	0	104/254 (41%)	94 (90%)	10 (10%)	8	20
All	All	7561/8690 (87%)	7424 (98%)	137 (2%)	51	78

All (137) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	j	221	LYS
41	r	112	GLN
45	a	3	GLN
45	a	9	ASP
45	a	10	LEU
45	a	25	ARG
45	a	27	SER
45	a	32	ILE
45	a	63	THR
45	a	77	VAL
45	a	89	LEU
45	a	102	VAL
45	a	113	VAL
45	a	121	ASN
45	a	139	LEU
45	a	156	LEU
45	a	199	ILE
45	a	285	ILE
45	a	293	TYR
45	a	316	ILE
45	a	384	LEU
45	a	450	VAL
45	a	565	LEU
45	a	589	MET
45	a	605	ILE
45	a	609	ASP

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Mol	Chain	Res	Type
45	a	630	VAL
45	a	649	TRP
45	a	665	VAL
45	a	692	LEU
45	a	696	GLN
45	a	697	LEU
45	a	837	VAL
45	a	868	THR
45	a	881	GLU
45	a	917	TYR
45	a	928	LEU
45	a	934	VAL
45	a	947	LEU
45	a	1003	GLN
45	a	1011	VAL
46	e	28	ASN
46	e	102	ASP
46	e	105	VAL
46	e	125	ILE
46	e	143	LEU
46	e	175	GLU
46	e	178	LEU
46	e	190	GLU
46	e	252	LEU
46	e	264	VAL
46	e	299	THR
46	e	310	LEU
46	e	328	ILE
46	e	358	VAL
46	e	394	SER
46	e	401	VAL
46	e	403	ASN
46	e	412	PHE
46	e	698	TYR
46	e	704	THR
46	e	707	LYS
46	e	731	LEU
46	e	733	HIS
46	e	754	ILE
46	e	770	ILE
46	e	780	ILE
46	e	782	TYR

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Mol	Chain	Res	Type
46	e	790	LEU
46	e	807	LYS
46	e	812	LEU
46	e	819	LEU
46	e	820	ASP
46	e	823	LEU
46	e	826	LEU
46	e	842	SER
46	e	893	MET
46	e	895	THR
46	e	904	VAL
46	e	921	ILE
46	e	933	LEU
46	e	987	ILE
46	e	990	VAL
46	e	1019	ILE
46	e	1047	THR
46	e	1050	LEU
46	e	1079	LEU
46	e	1084	LEU
46	e	1086	MET
46	e	1094	TYR
46	e	1102	CYS
46	e	1135	MET
46	e	1158	VAL
46	e	1179	LEU
46	e	1189	ASN
46	e	1193	LEU
46	e	1195	THR
46	e	1240	LEU
46	e	1248	VAL
46	e	1258	GLU
46	e	1269	LEU
46	e	1274	LEU
46	e	1286	MET
46	e	1300	ILE
46	e	1303	MET
46	e	1356	LEU
46	e	1358	GLN
46	e	1365	CYS
46	e	1367	THR
46	e	1379	LEU

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Mol	Chain	Res	Type
46	e	1391	ILE
46	e	1395	LEU
46	e	1409	ARG
46	e	1417	LEU
46	e	1421	LEU
46	e	1432	TYR
46	e	1439	LEU
46	e	1441	ILE
46	e	1454	ILE
46	e	1474	MET
46	e	1476	THR
46	e	1480	ILE
46	e	1491	LEU
46	e	1539	LEU
48	v	54	HIS
48	v	71	GLU
48	v	73	LEU
52	0	30	VAL
52	0	51	VAL
52	0	52	LEU
52	0	67	LEU
52	0	76	LEU
52	0	80	VAL
52	0	93	LEU
52	0	95	GLU
52	0	105	VAL
52	0	189	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (97) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	95	GLN
2	B	193[A]	GLN
3	C	55	GLN
3	C	97	ASN
4	D	5	HIS
5	E	150	GLN
7	G	66	ASN
7	G	149	GLN
8	H	87	ASN
8	H	101	ASN
11	K	65	GLN

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Mol	Chain	Res	Type
11	K	85	GLN
13	M	122	HIS
13	M	127	ASN
14	N	38	GLN
15	O	12	GLN
15	O	17	HIS
17	Q	15	ASN
17	Q	21	HIS
18	R	35	GLN
18	R	49	ASN
20	T	61	GLN
21	U	16	GLN
21	U	59	ASN
21	U	99	GLN
23	W	12	HIS
23	W	13	ASN
25	Y	4	GLN
25	Y	20	ASN
27	b	3	ASN
27	b	102	GLN
33	j	211	HIS
34	k	139	GLN
34	k	198	HIS
34	k	224	HIS
35	l	5	GLN
35	l	196	ASN
35	l	213	ASN
35	l	316	ASN
38	o	64	GLN
38	o	225	GLN
38	o	244	ASN
39	p	77	GLN
40	q	49	ASN
40	q	169	ASN
40	q	183	HIS
41	r	51	HIS
42	s	43	GLN
42	s	62	ASN
42	s	90	GLN
44	u	62	GLN
45	a	3	GLN
45	a	121	ASN

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Mol	Chain	Res	Type
45	a	141	HIS
45	a	290	ASN
45	a	382	GLN
45	a	395	ASN
45	a	413	GLN
45	a	417	ASN
45	a	532	GLN
45	a	599	GLN
45	a	664	ASN
45	a	691	HIS
45	a	696	GLN
45	a	957	GLN
45	a	1003	GLN
46	e	13	ASN
46	e	20	HIS
46	e	93	GLN
46	e	160	ASN
46	e	174	GLN
46	e	226	ASN
46	e	233	ASN
46	e	403	ASN
46	e	888	ASN
46	e	1111	GLN
46	e	1138	ASN
46	e	1141	GLN
46	e	1146	GLN
46	e	1153	GLN
46	e	1206	GLN
46	e	1273	HIS
46	e	1288	GLN
46	e	1293	GLN
46	e	1354	HIS
46	e	1358	GLN
46	e	1455	GLN
46	e	1457	ASN
46	e	1471	GLN
46	e	1484	ASN
46	e	1532	ASN
47	g	9	ASN
47	g	75	GLN
48	v	52	HIS
48	v	78	HIS

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Mol	Chain	Res	Type
49	w	27	ASN
52	0	36	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	f	3212/3395 (94%)	594 (18%)	0
31	h	120/121 (99%)	12 (10%)	0
32	i	157/158 (99%)	32 (20%)	0
50	y	71/76 (93%)	29 (40%)	0
All	All	3560/3750 (94%)	667 (18%)	0

All (667) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
30	f	6	A
30	f	13	A
30	f	14	U
30	f	26	A
30	f	40	A
30	f	43	A
30	f	49	A
30	f	59	G
30	f	60	A
30	f	65	A
30	f	66	A
30	f	92	G
30	f	99	A
30	f	109	A
30	f	110	G
30	f	111	C
30	f	116	A
30	f	120	G
30	f	121	A
30	f	122	A
30	f	133	U
30	f	134	U
30	f	135	C
30	f	136	G
30	f	156	G
30	f	157	A

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Mol	Chain	Res	Type
30	f	165	A
30	f	166	C
30	f	172	G
30	f	173	G
30	f	187	A
30	f	190	U
30	f	191	U
30	f	200	C
30	f	206	G
30	f	210	U
30	f	211	A
30	f	213	A
30	f	218	G
30	f	219	A
30	f	234	G
30	f	240	U
30	f	241	G
30	f	242	C
30	f	243	G
30	f	245	U
30	f	249	U
30	f	252	U
30	f	269	G
30	f	283	G
30	f	286	U
30	f	295	A
30	f	305	U
30	f	323	A
30	f	329	U
30	f	339	C
30	f	350	C
30	f	374	A
30	f	376	G
30	f	398	A
30	f	399	A
30	f	401	U
30	f	402	A
30	f	403	C
30	f	421	G
30	f	422	A
30	f	439	C
30	f	440	A

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Mol	Chain	Res	Type
30	f	441	U
30	f	442	G
30	f	443	G
30	f	445	G
30	f	446	U
30	f	447	U
30	f	448	U
30	f	450	G
30	f	487	U
30	f	488	U
30	f	489	U
30	f	490	C
30	f	494	G
30	f	518	G
30	f	520	U
30	f	521	A
30	f	523	A
30	f	535	G
30	f	536	U
30	f	543	C
30	f	544	C
30	f	546	C
30	f	547	G
30	f	548	G
30	f	551	A
30	f	552	G
30	f	555	U
30	f	557	A
30	f	559	A
30	f	578	A
30	f	579	G
30	f	589	A
30	f	597	G
30	f	604	G
30	f	608	A
30	f	609	G
30	f	611	A
30	f	620	U
30	f	621	A
30	f	622	A
30	f	637	C
30	f	638	C

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Mol	Chain	Res	Type
30	f	649	A
30	f	660	A
30	f	667	C
30	f	677	A
30	f	681	U
30	f	684	G
30	f	690	A
30	f	691	A
30	f	705	A
30	f	712	G
30	f	715	A
30	f	716	A
30	f	719	U
30	f	720	A
30	f	758	C
30	f	763	G
30	f	764	U
30	f	765	C
30	f	766	U
30	f	767	U
30	f	776	U
30	f	777	U
30	f	780	A
30	f	781	G
30	f	785	G
30	f	786	A
30	f	806	A
30	f	817	A
30	f	830	A
30	f	846	A
30	f	849	C
30	f	850	U
30	f	861	C
30	f	874	U
30	f	879	U
30	f	896	A
30	f	907	G
30	f	908	G
30	f	914	A
30	f	916	G
30	f	917	A
30	f	920	A

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Mol	Chain	Res	Type
30	f	921	A
30	f	924	G
30	f	925	A
30	f	937	G
30	f	944	C
30	f	959	C
30	f	960	U
30	f	981	U
30	f	982	C
30	f	991	G
30	f	994	G
30	f	1001	G
30	f	1002	A
30	f	1010	G
30	f	1015	U
30	f	1016	C
30	f	1017	C
30	f	1018	G
30	f	1021	G
30	f	1024	G
30	f	1025	A
30	f	1028	U
30	f	1036	A
30	f	1041	U
30	f	1047	A
30	f	1049	C
30	f	1063	G
30	f	1064	A
30	f	1065	A
30	f	1072	G
30	f	1081	U
30	f	1087	G
30	f	1093	A
30	f	1094	U
30	f	1095	U
30	f	1097	G
30	f	1098	A
30	f	1103	A
30	f	1104	G
30	f	1117	G
30	f	1131	G
30	f	1144	U

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Mol	Chain	Res	Type
30	f	1153	A
30	f	1159	A
30	f	1160	C
30	f	1177	G
30	f	1180	A
30	f	1181	U
30	f	1192	C
30	f	1193	A
30	f	1196	C
30	f	1197	A
30	f	1201	C
30	f	1202	A
30	f	1208	U
30	f	1217	A
30	f	1218	U
30	f	1219	C
30	f	1222	G
30	f	1225	A
30	f	1227	C
30	f	1235	U
30	f	1236	G
30	f	1238	C
30	f	1241	U
30	f	1242	G
30	f	1244	A
30	f	1245	A
30	f	1251	A
30	f	1252	A
30	f	1254	C
30	f	1258	U
30	f	1259	A
30	f	1263	A
30	f	1264	G
30	f	1265	U
30	f	1269	U
30	f	1272	C
30	f	1277	C
30	f	1278	A
30	f	1279	C
30	f	1282	G
30	f	1285	G
30	f	1286	A

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Mol	Chain	Res	Type
30	f	1287	A
30	f	1295	G
30	f	1307	G
30	f	1308	A
30	f	1309	U
30	f	1313	G
30	f	1330	A
30	f	1348	U
30	f	1349	G
30	f	1351	U
30	f	1352	A
30	f	1354	G
30	f	1355	A
30	f	1356	U
30	f	1357	G
30	f	1386	A
30	f	1392	G
30	f	1399	A
30	f	1400	G
30	f	1419	A
30	f	1434	G
30	f	1437	C
30	f	1446	A
30	f	1450	G
30	f	1481	A
30	f	1482	A
30	f	1483	G
30	f	1487	G
30	f	1488	G
30	f	1502	C
30	f	1508	C
30	f	1536	G
30	f	1539	A
30	f	1555	U
30	f	1556	C
30	f	1557	A
30	f	1560	G
30	f	1562	C
30	f	1563	C
30	f	1566	A
30	f	1568	U
30	f	1569	U

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Mol	Chain	Res	Type
30	f	1572	U
30	f	1573	G
30	f	1575	A
30	f	1576	G
30	f	1580	A
30	f	1581	C
30	f	1582	C
30	f	1583	A
30	f	1589	A
30	f	1590	G
30	f	1605	A
30	f	1607	U
30	f	1620	U
30	f	1629	U
30	f	1639	C
30	f	1642	A
30	f	1643	A
30	f	1645	U
30	f	1657	C
30	f	1683	A
30	f	1716	U
30	f	1717	U
30	f	1724	U
30	f	1725	C
30	f	1736	G
30	f	1741	A
30	f	1750	A
30	f	1751	G
30	f	1760	A
30	f	1761	C
30	f	1764	U
30	f	1765	U
30	f	1766	G
30	f	1770	G
30	f	1775	G
30	f	1780	G
30	f	1797	A
30	f	1814	A
30	f	1816	A
30	f	1819	U
30	f	1820	U
30	f	1821	U

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Mol	Chain	Res	Type
30	f	1835	A
30	f	1839	A
30	f	1840	U
30	f	1841	A
30	f	1842	A
30	f	1846	C
30	f	1849	C
30	f	1850	A
30	f	1866	C
30	f	1867	A
30	f	1880	U
30	f	1881	A
30	f	1893	A
30	f	1906	G
30	f	1943	C
30	f	1952	G
30	f	1953	G
30	f	1954	G
30	f	2094	C
30	f	2101	C
30	f	2102	U
30	f	2111	G
30	f	2112	U
30	f	2113	A
30	f	2114	C
30	f	2121	G
30	f	2122	G
30	f	2131	A
30	f	2134	G
30	f	2140	U
30	f	2144	A
30	f	2158	A
30	f	2160	G
30	f	2169	G
30	f	2176	U
30	f	2201	G
30	f	2206	G
30	f	2207	A
30	f	2208	A
30	f	2209	U
30	f	2222	A
30	f	2223	A

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Mol	Chain	Res	Type
30	f	2225	U
30	f	2228	A
30	f	2249	G
30	f	2270	A
30	f	2272	G
30	f	2273	G
30	f	2274	U
30	f	2281	A
30	f	2282	U
30	f	2288	G
30	f	2307	G
30	f	2308	C
30	f	2310	U
30	f	2313	A
30	f	2314	U
30	f	2315	G
30	f	2334	U
30	f	2335	G
30	f	2336	U
30	f	2373	A
30	f	2374	C
30	f	2375	G
30	f	2385	G
30	f	2388	U
30	f	2393	G
30	f	2397	A
30	f	2402	A
30	f	2403	G
30	f	2404	A
30	f	2411	U
30	f	2419	A
30	f	2437	G
30	f	2446	U
30	f	2447	A
30	f	2450	G
30	f	2461	A
30	f	2463	G
30	f	2464	U
30	f	2468	A
30	f	2469	G
30	f	2470	C
30	f	2471	U

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Mol	Chain	Res	Type
30	f	2472	U
30	f	2474	G
30	f	2479	C
30	f	2480	A
30	f	2484	A
30	f	2486	A
30	f	2487	U
30	f	2488	A
30	f	2494	A
30	f	2495	C
30	f	2496	C
30	f	2499	U
30	f	2501	U
30	f	2502	A
30	f	2503	G
30	f	2505	U
30	f	2514	U
30	f	2515	A
30	f	2522	G
30	f	2526	C
30	f	2531	C
30	f	2537	U
30	f	2538	U
30	f	2539	C
30	f	2540	A
30	f	2541	U
30	f	2542	U
30	f	2544	U
30	f	2547	A
30	f	2548	C
30	f	2549	G
30	f	2552	C
30	f	2554	A
30	f	2555	G
30	f	2561	A
30	f	2569	A
30	f	2570	U
30	f	2571	U
30	f	2572	C
30	f	2573	G
30	f	2581	U
30	f	2585	G

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Mol	Chain	Res	Type
30	f	2593	A
30	f	2594	C
30	f	2606	G
30	f	2607	G
30	f	2614	G
30	f	2648	G
30	f	2651	G
30	f	2652	U
30	f	2656	A
30	f	2674	A
30	f	2677	G
30	f	2678	A
30	f	2689	A
30	f	2691	A
30	f	2694	A
30	f	2696	A
30	f	2704	A
30	f	2714	G
30	f	2719	U
30	f	2728	G
30	f	2729	U
30	f	2740	A
30	f	2752	U
30	f	2753	G
30	f	2755	C
30	f	2772	C
30	f	2773	C
30	f	2777	G
30	f	2778	G
30	f	2788	C
30	f	2796	G
30	f	2800	G
30	f	2801	A
30	f	2803	A
30	f	2810	C
30	f	2814	G
30	f	2817	A
30	f	2818	U
30	f	2821	C
30	f	2834	G
30	f	2842	U
30	f	2844	C

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Mol	Chain	Res	Type
30	f	2845	A
30	f	2849	C
30	f	2860	U
30	f	2867	C
30	f	2871	G
30	f	2872	A
30	f	2875	U
30	f	2887	A
30	f	2898	G
30	f	2899	C
30	f	2911	A
30	f	2914	G
30	f	2923	U
30	f	2935	U
30	f	2936	A
30	f	2938	G
30	f	2941	A
30	f	2942	C
30	f	2947	G
30	f	2955	U
30	f	2971	A
30	f	2983	C
30	f	2990	G
30	f	2992	U
30	f	2996	U
30	f	2997	G
30	f	3006	A
30	f	3012	A
30	f	3056	U
30	f	3059	G
30	f	3078	U
30	f	3079	U
30	f	3080	G
30	f	3086	A
30	f	3092	C
30	f	3104	U
30	f	3113	A
30	f	3122	A
30	f	3130	A
30	f	3131	U
30	f	3142	A
30	f	3143	C

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Mol	Chain	Res	Type
30	f	3151	U
30	f	3154	C
30	f	3155	U
30	f	3156	U
30	f	3157	U
30	f	3165	A
30	f	3170	A
30	f	3173	G
30	f	3174	A
30	f	3175	U
30	f	3176	G
30	f	3179	U
30	f	3181	C
30	f	3186	A
30	f	3187	A
30	f	3196	U
30	f	3207	U
30	f	3209	A
30	f	3217	C
30	f	3218	A
30	f	3219	G
30	f	3228	C
30	f	3229	G
30	f	3243	A
30	f	3245	A
30	f	3247	G
30	f	3259	U
30	f	3263	G
30	f	3269	U
30	f	3270	U
30	f	3273	A
30	f	3276	G
30	f	3281	U
30	f	3287	U
30	f	3288	G
30	f	3289	G
30	f	3294	A
30	f	3295	A
30	f	3303	G
30	f	3304	U
30	f	3307	A
30	f	3313	U

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Mol	Chain	Res	Type
30	f	3316	A
30	f	3317	U
30	f	3318	G
30	f	3319	U
30	f	3320	A
30	f	3341	U
30	f	3342	A
30	f	3345	G
30	f	3351	U
30	f	3352	U
30	f	3353	G
30	f	3354	U
30	f	3355	U
30	f	3369	G
30	f	3375	A
30	f	3378	C
30	f	3382	U
30	f	3383	G
30	f	3386	G
30	f	3389	U
30	f	3390	G
30	f	3396	U
31	h	7	G
31	h	29	C
31	h	53	U
31	h	54	U
31	h	55	A
31	h	65	G
31	h	73	C
31	h	74	C
31	h	95	A
31	h	102	A
31	h	112	G
31	h	121	U
32	i	23	U
32	i	34	U
32	i	35	C
32	i	39	G
32	i	48	A
32	i	52	A
32	i	53	A
32	i	59	A

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Mol	Chain	Res	Type
32	i	62	C
32	i	63	G
32	i	80	A
32	i	81	U
32	i	82	U
32	i	83	C
32	i	84	C
32	i	85	G
32	i	86	U
32	i	87	G
32	i	90	U
32	i	95	G
32	i	104	A
32	i	105	A
32	i	106	C
32	i	111	A
32	i	113	U
32	i	125	U
32	i	126	A
32	i	138	A
32	i	151	C
32	i	152	G
32	i	157	U
32	i	158	U
50	y	7	G
50	y	8	U
50	y	9	G
50	y	10	G
50	y	13	U
50	y	16	U
50	y	17	C
50	y	22	G
50	y	23	C
50	y	31	C
50	y	34	A
50	y	35	G
50	y	36	C
50	y	38	U
50	y	42	A
50	y	43	G
50	y	44	A
50	y	45	G

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Mol	Chain	Res	Type
50	y	46	G
50	y	47	U
50	y	48	C
50	y	56	C
50	y	58	A
50	y	60	U
50	y	61	C
50	y	68	C
50	y	71	C
50	y	75	C
50	y	76	A

There are no RNA pucker outliers to report.

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
48	5CT	v	51	48	13,14,15	0.78	0	8,15,17	1.29	1 (12%)

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
48	5CT	v	51	48	-	9/13/14/16	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	v	51	5CT	C4-C3-C2	-2.19	108.85	113.47

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
48	v	51	5CT	NZ-C1-C2-C3
48	v	51	5CT	O1-C2-C3-C4
48	v	51	5CT	C2-C3-C4-N1
48	v	51	5CT	C-CA-CB-CG
48	v	51	5CT	N-CA-CB-CG
48	v	51	5CT	NZ-C1-C2-O1
48	v	51	5CT	C1-C2-C3-C4
48	v	51	5CT	C2-C1-NZ-CE
48	v	51	5CT	CE-CD-CG-CB

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
48	v	51	5CT	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 21 ligands modelled in this entry, 20 are monoatomic - leaving 1 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	$\# Z > 2$
56	SPD	f	3401	-	9,9,9	0.32	0	8,8,8	0.85	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
56	SPD	f	3401	-	-	5/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
56	f	3401	SPD	C3-C4-C5-N6
56	f	3401	SPD	N6-C7-C8-C9
56	f	3401	SPD	C2-C3-C4-C5
56	f	3401	SPD	C4-C5-N6-C7
56	f	3401	SPD	C8-C7-N6-C5

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	f	3401	SPD	1	0

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.

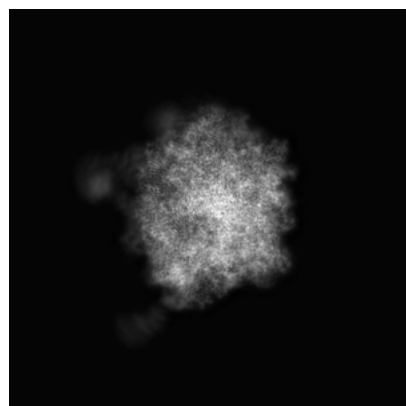
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15424. These allow visual inspection of the internal detail of the map and identification of artifacts.

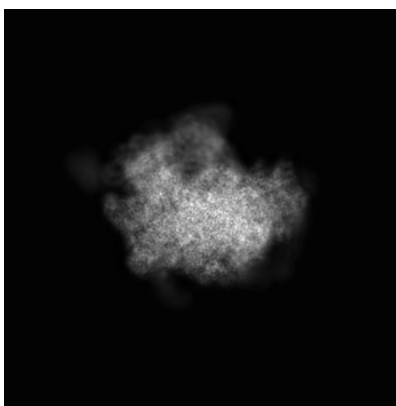
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

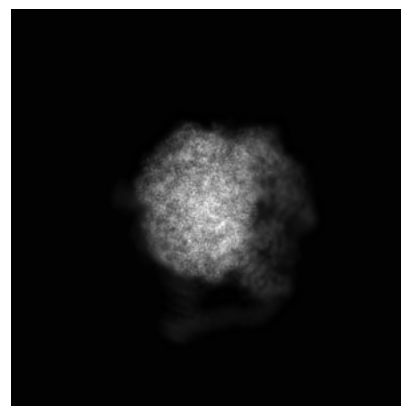
6.1.1 Primary map



X

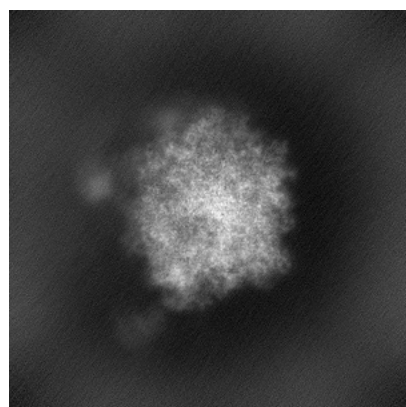


Y

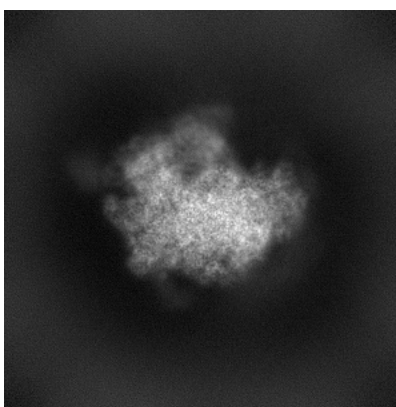


Z

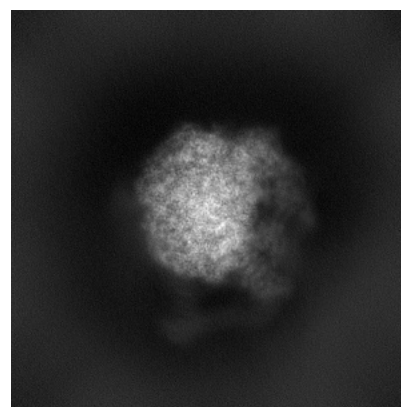
6.1.2 Raw map



X



Y

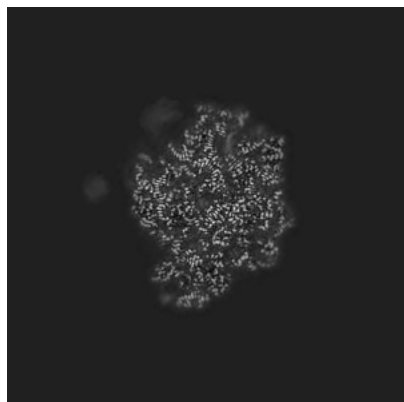


Z

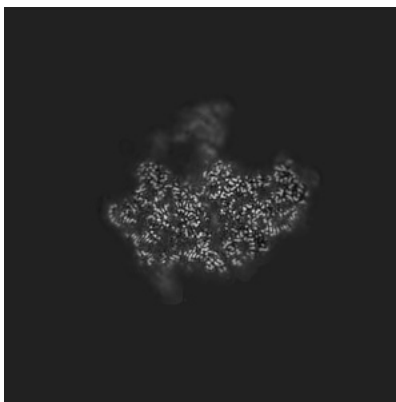
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

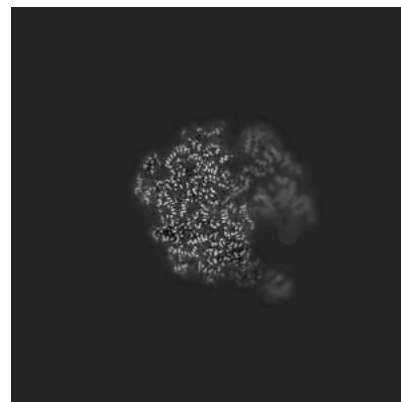
6.2.1 Primary map



X Index: 225

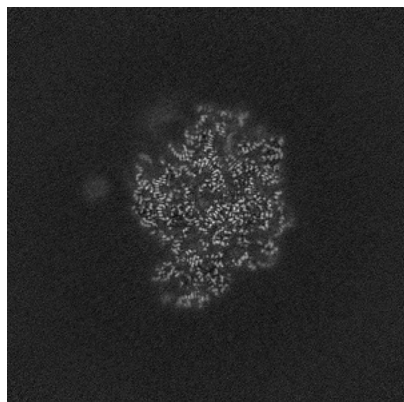


Y Index: 225

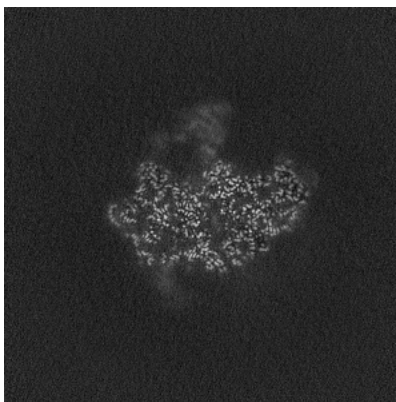


Z Index: 225

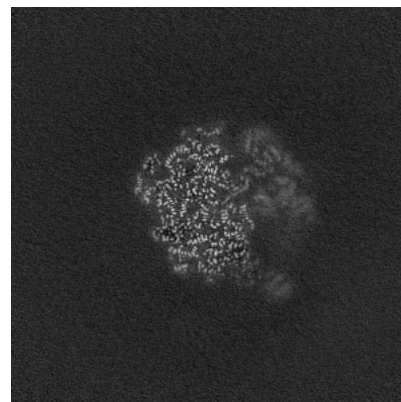
6.2.2 Raw map



X Index: 225



Y Index: 225

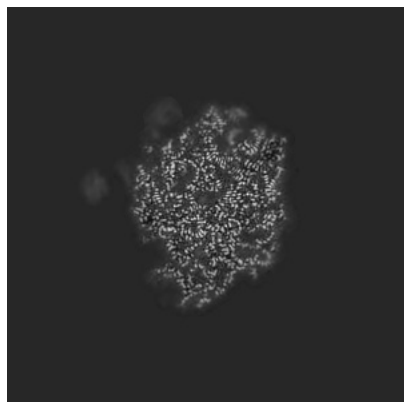


Z Index: 225

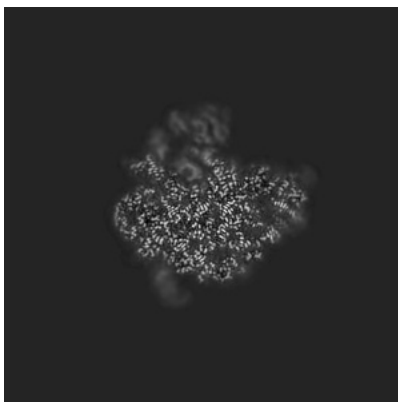
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

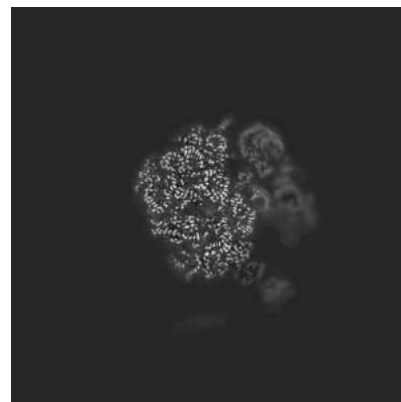
6.3.1 Primary map



X Index: 219

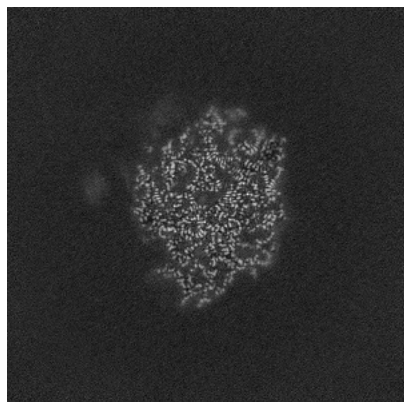


Y Index: 237

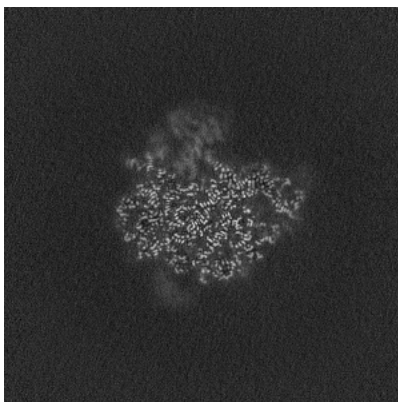


Z Index: 231

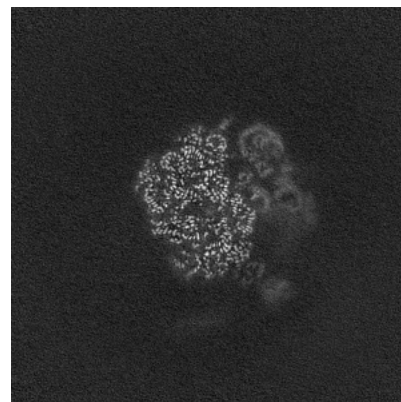
6.3.2 Raw map



X Index: 219



Y Index: 241

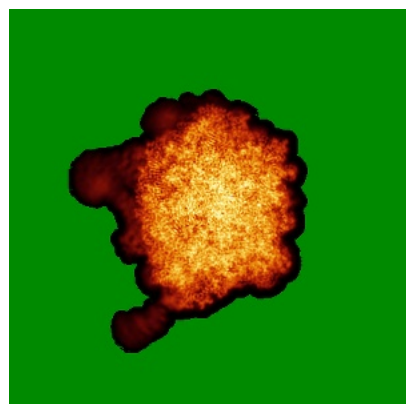


Z Index: 231

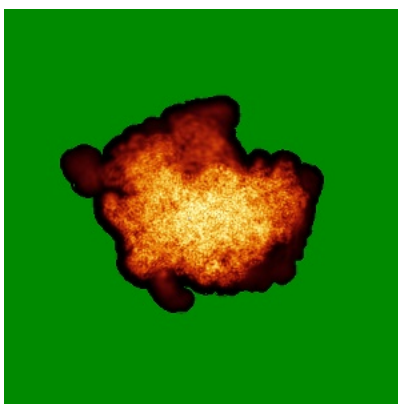
The images above show the largest variance slices of the map in three orthogonal directions.

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

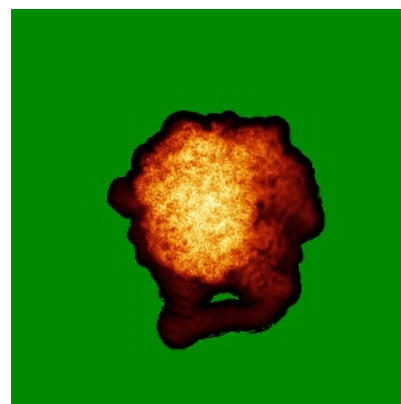
6.4.1 Primary map



X

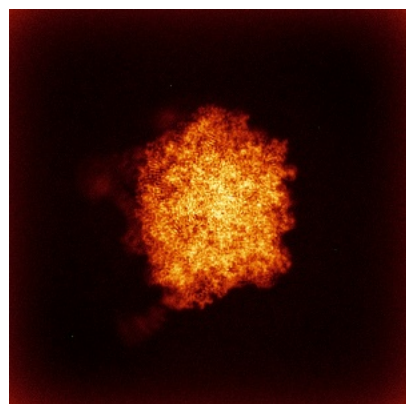


Y

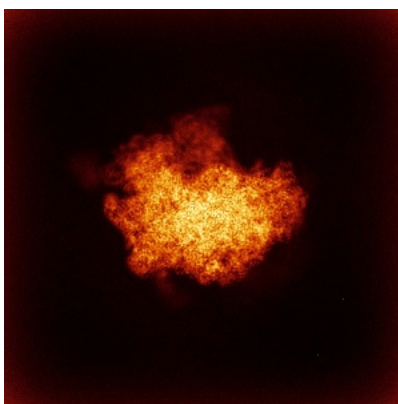


Z

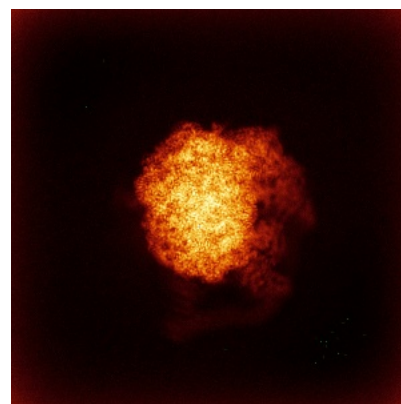
6.4.2 Raw map



X



Y

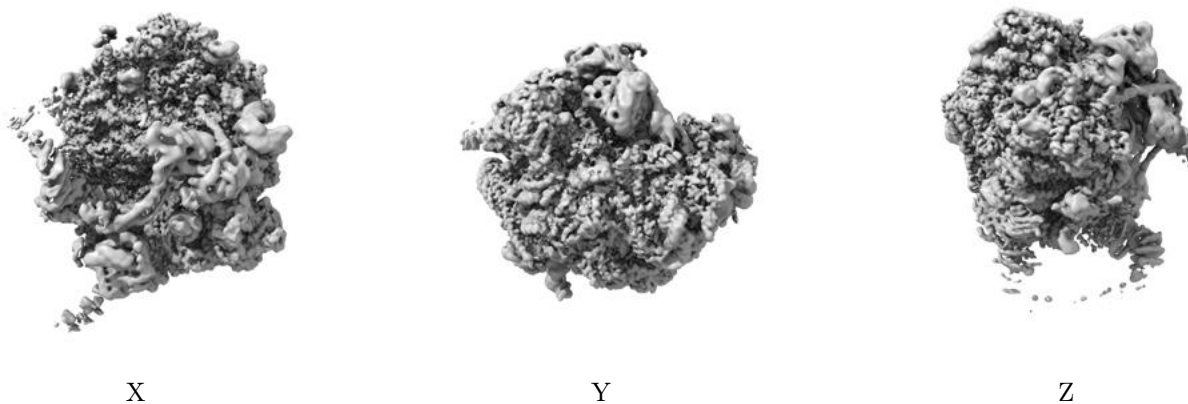


Z

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.

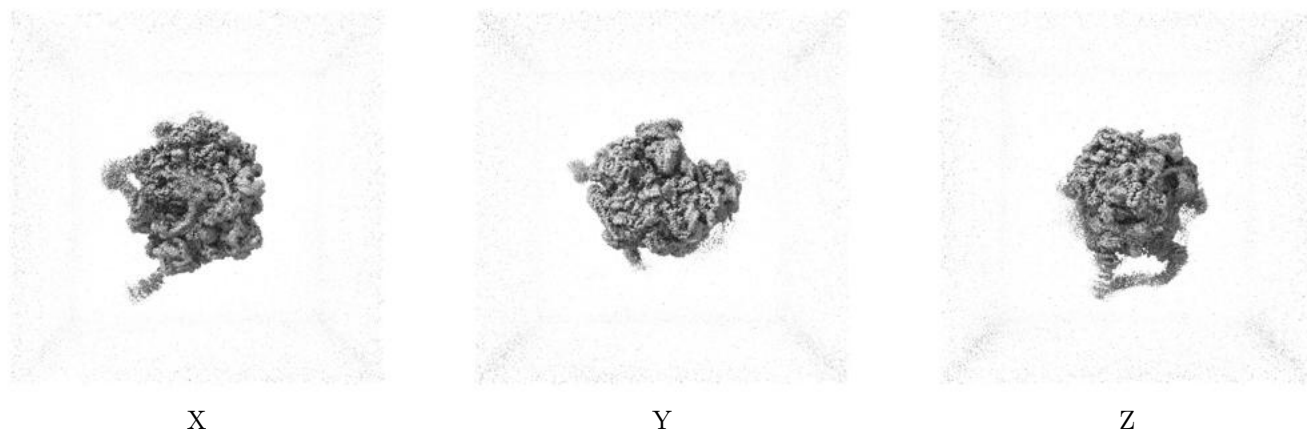
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

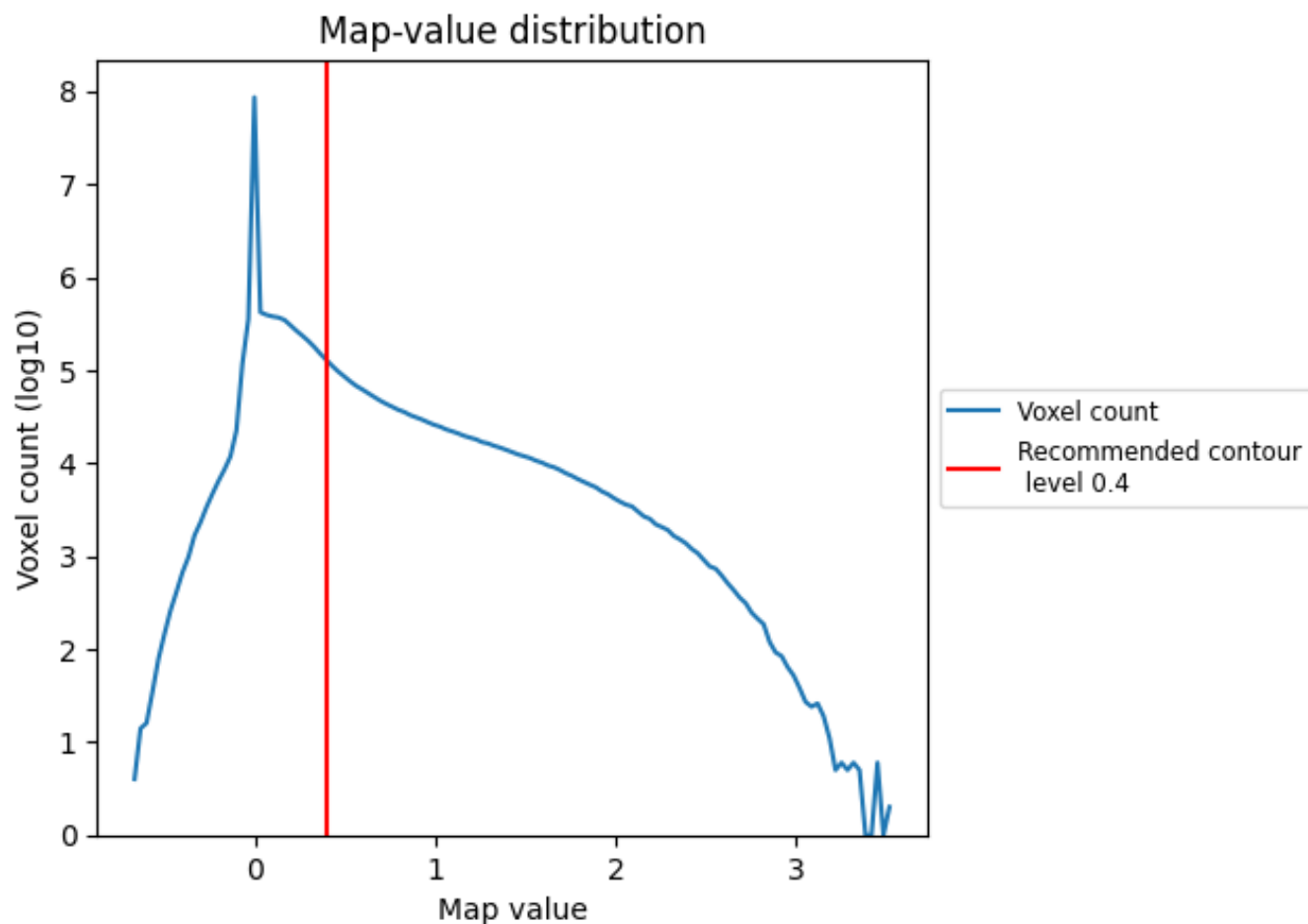
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

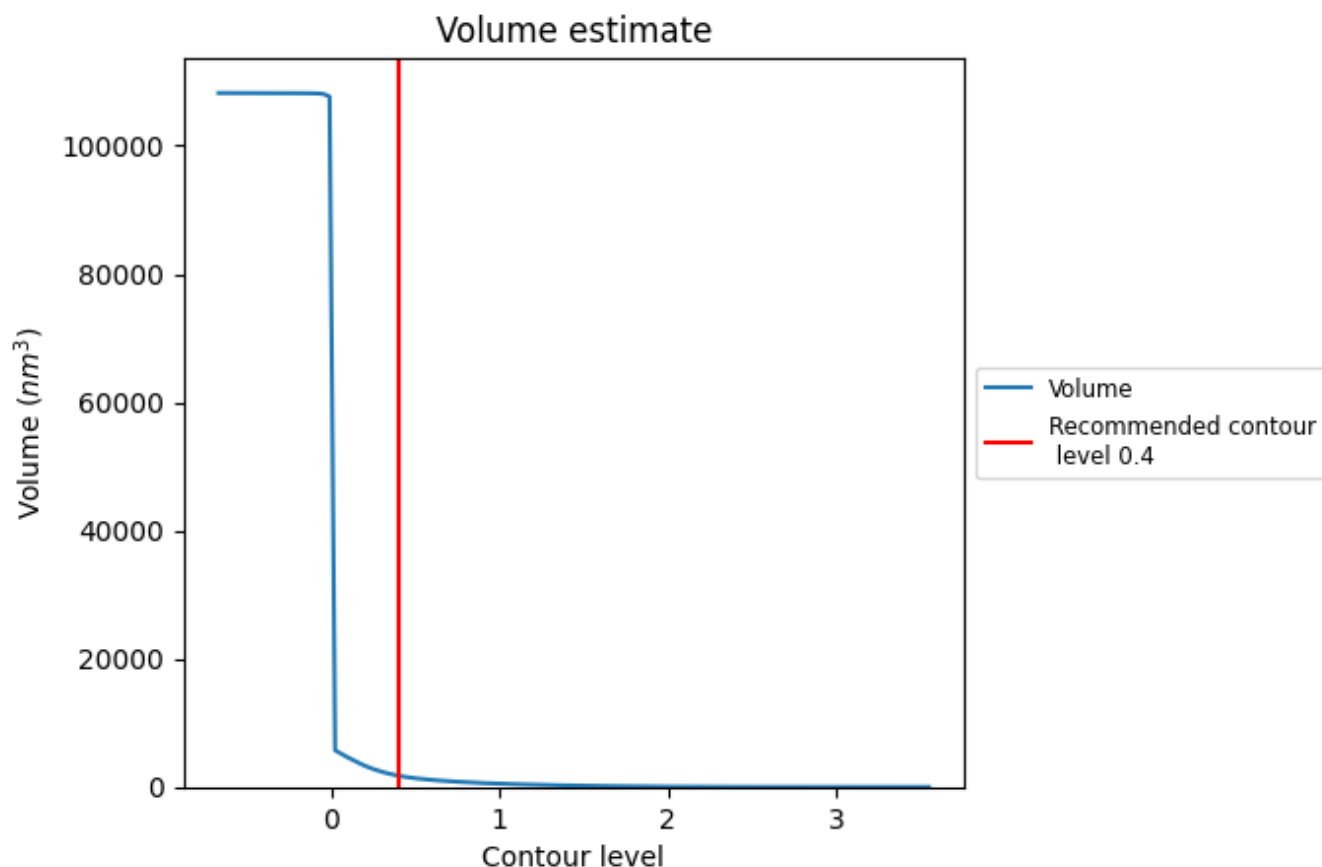
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

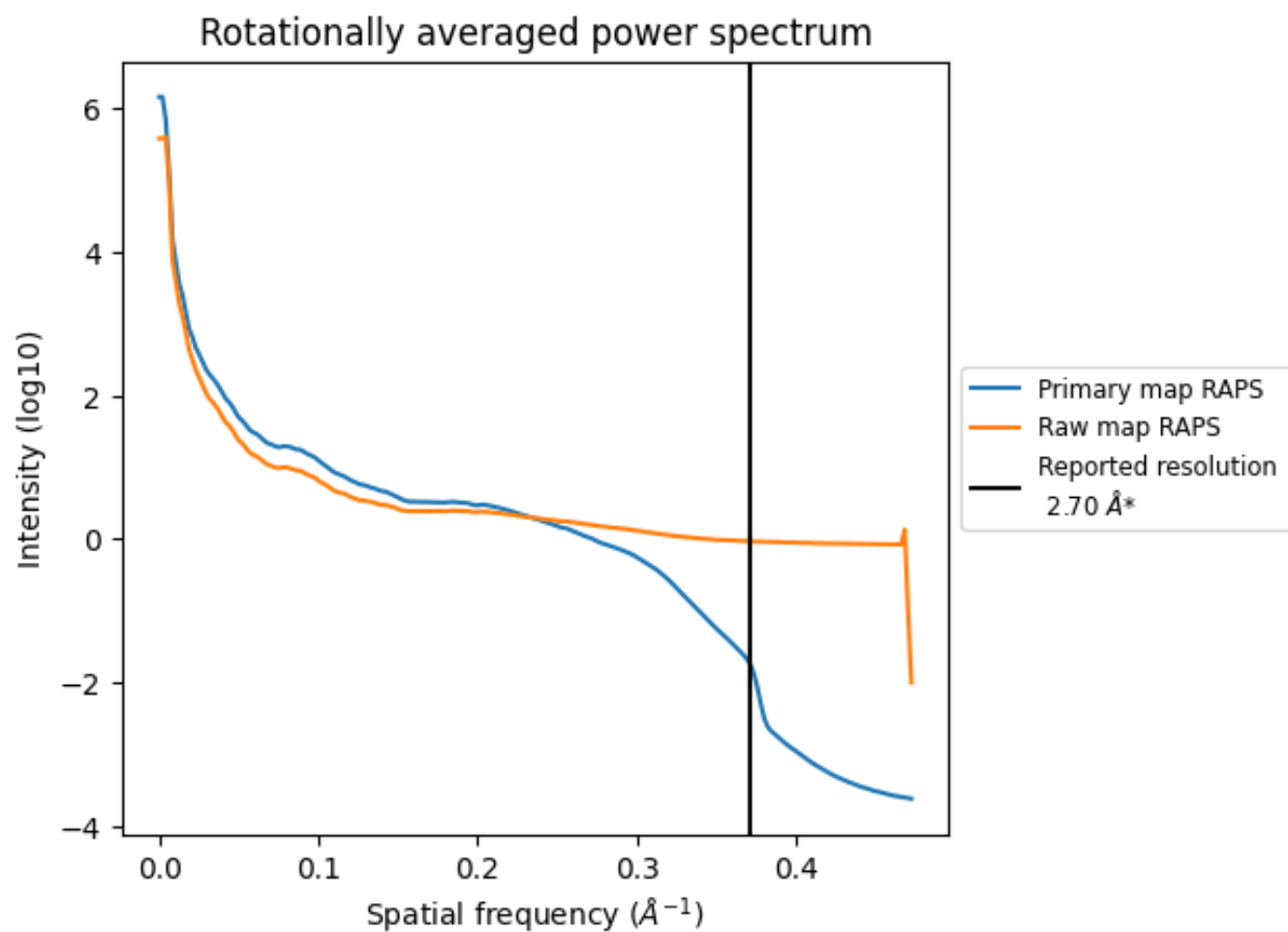
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1749 nm^3 ; this corresponds to an approximate mass of 1580 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 ⓘ

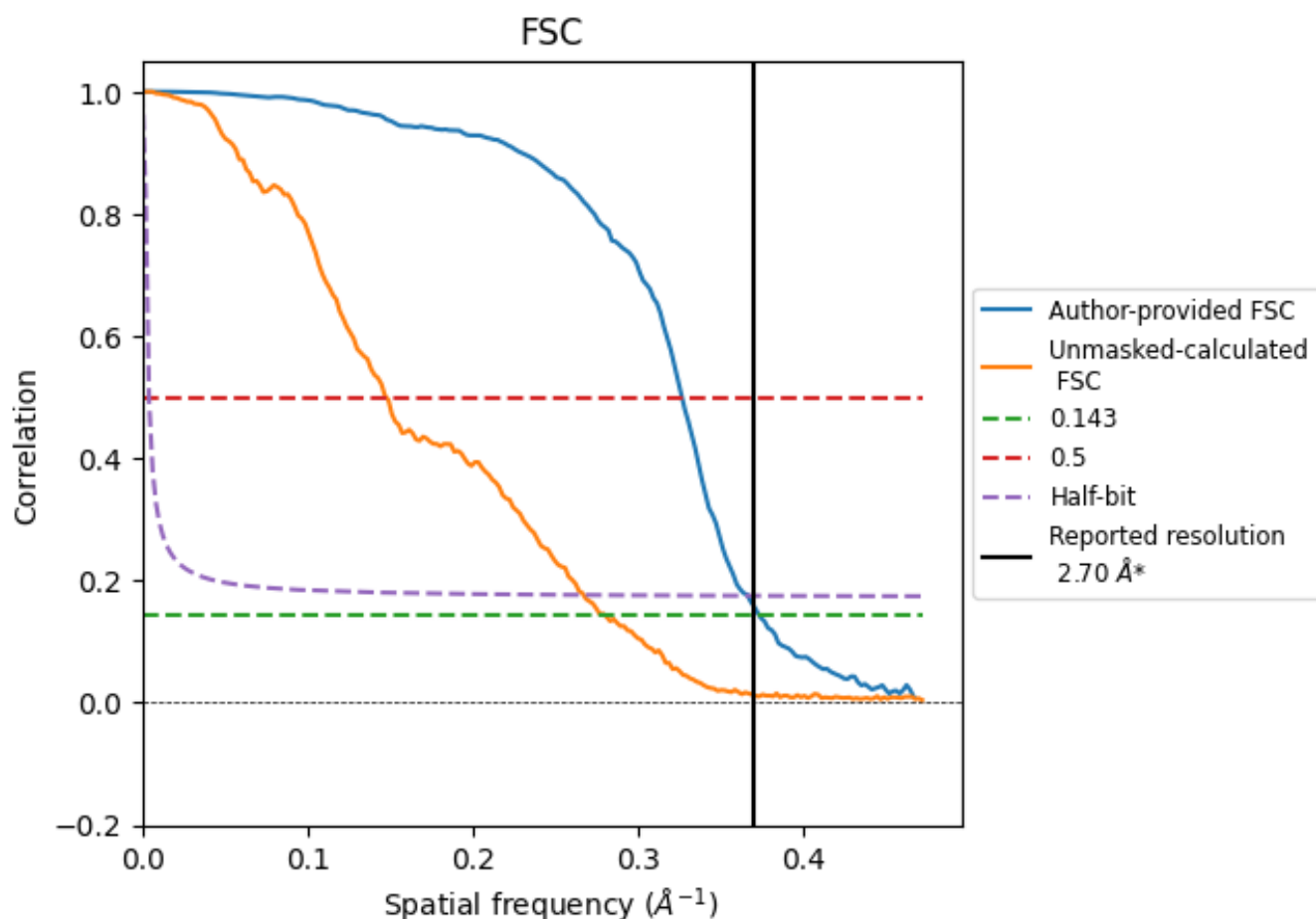


*Reported resolution corresponds to spatial frequency of $0.370 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

8.2 Resolution estimates [i](#)

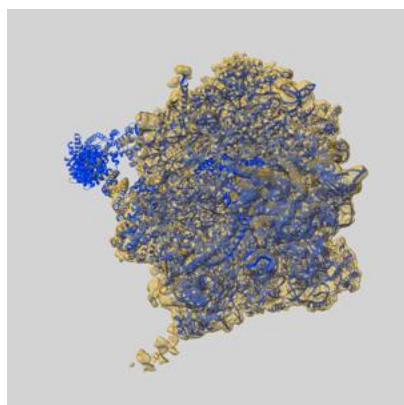
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.68	3.06	2.73
Unmasked-calculated*	3.57	6.78	3.74

*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 3.57 differs from the reported value 2.7 by more than 10 %

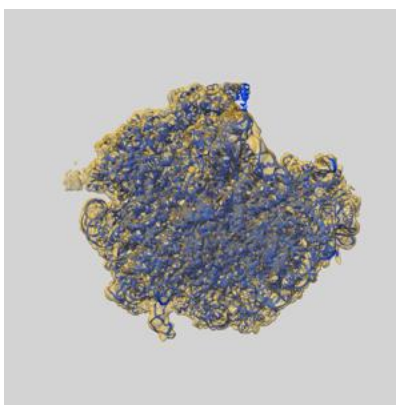
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-15424 and PDB model 8AGU. Per-residue inclusion information can be found in section [3](#) on page [15](#).

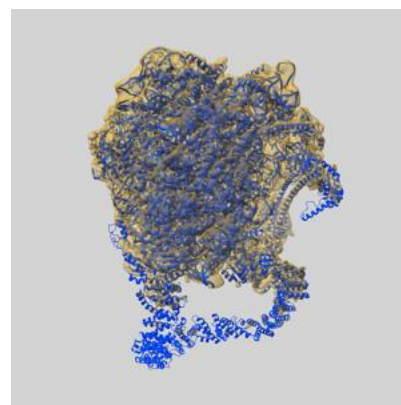
9.1 Map-model overlay [i](#)



X



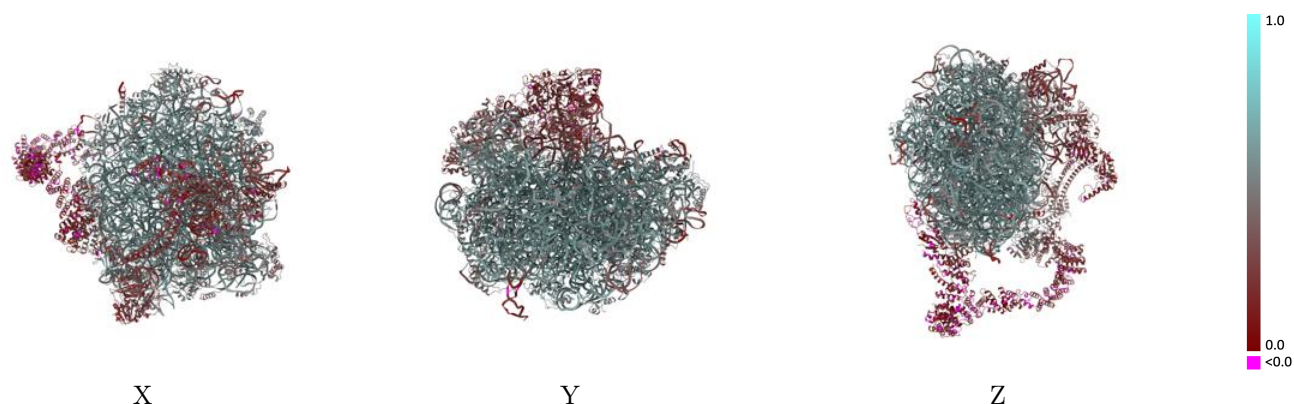
Y



Z

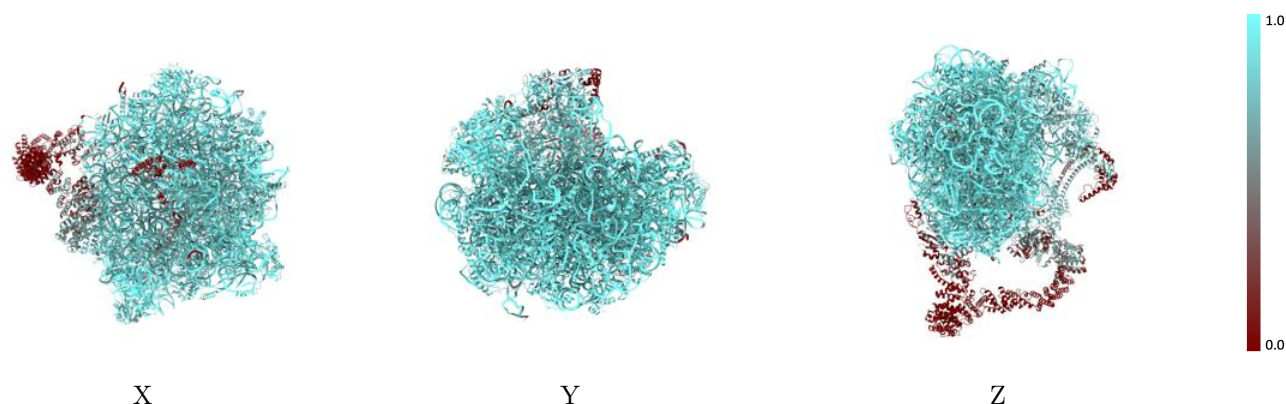
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



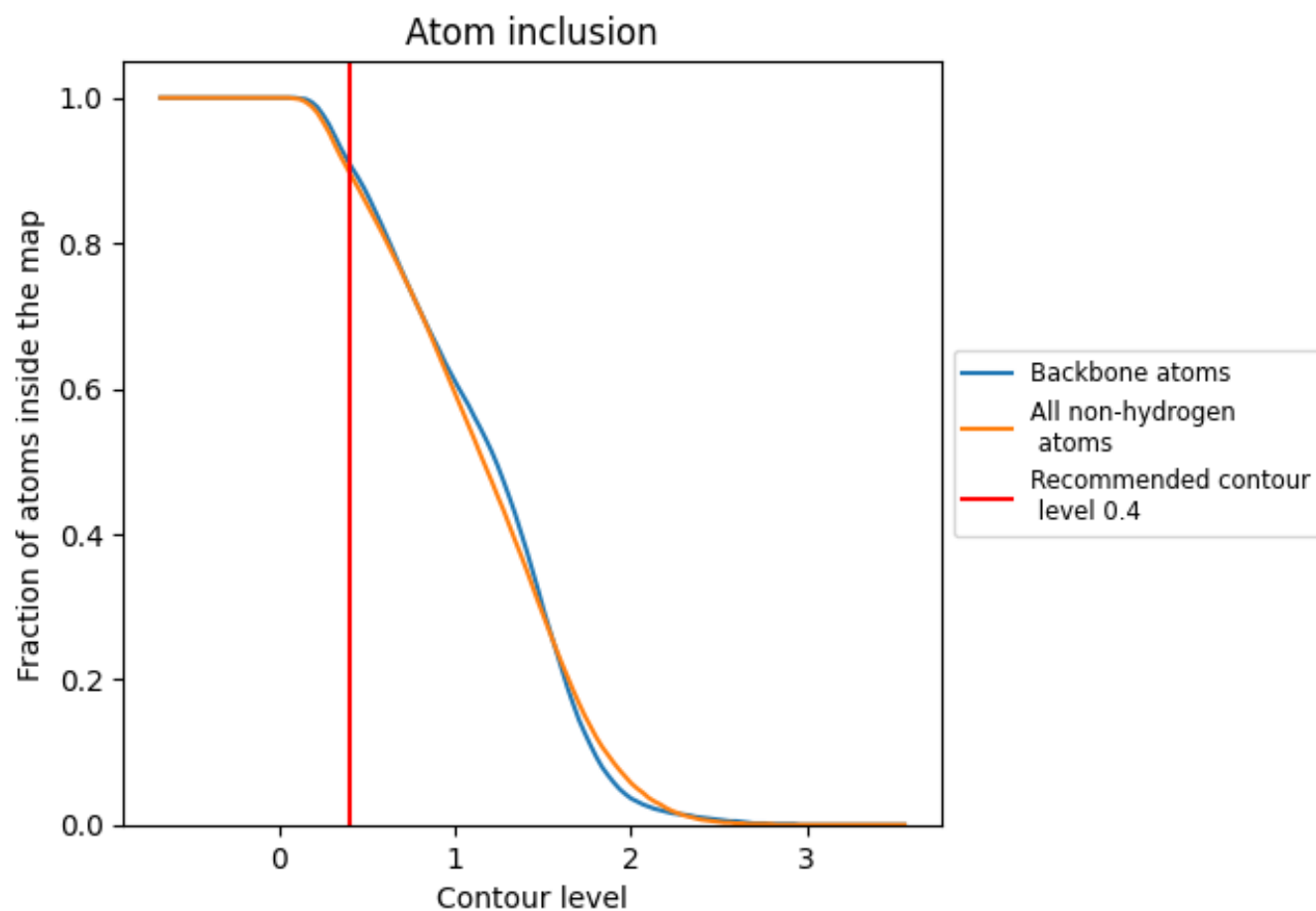
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 90% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8980	 0.4960
0	 0.8070	 0.2580
1	 0.9880	 0.4550
A	 0.9920	 0.5990
B	 0.9790	 0.5770
C	 0.9680	 0.5790
D	 0.9760	 0.5700
E	 0.9340	 0.5360
F	 0.9720	 0.5680
G	 0.9650	 0.5510
H	 0.9130	 0.4540
I	 0.9560	 0.5630
J	 0.9580	 0.5570
K	 0.9690	 0.5560
L	 0.9680	 0.5530
M	 0.9400	 0.5040
N	 0.9750	 0.5820
O	 0.9450	 0.5240
P	 0.9370	 0.5070
Q	 0.9200	 0.5350
R	 0.9770	 0.5880
S	 0.9900	 0.6100
T	 0.9700	 0.5620
U	 0.9620	 0.5400
V	 0.9540	 0.5170
W	 1.0000	 0.6140
X	 0.9080	 0.4740
Y	 0.9980	 0.5930
Z	 0.9650	 0.5610
a	 0.6670	 0.2240
b	 0.9630	 0.5560
c	 0.9670	 0.5530
d	 0.7180	 0.3780
e	 0.2490	 0.1560
f	 0.9900	 0.5600



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Chain	Atom inclusion	Q-score
g	 0.3760	 0.3870
h	 0.9990	 0.5570
i	 0.9940	 0.5870
j	 0.9820	 0.5950
k	 0.9720	 0.5730
l	 0.9720	 0.5620
m	 0.9380	 0.4740
n	 0.9510	 0.5130
o	 0.9700	 0.5580
p	 0.9370	 0.5060
q	 0.9560	 0.5330
r	 0.9510	 0.5240
s	 0.9210	 0.4230
t	 0.9650	 0.5490
u	 0.9680	 0.5350
v	 0.8410	 0.3850
w	 0.8050	 0.2370
y	 0.9700	 0.2580
z	 0.9080	 0.2700