Full wwPDB EM Validation Report (i)

Apr 29, 2024 – 03:18 pm BST

PDB ID	:	2J37
EMDB ID	:	EMD-1264
Title	:	MODEL OF MAMMALIAN SRP BOUND TO 80S RNCS
Authors	:	Halic, M.; Blau, M.; Becker, T.; Mielke, T.; Pool, M.R.; Wild, K.; Sinning, I.; Beckmann, R.
Deposited on	:	2006-08-18
Resolution	:	8.70 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 (i) 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 (i)) were used in the production of this report:

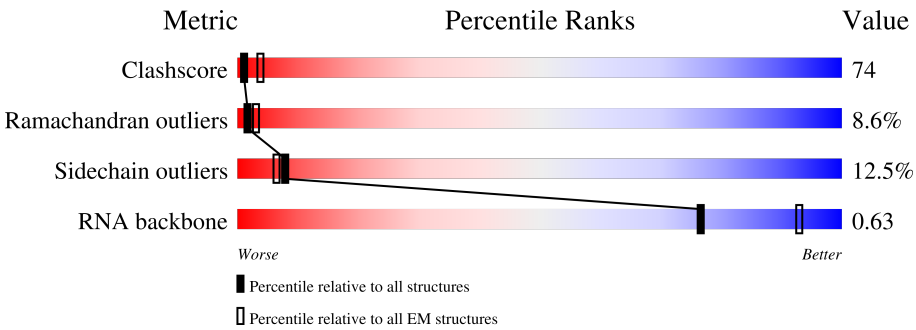
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 8.70 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	4	152	16% 22% 9% 6% 47%
2	5	124	16% 24% 8% • 48%
3	6	123	22% 27% 9% 8% 34%
4	A	128	15% 37% 51% 12%
5	B	108	13% 40% 52% 6% ••
6	S	17	29% 18% 82%
7	W	504	18% 28% 40% 18% 9% 5%

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Mol	Chain	Length	Quality of chain
8	Z	280	45% 43% 10%

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 15110 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 L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	4	81	652	423	108	119	2	0	0

- Molecule 2 is a protein called RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	5	64	504	314	99	91	0	0

- Molecule 3 is a protein called RIBOSOMAL PROTEIN L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	6	81	671	416	138	115	2	0	0

- Molecule 4 is a RNA chain called SRP RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	A	128	2748	1226	511	884	127	0	0

- Molecule 5 is a protein called SIGNAL RECOGNITION PARTICLE 19 KDA PROTEIN (SRP19).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	B	107	869	549	159	155	6	0	0

- Molecule 6 is a protein called SIGNAL SEQUENCE.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	S	17	141	97	22	22	0	0

- Molecule 7 is a protein called SIGNAL RECOGNITION PARTICLE 54 KDA PROTEIN (SRP54).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	W	479	3517	2196	614	683	24	0	0

- Molecule 8 is a RNA chain called RIBOSOMAL RNA.

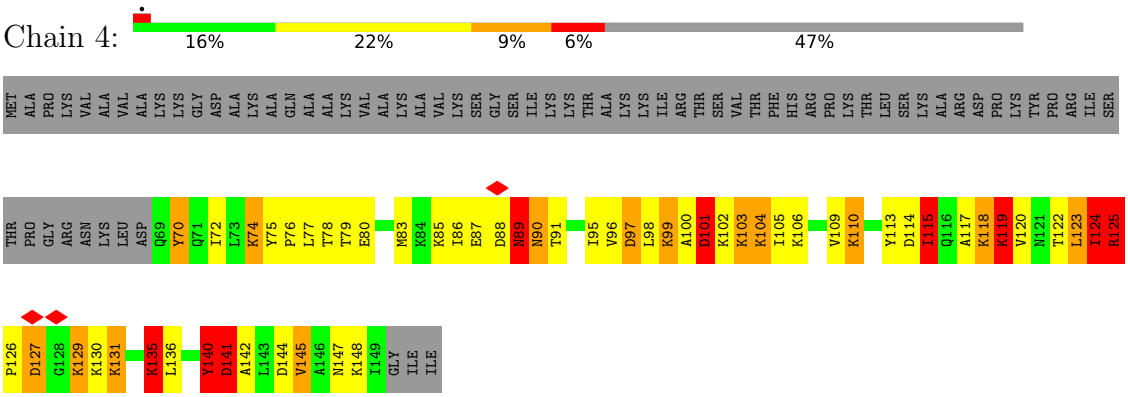
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	Z	280	6008	2681	1115	1932	280	0	0

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.

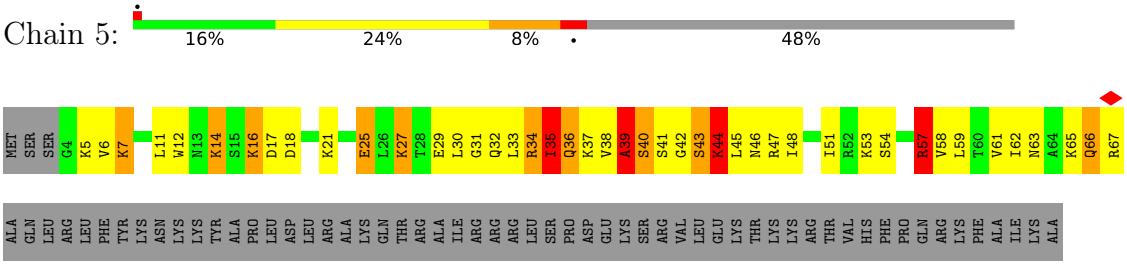
- Molecule 1: 60S RIBOSOMAL PROTEIN L23

Chain 4:



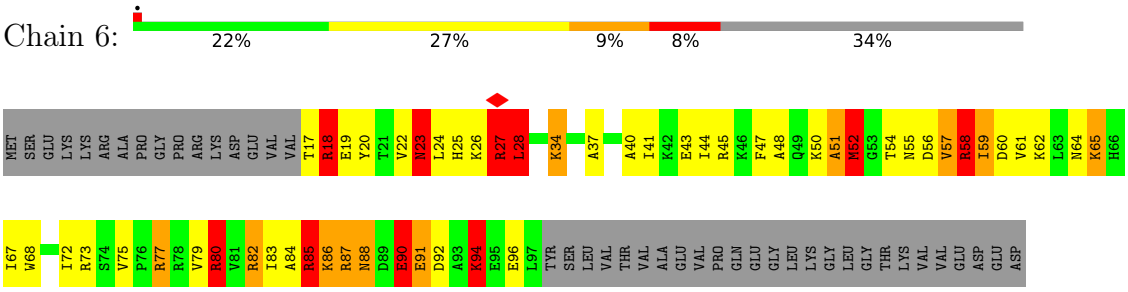
- Molecule 2: RIBOSOMAL PROTEIN L35

Chain 5:



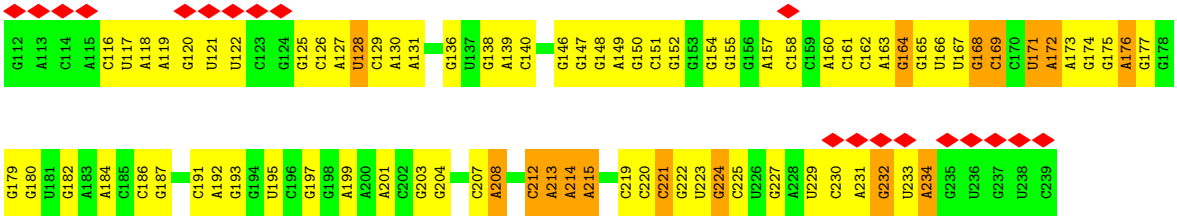
- Molecule 3: RIBOSOMAL PROTEIN L31

Chain 6:



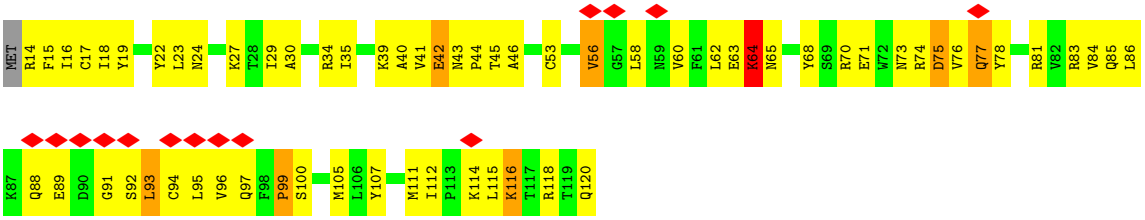
- Molecule 4: SRP RNA

Chain A:



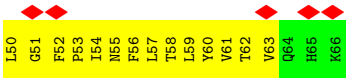
• Molecule 5: SIGNAL RECOGNITION PARTICLE 19 KDA PROTEIN (SRP19)

Chain B:



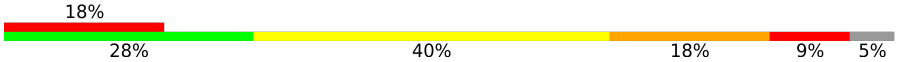
• Molecule 6: SIGNAL SEQUENCE

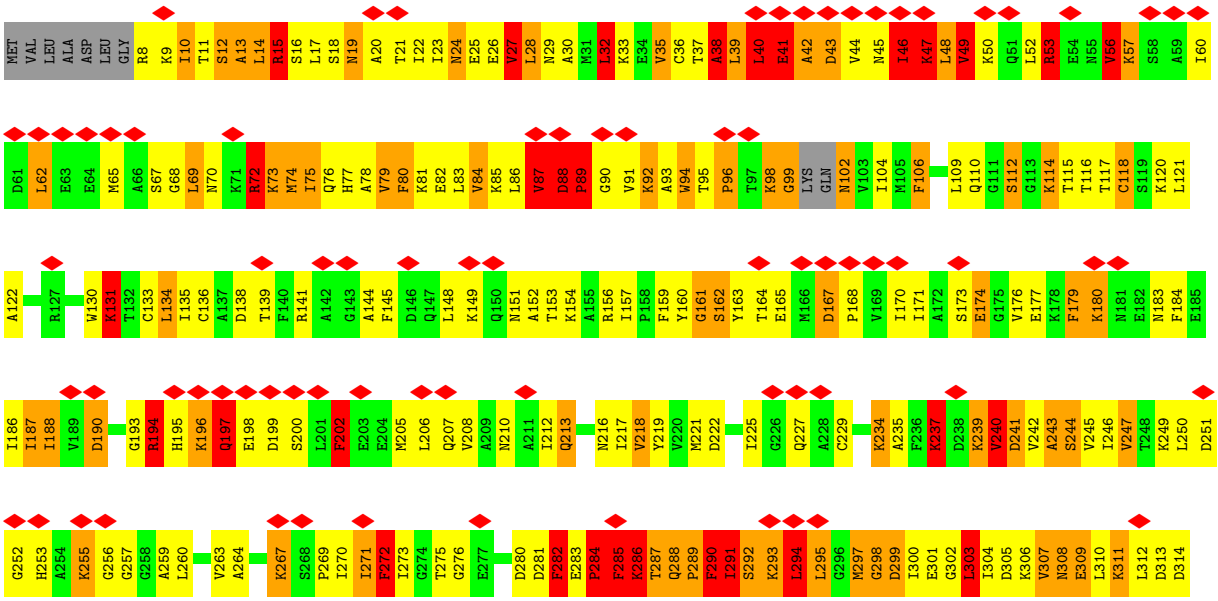
Chain S:



• Molecule 7: SIGNAL RECOGNITION PARTICLE 54 KDA PROTEIN (SRP54)

Chain W:





N315 E316 A317 L318 I319 E320 K321 L322 K323 H324 G325 Q326 F327 T328 L329 R330 D331 M332 Y333 E334 Q335 F336 Q337 N338 I339 M340 K341 M342 G343 P344 F345 S346 Q347 I348 L349 G350 M351 I352 P353 G354 F355 G356 T357 D358 F359 M360 S361 K362 G363 N364 E365 Q366 E367 S368 M369 A370 R371 L372 K373

T377 I378 M379 D380 S381 M382 N383 L387 D388 D391 G392 A393 K394 V395 F396 S397 R405 G409 S410 G411 V412 D416 Q423 Y424 F427 A428 Q429 M430 V431 K432 K433 M434 G435 G436 I437 K438 G439 L440 F441 K442 G443 G444 D445 M446 S447 K448 N449 V450 S451 Q452 S453 Q454 M455

A456 K457 L458 N459 Q460 Q461 G475 G476 M477 A478 G479 L480 Q481 S482 Q488 GLN GLY ALA ALA GLY ASN MET LYS GLY MET MET GLY PHE ASN ASN MET

- Molecule 8: RIBOSOMAL RNA

Chain Z: 45% 43% 10%

C1 U2 G3 C4 A5 A6 A7 G8 C12 C13 U14 G17 A18 A19 G24 G25 C26 G27 A28 A29 A30 U31 A32 G33 A34 G35 C36 G40 C41 G42 A43 U44 A45 G46 U47 C48 G49 G50 G51 G55 A56 G62 A63 C64 G65 A70 A71 U72 G73 G81 U86

C87 A88 G89 C90 A91 G94 C95 U96 G97 A98 U104 G105 A106 G109 U110 U111 A112 G113 C114 C115 G116 G117 U118 U121 A122 U125 C126 A127 U128 A135 C136 U137 C138 C141 U142 A149 U152 A156 A157 A158 C159 G160 G161 U167 A168 U169 U170 C171 C172

C173 G174 U175 G176 A179 C180 G181 G182 U185 C186 G187 G193 C194 U195 G196 G197 G198 C199 A200 U201 C202 G203 C204 G208 U209 C210 G211 A212 A213 C214 U217 C218 C219 A220 G226 U227 G228 G229 A230 A231 G232 C233 C234 G235 A243 G244 G245 A246 A247 G248 C249 G250

C253 G254 A255 A256 C257 G258 A264 U265 A266 G267 A270 C273 G274 U275 G276 A277 C280

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	Not provided	
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	20	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	0.707	Depositor
Minimum map value	-0.317	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.054	Depositor
Recommended contour level	0.0602	Depositor
Map size (Å)	452.64, 452.64, 452.64	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles (°)	90, 90, 90	wwPDB
Pixel spacing (Å)	1.23, 1.23, 1.23	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	4	1.34	7/658 (1.1%)	3.28	37/879 (4.2%)
2	5	1.39	4/506 (0.8%)	2.45	20/673 (3.0%)
3	6	1.35	3/680 (0.4%)	1.95	24/906 (2.6%)
4	A	0.46	0/3077	0.71	0/4800
5	B	0.46	0/883	0.70	0/1188
6	S	0.54	0/145	0.72	0/197
7	W	4.09	89/3545 (2.5%)	3.39	180/4707 (3.8%)
8	Z	0.45	0/6723	0.73	6/10473 (0.1%)
All	All	2.00	103/16217 (0.6%)	1.83	267/23823 (1.1%)

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
1	4	2	7
2	5	0	4
3	6	0	11
4	A	0	3
7	W	3	38
8	Z	0	6
All	All	5	69

All (103) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	W	284	PRO	N-CD	139.54	3.43	1.47
7	W	92	LYS	CB-CG	66.27	3.31	1.52
7	W	294	LEU	CB-CG	61.58	3.31	1.52
7	W	331	ASP	CB-CG	57.69	2.72	1.51
7	W	286	LYS	CB-CG	55.40	3.02	1.52
7	W	340	MET	CB-CG	48.81	3.07	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	W	342	MET	CB-CG	45.13	2.95	1.51
7	W	285	PHE	CB-CG	44.49	2.27	1.51
7	W	430	MET	CB-CG	44.00	2.92	1.51
7	W	431	VAL	CB-CG1	39.90	2.36	1.52
7	W	321	LYS	C-N	-33.57	0.56	1.34
7	W	292	SER	CB-OG	27.86	1.78	1.42
7	W	239	LYS	CA-CB	-27.78	0.92	1.53
7	W	293	LYS	CB-CG	24.62	2.19	1.52
7	W	202	PHE	CE1-CZ	-19.63	1.00	1.37
7	W	365	GLU	C-N	19.36	1.78	1.34
7	W	366	GLN	N-CA	-19.02	1.08	1.46
7	W	239	LYS	CB-CG	18.78	2.03	1.52
7	W	289	PRO	N-CD	18.58	1.73	1.47
7	W	351	MET	C-N	-18.39	0.91	1.34
7	W	354	GLY	C-N	-18.11	0.92	1.34
7	W	360	MET	C-N	-17.82	0.93	1.34
7	W	298	GLY	C-N	17.15	1.73	1.34
7	W	202	PHE	CE2-CZ	16.55	1.68	1.37
7	W	357	THR	C-N	-15.85	0.97	1.34
7	W	432	LYS	CB-CG	15.46	1.94	1.52
7	W	341	LYS	CB-CG	-15.40	1.10	1.52
7	W	40	LEU	C-N	14.14	1.66	1.34
2	5	39	ALA	C-N	-14.08	1.01	1.34
7	W	287	THR	CB-CG2	-13.52	1.07	1.52
7	W	363	GLY	C-N	-12.98	1.04	1.34
7	W	41	GLU	N-CA	12.96	1.72	1.46
7	W	40	LEU	CA-C	-12.68	1.20	1.52
7	W	297	MET	CB-CG	12.31	1.90	1.51
7	W	289	PRO	CG-CD	-12.27	1.10	1.50
7	W	303	LEU	C-N	12.11	1.61	1.34
7	W	431	VAL	CB-CG2	-11.93	1.27	1.52
7	W	112	SER	CB-OG	-11.79	1.26	1.42
7	W	243	ALA	C-N	-11.51	1.07	1.34
7	W	40	LEU	CA-CB	11.23	1.79	1.53
7	W	448	LYS	C-N	-11.12	1.08	1.34
7	W	161	GLY	C-N	10.80	1.58	1.34
7	W	318	LEU	C-N	10.41	1.57	1.34
7	W	282	PHE	CD2-CE2	-10.00	1.19	1.39
7	W	240	VAL	C-N	-9.92	1.11	1.34
2	5	35	ILE	C-N	9.74	1.56	1.34
7	W	40	LEU	CB-CG	9.52	1.80	1.52
7	W	348	ILE	C-N	-9.41	1.12	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	W	202	PHE	CD2-CE2	-9.35	1.20	1.39
7	W	99	GLY	CA-C	-9.24	1.37	1.51
7	W	202	PHE	CB-CG	-9.17	1.35	1.51
1	4	125	ARG	CZ-NH2	9.02	1.44	1.33
7	W	239	LYS	CG-CD	8.98	1.82	1.52
7	W	299	ASP	C-N	8.94	1.54	1.34
7	W	41	GLU	CA-CB	8.87	1.73	1.53
7	W	272	PHE	CA-CB	-8.30	1.35	1.53
1	4	131	LYS	CD-CE	8.06	1.71	1.51
1	4	140	TYR	CE2-CZ	-7.89	1.28	1.38
7	W	188	ILE	CB-CG2	-7.80	1.28	1.52
7	W	42	ALA	CA-C	-7.80	1.32	1.52
7	W	442	LYS	C-N	-7.78	1.19	1.33
7	W	237	LYS	CE-NZ	-7.68	1.29	1.49
7	W	480	LEU	C-N	7.65	1.51	1.34
7	W	41	GLU	CB-CG	7.32	1.66	1.52
7	W	197	GLN	C-O	-7.17	1.09	1.23
7	W	291	ILE	CB-CG2	7.09	1.74	1.52
7	W	40	LEU	N-CA	7.03	1.60	1.46
7	W	131	LYS	C-N	6.95	1.50	1.34
1	4	135	LYS	CD-CE	6.86	1.68	1.51
7	W	354	GLY	N-CA	6.69	1.56	1.46
7	W	437	ILE	C-N	-6.64	1.18	1.34
7	W	106	PHE	CE1-CZ	-6.63	1.24	1.37
7	W	40	LEU	C-O	6.51	1.35	1.23
7	W	272	PHE	CG-CD2	6.42	1.48	1.38
7	W	272	PHE	CG-CD1	6.41	1.48	1.38
7	W	106	PHE	CD1-CE1	-6.34	1.26	1.39
7	W	451	SER	C-N	-6.33	1.19	1.34
7	W	282	PHE	CD1-CE1	-6.29	1.26	1.39
2	5	42	GLY	C-N	6.25	1.48	1.34
7	W	287	THR	CB-OG1	6.24	1.55	1.43
7	W	284	PRO	CB-CG	6.22	1.81	1.50
7	W	244	SER	N-CA	-6.08	1.34	1.46
2	5	34	ARG	CZ-NH2	6.01	1.40	1.33
7	W	174	GLU	CA-CB	-5.93	1.40	1.53
7	W	367	GLU	N-CA	5.90	1.58	1.46
7	W	194	ARG	CZ-NH2	-5.78	1.25	1.33
1	4	131	LYS	CE-NZ	5.78	1.63	1.49
7	W	218	VAL	CB-CG2	-5.73	1.40	1.52
7	W	102	ASN	N-CA	-5.65	1.35	1.46
3	6	85	ARG	CZ-NH1	5.62	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	4	135	LYS	CE-NZ	5.59	1.63	1.49
7	W	352	ILE	N-CA	-5.58	1.35	1.46
7	W	118	CYS	CA-CB	-5.50	1.41	1.53
7	W	324	HIS	C-N	-5.44	1.23	1.33
3	6	58	ARG	CZ-NH2	5.40	1.40	1.33
3	6	27	ARG	CZ-NH1	5.36	1.40	1.33
1	4	125	ARG	CD-NE	-5.31	1.37	1.46
7	W	289	PRO	CB-CG	5.28	1.76	1.50
7	W	94	TRP	CE2-CZ2	-5.26	1.30	1.39
7	W	247	VAL	CB-CG1	-5.25	1.41	1.52
7	W	96	PRO	N-CD	5.21	1.55	1.47
7	W	106	PHE	CD2-CE2	-5.17	1.28	1.39
7	W	84	VAL	C-N	5.07	1.45	1.34

All (267) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	W	285	PHE	CB-CG-CD1	-73.05	69.66	120.80
1	4	125	ARG	NE-CZ-NH2	-72.81	83.89	120.30
7	W	285	PHE	CB-CG-CD2	66.74	167.52	120.80
7	W	352	ILE	C-N-CD	-49.65	11.38	120.60
7	W	284	PRO	CA-N-CD	-43.64	50.41	111.50
7	W	331	ASP	CB-CG-OD1	-38.10	84.00	118.30
7	W	298	GLY	O-C-N	-36.68	64.01	122.70
7	W	430	MET	CA-CB-CG	-34.60	54.48	113.30
7	W	340	MET	CA-CB-CG	-34.59	54.50	113.30
7	W	480	LEU	O-C-N	-34.09	68.15	122.70
7	W	321	LYS	O-C-N	-33.85	68.54	122.70
7	W	40	LEU	CB-CA-C	-32.71	48.04	110.20
7	W	342	MET	CA-CB-CG	-31.50	59.75	113.30
2	5	35	ILE	O-C-N	-29.92	74.83	122.70
7	W	331	ASP	CB-CG-OD2	28.38	143.84	118.30
7	W	40	LEU	O-C-N	25.74	163.89	122.70
7	W	285	PHE	CB-CA-C	25.57	161.53	110.40
7	W	321	LYS	CA-C-N	25.23	172.69	117.20
7	W	303	LEU	CB-CG-CD2	-24.83	68.79	111.00
7	W	202	PHE	CD1-CE1-CZ	-24.73	90.43	120.10
7	W	432	LYS	CA-CB-CG	-23.30	62.15	113.40
7	W	442	LYS	O-C-N	-22.92	84.23	123.20
7	W	437	ILE	CA-C-N	-22.05	68.70	117.20
7	W	303	LEU	CB-CG-CD1	21.66	147.81	111.00
7	W	285	PHE	CG-CD2-CE2	-21.33	97.34	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	W	294	LEU	CA-CB-CG	-21.06	66.87	115.30
7	W	287	THR	CA-CB-CG2	20.59	141.23	112.40
1	4	125	ARG	NE-CZ-NH1	20.51	130.55	120.30
7	W	99	GLY	CA-C-O	20.50	157.50	120.60
7	W	293	LYS	CA-CB-CG	-20.42	68.47	113.40
7	W	286	LYS	CB-CG-CD	-20.37	58.63	111.60
2	5	34	ARG	NE-CZ-NH1	-20.27	110.16	120.30
7	W	40	LEU	CA-C-O	-20.15	77.79	120.10
7	W	285	PHE	CA-CB-CG	-20.09	65.70	113.90
7	W	431	VAL	CA-CB-CG1	-19.98	80.94	110.90
7	W	294	LEU	CB-CG-CD1	-19.96	77.06	111.00
7	W	431	VAL	CG1-CB-CG2	-18.78	80.85	110.90
7	W	303	LEU	O-C-N	-18.37	93.31	122.70
7	W	340	MET	O-C-N	-18.35	93.34	122.70
7	W	106	PHE	CD1-CE1-CZ	18.26	142.01	120.10
7	W	92	LYS	CA-CB-CG	-17.91	74.00	113.40
7	W	84	VAL	O-C-N	17.59	150.84	122.70
2	5	42	GLY	O-C-N	17.58	150.82	122.70
7	W	324	HIS	O-C-N	-16.58	95.01	123.20
7	W	290	PHE	CB-CG-CD2	-16.50	109.25	120.80
2	5	39	ALA	C-N-CA	16.20	162.21	121.70
7	W	27	VAL	CG1-CB-CG2	-16.19	85.00	110.90
7	W	240	VAL	O-C-N	-15.73	97.53	122.70
7	W	363	GLY	O-C-N	-15.36	98.13	122.70
7	W	331	ASP	CA-CB-CG	-15.18	80.00	113.40
7	W	363	GLY	C-N-CA	14.96	159.11	121.70
7	W	365	GLU	CA-C-N	-14.72	84.81	117.20
7	W	294	LEU	CB-CG-CD2	14.68	135.95	111.00
3	6	18	ARG	NE-CZ-NH2	-14.67	112.96	120.30
7	W	357	THR	C-N-CA	-14.49	85.47	121.70
2	5	39	ALA	O-C-N	-14.39	99.67	122.70
7	W	285	PHE	CZ-CE2-CD2	14.23	137.18	120.10
7	W	285	PHE	N-CA-CB	-14.20	85.04	110.60
7	W	284	PRO	CB-CG-CD	-14.12	51.44	106.50
7	W	286	LYS	CA-CB-CG	-13.68	83.30	113.40
7	W	40	LEU	N-CA-C	-13.65	74.16	111.00
2	5	43	SER	N-CA-CB	-13.21	90.69	110.50
7	W	348	ILE	O-C-N	13.06	143.59	122.70
7	W	88	ASP	C-N-CD	-13.05	91.90	120.60
3	6	18	ARG	NE-CZ-NH1	12.94	126.77	120.30
7	W	342	MET	CB-CG-SD	12.90	151.09	112.40
7	W	24	ASN	CB-CA-C	-12.83	84.75	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	W	243	ALA	O-C-N	-12.80	102.22	122.70
7	W	197	GLN	O-C-N	-12.52	102.66	122.70
1	4	125	ARG	NH1-CZ-NH2	12.50	133.15	119.40
7	W	437	ILE	C-N-CA	-12.49	90.47	121.70
7	W	239	LYS	CD-CE-NZ	12.40	140.23	111.70
7	W	480	LEU	CA-C-N	-11.92	90.97	117.20
2	5	35	ILE	CA-C-N	11.89	143.36	117.20
7	W	321	LYS	C-N-CA	11.84	151.29	121.70
7	W	92	LYS	CB-CG-CD	-11.82	80.86	111.60
7	W	293	LYS	CB-CG-CD	-11.55	81.57	111.60
7	W	202	PHE	CZ-CE2-CD2	-11.53	106.26	120.10
7	W	40	LEU	C-N-CA	11.53	150.53	121.70
7	W	351	MET	C-N-CA	11.51	150.48	121.70
2	5	42	GLY	CA-C-N	-11.45	92.01	117.20
1	4	90	ASN	CB-CG-OD1	-11.35	98.89	121.60
7	W	289	PRO	CA-N-CD	-11.27	95.72	111.50
7	W	202	PHE	CB-CG-CD2	-11.23	112.94	120.80
7	W	84	VAL	CA-C-N	-11.22	92.51	117.20
7	W	72	ARG	NE-CZ-NH1	11.22	125.91	120.30
7	W	285	PHE	CE1-CZ-CE2	-11.20	99.83	120.00
1	4	141	ASP	C-N-CA	11.16	149.60	121.70
7	W	348	ILE	CA-C-N	-11.03	92.93	117.20
7	W	49	VAL	CA-CB-CG2	-10.94	94.48	110.90
2	5	43	SER	N-CA-C	10.90	140.44	111.00
7	W	348	ILE	C-N-CA	-10.89	94.47	121.70
7	W	340	MET	CB-CG-SD	-10.86	79.81	112.40
7	W	40	LEU	CA-C-N	-10.58	93.92	117.20
7	W	366	GLN	N-CA-C	10.47	139.26	111.00
7	W	106	PHE	CG-CD1-CE1	-10.43	109.33	120.80
7	W	324	HIS	C-N-CA	10.31	143.96	122.30
7	W	366	GLN	CB-CA-C	-10.12	90.15	110.40
3	6	52	MET	CG-SD-CE	-10.06	84.10	100.20
7	W	357	THR	CA-C-N	-9.93	95.36	117.20
2	5	43	SER	C-N-CA	9.85	146.31	121.70
1	4	131	LYS	CD-CE-NZ	9.66	133.93	111.70
2	5	17	ASP	CB-CG-OD2	9.59	126.94	118.30
1	4	142	ALA	CB-CA-C	-9.59	95.72	110.10
7	W	290	PHE	CB-CG-CD1	9.56	127.49	120.80
1	4	101	ASP	C-N-CA	9.47	145.37	121.70
7	W	282	PHE	CD1-CE1-CZ	-9.37	108.86	120.10
1	4	115	ILE	CA-CB-CG1	9.31	128.69	111.00
7	W	363	GLY	CA-C-N	9.24	137.53	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	W	480	LEU	C-N-CA	9.15	144.58	121.70
7	W	87	VAL	C-N-CA	9.09	144.42	121.70
2	5	39	ALA	CA-C-N	8.98	136.96	117.20
7	W	324	HIS	CA-C-N	8.98	134.15	116.20
2	5	57	ARG	NE-CZ-NH1	-8.93	115.83	120.30
1	4	101	ASP	N-CA-C	8.87	134.96	111.00
3	6	57	VAL	CB-CA-C	8.61	127.77	111.40
7	W	41	GLU	CB-CA-C	-8.59	93.23	110.40
7	W	303	LEU	CA-C-N	-8.51	98.48	117.20
7	W	341	LYS	CB-CG-CD	-8.51	89.49	111.60
1	4	145	VAL	CA-CB-CG2	-8.48	98.17	110.90
7	W	190	ASP	CB-CG-OD1	-8.47	110.68	118.30
7	W	56	VAL	CG1-CB-CG2	-8.38	97.50	110.90
8	Z	1	C	C2'-C3'-O3'	8.35	127.86	109.50
7	W	106	PHE	CE1-CZ-CE2	-8.33	105.01	120.00
7	W	327	PHE	O-C-N	8.33	136.02	122.70
7	W	239	LYS	CA-CB-CG	8.32	131.71	113.40
1	4	115	ILE	CA-CB-CG2	-8.20	94.51	110.90
1	4	140	TYR	CG-CD1-CE1	-8.19	114.75	121.30
8	Z	70	A	C2'-C3'-O3'	8.17	127.47	109.50
1	4	135	LYS	CA-CB-CG	8.11	131.25	113.40
7	W	41	GLU	CA-CB-CG	8.08	131.18	113.40
2	5	44	LYS	N-CA-CB	8.05	125.09	110.60
7	W	80	PHE	O-C-N	8.04	135.56	122.70
7	W	289	PRO	N-CA-CB	8.03	112.93	103.30
3	6	58	ARG	NE-CZ-NH2	-8.02	116.29	120.30
7	W	41	GLU	N-CA-C	8.01	132.63	111.00
1	4	131	LYS	CG-CD-CE	8.00	135.88	111.90
7	W	212	ILE	O-C-N	-7.98	109.93	122.70
7	W	46	ILE	O-C-N	-7.96	109.95	122.70
7	W	49	VAL	CG1-CB-CG2	-7.93	98.22	110.90
3	6	90	GLU	CA-CB-CG	7.87	130.72	113.40
1	4	90	ASN	CB-CG-ND2	7.87	135.58	116.70
7	W	448	LYS	O-C-N	-7.76	110.29	122.70
7	W	430	MET	CB-CG-SD	-7.70	89.31	112.40
7	W	354	GLY	C-N-CA	7.68	140.89	121.70
7	W	291	ILE	CG1-CB-CG2	-7.64	94.59	111.40
7	W	46	ILE	N-CA-C	-7.62	90.44	111.00
7	W	365	GLU	O-C-N	-7.61	110.52	122.70
7	W	42	ALA	N-CA-CB	7.57	120.69	110.10
7	W	318	LEU	O-C-N	7.52	134.73	122.70
8	Z	170	U	C2'-C3'-O3'	7.47	125.94	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	W	289	PRO	CA-CB-CG	-7.45	89.84	104.00
3	6	28	LEU	CB-CA-C	-7.42	96.11	110.20
7	W	167	ASP	O-C-N	-7.38	107.08	121.10
1	4	135	LYS	CD-CE-NZ	7.33	128.56	111.70
7	W	49	VAL	CA-CB-CG1	7.31	121.86	110.90
7	W	295	LEU	CB-CG-CD2	-7.30	98.59	111.00
1	4	101	ASP	CA-C-N	-7.29	101.17	117.20
7	W	292	SER	CA-CB-OG	-7.28	91.55	111.20
7	W	202	PHE	CG-CD2-CE2	-7.27	112.81	120.80
7	W	291	ILE	CA-CB-CG1	-7.26	97.21	111.00
7	W	202	PHE	CE1-CZ-CE2	7.25	133.06	120.00
1	4	135	LYS	CB-CG-CD	7.22	130.37	111.60
7	W	456	ALA	O-C-N	7.11	134.08	122.70
2	5	43	SER	O-C-N	7.10	134.06	122.70
1	4	101	ASP	CB-CG-OD2	-7.07	111.94	118.30
1	4	119	LYS	CD-CE-NZ	7.07	127.95	111.70
3	6	52	MET	CA-CB-CG	7.03	125.24	113.30
3	6	85	ARG	CB-CA-C	-7.02	96.36	110.40
7	W	239	LYS	CB-CG-CD	6.97	129.73	111.60
7	W	282	PHE	CE1-CZ-CE2	6.95	132.51	120.00
2	5	34	ARG	NH1-CZ-NH2	6.94	127.03	119.40
8	Z	43	A	C2'-C3'-O3'	6.93	124.80	113.70
7	W	41	GLU	N-CA-CB	6.93	123.08	110.60
7	W	327	PHE	CA-C-N	-6.89	102.03	117.20
3	6	85	ARG	N-CA-CB	6.89	123.01	110.60
7	W	53	ARG	NE-CZ-NH2	6.89	123.74	120.30
3	6	23	ASN	N-CA-C	-6.84	92.54	111.00
7	W	99	GLY	N-CA-C	-6.83	96.02	113.10
3	6	27	ARG	NE-CZ-NH1	-6.80	116.90	120.30
7	W	303	LEU	CA-CB-CG	6.74	130.80	115.30
3	6	85	ARG	NE-CZ-NH1	-6.71	116.95	120.30
7	W	243	ALA	CA-C-O	6.66	134.09	120.10
7	W	431	VAL	CA-CB-CG2	-6.64	100.94	110.90
7	W	84	VAL	C-N-CA	-6.63	105.13	121.70
7	W	167	ASP	CA-C-N	6.62	135.62	117.10
1	4	141	ASP	N-CA-C	6.58	128.75	111.00
7	W	102	ASN	N-CA-C	-6.55	93.30	111.00
1	4	70	TYR	CB-CG-CD1	6.51	124.91	121.00
7	W	42	ALA	CB-CA-C	-6.48	100.38	110.10
1	4	141	ASP	CA-C-N	-6.46	102.98	117.20
7	W	89	PRO	CB-CA-C	6.44	128.09	112.00
7	W	53	ARG	NE-CZ-NH1	-6.41	117.10	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	W	46	ILE	CA-C-N	6.39	131.27	117.20
3	6	80	ARG	N-CA-C	-6.32	93.94	111.00
1	4	115	ILE	CB-CA-C	-6.30	98.99	111.60
7	W	38	ALA	CB-CA-C	-6.29	100.66	110.10
7	W	42	ALA	O-C-N	6.25	132.70	122.70
3	6	90	GLU	N-CA-CB	6.23	121.82	110.60
2	5	17	ASP	CB-CG-OD1	-6.21	112.71	118.30
7	W	80	PHE	CA-C-N	-6.17	103.63	117.20
7	W	432	LYS	CB-CG-CD	-6.07	95.82	111.60
7	W	43	ASP	CB-CG-OD2	-6.03	112.87	118.30
2	5	43	SER	CA-C-N	-6.02	103.95	117.20
7	W	197	GLN	OE1-CD-NE2	-6.00	108.09	121.90
1	4	140	TYR	CG-CD2-CE2	-5.99	116.51	121.30
1	4	141	ASP	O-C-N	5.97	132.26	122.70
7	W	318	LEU	CA-C-N	-5.93	104.14	117.20
7	W	367	GLU	N-CA-CB	-5.90	99.98	110.60
7	W	450	VAL	CA-C-N	-5.88	104.28	117.20
7	W	40	LEU	N-CA-CB	5.85	122.11	110.40
1	4	89	ASN	CB-CG-OD1	5.80	133.20	121.60
7	W	179	PHE	CD1-CE1-CZ	5.79	127.05	120.10
7	W	442	LYS	CA-C-N	5.76	127.72	116.20
3	6	94	LYS	N-CA-CB	5.73	120.92	110.60
7	W	24	ASN	CB-CG-OD1	-5.72	110.15	121.60
1	4	125	ARG	CB-CA-C	5.71	121.83	110.40
2	5	41	SER	CB-CA-C	5.71	120.96	110.10
1	4	102	LYS	CB-CA-C	-5.70	99.00	110.40
7	W	40	LEU	CB-CG-CD1	5.69	120.67	111.00
8	Z	112	A	C2'-C3'-O3'	5.67	122.78	113.70
2	5	57	ARG	NE-CZ-NH2	5.66	123.13	120.30
3	6	85	ARG	NE-CZ-NH2	5.66	123.13	120.30
7	W	32	LEU	CB-CG-CD1	5.61	120.53	111.00
7	W	24	ASN	CA-CB-CG	5.59	125.71	113.40
7	W	39	LEU	C-N-CA	5.59	135.68	121.70
1	4	125	ARG	N-CA-CB	5.54	120.57	110.60
7	W	35	VAL	CA-CB-CG1	5.53	119.20	110.90
3	6	58	ARG	NE-CZ-NH1	5.51	123.05	120.30
3	6	96	GLU	N-CA-C	-5.50	96.15	111.00
1	4	124	ILE	N-CA-C	-5.49	96.17	111.00
1	4	140	TYR	CE1-CZ-OH	5.49	134.92	120.10
3	6	82	ARG	N-CA-C	-5.46	96.26	111.00
7	W	15	ARG	NE-CZ-NH2	5.44	123.02	120.30
3	6	88	ASN	N-CA-C	-5.43	96.35	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	W	288	GLN	C-N-CD	-5.42	108.67	120.60
7	W	282	PHE	CG-CD2-CE2	-5.42	114.84	120.80
7	W	450	VAL	O-C-N	5.41	131.36	122.70
1	4	123	LEU	CB-CG-CD1	5.39	120.17	111.00
7	W	13	ALA	N-CA-CB	5.39	117.64	110.10
7	W	320	GLU	O-C-N	5.39	131.32	122.70
7	W	24	ASN	O-C-N	-5.36	114.12	122.70
1	4	124	ILE	O-C-N	-5.36	114.13	122.70
7	W	243	ALA	CA-C-N	-5.32	105.49	117.20
7	W	272	PHE	CB-CG-CD1	-5.32	117.08	120.80
7	W	456	ALA	CA-C-N	-5.32	105.51	117.20
7	W	134	LEU	CB-CG-CD1	-5.31	101.97	111.00
3	6	19	GLU	N-CA-C	-5.29	96.70	111.00
7	W	20	ALA	O-C-N	-5.29	114.24	122.70
1	4	101	ASP	N-CA-CB	5.26	120.07	110.60
3	6	52	MET	N-CA-C	-5.26	96.81	111.00
7	W	323	LYS	CB-CA-C	5.25	120.90	110.40
7	W	284	PRO	N-CA-CB	5.25	109.59	103.30
7	W	187	ILE	CB-CG1-CD1	5.24	128.57	113.90
7	W	311	LYS	N-CA-C	-5.20	96.95	111.00
7	W	24	ASN	N-CA-C	5.18	124.98	111.00
7	W	194	ARG	NE-CZ-NH1	5.17	122.89	120.30
7	W	194	ARG	NE-CZ-NH2	5.17	122.89	120.30
7	W	197	GLN	CA-C-N	5.17	128.57	117.20
1	4	119	LYS	CG-CD-CE	5.14	127.31	111.90
8	Z	255	A	C5'-C4'-C3'	5.14	124.22	116.00
7	W	47	LYS	N-CA-C	-5.11	97.20	111.00
7	W	290	PHE	N-CA-CB	-5.11	101.41	110.60
7	W	287	THR	CA-CB-OG1	-5.09	98.30	109.00
3	6	85	ARG	CD-NE-CZ	-5.09	116.48	123.60
7	W	72	ARG	NH1-CZ-NH2	-5.07	113.82	119.40
7	W	453	SER	O-C-N	5.01	130.71	122.70

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	4	125	ARG	CA
1	4	141	ASP	CA
7	W	40	LEU	CA
7	W	285	PHE	CA
7	W	287	THR	CB

All (69) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	4	101	ASP	Peptide,Mainchain
1	4	124	ILE	Peptide
1	4	125	ARG	Sidechain
1	4	140	TYR	Sidechain
1	4	141	ASP	Peptide
1	4	89	ASN	Peptide
2	5	35	ILE	Mainchain
2	5	39	ALA	Peptide,Mainchain
2	5	43	SER	Peptide
3	6	18	ARG	Sidechain
3	6	27	ARG	Sidechain
3	6	47	PHE	Sidechain
3	6	50	LYS	Peptide
3	6	51	ALA	Peptide
3	6	58	ARG	Sidechain
3	6	77	ARG	Sidechain
3	6	80	ARG	Sidechain
3	6	86	LYS	Peptide
3	6	87	ARG	Peptide,Sidechain
4	A	197	G	Sidechain
4	A	201	A	Sidechain
4	A	208	A	Sidechain
7	W	15	ARG	Sidechain
7	W	161	GLY	Mainchain
7	W	167	ASP	Peptide
7	W	202	PHE	Sidechain
7	W	240	VAL	Mainchain
7	W	243	ALA	Mainchain
7	W	272	PHE	Sidechain
7	W	282	PHE	Sidechain
7	W	285	PHE	Sidechain
7	W	290	PHE	Sidechain
7	W	303	LEU	Peptide,Mainchain
7	W	321	LYS	Mainchain
7	W	324	HIS	Mainchain
7	W	331	ASP	Sidechain
7	W	340	MET	Peptide,Mainchain
7	W	351	MET	Peptide,Mainchain
7	W	352	ILE	Mainchain
7	W	354	GLY	Peptide
7	W	357	THR	Mainchain
7	W	360	MET	Peptide,Mainchain

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Mol	Chain	Res	Type	Group
7	W	363	GLY	Peptide,Mainchain
7	W	437	ILE	Peptide,Mainchain
7	W	442	LYS	Mainchain
7	W	448	LYS	Peptide,Mainchain
7	W	450	VAL	Mainchain
7	W	451	SER	Peptide,Mainchain
7	W	46	ILE	Peptide
7	W	480	LEU	Peptide,Mainchain
7	W	87	VAL	Peptide
8	Z	196	G	Sidechain
8	Z	254	G	Sidechain
8	Z	3	G	Sidechain
8	Z	6	A	Sidechain
8	Z	81	G	Sidechain
8	Z	94	G	Sidechain

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	4	652	0	703	156	0
2	5	504	0	550	95	0
3	6	671	0	704	117	0
4	A	2748	0	1389	87	0
5	B	869	0	901	80	0
6	S	141	0	146	107	0
7	W	3517	0	3388	1251	0
8	Z	6008	0	3033	302	0
All	All	15110	0	10814	1922	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 74.

All (1922) 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)
7:W:432:LYS:HA	7:W:436:GLY:CA	1.16	1.63
1:4:89:ASN:CB	8:Z:172:C:C5'	1.80	1.60
7:W:52:LEU:CD1	7:W:86:LEU:HD21	1.18	1.57
3:6:65:LYS:HD2	8:Z:64:C:C2'	1.23	1.56
7:W:87:VAL:HG22	7:W:257:GLY:CA	1.19	1.56
3:6:68:TRP:HZ3	8:Z:46:G:C2	1.23	1.55
6:S:50:LEU:HD12	7:W:478:ALA:CA	1.09	1.55
7:W:239:LYS:CG	7:W:239:LYS:CD	1.83	1.55
7:W:52:LEU:CG	7:W:86:LEU:HD11	1.31	1.55
7:W:40:LEU:CB	7:W:40:LEU:CG	1.80	1.54
7:W:52:LEU:HG	7:W:86:LEU:CD1	1.11	1.54
1:4:89:ASN:CA	8:Z:172:C:H5"	1.32	1.54
6:S:58:THR:CG2	7:W:339:ILE:HD13	1.35	1.53
7:W:52:LEU:HD11	7:W:86:LEU:CD2	1.19	1.53
3:6:68:TRP:CZ3	8:Z:46:G:N3	1.78	1.51
7:W:41:GLU:N	7:W:41:GLU:CA	1.72	1.50
7:W:52:LEU:HD21	7:W:86:LEU:CD2	1.25	1.50
7:W:432:LYS:CG	7:W:432:LYS:CA	1.82	1.50
6:S:57:LEU:HD22	7:W:430:MET:CE	1.03	1.49
7:W:297:MET:CB	7:W:297:MET:CG	1.90	1.49
6:S:57:LEU:CD2	7:W:430:MET:CE	1.90	1.48
7:W:52:LEU:HD11	7:W:86:LEU:CG	1.39	1.48
8:Z:159:C:C4'	8:Z:213:A:H1'	1.41	1.48
3:6:68:TRP:HZ3	8:Z:46:G:N3	1.09	1.48
7:W:87:VAL:CG2	7:W:257:GLY:HA2	1.43	1.48
8:Z:159:C:C1'	8:Z:213:A:N3	1.74	1.47
7:W:52:LEU:CD2	7:W:86:LEU:CD2	1.92	1.46
8:Z:159:C:H1'	8:Z:213:A:C2	1.48	1.45
7:W:432:LYS:CG	7:W:432:LYS:CB	1.94	1.45
1:4:89:ASN:HB2	8:Z:172:C:C5'	1.35	1.45
7:W:332:MET:SD	7:W:424:TYR:CD1	2.10	1.45
2:5:34:ARG:CG	2:5:37:LYS:HZ3	1.28	1.44
7:W:430:MET:N	7:W:430:MET:CG	1.82	1.43
8:Z:159:C:H4'	8:Z:213:A:C1'	1.44	1.43
3:6:64:ASN:HD21	8:Z:48:C:C5'	1.32	1.43
7:W:283:GLU:C	7:W:284:PRO:HB2	1.35	1.43
6:S:63:VAL:HG11	7:W:361:SER:CB	1.49	1.42
6:S:62:THR:CG2	7:W:371:ARG:HD3	1.45	1.42
7:W:327:PHE:HB3	7:W:333:TYR:CD2	1.54	1.42
1:4:89:ASN:HD22	8:Z:171:C:C3'	1.31	1.41
7:W:432:LYS:HG3	7:W:436:GLY:CA	1.50	1.41
3:6:65:LYS:CD	8:Z:64:C:C2'	1.80	1.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:298:GLY:C	7:W:299:ASP:N	1.73	1.40
8:Z:159:C:C4'	8:Z:213:A:C1'	1.99	1.39
8:Z:159:C:H1'	8:Z:213:A:N3	1.22	1.38
7:W:429:GLN:O	7:W:432:LYS:CB	1.70	1.37
3:6:64:ASN:ND2	8:Z:48:C:H5'	1.35	1.36
7:W:365:GLU:O	7:W:368:SER:N	1.57	1.36
7:W:365:GLU:C	7:W:366:GLN:N	1.78	1.36
6:S:50:LEU:CD1	7:W:478:ALA:CA	1.97	1.35
7:W:239:LYS:CG	7:W:239:LYS:CB	2.03	1.35
7:W:16:SER:CA	7:W:17:LEU:HB3	1.22	1.34
7:W:77:HIS:O	7:W:81:LYS:CG	1.73	1.34
7:W:250:LEU:CD2	7:W:290:PHE:CZ	2.11	1.34
7:W:239:LYS:CB	7:W:239:LYS:N	1.86	1.33
7:W:432:LYS:CA	7:W:436:GLY:HA2	1.58	1.33
7:W:344:PRO:N	7:W:345:PHE:CD2	1.74	1.33
7:W:441:PHE:O	7:W:444:GLY:C	1.66	1.32
7:W:52:LEU:CD2	7:W:86:LEU:HD22	1.56	1.31
7:W:287:THR:O	7:W:291:ILE:HD12	1.22	1.31
7:W:293:LYS:C	7:W:294:LEU:CB	1.99	1.31
7:W:338:ASN:O	7:W:342:MET:CB	1.78	1.31
8:Z:160:G:H5'	8:Z:212:A:C4	1.64	1.31
7:W:271:ILE:HD12	7:W:272:PHE:CD1	1.66	1.30
7:W:314:ASP:OD2	7:W:319:ILE:HD11	1.13	1.30
3:6:68:TRP:CZ3	8:Z:46:G:N2	1.99	1.30
7:W:285:PHE:CG	7:W:285:PHE:CA	2.14	1.30
7:W:88:ASP:CG	7:W:259:ALA:HB1	1.50	1.30
7:W:306:LYS:HA	7:W:347:GLN:NE2	1.47	1.30
7:W:336:PHE:CD2	7:W:379:MET:HE1	1.64	1.29
1:4:96:VAL:O	1:4:97:ASP:CG	1.69	1.29
7:W:45:ASN:O	7:W:227:GLN:HG3	1.30	1.29
7:W:87:VAL:O	7:W:259:ALA:CB	1.78	1.29
7:W:52:LEU:CD1	7:W:86:LEU:CG	2.07	1.29
7:W:239:LYS:CB	7:W:239:LYS:C	1.98	1.29
6:S:52:PHE:CE2	7:W:351:MET:SD	2.24	1.28
2:5:33:LEU:O	2:5:37:LYS:CG	1.63	1.28
3:6:68:TRP:CZ3	8:Z:46:G:C2	2.15	1.28
8:Z:1:C:O3'	8:Z:2:U:H5"	1.19	1.28
1:4:89:ASN:ND2	8:Z:171:C:C3'	1.89	1.28
3:6:65:LYS:CE	8:Z:64:C:O2'	1.82	1.28
7:W:298:GLY:O	7:W:299:ASP:N	1.63	1.28
1:4:72:ILE:HA	1:4:97:ASP:OD2	1.28	1.28

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:294:LEU:CG	7:W:294:LEU:N	1.97	1.28
6:S:56:PHE:O	7:W:352:ILE:CG2	1.82	1.27
7:W:340:MET:N	7:W:372:LEU:CD1	1.89	1.27
7:W:289:PRO:CD	7:W:289:PRO:N	1.73	1.26
7:W:366:GLN:N	7:W:367:GLU:N	1.83	1.26
7:W:40:LEU:CG	7:W:40:LEU:C	2.01	1.26
7:W:285:PHE:CG	7:W:285:PHE:HA	1.69	1.26
2:5:34:ARG:HG2	2:5:37:LYS:NZ	0.94	1.26
7:W:338:ASN:O	7:W:342:MET:HB2	1.18	1.26
7:W:345:PHE:CE1	7:W:365:GLU:OE1	1.89	1.25
7:W:429:GLN:O	7:W:432:LYS:CA	1.84	1.25
7:W:432:LYS:CG	7:W:436:GLY:HA3	1.64	1.25
7:W:339:ILE:C	7:W:372:LEU:HD11	1.55	1.25
7:W:52:LEU:CG	7:W:86:LEU:HD21	1.66	1.25
7:W:432:LYS:CG	7:W:432:LYS:C	2.05	1.25
7:W:432:LYS:CA	7:W:436:GLY:CA	2.12	1.25
6:S:60:TYR:HB2	7:W:352:ILE:CG2	1.67	1.25
7:W:16:SER:C	7:W:17:LEU:CA	2.05	1.25
7:W:432:LYS:CG	7:W:432:LYS:O	1.85	1.25
7:W:340:MET:HE3	7:W:373:LYS:N	1.49	1.24
2:5:34:ARG:CG	2:5:37:LYS:NZ	1.90	1.24
7:W:87:VAL:O	7:W:259:ALA:HB3	1.09	1.24
7:W:179:PHE:CE2	7:W:187:ILE:HG12	1.73	1.24
6:S:58:THR:HG21	7:W:339:ILE:CD1	1.68	1.23
7:W:16:SER:C	7:W:17:LEU:CG	2.04	1.23
7:W:285:PHE:CB	7:W:285:PHE:CD1	2.21	1.23
3:6:65:LYS:CG	8:Z:64:C:O2'	1.83	1.23
6:S:58:THR:CG2	7:W:339:ILE:HG21	1.66	1.23
7:W:179:PHE:CZ	7:W:187:ILE:HG12	1.75	1.22
7:W:250:LEU:HD21	7:W:290:PHE:CE1	1.74	1.22
7:W:283:GLU:O	7:W:284:PRO:N	1.72	1.22
7:W:87:VAL:C	7:W:259:ALA:HB3	1.59	1.22
7:W:287:THR:O	7:W:291:ILE:CD1	1.84	1.22
6:S:58:THR:CB	7:W:339:ILE:HD13	1.69	1.21
1:4:75:TYR:CD1	2:5:34:ARG:O	1.94	1.21
7:W:293:LYS:CA	7:W:293:LYS:CG	2.16	1.21
7:W:342:MET:HA	7:W:342:MET:CG	1.70	1.21
2:5:25:GLU:OE2	7:W:22:ILE:CG2	1.88	1.20
7:W:250:LEU:HD21	7:W:290:PHE:CZ	1.71	1.20
7:W:283:GLU:C	7:W:284:PRO:CB	2.09	1.20
8:Z:160:G:H5'	8:Z:212:A:N9	1.52	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S:63:VAL:CG1	7:W:361:SER:HB2	1.72	1.20
7:W:342:MET:HE1	7:W:347:GLN:NE2	1.55	1.20
7:W:52:LEU:CG	7:W:86:LEU:CD1	1.93	1.19
7:W:293:LYS:CG	7:W:293:LYS:CB	2.19	1.19
7:W:441:PHE:O	7:W:445:ASP:N	1.75	1.19
7:W:52:LEU:CD1	7:W:86:LEU:CD2	1.84	1.18
7:W:89:PRO:CA	7:W:287:THR:OG1	1.91	1.18
7:W:285:PHE:CG	7:W:285:PHE:CB	2.27	1.18
7:W:56:VAL:HA	7:W:82:GLU:OE2	1.42	1.18
7:W:52:LEU:CG	7:W:86:LEU:CD2	2.18	1.18
7:W:106:PHE:HE1	7:W:188:ILE:CG2	1.56	1.17
1:4:89:ASN:CB	8:Z:172:C:H5'	1.53	1.17
7:W:297:MET:HB3	7:W:300:ILE:HD12	1.25	1.17
7:W:336:PHE:CD2	7:W:379:MET:CE	2.26	1.17
7:W:432:LYS:O	7:W:432:LYS:HG2	0.99	1.17
7:W:40:LEU:C	7:W:40:LEU:HG	1.65	1.16
7:W:345:PHE:CD1	7:W:365:GLU:HB3	1.80	1.16
7:W:314:ASP:CG	7:W:319:ILE:HD11	1.66	1.16
8:Z:159:C:H4'	8:Z:213:A:O4'	1.46	1.16
3:6:60:ASP:C	8:Z:48:C:O2'	1.84	1.16
7:W:432:LYS:HA	7:W:432:LYS:CG	1.68	1.16
7:W:350:GLY:O	7:W:352:ILE:HG13	1.44	1.15
7:W:284:PRO:O	7:W:286:LYS:HD3	1.47	1.15
7:W:344:PRO:N	7:W:345:PHE:CE2	2.15	1.15
7:W:335:GLN:HB3	7:W:427:PHE:CZ	1.79	1.15
3:6:65:LYS:HD3	8:Z:64:C:O2'	1.36	1.14
8:Z:159:C:H1'	8:Z:213:A:C4	1.81	1.14
3:6:59:ILE:CG1	8:Z:48:C:O3'	1.93	1.14
7:W:271:ILE:HD12	7:W:272:PHE:CE1	1.82	1.14
7:W:325:GLY:O	7:W:328:THR:HB	1.45	1.14
1:4:89:ASN:CB	8:Z:172:C:H5"	1.52	1.14
3:6:60:ASP:CA	8:Z:48:C:O2'	1.95	1.14
7:W:327:PHE:HB3	7:W:333:TYR:CE2	1.83	1.14
2:5:34:ARG:HD3	2:5:37:LYS:HD3	1.14	1.13
3:6:41:ILE:HG21	8:Z:47:U:O3'	1.48	1.13
1:4:72:ILE:O	1:4:96:VAL:O	1.64	1.13
6:S:63:VAL:CG1	7:W:361:SER:CB	2.26	1.13
7:W:23:ILE:HG23	7:W:26:GLU:OE2	1.49	1.13
7:W:293:LYS:C	7:W:294:LEU:CA	2.17	1.13
7:W:52:LEU:CD2	7:W:86:LEU:HD21	1.62	1.12
8:Z:161:G:C1'	8:Z:267:G:H4'	1.77	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4:95:ILE:HG22	1:4:96:VAL:HG11	1.30	1.12
7:W:87:VAL:HG22	7:W:257:GLY:N	1.64	1.12
7:W:432:LYS:C	7:W:432:LYS:HG2	1.67	1.12
6:S:60:TYR:HB2	7:W:352:ILE:HG21	1.29	1.11
1:4:89:ASN:CA	8:Z:172:C:C5'	2.19	1.11
1:4:98:LEU:HD11	1:4:101:ASP:OD1	1.47	1.11
7:W:202:PHE:CD2	7:W:239:LYS:HD2	1.85	1.11
7:W:239:LYS:CB	7:W:239:LYS:HA	1.63	1.11
7:W:306:LYS:HB2	7:W:347:GLN:OE1	1.50	1.11
7:W:432:LYS:HA	7:W:432:LYS:HG3	1.23	1.11
1:4:85:LYS:HE2	8:Z:171:C:H4'	1.19	1.11
7:W:345:PHE:CD1	7:W:365:GLU:OE1	2.03	1.10
6:S:56:PHE:O	7:W:352:ILE:HG23	0.94	1.10
7:W:337:GLN:HA	7:W:340:MET:HB2	1.33	1.10
8:Z:159:C:C1'	8:Z:213:A:C4	2.35	1.10
7:W:52:LEU:HD11	7:W:86:LEU:HG	1.32	1.10
7:W:314:ASP:C	7:W:315:ASN:N	2.05	1.10
1:4:98:LEU:HD12	1:4:130:LYS:HZ3	0.98	1.10
7:W:84:VAL:HG13	7:W:88:ASP:O	1.49	1.10
7:W:432:LYS:HA	7:W:436:GLY:HA3	1.16	1.10
7:W:94:TRP:CH2	7:W:218:VAL:HG21	1.87	1.09
1:4:140:TYR:CZ	1:4:145:VAL:HG21	1.88	1.09
7:W:313:ASP:HA	7:W:319:ILE:HD11	1.30	1.09
3:6:68:TRP:CZ2	8:Z:47:U:O4'	2.04	1.09
6:S:62:THR:HG21	7:W:371:ARG:CD	1.80	1.09
7:W:430:MET:N	7:W:430:MET:HG3	1.57	1.09
3:6:61:VAL:HG21	8:Z:62:G:H22	1.08	1.08
7:W:306:LYS:CA	7:W:347:GLN:NE2	2.14	1.08
7:W:194:ARG:NH2	7:W:202:PHE:HB2	1.66	1.08
7:W:330:ARG:HB2	7:W:333:TYR:CB	1.83	1.08
8:Z:159:C:O4'	8:Z:213:A:H1'	1.50	1.08
2:5:36:GLN:O	2:5:40:SER:O	1.71	1.08
7:W:89:PRO:HA	7:W:287:THR:CG2	1.82	1.08
7:W:77:HIS:C	7:W:81:LYS:HG3	1.72	1.08
7:W:106:PHE:CZ	7:W:121:LEU:HD12	1.88	1.08
7:W:431:VAL:O	7:W:436:GLY:HA2	1.50	1.08
6:S:58:THR:HG21	7:W:339:ILE:CG2	1.84	1.07
8:Z:160:G:P	8:Z:212:A:H1'	1.94	1.07
2:5:33:LEU:O	2:5:37:LYS:HG2	1.30	1.07
3:6:61:VAL:HG21	8:Z:62:G:N2	1.66	1.07
2:5:34:ARG:HG2	2:5:37:LYS:CE	1.77	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:134:LEU:HD11	7:W:157:ILE:CD1	1.85	1.07
2:5:25:GLU:OE2	7:W:22:ILE:HG22	1.51	1.07
7:W:134:LEU:HD11	7:W:157:ILE:HD11	1.27	1.07
7:W:202:PHE:CZ	7:W:239:LYS:CB	2.37	1.07
7:W:337:GLN:CA	7:W:340:MET:HB2	1.85	1.07
7:W:330:ARG:HB2	7:W:333:TYR:H	1.13	1.06
7:W:202:PHE:CZ	7:W:239:LYS:HB2	1.90	1.06
7:W:332:MET:SD	7:W:424:TYR:CG	2.47	1.06
7:W:479:GLY:C	7:W:480:LEU:N	2.07	1.06
8:Z:159:C:O4'	8:Z:213:A:N3	1.85	1.06
6:S:58:THR:HG21	7:W:339:ILE:HG21	1.16	1.06
7:W:306:LYS:HA	7:W:347:GLN:HE22	0.94	1.06
7:W:52:LEU:HG	7:W:86:LEU:HD13	1.33	1.06
7:W:429:GLN:O	7:W:432:LYS:HB3	1.37	1.06
3:6:65:LYS:HD3	8:Z:64:C:C3'	1.84	1.06
6:S:57:LEU:HD22	7:W:430:MET:HE2	1.08	1.06
1:4:123:LEU:HD21	8:Z:111:U:H5'	1.36	1.05
3:6:65:LYS:HD3	8:Z:64:C:O3'	1.53	1.05
7:W:332:MET:SD	7:W:424:TYR:HB2	1.96	1.05
7:W:477:MET:O	7:W:479:GLY:N	1.88	1.05
7:W:338:ASN:C	7:W:342:MET:HB2	1.76	1.05
6:S:54:ILE:HG23	7:W:427:PHE:CE2	1.91	1.05
1:4:75:TYR:CE1	2:5:34:ARG:O	2.08	1.05
6:S:58:THR:CG2	7:W:339:ILE:CD1	2.28	1.05
7:W:42:ALA:HA	7:W:49:VAL:HG21	1.11	1.05
7:W:106:PHE:HE1	7:W:188:ILE:HG23	1.20	1.05
7:W:136:CYS:SG	7:W:148:LEU:HB3	1.96	1.05
7:W:319:ILE:HA	7:W:323:LYS:CE	1.84	1.04
7:W:366:GLN:CD	7:W:369:MET:N	1.79	1.04
6:S:57:LEU:CD2	7:W:430:MET:HE3	1.86	1.04
7:W:87:VAL:CG2	7:W:257:GLY:CA	2.13	1.04
2:5:34:ARG:CD	2:5:37:LYS:HD3	1.76	1.04
7:W:450:VAL:O	7:W:454:GLN:N	1.87	1.04
7:W:325:GLY:O	7:W:328:THR:CB	2.05	1.04
7:W:340:MET:CE	7:W:373:LYS:N	2.20	1.04
7:W:342:MET:CE	7:W:347:GLN:NE2	2.19	1.04
7:W:84:VAL:HG12	7:W:89:PRO:HB3	1.40	1.04
3:6:68:TRP:HH2	8:Z:46:G:H2'	1.21	1.03
6:S:61:VAL:HG11	7:W:423:GLN:HG2	1.34	1.03
7:W:429:GLN:C	7:W:432:LYS:HB3	1.77	1.03
8:Z:161:G:H1'	8:Z:267:G:H4'	1.39	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:430:MET:HA	7:W:433:LYS:HB2	1.38	1.03
7:W:330:ARG:HD2	7:W:333:TYR:HB2	1.41	1.03
7:W:443:GLY:O	7:W:447:SER:CA	2.05	1.03
7:W:41:GLU:N	7:W:41:GLU:HA	1.67	1.03
7:W:77:HIS:CB	7:W:81:LYS:HE3	1.88	1.03
7:W:430:MET:O	7:W:433:LYS:HB2	1.57	1.03
7:W:330:ARG:CB	7:W:333:TYR:H	1.71	1.03
7:W:52:LEU:HD13	7:W:86:LEU:HD21	1.35	1.02
7:W:358:ASP:CB	7:W:361:SER:OG	2.07	1.02
1:4:85:LYS:CE	8:Z:171:C:H4'	1.88	1.02
7:W:52:LEU:CD1	7:W:86:LEU:HD11	1.90	1.02
7:W:283:GLU:C	7:W:284:PRO:N	2.13	1.02
6:S:58:THR:OG1	7:W:339:ILE:CD1	2.05	1.02
7:W:340:MET:N	7:W:372:LEU:HD12	1.18	1.02
7:W:285:PHE:HE1	7:W:304:ILE:HD12	1.24	1.02
7:W:431:VAL:CB	7:W:431:VAL:CG1	2.36	1.02
8:Z:159:C:C5'	8:Z:213:A:H1'	1.88	1.02
7:W:88:ASP:OD2	7:W:259:ALA:HB1	1.58	1.01
7:W:84:VAL:CG1	7:W:89:PRO:HB3	1.91	1.01
7:W:94:TRP:CZ2	7:W:218:VAL:HG21	1.94	1.01
7:W:16:SER:O	7:W:17:LEU:HB2	0.85	1.01
7:W:330:ARG:CG	7:W:333:TYR:HB2	1.90	1.01
7:W:430:MET:CA	7:W:433:LYS:HB2	1.89	1.01
7:W:299:ASP:HB3	7:W:348:ILE:HA	1.01	1.01
7:W:323:LYS:N	7:W:337:GLN:HE22	1.58	1.01
7:W:358:ASP:HB3	7:W:361:SER:OG	1.58	1.01
7:W:430:MET:CG	7:W:430:MET:CA	2.38	1.01
7:W:106:PHE:CE2	7:W:121:LEU:HD12	1.96	1.00
7:W:429:GLN:CA	7:W:432:LYS:HB3	1.90	1.00
7:W:88:ASP:OD1	7:W:259:ALA:C	1.99	1.00
2:5:33:LEU:O	2:5:37:LYS:HG3	1.32	1.00
7:W:330:ARG:HB2	7:W:333:TYR:HB2	1.42	1.00
7:W:330:ARG:CB	7:W:333:TYR:HB2	1.92	1.00
7:W:239:LYS:HB2	7:W:239:LYS:CA	1.49	1.00
7:W:272:PHE:CG	7:W:282:PHE:CZ	2.50	1.00
7:W:337:GLN:O	7:W:340:MET:HB2	1.62	1.00
8:Z:159:C:C1'	8:Z:213:A:C2	2.31	1.00
7:W:239:LYS:CA	7:W:239:LYS:HB3	1.49	0.99
1:4:85:LYS:HE2	8:Z:171:C:C4'	1.92	0.99
7:W:77:HIS:HB3	7:W:81:LYS:HE3	1.00	0.99
7:W:284:PRO:O	7:W:286:LYS:CD	2.10	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6:59:ILE:HD13	8:Z:49:G:P	2.02	0.99
7:W:314:ASP:OD2	7:W:319:ILE:CD1	2.09	0.99
1:4:72:ILE:CA	1:4:97:ASP:OD2	2.10	0.99
7:W:330:ARG:HB2	7:W:333:TYR:N	1.76	0.99
1:4:98:LEU:HD12	1:4:130:LYS:NZ	1.75	0.99
7:W:327:PHE:O	7:W:333:TYR:HB3	1.63	0.99
7:W:365:GLU:CA	7:W:366:GLN:N	2.24	0.99
7:W:394:LYS:HD2	8:Z:14:U:OP1	1.62	0.99
7:W:77:HIS:HB3	7:W:81:LYS:CE	1.93	0.98
7:W:87:VAL:CG2	7:W:257:GLY:N	2.25	0.98
7:W:250:LEU:CD2	7:W:290:PHE:HZ	1.63	0.98
7:W:299:ASP:CB	7:W:348:ILE:HA	1.93	0.98
7:W:432:LYS:HG3	7:W:436:GLY:HA3	1.02	0.98
7:W:84:VAL:HG12	7:W:89:PRO:CB	1.93	0.98
7:W:330:ARG:CD	7:W:333:TYR:HB2	1.93	0.98
3:6:65:LYS:HD3	8:Z:64:C:C2'	1.78	0.98
7:W:432:LYS:HG3	7:W:436:GLY:N	1.79	0.98
7:W:293:LYS:CG	7:W:293:LYS:HA	1.88	0.98
7:W:365:GLU:C	7:W:366:GLN:CB	2.32	0.98
7:W:89:PRO:HA	7:W:287:THR:HG21	1.46	0.98
1:4:136:LEU:HD13	1:4:140:TYR:CE2	1.98	0.97
7:W:429:GLN:C	7:W:432:LYS:CB	2.30	0.97
3:6:68:TRP:HZ3	8:Z:46:G:N2	1.48	0.97
3:6:58:ARG:HH11	8:Z:49:G:P	1.87	0.97
6:S:56:PHE:CE1	7:W:350:GLY:O	2.17	0.97
7:W:84:VAL:CG1	7:W:88:ASP:O	2.13	0.97
7:W:297:MET:CB	7:W:300:ILE:HD12	1.95	0.97
7:W:431:VAL:CG1	7:W:431:VAL:HG22	1.93	0.97
7:W:475:GLY:O	7:W:476:GLY:N	1.98	0.97
3:6:68:TRP:CH2	8:Z:46:G:N3	2.33	0.97
6:S:62:THR:HG21	7:W:371:ARG:HD3	1.00	0.97
6:S:62:THR:CG2	7:W:371:ARG:CD	2.40	0.97
7:W:89:PRO:CA	7:W:287:THR:HG21	1.95	0.97
7:W:106:PHE:CE1	7:W:188:ILE:HG23	2.00	0.97
3:6:72:ILE:HD11	8:Z:45:A:C5	2.00	0.97
7:W:106:PHE:CE1	7:W:188:ILE:CG2	2.48	0.96
7:W:272:PHE:CE2	7:W:282:PHE:CE2	2.53	0.96
7:W:80:PHE:CE2	7:W:291:ILE:HG12	1.93	0.96
7:W:202:PHE:CE2	7:W:239:LYS:HB3	2.00	0.96
7:W:285:PHE:CB	7:W:285:PHE:HD1	1.70	0.96
7:W:342:MET:CE	7:W:347:GLN:CD	2.34	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:431:VAL:C	7:W:436:GLY:HA2	1.86	0.96
6:S:57:LEU:HD22	7:W:430:MET:HE1	0.97	0.96
7:W:80:PHE:CE2	7:W:291:ILE:CG1	2.23	0.96
7:W:306:LYS:CA	7:W:347:GLN:HE22	1.76	0.96
2:5:34:ARG:HG2	2:5:37:LYS:HZ2	1.23	0.96
7:W:77:HIS:O	7:W:81:LYS:HG3	0.79	0.96
8:Z:159:C:O5'	8:Z:213:A:C1'	2.12	0.96
7:W:342:MET:HE1	7:W:347:GLN:HE21	1.21	0.96
4:A:220:C:H2'	4:A:221:C:H5"	1.45	0.96
1:4:123:LEU:HD11	8:Z:111:U:C5'	1.96	0.95
2:5:34:ARG:HH12	2:5:48:ILE:HG23	1.29	0.95
7:W:249:LYS:O	7:W:249:LYS:HD3	1.65	0.95
7:W:272:PHE:HB3	7:W:282:PHE:CE1	2.01	0.95
7:W:337:GLN:HA	7:W:340:MET:CB	1.95	0.95
7:W:339:ILE:HA	7:W:342:MET:CB	1.94	0.95
7:W:431:VAL:O	7:W:436:GLY:CA	2.14	0.95
1:4:119:LYS:HD3	1:4:135:LYS:HZ3	1.30	0.95
7:W:337:GLN:C	7:W:340:MET:HB2	1.87	0.95
7:W:323:LYS:H	7:W:337:GLN:HE22	1.07	0.95
2:5:25:GLU:OE2	7:W:22:ILE:HG23	1.64	0.95
7:W:339:ILE:C	7:W:372:LEU:CD1	2.35	0.95
7:W:89:PRO:HA	7:W:287:THR:CB	1.95	0.95
7:W:342:MET:HE1	7:W:347:GLN:CD	1.87	0.95
7:W:345:PHE:HD1	7:W:365:GLU:CG	1.79	0.95
3:6:65:LYS:CD	8:Z:64:C:O2'	0.65	0.95
5:B:60:VAL:HG23	5:B:83:ARG:O	1.67	0.95
1:4:89:ASN:HA	8:Z:172:C:H5"	0.97	0.95
7:W:330:ARG:NE	7:W:387:LEU:HD22	1.81	0.95
3:6:61:VAL:HA	8:Z:48:C:H1'	1.46	0.95
7:W:293:LYS:HG2	7:W:293:LYS:O	1.67	0.94
1:4:88:ASP:O	8:Z:172:C:H4'	1.66	0.94
7:W:45:ASN:C	7:W:227:GLN:HG3	1.86	0.94
7:W:430:MET:O	7:W:433:LYS:CB	2.15	0.94
1:4:75:TYR:OH	2:5:39:ALA:N	1.78	0.94
6:S:56:PHE:CD1	7:W:350:GLY:C	2.40	0.94
7:W:250:LEU:CD2	7:W:290:PHE:CE1	2.43	0.94
7:W:441:PHE:O	7:W:444:GLY:CA	2.15	0.94
3:6:68:TRP:CH2	8:Z:46:G:H2'	2.02	0.94
7:W:340:MET:HE1	7:W:373:LYS:HB2	1.49	0.94
7:W:429:GLN:HA	7:W:432:LYS:HB3	1.48	0.94
2:5:30:LEU:O	2:5:37:LYS:NZ	2.01	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:250:LEU:O	7:W:250:LEU:HD13	1.67	0.94
7:W:327:PHE:CD2	7:W:333:TYR:CE2	2.55	0.94
7:W:336:PHE:CE2	7:W:379:MET:HE2	2.03	0.94
7:W:460:GLN:CA	7:W:461:GLN:N	2.30	0.94
8:Z:160:G:H5'	8:Z:212:A:C1'	1.98	0.94
7:W:286:LYS:CB	7:W:286:LYS:HD2	1.98	0.94
7:W:364:ASN:ND2	7:W:367:GLU:OE2	2.01	0.94
7:W:299:ASP:HB3	7:W:348:ILE:CA	1.96	0.94
7:W:88:ASP:OD1	7:W:259:ALA:O	1.86	0.93
7:W:345:PHE:HD1	7:W:365:GLU:CD	1.72	0.93
7:W:272:PHE:CD2	7:W:282:PHE:CE2	2.56	0.93
3:6:58:ARG:NH1	8:Z:48:C:H2'	1.84	0.93
7:W:42:ALA:HA	7:W:49:VAL:CG2	1.99	0.93
6:S:60:TYR:HB2	7:W:352:ILE:HG22	1.44	0.93
7:W:429:GLN:HA	7:W:432:LYS:CB	1.98	0.93
7:W:327:PHE:HB3	7:W:333:TYR:HD2	1.12	0.93
7:W:202:PHE:CE2	7:W:239:LYS:CB	2.52	0.93
7:W:358:ASP:O	7:W:361:SER:HB3	1.69	0.93
7:W:340:MET:HE3	7:W:373:LYS:H	1.07	0.93
6:S:58:THR:OG1	7:W:339:ILE:HD11	1.68	0.92
7:W:293:LYS:C	7:W:294:LEU:HA	1.89	0.92
7:W:331:ASP:C	7:W:331:ASP:CG	2.28	0.92
7:W:42:ALA:CA	7:W:49:VAL:HG21	2.00	0.92
7:W:89:PRO:N	7:W:287:THR:OG1	2.01	0.92
7:W:358:ASP:HB3	7:W:361:SER:CB	1.98	0.92
7:W:432:LYS:CG	7:W:436:GLY:CA	2.34	0.92
7:W:293:LYS:O	7:W:294:LEU:HB2	1.69	0.92
7:W:239:LYS:CB	7:W:239:LYS:CA	0.92	0.92
7:W:475:GLY:C	7:W:476:GLY:N	2.22	0.92
7:W:327:PHE:CB	7:W:333:TYR:CD2	2.49	0.92
7:W:345:PHE:CD1	7:W:365:GLU:CD	2.43	0.92
7:W:293:LYS:CB	7:W:293:LYS:CD	2.47	0.92
7:W:430:MET:C	7:W:433:LYS:HB2	1.90	0.92
3:6:58:ARG:HH12	8:Z:49:G:H8	1.18	0.92
7:W:336:PHE:HD2	7:W:379:MET:CE	1.80	0.92
1:4:98:LEU:CD1	1:4:130:LYS:HZ3	1.83	0.91
7:W:250:LEU:HD11	7:W:290:PHE:HE1	1.34	0.91
7:W:272:PHE:CD1	7:W:282:PHE:HZ	1.87	0.91
7:W:366:GLN:CD	7:W:369:MET:H	1.45	0.91
6:S:52:PHE:CD2	7:W:351:MET:SD	2.64	0.91
7:W:18:SER:O	7:W:19:ASN:OD1	1.88	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:302:GLY:O	7:W:305:ASP:N	2.03	0.91
7:W:330:ARG:HD2	7:W:333:TYR:CD1	2.06	0.91
7:W:250:LEU:HD23	7:W:290:PHE:CZ	2.03	0.91
7:W:332:MET:SD	7:W:424:TYR:CB	2.58	0.91
7:W:440:LEU:O	7:W:444:GLY:HA3	1.70	0.91
7:W:272:PHE:CD1	7:W:282:PHE:CZ	2.59	0.90
6:S:63:VAL:CG1	7:W:361:SER:HB3	2.02	0.90
7:W:270:ILE:O	7:W:270:ILE:HD12	1.71	0.90
7:W:449:ASN:O	7:W:452:GLN:N	2.05	0.90
7:W:314:ASP:CG	7:W:319:ILE:CD1	2.39	0.90
7:W:345:PHE:CD1	7:W:365:GLU:CB	2.55	0.90
3:6:68:TRP:CE3	8:Z:46:G:N2	2.24	0.90
7:W:365:GLU:C	7:W:366:GLN:CA	2.39	0.90
3:6:58:ARG:NH1	8:Z:49:G:H8	1.68	0.90
7:W:345:PHE:HE1	7:W:365:GLU:OE1	1.47	0.90
7:W:117:THR:HG21	7:W:246:ILE:HD13	1.53	0.90
7:W:285:PHE:CE1	7:W:304:ILE:HD12	2.06	0.90
7:W:429:GLN:CA	7:W:432:LYS:CB	2.48	0.90
7:W:443:GLY:O	7:W:447:SER:C	2.09	0.90
4:A:127:A:C2'	4:A:128:U:H5"	2.02	0.90
7:W:202:PHE:CZ	7:W:239:LYS:CG	2.55	0.90
8:Z:160:G:C5'	8:Z:212:A:C4	2.53	0.90
1:4:76:PRO:O	2:5:38:VAL:HG11	1.71	0.89
3:6:61:VAL:CG2	8:Z:62:G:H22	1.85	0.89
7:W:332:MET:SD	7:W:424:TYR:HD1	1.69	0.89
8:Z:1:C:O3'	8:Z:2:U:C5'	2.14	0.89
6:S:58:THR:HG21	7:W:339:ILE:HD13	0.99	0.89
6:S:57:LEU:CD2	7:W:430:MET:HE1	1.79	0.89
7:W:165:GLU:OE1	7:W:171:ILE:HD11	1.72	0.89
1:4:123:LEU:CD1	8:Z:111:U:H4'	2.01	0.89
7:W:89:PRO:HA	7:W:287:THR:OG1	1.67	0.89
7:W:339:ILE:CA	7:W:342:MET:HB2	2.03	0.89
7:W:431:VAL:CG1	7:W:431:VAL:CG2	2.50	0.89
5:B:64:LYS:HD3	5:B:64:LYS:N	1.88	0.89
7:W:202:PHE:CZ	7:W:239:LYS:CD	2.56	0.89
7:W:336:PHE:CE2	7:W:379:MET:CE	2.55	0.89
7:W:394:LYS:HA	8:Z:13:C:OP1	1.71	0.89
7:W:429:GLN:O	7:W:432:LYS:C	2.11	0.89
6:S:62:THR:HG22	7:W:371:ARG:HD3	1.51	0.88
6:S:63:VAL:HG11	7:W:361:SER:HB2	0.90	0.88
7:W:52:LEU:CG	7:W:86:LEU:CG	2.43	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:16:SER:C	7:W:17:LEU:CB	0.79	0.88
2:5:35:ILE:C	2:5:37:LYS:H	1.77	0.88
7:W:250:LEU:CG	7:W:290:PHE:CZ	2.56	0.88
7:W:272:PHE:CE2	7:W:282:PHE:HE2	1.90	0.88
7:W:272:PHE:CD2	7:W:282:PHE:CZ	2.62	0.88
7:W:342:MET:CE	7:W:347:GLN:HG3	2.02	0.88
7:W:207:GLN:HA	7:W:210:ASN:ND2	1.89	0.88
8:Z:159:C:C5'	8:Z:213:A:C1'	2.50	0.88
8:Z:161:G:C4'	8:Z:267:G:C1'	2.27	0.88
7:W:297:MET:HB3	7:W:300:ILE:CD1	2.03	0.88
7:W:429:GLN:O	7:W:432:LYS:N	2.05	0.88
7:W:202:PHE:CE2	7:W:239:LYS:HD2	2.08	0.87
7:W:365:GLU:O	7:W:367:GLU:N	2.07	0.87
4:A:127:A:H2'	4:A:128:U:H5"	1.56	0.87
7:W:337:GLN:O	7:W:341:LYS:N	2.07	0.87
6:S:56:PHE:C	7:W:352:ILE:HG23	1.93	0.87
7:W:11:THR:HA	7:W:14:LEU:HD23	1.57	0.87
7:W:16:SER:N	7:W:17:LEU:HB3	1.88	0.87
7:W:194:ARG:NH1	7:W:196:LYS:HA	1.89	0.87
7:W:285:PHE:HE1	7:W:304:ILE:CD1	1.87	0.87
1:4:89:ASN:HA	8:Z:172:C:C5'	1.92	0.87
5:B:94:CYS:O	5:B:95:LEU:HD23	1.74	0.87
7:W:87:VAL:O	7:W:87:VAL:HG12	1.73	0.86
7:W:133:CYS:SG	7:W:179:PHE:HE1	1.97	0.86
8:Z:161:G:H5'	8:Z:267:G:H1'	1.57	0.86
7:W:23:ILE:CG2	7:W:26:GLU:OE2	2.24	0.86
7:W:432:LYS:HG3	7:W:435:GLY:C	1.96	0.86
1:4:122:THR:HG23	1:4:130:LYS:HD3	1.56	0.86
7:W:271:ILE:CD1	7:W:272:PHE:CE1	2.59	0.86
7:W:106:PHE:CE2	7:W:121:LEU:CD1	2.58	0.86
7:W:319:ILE:HA	7:W:323:LYS:NZ	1.90	0.86
1:4:123:LEU:HD11	8:Z:111:U:H4'	1.57	0.86
7:W:88:ASP:CG	7:W:259:ALA:CB	2.43	0.86
7:W:225:ILE:CG2	7:W:229:CYS:SG	2.64	0.86
7:W:272:PHE:CB	7:W:282:PHE:CE1	2.58	0.86
7:W:202:PHE:CE2	7:W:239:LYS:CG	2.59	0.85
7:W:225:ILE:HG22	7:W:229:CYS:SG	2.16	0.85
7:W:432:LYS:N	7:W:436:GLY:HA2	1.90	0.85
1:4:96:VAL:O	1:4:97:ASP:OD1	1.93	0.85
4:A:184:A:N3	7:W:405:ARG:NH1	2.24	0.85
2:5:34:ARG:NH1	2:5:37:LYS:NZ	2.24	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:76:GLN:HA	7:W:79:VAL:HG22	1.56	0.85
7:W:366:GLN:HG3	7:W:367:GLU:N	1.91	0.85
7:W:94:TRP:CZ2	7:W:218:VAL:CG2	2.58	0.85
7:W:340:MET:CE	7:W:373:LYS:HB2	2.06	0.85
5:B:24:ASN:HD22	5:B:27:LYS:HG3	1.42	0.85
7:W:90:GLY:HA3	7:W:286:LYS:HB3	1.58	0.84
1:4:98:LEU:CD1	1:4:130:LYS:NZ	2.39	0.84
7:W:428:ALA:O	7:W:432:LYS:HB2	1.76	0.84
3:6:68:TRP:CH2	8:Z:47:U:O4'	2.30	0.84
7:W:339:ILE:HD12	7:W:427:PHE:HE1	1.42	0.84
6:S:58:THR:CB	7:W:339:ILE:CD1	2.53	0.84
7:W:24:ASN:O	7:W:27:VAL:HG12	1.78	0.84
7:W:52:LEU:CD1	7:W:86:LEU:CD1	2.37	0.84
7:W:118:CYS:HB3	7:W:190:ASP:OD1	1.76	0.84
7:W:315:ASN:O	7:W:318:LEU:HG	1.78	0.84
7:W:350:GLY:C	7:W:352:ILE:HG13	1.98	0.84
6:S:58:THR:OG1	7:W:339:ILE:HD13	1.70	0.83
7:W:250:LEU:CG	7:W:290:PHE:CE1	2.60	0.83
3:6:54:THR:HA	3:6:90:GLU:HB2	1.61	0.83
7:W:313:ASP:CA	7:W:319:ILE:HD11	2.04	0.83
8:Z:27:G:H22	8:Z:30:A:H5'	1.42	0.83
6:S:58:THR:HG22	7:W:339:ILE:HG21	1.58	0.83
7:W:173:SER:O	7:W:176:VAL:HG12	1.78	0.83
7:W:271:ILE:HD12	7:W:272:PHE:CG	2.13	0.83
7:W:453:SER:O	7:W:456:ALA:N	2.10	0.83
7:W:293:LYS:C	7:W:294:LEU:HB2	1.95	0.83
6:S:58:THR:CG2	7:W:339:ILE:CG2	2.51	0.83
8:Z:158:A:OP1	8:Z:214:C:C5'	2.27	0.83
8:Z:159:C:O4'	8:Z:213:A:C4	2.32	0.83
7:W:84:VAL:CG1	7:W:89:PRO:CA	2.55	0.83
7:W:194:ARG:HH11	7:W:196:LYS:HA	1.44	0.83
7:W:342:MET:CE	7:W:347:GLN:CG	2.57	0.83
7:W:88:ASP:C	7:W:287:THR:OG1	2.16	0.83
8:Z:159:C:H4'	8:Z:213:A:N9	1.93	0.83
7:W:286:LYS:CD	7:W:286:LYS:CB	2.58	0.82
7:W:306:LYS:CB	7:W:347:GLN:OE1	2.28	0.82
7:W:324:HIS:CE1	7:W:338:ASN:N	2.47	0.82
7:W:348:ILE:HG22	7:W:349:LEU:N	1.94	0.82
7:W:84:VAL:CG1	7:W:89:PRO:CB	2.55	0.82
7:W:283:GLU:C	7:W:284:PRO:CD	2.47	0.82
7:W:339:ILE:HA	7:W:342:MET:HB2	1.55	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:14:LEU:CD1	7:W:295:LEU:CD2	2.57	0.82
7:W:341:LYS:O	7:W:341:LYS:HG2	1.78	0.82
7:W:348:ILE:CG2	7:W:349:LEU:N	2.37	0.82
2:5:27:LYS:HE3	2:5:27:LYS:O	1.80	0.82
2:5:30:LEU:HD23	2:5:37:LYS:NZ	1.94	0.82
7:W:179:PHE:CZ	7:W:187:ILE:CG1	2.62	0.82
7:W:293:LYS:C	7:W:293:LYS:CG	2.47	0.82
7:W:338:ASN:O	7:W:342:MET:N	2.12	0.82
6:S:57:LEU:CD2	7:W:430:MET:HE2	1.80	0.82
7:W:89:PRO:CB	7:W:287:THR:HG21	2.09	0.82
7:W:330:ARG:HD2	7:W:333:TYR:CB	2.08	0.82
7:W:358:ASP:HB2	7:W:361:SER:OG	1.80	0.82
7:W:430:MET:CA	7:W:433:LYS:CB	2.54	0.82
7:W:87:VAL:CG2	7:W:256:GLY:C	2.46	0.82
6:S:54:ILE:CG2	7:W:427:PHE:CE2	2.63	0.81
7:W:285:PHE:CE1	7:W:304:ILE:CD1	2.63	0.81
7:W:284:PRO:O	7:W:286:LYS:CG	2.28	0.81
7:W:442:LYS:C	7:W:444:GLY:N	2.32	0.81
7:W:479:GLY:CA	7:W:480:LEU:N	2.43	0.81
7:W:342:MET:CG	7:W:342:MET:CA	2.55	0.81
1:4:136:LEU:HD13	1:4:140:TYR:HE2	1.43	0.81
7:W:15:ARG:NH2	7:W:18:SER:O	2.12	0.81
7:W:319:ILE:O	7:W:323:LYS:HG3	1.80	0.81
7:W:299:ASP:HA	7:W:347:GLN:O	1.81	0.81
3:6:61:VAL:HG11	8:Z:63:A:N3	1.94	0.81
7:W:430:MET:HA	7:W:433:LYS:CB	1.91	0.81
7:W:348:ILE:CG2	7:W:349:LEU:H	1.93	0.81
7:W:365:GLU:C	7:W:366:GLN:HB2	2.00	0.81
2:5:12:TRP:HE1	2:5:61:VAL:HG22	1.45	0.81
2:5:34:ARG:HH11	2:5:37:LYS:NZ	1.77	0.81
1:4:123:LEU:HD11	8:Z:111:U:H5'	1.61	0.81
8:Z:159:C:O3'	8:Z:212:A:H1'	1.81	0.81
7:W:432:LYS:CB	7:W:432:LYS:CD	2.58	0.80
7:W:293:LYS:CB	7:W:293:LYS:HD2	2.10	0.80
2:5:34:ARG:CD	2:5:37:LYS:HZ3	1.93	0.80
6:S:59:LEU:HG	7:W:352:ILE:HD13	1.64	0.80
3:6:58:ARG:NH1	8:Z:49:G:P	2.54	0.80
7:W:288:GLN:C	7:W:289:PRO:CD	2.49	0.80
7:W:366:GLN:CA	7:W:367:GLU:N	2.42	0.80
8:Z:160:G:OP1	8:Z:212:A:H1'	1.80	0.80
1:4:75:TYR:HE1	2:5:35:ILE:HA	1.46	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:106:PHE:CZ	7:W:121:LEU:CD1	2.64	0.80
7:W:337:GLN:O	7:W:340:MET:CB	2.30	0.80
1:4:123:LEU:HD11	8:Z:111:U:C4'	2.11	0.80
6:S:60:TYR:CB	7:W:352:ILE:CG2	2.58	0.80
7:W:134:LEU:CD1	7:W:157:ILE:CD1	2.59	0.80
7:W:345:PHE:HD1	7:W:365:GLU:CB	1.92	0.80
3:6:65:LYS:HD2	8:Z:64:C:C1'	2.10	0.80
7:W:149:LYS:HG2	7:W:159:PHE:CD1	2.16	0.79
3:6:58:ARG:NH1	8:Z:49:G:C8	2.50	0.79
6:S:63:VAL:HG11	7:W:358:ASP:HB3	1.62	0.79
7:W:84:VAL:O	7:W:88:ASP:C	2.21	0.79
7:W:365:GLU:C	7:W:367:GLU:N	2.35	0.79
1:4:76:PRO:O	2:5:38:VAL:CG1	2.30	0.79
3:6:61:VAL:CA	8:Z:48:C:H1'	2.13	0.79
5:B:14:ARG:HB3	5:B:14:ARG:NH1	1.96	0.79
7:W:291:ILE:HD12	7:W:291:ILE:H	1.47	0.79
7:W:302:GLY:O	7:W:304:ILE:N	2.15	0.79
7:W:327:PHE:CB	7:W:333:TYR:CE2	2.65	0.79
7:W:339:ILE:CA	7:W:342:MET:CB	2.60	0.79
7:W:299:ASP:CA	7:W:347:GLN:O	2.29	0.79
8:Z:160:G:C5'	8:Z:212:A:N9	2.43	0.79
3:6:68:TRP:CH2	8:Z:46:G:C2'	2.65	0.79
7:W:365:GLU:O	7:W:366:GLN:HG3	1.83	0.79
7:W:250:LEU:CG	7:W:290:PHE:HZ	1.95	0.79
7:W:339:ILE:HA	7:W:342:MET:HB3	1.63	0.79
7:W:432:LYS:CB	7:W:432:LYS:NZ	2.46	0.79
8:Z:160:G:C5'	8:Z:212:A:C1'	2.61	0.79
1:4:115:ILE:HG21	1:4:140:TYR:OH	1.81	0.79
7:W:297:MET:O	7:W:300:ILE:N	2.15	0.79
7:W:81:LYS:O	7:W:85:LYS:HG3	1.82	0.79
7:W:339:ILE:C	7:W:340:MET:O	2.20	0.79
7:W:205:MET:O	7:W:208:VAL:HG12	1.83	0.78
7:W:338:ASN:O	7:W:342:MET:CA	2.30	0.78
1:4:95:ILE:HG22	1:4:96:VAL:CG1	2.10	0.78
7:W:21:THR:HG22	7:W:21:THR:O	1.82	0.78
7:W:56:VAL:CA	7:W:82:GLU:OE2	2.28	0.78
7:W:448:LYS:H	7:W:451:SER:CA	1.96	0.78
2:5:34:ARG:HH11	2:5:37:LYS:CE	1.97	0.78
7:W:15:ARG:NE	7:W:18:SER:O	2.15	0.78
8:Z:6:A:N3	8:Z:8:G:H5"	1.98	0.78
7:W:453:SER:O	7:W:457:LYS:N	2.16	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:161:G:C4'	8:Z:267:G:H1'	2.12	0.78
7:W:234:LYS:NZ	7:W:237:LYS:HZ2	1.81	0.78
7:W:250:LEU:HD23	7:W:290:PHE:HZ	1.39	0.78
1:4:98:LEU:HA	1:4:99:LYS:N	1.97	0.78
3:6:59:ILE:HD13	8:Z:49:G:OP2	1.84	0.78
7:W:431:VAL:CG1	7:W:431:VAL:CA	2.61	0.78
1:4:136:LEU:HD13	1:4:140:TYR:CD2	2.18	0.78
7:W:122:ALA:CB	7:W:157:ILE:HD13	2.13	0.78
7:W:133:CYS:HG	7:W:179:PHE:HE1	1.31	0.78
7:W:149:LYS:HG2	7:W:159:PHE:CE1	2.18	0.78
7:W:202:PHE:CE2	7:W:239:LYS:CD	2.65	0.78
8:Z:230:A:N6	8:Z:245:G:H1'	1.99	0.78
7:W:250:LEU:CD1	7:W:290:PHE:HE1	1.96	0.78
7:W:250:LEU:HG	7:W:290:PHE:CZ	2.17	0.78
7:W:342:MET:HE2	7:W:347:GLN:CD	2.03	0.78
7:W:447:SER:CA	7:W:451:SER:CA	2.62	0.78
7:W:293:LYS:CG	7:W:293:LYS:O	2.32	0.77
7:W:202:PHE:CE1	7:W:239:LYS:NZ	2.52	0.77
8:Z:161:G:C5'	8:Z:267:G:H1'	2.14	0.77
2:5:35:ILE:C	2:5:37:LYS:N	2.37	0.77
3:6:58:ARG:HH12	8:Z:48:C:H2'	1.48	0.77
7:W:52:LEU:CD1	7:W:86:LEU:HG	1.97	0.77
7:W:366:GLN:CG	7:W:369:MET:H	1.97	0.77
2:5:25:GLU:CD	7:W:22:ILE:HG23	2.04	0.77
4:A:220:C:C2'	4:A:221:C:H5"	2.14	0.77
6:S:60:TYR:CE1	7:W:354:GLY:HA3	2.20	0.77
7:W:202:PHE:CZ	7:W:239:LYS:CE	2.67	0.77
7:W:49:VAL:HG23	7:W:50:LYS:H	1.50	0.77
7:W:339:ILE:CD1	7:W:427:PHE:CE1	2.67	0.77
7:W:14:LEU:HD12	7:W:295:LEU:CD2	2.14	0.77
7:W:56:VAL:HB	7:W:82:GLU:OE1	1.85	0.77
7:W:138:ASP:OD1	7:W:144:ALA:HB1	1.85	0.77
6:S:52:PHE:HB3	6:S:53:PRO:HD3	1.65	0.76
7:W:247:VAL:HG12	7:W:273:ILE:HD13	1.66	0.76
7:W:306:LYS:HB2	7:W:347:GLN:CD	2.06	0.76
7:W:80:PHE:CD2	7:W:291:ILE:HG12	2.10	0.76
7:W:366:GLN:CG	7:W:367:GLU:N	2.48	0.76
4:A:175:G:H3'	4:A:176:A:H5'	1.68	0.76
7:W:145:PHE:O	7:W:149:LYS:HG3	1.85	0.76
7:W:202:PHE:CD1	7:W:239:LYS:NZ	2.53	0.76
7:W:365:GLU:HB2	7:W:366:GLN:CA	2.15	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4:98:LEU:CD1	1:4:101:ASP:OD1	2.32	0.76
7:W:41:GLU:HG2	7:W:42:ALA:H	1.50	0.76
8:Z:27:G:H22	8:Z:30:A:C5'	1.97	0.76
7:W:365:GLU:HB2	7:W:366:GLN:N	2.01	0.76
7:W:299:ASP:C	7:W:347:GLN:O	2.23	0.76
7:W:340:MET:SD	7:W:372:LEU:C	2.64	0.76
7:W:432:LYS:CG	7:W:435:GLY:O	2.33	0.76
7:W:117:THR:CG2	7:W:246:ILE:HD13	2.14	0.76
7:W:293:LYS:HA	7:W:293:LYS:HG3	1.66	0.76
1:4:75:TYR:CE1	2:5:35:ILE:HA	2.20	0.76
2:5:54:SER:HA	2:5:57:ARG:HE	1.51	0.76
7:W:339:ILE:CD1	7:W:427:PHE:HE1	1.99	0.76
7:W:115:THR:O	7:W:118:CYS:SG	2.43	0.76
7:W:133:CYS:HB2	7:W:184:PHE:CD2	2.20	0.76
6:S:60:TYR:CB	7:W:352:ILE:HG21	2.13	0.76
7:W:429:GLN:C	7:W:432:LYS:H	1.89	0.76
7:W:348:ILE:O	7:W:349:LEU:C	2.20	0.75
7:W:327:PHE:HD2	7:W:333:TYR:CE2	2.02	0.75
7:W:330:ARG:HB2	7:W:333:TYR:CA	2.15	0.75
7:W:342:MET:HE1	7:W:347:GLN:CG	2.15	0.75
7:W:366:GLN:HG3	7:W:368:SER:N	2.01	0.75
7:W:432:LYS:HA	7:W:436:GLY:HA2	0.92	0.75
7:W:440:LEU:O	7:W:444:GLY:CA	2.34	0.75
8:Z:160:G:C5'	8:Z:212:A:H1'	2.16	0.75
3:6:59:ILE:CD1	8:Z:48:C:O3'	2.34	0.75
7:W:313:ASP:O	7:W:315:ASN:N	2.19	0.75
7:W:340:MET:CE	7:W:373:LYS:CA	2.64	0.75
1:4:115:ILE:HG21	1:4:140:TYR:CZ	2.21	0.75
7:W:339:ILE:HD11	7:W:427:PHE:CE1	2.22	0.75
4:A:127:A:H2'	4:A:128:U:C5'	2.17	0.75
1:4:119:LYS:HD3	1:4:135:LYS:NZ	2.02	0.75
1:4:140:TYR:CE2	1:4:145:VAL:HG21	2.22	0.75
7:W:122:ALA:CB	7:W:157:ILE:CD1	2.64	0.75
7:W:88:ASP:OD1	7:W:259:ALA:HB1	1.86	0.75
7:W:319:ILE:CA	7:W:323:LYS:CE	2.64	0.75
7:W:432:LYS:HB3	7:W:432:LYS:HZ3	1.51	0.75
7:W:285:PHE:CG	7:W:285:PHE:C	2.60	0.75
7:W:330:ARG:HD2	7:W:333:TYR:HD1	1.52	0.74
7:W:94:TRP:HH2	7:W:218:VAL:HG21	1.49	0.74
7:W:365:GLU:CB	7:W:366:GLN:N	2.49	0.74
7:W:15:ARG:CZ	7:W:18:SER:O	2.35	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:360:MET:O	7:W:362:LYS:HG3	1.87	0.74
7:W:314:ASP:C	7:W:315:ASN:CA	2.54	0.74
1:4:96:VAL:O	1:4:97:ASP:CB	2.35	0.74
3:6:59:ILE:CD1	8:Z:48:C:C3'	2.55	0.74
7:W:87:VAL:HA	7:W:260:LEU:H	1.53	0.74
7:W:130:TRP:CG	7:W:186:ILE:HD11	2.22	0.74
7:W:202:PHE:HZ	7:W:239:LYS:CG	1.97	0.74
7:W:432:LYS:O	7:W:434:MET:HA	1.87	0.74
2:5:16:LYS:HG3	2:5:67:ARG:C	2.08	0.74
7:W:207:GLN:HA	7:W:210:ASN:HD21	1.52	0.74
1:4:105:ILE:HD11	1:4:130:LYS:HE3	1.70	0.74
7:W:131:LYS:HB3	7:W:184:PHE:HA	1.67	0.74
7:W:319:ILE:HA	7:W:323:LYS:HE3	1.70	0.74
1:4:115:ILE:HG22	1:4:140:TYR:CE1	2.23	0.74
3:6:25:HIS:CE1	3:6:79:VAL:HG12	2.23	0.74
3:6:58:ARG:NH1	8:Z:49:G:O5'	1.93	0.74
7:W:202:PHE:HE2	7:W:239:LYS:HB3	1.50	0.74
7:W:293:LYS:O	7:W:294:LEU:CB	2.30	0.74
7:W:88:ASP:OD2	7:W:270:ILE:HG21	1.85	0.74
7:W:325:GLY:O	7:W:334:GLU:OE2	2.05	0.74
7:W:477:MET:O	7:W:478:ALA:C	2.24	0.74
7:W:452:GLN:O	7:W:456:ALA:N	2.21	0.73
7:W:323:LYS:N	7:W:337:GLN:NE2	2.36	0.73
7:W:336:PHE:CD2	7:W:379:MET:HE2	2.17	0.73
7:W:52:LEU:CB	7:W:86:LEU:HD11	2.18	0.73
7:W:88:ASP:O	7:W:287:THR:CB	2.35	0.73
7:W:202:PHE:CG	7:W:239:LYS:HD2	2.22	0.73
7:W:336:PHE:O	7:W:372:LEU:HD13	1.88	0.73
1:4:75:TYR:HE1	2:5:35:ILE:CA	2.00	0.73
7:W:110:GLN:HE22	7:W:141:ARG:NH1	1.87	0.73
7:W:327:PHE:CD2	7:W:333:TYR:HE2	2.03	0.73
2:5:33:LEU:HB2	2:5:37:LYS:CE	2.18	0.73
2:5:34:ARG:CD	2:5:37:LYS:CD	2.49	0.73
7:W:84:VAL:O	7:W:88:ASP:O	2.05	0.73
7:W:366:GLN:HG3	7:W:367:GLU:C	2.08	0.73
5:B:14:ARG:HB3	5:B:14:ARG:CZ	2.17	0.73
7:W:94:TRP:CH2	7:W:218:VAL:CG2	2.71	0.73
7:W:285:PHE:HD2	7:W:286:LYS:O	1.71	0.73
7:W:319:ILE:O	7:W:319:ILE:HG22	1.88	0.73
7:W:328:THR:O	7:W:328:THR:HG22	1.88	0.73
3:6:65:LYS:NZ	8:Z:65:G:O4'	2.12	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6:61:VAL:N	8:Z:48:C:O2'	2.22	0.72
7:W:99:GLY:C	7:W:102:ASN:N	2.43	0.72
8:Z:229:G:N2	8:Z:245:G:H2'	2.05	0.72
7:W:84:VAL:HG12	7:W:89:PRO:CA	2.19	0.72
2:5:34:ARG:HD3	2:5:37:LYS:CD	2.05	0.72
7:W:106:PHE:HE2	7:W:121:LEU:CD1	1.99	0.72
7:W:283:GLU:C	7:W:284:PRO:CA	2.58	0.72
3:6:65:LYS:CE	8:Z:64:C:C2'	2.56	0.72
4:A:151:C:OP1	4:A:204:G:H4'	1.90	0.72
3:6:65:LYS:CD	8:Z:64:C:C3'	2.52	0.72
7:W:365:GLU:C	7:W:366:GLN:HG3	2.10	0.72
1:4:115:ILE:CG2	1:4:140:TYR:CZ	2.73	0.72
8:Z:105:G:O2'	8:Z:106:A:H5'	1.90	0.72
1:4:110:LYS:HG2	1:4:115:ILE:O	1.88	0.72
2:5:25:GLU:OE1	7:W:22:ILE:HA	1.89	0.72
2:5:30:LEU:HD23	2:5:37:LYS:HZ2	1.54	0.72
5:B:64:LYS:HZ2	5:B:65:ASN:H	1.38	0.72
7:W:444:GLY:HA2	7:W:447:SER:O	1.90	0.72
7:W:148:LEU:O	7:W:148:LEU:HD13	1.89	0.71
7:W:300:ILE:O	7:W:303:LEU:HG	1.90	0.71
4:A:148:G:H4'	5:B:15:PHE:O	1.89	0.71
7:W:302:GLY:C	7:W:304:ILE:H	1.94	0.71
8:Z:158:A:OP1	8:Z:214:C:H5"	1.88	0.71
3:6:41:ILE:CG2	8:Z:47:U:O3'	2.35	0.71
7:W:326:GLN:O	7:W:329:LEU:HG	1.90	0.71
3:6:83:ILE:HG22	3:6:94:LYS:HB2	1.71	0.71
1:4:98:LEU:HB2	1:4:130:LYS:HB2	1.73	0.71
7:W:151:ASN:HA	7:W:154:LYS:HZ2	1.55	0.71
7:W:247:VAL:CG1	7:W:273:ILE:CD1	2.68	0.71
4:A:117:U:H3	4:A:234:A:H61	1.36	0.71
2:5:33:LEU:CB	2:5:37:LYS:HE2	2.21	0.71
2:5:34:ARG:NH1	2:5:48:ILE:HG23	2.06	0.71
7:W:432:LYS:HG3	7:W:435:GLY:O	1.91	0.71
7:W:340:MET:HE1	7:W:373:LYS:CB	2.20	0.71
2:5:34:ARG:HH12	2:5:48:ILE:CG2	2.04	0.71
3:6:55:ASN:HD22	3:6:92:ASP:HB2	1.56	0.71
7:W:197:GLN:NE2	7:W:197:GLN:O	2.24	0.71
7:W:234:LYS:NZ	7:W:234:LYS:HA	2.06	0.71
6:S:58:THR:HG21	7:W:339:ILE:CG1	2.21	0.70
7:W:18:SER:O	7:W:19:ASN:CG	2.29	0.70
1:4:122:THR:O	1:4:123:LEU:HD12	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4:140:TYR:CZ	1:4:145:VAL:CG2	2.71	0.70
5:B:73:ASN:ND2	5:B:75:ASP:H	1.89	0.70
6:S:61:VAL:HG12	7:W:423:GLN:HE21	1.56	0.70
7:W:122:ALA:HB3	7:W:157:ILE:HD13	1.71	0.70
7:W:394:LYS:HD2	8:Z:14:U:P	2.31	0.70
7:W:428:ALA:O	7:W:432:LYS:CB	2.38	0.70
3:6:64:ASN:HD21	8:Z:48:C:C4'	2.03	0.70
7:W:16:SER:O	7:W:17:LEU:CB	1.64	0.70
4:A:125:G:H1	4:A:225:C:H42	1.39	0.70
7:W:136:CYS:O	7:W:145:PHE:HE2	1.75	0.70
7:W:271:ILE:CD1	7:W:272:PHE:CD1	2.61	0.70
7:W:432:LYS:HA	7:W:436:GLY:N	2.05	0.70
8:Z:160:G:O2'	8:Z:266:A:C2	2.40	0.70
8:Z:161:G:C1'	8:Z:267:G:C4'	2.64	0.70
7:W:314:ASP:C	7:W:315:ASN:HA	2.13	0.69
4:A:130:A:H2'	4:A:131:A:C8	2.26	0.69
6:S:57:LEU:CB	7:W:430:MET:HE3	2.22	0.69
7:W:14:LEU:CD1	7:W:295:LEU:HD23	2.22	0.69
7:W:109:LEU:HD23	7:W:109:LEU:H	1.57	0.69
7:W:327:PHE:CB	7:W:333:TYR:HD2	1.95	0.69
8:Z:159:C:C4'	8:Z:213:A:N9	2.54	0.69
7:W:325:GLY:O	7:W:328:THR:OG1	2.09	0.69
1:4:79:THR:HG21	8:Z:109:G:OP1	1.92	0.69
7:W:336:PHE:HE2	7:W:379:MET:HE2	1.57	0.69
3:6:68:TRP:HE3	8:Z:46:G:H21	1.31	0.69
5:B:93:LEU:N	5:B:93:LEU:HD23	2.08	0.69
8:Z:159:C:C4'	8:Z:213:A:O4'	2.26	0.69
7:W:289:PRO:O	7:W:301:GLU:OE1	2.10	0.69
7:W:328:THR:O	7:W:334:GLU:OE1	2.11	0.69
7:W:444:GLY:C	7:W:445:ASP:CA	2.61	0.69
7:W:14:LEU:HD11	7:W:295:LEU:HD23	1.73	0.69
7:W:24:ASN:O	7:W:28:LEU:HD13	1.93	0.69
7:W:138:ASP:OD1	7:W:144:ALA:CB	2.40	0.69
7:W:260:LEU:O	7:W:263:VAL:HG12	1.92	0.69
7:W:339:ILE:O	7:W:342:MET:C	2.31	0.69
7:W:365:GLU:C	7:W:366:GLN:CG	2.61	0.69
8:Z:160:G:H5'	8:Z:212:A:H1'	1.74	0.69
1:4:103:LYS:O	1:4:103:LYS:HE3	1.93	0.69
3:6:64:ASN:ND2	8:Z:48:C:C4'	2.56	0.69
3:6:64:ASN:ND2	8:Z:48:C:C5'	2.16	0.69
7:W:330:ARG:CB	7:W:333:TYR:N	2.44	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:340:MET:HE3	7:W:373:LYS:CA	2.23	0.69
7:W:14:LEU:HD11	7:W:295:LEU:CD2	2.23	0.69
7:W:89:PRO:HB3	7:W:287:THR:HG21	1.62	0.69
3:6:72:ILE:HD11	8:Z:45:A:C4	2.28	0.68
7:W:179:PHE:CD2	7:W:187:ILE:HG12	2.28	0.68
8:Z:44:U:O2	8:Z:44:U:H2'	1.92	0.68
1:4:98:LEU:CA	1:4:99:LYS:N	2.55	0.68
7:W:114:LYS:H	7:W:114:LYS:HD3	1.57	0.68
7:W:323:LYS:H	7:W:337:GLN:NE2	1.88	0.68
7:W:109:LEU:CD2	7:W:112:SER:OG	2.41	0.68
3:6:64:ASN:HD21	8:Z:48:C:H5'	0.55	0.68
2:5:33:LEU:CB	2:5:37:LYS:CE	2.71	0.68
6:S:56:PHE:CD1	7:W:350:GLY:O	2.44	0.68
1:4:76:PRO:N	2:5:38:VAL:HG21	2.09	0.68
3:6:25:HIS:HE1	3:6:79:VAL:HG12	1.58	0.68
1:4:119:LYS:HG3	1:4:135:LYS:HB2	1.75	0.68
7:W:16:SER:N	7:W:17:LEU:HD22	2.09	0.68
7:W:202:PHE:CZ	7:W:239:LYS:NZ	2.61	0.68
7:W:136:CYS:SG	7:W:148:LEU:CB	2.78	0.68
7:W:234:LYS:CE	7:W:237:LYS:HZ1	2.06	0.68
4:A:154:G:O2'	4:A:155:G:H5'	1.93	0.67
7:W:289:PRO:HA	7:W:301:GLU:OE1	1.94	0.67
2:5:29:GLU:HG2	7:W:22:ILE:N	2.08	0.67
4:A:127:A:O2'	4:A:128:U:H5"	1.93	0.67
7:W:429:GLN:HA	7:W:432:LYS:HB2	1.74	0.67
8:Z:159:C:O5'	8:Z:213:A:O4'	2.10	0.67
2:5:29:GLU:HG2	7:W:21:THR:C	2.15	0.67
7:W:271:ILE:HG23	7:W:272:PHE:CD1	2.29	0.67
7:W:430:MET:O	7:W:432:LYS:N	2.28	0.67
1:4:89:ASN:CG	8:Z:172:C:C5'	2.29	0.67
4:A:175:G:H1	4:A:221:C:H42	1.42	0.67
7:W:90:GLY:CA	7:W:286:LYS:HB3	2.24	0.67
7:W:340:MET:CE	7:W:373:LYS:CB	2.72	0.67
8:Z:230:A:H61	8:Z:245:G:H1'	1.58	0.67
2:5:44:LYS:NZ	2:5:44:LYS:HA	2.08	0.67
3:6:59:ILE:CD1	8:Z:48:C:H3'	2.24	0.67
7:W:48:LEU:CD2	7:W:52:LEU:HD23	2.25	0.67
7:W:131:LYS:HG2	7:W:183:ASN:O	1.95	0.67
7:W:234:LYS:HZ1	7:W:237:LYS:HZ2	1.41	0.67
7:W:290:PHE:HA	7:W:293:LYS:CB	2.25	0.67
7:W:299:ASP:O	7:W:347:GLN:O	2.12	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:215:A:H8	4:A:215:A:O5'	1.78	0.67
7:W:245:VAL:CG2	7:W:270:ILE:HA	2.25	0.67
3:6:22:VAL:HG12	3:6:23:ASN:O	1.95	0.67
7:W:14:LEU:HD12	7:W:295:LEU:HD22	1.74	0.67
7:W:239:LYS:CG	7:W:239:LYS:CA	2.73	0.67
7:W:330:ARG:NH1	7:W:379:MET:HB3	2.09	0.67
6:S:60:TYR:CD1	7:W:354:GLY:HA3	2.30	0.67
7:W:87:VAL:HG23	7:W:257:GLY:HA2	1.70	0.67
7:W:339:ILE:N	7:W:342:MET:HB2	2.09	0.67
7:W:432:LYS:CB	7:W:432:LYS:HZ3	2.06	0.67
7:W:84:VAL:HG11	7:W:89:PRO:HA	1.72	0.66
7:W:245:VAL:HG23	7:W:270:ILE:HA	1.75	0.66
5:B:15:PHE:CE1	5:B:85:GLN:HB2	2.30	0.66
7:W:443:GLY:O	7:W:447:SER:N	2.28	0.66
8:Z:159:C:O5'	8:Z:213:A:C4'	2.43	0.66
8:Z:159:C:O5'	8:Z:213:A:H1'	1.86	0.66
2:5:34:ARG:NH1	2:5:37:LYS:HZ1	1.93	0.66
7:W:118:CYS:CB	7:W:190:ASP:OD1	2.43	0.66
7:W:271:ILE:CD1	7:W:272:PHE:CG	2.79	0.66
7:W:340:MET:CE	7:W:369:MET:O	2.44	0.66
8:Z:201:U:H2'	8:Z:202:C:H6	1.60	0.66
7:W:10:ILE:HD11	7:W:38:ALA:HB2	1.78	0.66
7:W:339:ILE:HG22	7:W:372:LEU:HD21	1.77	0.66
7:W:347:GLN:O	7:W:348:ILE:HG13	1.96	0.66
3:6:37:ALA:HB1	3:6:68:TRP:CD1	2.31	0.66
7:W:330:ARG:CZ	7:W:387:LEU:HD22	2.26	0.66
7:W:41:GLU:HG2	7:W:42:ALA:N	2.11	0.66
7:W:84:VAL:O	7:W:89:PRO:HD3	1.96	0.66
7:W:130:TRP:CB	7:W:186:ILE:HD12	2.25	0.66
8:Z:253:C:H2'	8:Z:254:G:O4'	1.96	0.65
1:4:85:LYS:HD2	8:Z:171:C:O2'	1.97	0.65
7:W:117:THR:HG21	7:W:246:ILE:CD1	2.26	0.65
7:W:130:TRP:HB3	7:W:186:ILE:HD12	1.77	0.65
7:W:267:LYS:HA	7:W:267:LYS:NZ	2.11	0.65
7:W:16:SER:C	7:W:17:LEU:HB3	0.60	0.65
7:W:250:LEU:HG	7:W:290:PHE:CE1	2.31	0.65
7:W:324:HIS:HE1	7:W:338:ASN:N	1.67	0.65
7:W:432:LYS:CA	7:W:436:GLY:HA3	2.00	0.65
7:W:448:LYS:H	7:W:451:SER:N	1.93	0.65
7:W:194:ARG:NH1	7:W:196:LYS:CA	2.59	0.65
7:W:330:ARG:HD2	7:W:333:TYR:CG	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:234:LYS:CE	7:W:237:LYS:NZ	2.59	0.65
7:W:289:PRO:O	7:W:293:LYS:N	2.29	0.65
5:B:14:ARG:O	5:B:14:ARG:HG2	1.95	0.65
7:W:104:ILE:HG22	7:W:216:ASN:HB2	1.78	0.65
7:W:432:LYS:HD2	7:W:435:GLY:O	1.97	0.65
8:Z:112:A:H5'	8:Z:171:C:OP1	1.96	0.65
8:Z:159:C:C2	8:Z:213:A:C2	2.84	0.65
7:W:46:ILE:HD12	7:W:227:GLN:HB3	1.79	0.65
7:W:240:VAL:O	7:W:240:VAL:HG12	1.97	0.65
7:W:432:LYS:HB3	7:W:432:LYS:NZ	2.09	0.65
8:Z:159:C:O4'	8:Z:213:A:C1'	2.28	0.65
4:A:157:A:H2'	4:A:158:C:C6	2.32	0.65
3:6:44:ILE:CD1	3:6:67:ILE:HD11	2.26	0.65
6:S:57:LEU:HD23	7:W:430:MET:CE	2.19	0.65
7:W:152:ALA:HB1	7:W:157:ILE:O	1.97	0.65
7:W:250:LEU:HD11	7:W:290:PHE:CE1	2.25	0.65
7:W:288:GLN:HB2	7:W:289:PRO:CD	2.26	0.65
1:4:85:LYS:NZ	8:Z:171:C:H4'	2.13	0.65
3:6:67:ILE:HG23	3:6:75:VAL:HG23	1.77	0.65
7:W:179:PHE:CE2	7:W:187:ILE:CG1	2.67	0.65
7:W:449:ASN:O	7:W:453:SER:N	2.25	0.65
4:A:157:A:H2'	4:A:158:C:H6	1.62	0.64
8:Z:219:C:H2'	8:Z:220:A:C8	2.33	0.64
3:6:56:ASP:O	3:6:92:ASP:HB3	1.97	0.64
7:W:160:TYR:CZ	7:W:174:GLU:HB3	2.33	0.64
7:W:270:ILE:O	7:W:270:ILE:CD1	2.44	0.64
3:6:59:ILE:HD11	8:Z:48:C:P	2.32	0.64
7:W:194:ARG:NH2	7:W:198:GLU:O	2.31	0.64
7:W:247:VAL:CG1	7:W:273:ILE:HD13	2.27	0.64
7:W:308:ASN:O	7:W:309:GLU:HB2	1.98	0.64
3:6:60:ASP:HA	8:Z:48:C:O2'	1.91	0.64
7:W:88:ASP:O	7:W:287:THR:OG1	2.16	0.64
7:W:217:ILE:CG2	7:W:242:VAL:HG22	2.28	0.64
7:W:87:VAL:HG22	7:W:257:GLY:HA2	0.64	0.64
7:W:283:GLU:CA	7:W:284:PRO:HB2	2.23	0.64
7:W:290:PHE:HA	7:W:293:LYS:HB2	1.80	0.64
1:4:125:ARG:HH22	1:4:131:LYS:HZ3	1.45	0.64
2:5:32:GLN:NE2	7:W:70:ASN:HB2	2.14	0.64
7:W:45:ASN:O	7:W:227:GLN:CG	2.26	0.64
7:W:94:TRP:HZ2	7:W:218:VAL:HG21	1.62	0.64
7:W:218:VAL:HG11	7:W:246:ILE:HG13	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:287:THR:O	7:W:291:ILE:HD13	1.90	0.64
7:W:428:ALA:HA	7:W:431:VAL:HB	1.80	0.64
7:W:430:MET:O	7:W:433:LYS:HB3	1.97	0.64
7:W:98:LYS:HA	7:W:98:LYS:NZ	2.14	0.63
7:W:247:VAL:HG13	7:W:247:VAL:O	1.97	0.63
5:B:60:VAL:HG23	5:B:83:ARG:C	2.18	0.63
7:W:29:ASN:HA	7:W:32:LEU:HD22	1.81	0.63
7:W:206:LEU:O	7:W:206:LEU:HD23	1.98	0.63
7:W:40:LEU:HD23	7:W:41:GLU:CB	2.28	0.63
7:W:340:MET:SD	7:W:373:LYS:N	2.71	0.63
7:W:430:MET:CG	7:W:430:MET:HA	2.26	0.63
1:4:98:LEU:HB2	1:4:130:LYS:CB	2.28	0.63
7:W:327:PHE:CG	7:W:333:TYR:CE2	2.86	0.63
4:A:148:G:O2'	5:B:83:ARG:NH2	2.31	0.63
7:W:88:ASP:OD1	7:W:259:ALA:CB	2.45	0.63
7:W:136:CYS:O	7:W:145:PHE:CE2	2.52	0.63
7:W:318:LEU:C	7:W:320:GLU:H	2.01	0.63
7:W:340:MET:HE3	7:W:369:MET:O	1.98	0.63
3:6:28:LEU:HD23	3:6:75:VAL:HG11	1.80	0.63
7:W:431:VAL:HG22	7:W:431:VAL:HG13	1.78	0.63
8:Z:158:A:OP1	8:Z:214:C:H5'	1.97	0.63
7:W:340:MET:O	7:W:342:MET:N	2.31	0.63
1:4:119:LYS:C	1:4:119:LYS:HD2	2.18	0.63
7:W:109:LEU:HD21	7:W:112:SER:OG	1.98	0.63
1:4:89:ASN:HB2	8:Z:172:C:H5'	0.65	0.62
5:B:76:VAL:HG13	5:B:77:GLN:N	2.14	0.62
7:W:11:THR:CA	7:W:14:LEU:HD23	2.27	0.62
7:W:15:ARG:O	7:W:18:SER:N	2.31	0.62
7:W:83:LEU:CD1	7:W:294:LEU:N	2.62	0.62
7:W:87:VAL:O	7:W:87:VAL:CG1	2.43	0.62
7:W:222:ASP:O	7:W:225:ILE:HG12	1.99	0.62
7:W:234:LYS:NZ	7:W:237:LYS:NZ	2.47	0.62
3:6:72:ILE:CD1	8:Z:45:A:C5	2.80	0.62
7:W:53:ARG:O	7:W:56:VAL:HG12	2.00	0.62
7:W:235:ALA:HB1	7:W:239:LYS:HE3	1.81	0.62
7:W:431:VAL:O	7:W:431:VAL:HG12	2.00	0.62
8:Z:114:C:O2'	8:Z:157:A:H2'	2.00	0.62
1:4:123:LEU:CD1	8:Z:111:U:C4'	2.74	0.62
5:B:88:GLN:HE21	5:B:92:SER:HB2	1.63	0.62
7:W:82:GLU:O	7:W:85:LYS:HB2	1.99	0.62
7:W:179:PHE:CZ	7:W:187:ILE:CG2	2.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4:98:LEU:O	1:4:129:LYS:C	2.38	0.62
4:A:120:G:N2	4:A:230:C:O2	2.32	0.62
7:W:359:PHE:O	7:W:360:MET:HB2	1.99	0.62
4:A:139:A:H2'	4:A:140:C:H6	1.63	0.62
7:W:22:ILE:HG22	7:W:22:ILE:O	2.00	0.62
7:W:95:THR:HG23	7:W:95:THR:O	1.98	0.62
7:W:339:ILE:CG2	7:W:372:LEU:HD21	2.29	0.62
1:4:89:ASN:HD22	8:Z:171:C:C2'	2.10	0.62
4:A:195:U:O4'	7:W:411:GLY:HA3	1.99	0.62
7:W:40:LEU:CG	7:W:41:GLU:N	2.63	0.62
7:W:87:VAL:C	7:W:259:ALA:CB	2.45	0.62
7:W:160:TYR:OH	7:W:174:GLU:HG3	2.00	0.62
7:W:285:PHE:HA	7:W:285:PHE:CD1	2.31	0.62
8:Z:161:G:C2'	8:Z:267:G:H4'	2.07	0.62
3:6:34:LYS:HG3	8:Z:44:U:C5	2.34	0.62
7:W:77:HIS:O	7:W:81:LYS:CB	2.47	0.62
7:W:96:PRO:HG2	7:W:130:TRP:CZ2	2.35	0.62
7:W:443:GLY:O	7:W:447:SER:O	2.18	0.62
4:A:117:U:H3	4:A:234:A:N6	1.98	0.62
7:W:449:ASN:O	7:W:451:SER:N	2.33	0.62
1:4:122:THR:HG23	1:4:130:LYS:CD	2.30	0.62
7:W:297:MET:HB3	7:W:300:ILE:HB	1.81	0.62
7:W:453:SER:O	7:W:454:GLN:C	2.37	0.62
1:4:96:VAL:HG12	1:4:97:ASP:N	2.15	0.62
1:4:119:LYS:NZ	1:4:135:LYS:HD3	2.14	0.62
3:6:59:ILE:HD13	8:Z:48:C:O3'	1.94	0.62
7:W:306:LYS:CB	7:W:347:GLN:NE2	2.63	0.62
3:6:58:ARG:CZ	8:Z:48:C:H2'	2.29	0.61
7:W:10:ILE:CD1	7:W:38:ALA:HB2	2.30	0.61
7:W:207:GLN:CA	7:W:210:ASN:ND2	2.62	0.61
7:W:294:LEU:N	7:W:294:LEU:HG	2.06	0.61
8:Z:138:C:H5'	8:Z:138:C:H6	1.65	0.61
7:W:84:VAL:O	7:W:260:LEU:HD11	2.00	0.61
7:W:94:TRP:HZ2	7:W:218:VAL:CG2	2.11	0.61
7:W:271:ILE:O	7:W:271:ILE:HD13	2.00	0.61
7:W:365:GLU:HB2	7:W:366:GLN:C	2.21	0.61
8:Z:159:C:C5'	8:Z:213:A:O4'	2.47	0.61
1:4:88:ASP:O	8:Z:172:C:C4'	2.44	0.61
1:4:123:LEU:CD2	8:Z:111:U:H5'	2.21	0.61
7:W:255:LYS:HA	7:W:255:LYS:NZ	2.14	0.61
4:A:149:A:H4'	5:B:17:CYS:SG	2.39	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:107:TYR:CZ	5:B:111:MET:HG3	2.35	0.61
6:S:58:THR:HG21	7:W:339:ILE:CB	2.31	0.61
6:S:60:TYR:OH	7:W:355:PHE:C	2.39	0.61
7:W:136:CYS:SG	7:W:148:LEU:HD12	2.41	0.61
7:W:337:GLN:O	7:W:340:MET:C	2.39	0.61
1:4:89:ASN:ND2	8:Z:171:C:H3'	2.06	0.61
6:S:56:PHE:CE2	7:W:351:MET:O	2.50	0.61
7:W:272:PHE:CG	7:W:282:PHE:CE1	2.89	0.61
6:S:63:VAL:CG1	7:W:358:ASP:HB3	2.29	0.61
7:W:327:PHE:CG	7:W:333:TYR:HE2	2.18	0.61
7:W:366:GLN:HG3	7:W:367:GLU:CA	2.30	0.61
7:W:330:ARG:HH21	7:W:387:LEU:HD13	1.66	0.61
7:W:340:MET:N	7:W:372:LEU:HD13	2.07	0.61
7:W:304:ILE:O	7:W:308:ASN:N	2.33	0.61
6:S:57:LEU:CG	7:W:430:MET:CE	2.75	0.61
6:S:61:VAL:CG1	7:W:423:GLN:HG2	2.21	0.61
7:W:52:LEU:HG	7:W:86:LEU:HD11	0.61	0.61
7:W:202:PHE:HZ	7:W:239:LYS:CE	2.14	0.61
7:W:84:VAL:HG11	7:W:89:PRO:HB3	1.78	0.60
7:W:441:PHE:C	7:W:445:ASP:N	2.52	0.60
1:4:98:LEU:HB2	1:4:130:LYS:HG3	1.83	0.60
4:A:139:A:H2'	4:A:140:C:C6	2.35	0.60
7:W:57:LYS:HE3	7:W:57:LYS:HA	1.83	0.60
7:W:303:LEU:CG	7:W:348:ILE:HD11	2.32	0.60
8:Z:161:G:C5'	8:Z:267:G:C1'	2.75	0.60
8:Z:41:C:H5'	8:Z:41:C:H6	1.66	0.60
7:W:202:PHE:HZ	7:W:239:LYS:CD	2.11	0.60
3:6:45:ARG:HD2	8:Z:48:C:OP1	2.02	0.60
6:S:59:LEU:HD21	7:W:352:ILE:HD11	1.84	0.60
6:S:62:THR:HG22	7:W:371:ARG:NH1	2.15	0.60
1:4:110:LYS:O	1:4:110:LYS:HE3	2.01	0.60
7:W:138:ASP:OD1	7:W:138:ASP:O	2.19	0.60
6:S:57:LEU:CG	7:W:430:MET:HE1	2.30	0.60
7:W:62:LEU:HD23	7:W:62:LEU:O	2.02	0.60
7:W:76:GLN:CA	7:W:79:VAL:HG22	2.31	0.60
7:W:271:ILE:HG23	7:W:272:PHE:N	2.17	0.60
7:W:477:MET:C	7:W:479:GLY:N	2.55	0.60
4:A:193:G:N1	7:W:409:GLY:O	2.32	0.60
6:S:60:TYR:CB	7:W:352:ILE:HG22	2.25	0.60
7:W:12:SER:O	7:W:17:LEU:HD22	2.02	0.60
7:W:247:VAL:CG1	7:W:273:ILE:HD12	2.30	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:290:PHE:O	7:W:294:LEU:HA	2.02	0.60
8:Z:35:G:OP1	8:Z:35:G:H3'	2.02	0.60
2:5:33:LEU:HB2	2:5:37:LYS:HE2	1.83	0.60
7:W:88:ASP:CG	7:W:270:ILE:HG21	2.21	0.60
7:W:92:LYS:HD2	7:W:269:PRO:HB2	1.83	0.60
7:W:365:GLU:CB	7:W:366:GLN:CA	2.78	0.60
8:Z:198:G:O2'	8:Z:199:C:H5'	2.02	0.60
1:4:83:MET:HA	1:4:86:ILE:HG22	1.84	0.59
1:4:91:THR:HG22	1:4:135:LYS:HG3	1.83	0.59
6:S:51:GLY:O	6:S:55:ASN:HB2	2.01	0.59
1:4:114:ASP:C	1:4:115:ILE:HG23	2.15	0.59
3:6:58:ARG:NH1	8:Z:48:C:C2'	2.63	0.59
7:W:340:MET:CA	7:W:372:LEU:HD12	2.26	0.59
7:W:444:GLY:C	7:W:445:ASP:N	2.55	0.59
1:4:72:ILE:O	1:4:97:ASP:CG	2.40	0.59
7:W:213:GLN:O	7:W:213:GLN:NE2	2.35	0.59
7:W:298:GLY:CA	7:W:299:ASP:N	2.64	0.59
7:W:217:ILE:HB	7:W:242:VAL:HA	1.83	0.59
8:Z:276:G:O2'	8:Z:277:A:H5'	2.02	0.59
7:W:87:VAL:HG21	7:W:257:GLY:N	2.15	0.59
7:W:310:LEU:C	7:W:312:LEU:N	2.52	0.59
8:Z:141:C:O2'	8:Z:142:U:H5'	2.03	0.59
2:5:31:GLY:O	2:5:35:ILE:HG12	2.03	0.59
7:W:48:LEU:CD2	7:W:52:LEU:CD2	2.81	0.59
7:W:271:ILE:HD13	7:W:271:ILE:C	2.23	0.59
1:4:113:TYR:HB2	1:4:115:ILE:HD12	1.84	0.59
7:W:114:LYS:HG2	7:W:115:THR:N	2.18	0.59
1:4:88:ASP:C	8:Z:172:C:H4'	2.22	0.59
2:5:30:LEU:O	2:5:37:LYS:CE	2.50	0.59
7:W:194:ARG:CZ	7:W:195:HIS:O	2.51	0.58
7:W:323:LYS:CA	7:W:337:GLN:NE2	2.66	0.58
1:4:125:ARG:HD3	1:4:127:ASP:HB3	1.84	0.58
7:W:240:VAL:O	7:W:240:VAL:CG1	2.51	0.58
1:4:76:PRO:O	2:5:38:VAL:HG21	2.03	0.58
1:4:89:ASN:ND2	8:Z:171:C:O3'	0.74	0.58
6:S:60:TYR:HE2	7:W:355:PHE:HA	1.68	0.58
7:W:430:MET:C	7:W:432:LYS:N	2.56	0.58
7:W:240:VAL:O	7:W:241:ASP:O	2.21	0.58
8:Z:179:A:H2'	8:Z:180:C:H6	1.69	0.58
3:6:65:LYS:CE	8:Z:64:C:H2'	2.33	0.58
4:A:233:U:H2'	4:A:234:A:H5"	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:286:LYS:CB	7:W:286:LYS:CE	2.81	0.58
4:A:163:A:H8	4:A:163:A:O5'	1.87	0.58
4:A:212:C:H4'	4:A:213:A:OP1	2.03	0.58
7:W:8:ARG:N	7:W:253:HIS:CE1	2.72	0.58
7:W:32:LEU:CD2	7:W:57:LYS:HZ3	2.17	0.58
7:W:84:VAL:CG1	7:W:88:ASP:C	2.71	0.58
7:W:293:LYS:C	7:W:294:LEU:HB3	2.14	0.58
8:Z:170:U:H6	8:Z:170:U:H5'	1.67	0.58
4:A:233:U:H3'	4:A:234:A:H5'	1.86	0.58
7:W:52:LEU:HD21	7:W:86:LEU:HD22	0.61	0.58
7:W:347:GLN:C	7:W:348:ILE:HG13	2.24	0.58
8:Z:179:A:H2'	8:Z:180:C:C6	2.38	0.58
6:S:60:TYR:CE2	7:W:355:PHE:HA	2.39	0.58
4:A:128:U:H6	4:A:128:U:H5'	1.68	0.58
7:W:122:ALA:HB1	7:W:157:ILE:HG21	1.85	0.58
1:4:123:LEU:HD13	8:Z:111:U:H4'	1.82	0.58
4:A:214:A:H5'	4:A:215:A:P	2.43	0.58
7:W:23:ILE:HG23	7:W:26:GLU:CD	2.23	0.58
7:W:179:PHE:HZ	7:W:187:ILE:HG23	1.69	0.58
7:W:397:SER:OG	8:Z:12:C:O3'	2.17	0.58
8:Z:159:C:N1	8:Z:213:A:C2	2.72	0.58
3:6:65:LYS:CB	8:Z:64:C:HO2'	2.17	0.57
6:S:60:TYR:CZ	7:W:354:GLY:HA3	2.39	0.57
7:W:335:GLN:HB3	7:W:427:PHE:CE2	2.38	0.57
7:W:431:VAL:CG1	7:W:431:VAL:HA	2.33	0.57
7:W:432:LYS:CD	7:W:436:GLY:HA3	2.32	0.57
8:Z:159:C:O2	8:Z:213:A:C2	2.57	0.57
8:Z:160:G:OP1	8:Z:212:A:C1'	2.51	0.57
5:B:73:ASN:HD21	5:B:75:ASP:H	1.50	0.57
7:W:41:GLU:CG	7:W:42:ALA:H	2.17	0.57
7:W:118:CYS:SG	7:W:190:ASP:OD2	2.62	0.57
7:W:194:ARG:CZ	7:W:202:PHE:HB2	2.29	0.57
5:B:73:ASN:HD21	5:B:75:ASP:CB	2.16	0.57
6:S:60:TYR:OH	7:W:356:GLY:N	2.37	0.57
7:W:49:VAL:HG23	7:W:50:LYS:N	2.14	0.57
7:W:52:LEU:HD11	7:W:86:LEU:HD23	1.61	0.57
7:W:139:THR:HA	7:W:145:PHE:CE1	2.39	0.57
7:W:194:ARG:NH1	7:W:195:HIS:O	2.38	0.57
1:4:115:ILE:CG2	1:4:140:TYR:CE1	2.85	0.57
7:W:221:MET:HE2	7:W:247:VAL:HB	1.85	0.57
5:B:73:ASN:ND2	5:B:75:ASP:N	2.51	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:53:ARG:C	7:W:56:VAL:HG12	2.25	0.57
7:W:429:GLN:C	7:W:432:LYS:N	2.54	0.57
7:W:122:ALA:HB1	7:W:157:ILE:HD13	1.86	0.57
7:W:202:PHE:CE1	7:W:239:LYS:HB2	2.30	0.57
7:W:331:ASP:CG	7:W:331:ASP:CB	2.72	0.57
7:W:160:TYR:OH	7:W:174:GLU:CB	2.53	0.57
7:W:194:ARG:HH12	7:W:196:LYS:C	2.08	0.57
7:W:267:LYS:HA	7:W:267:LYS:HZ2	1.69	0.57
7:W:330:ARG:CD	7:W:387:LEU:HD22	2.35	0.57
7:W:432:LYS:CD	7:W:435:GLY:O	2.52	0.57
4:A:220:C:H2'	4:A:221:C:C5'	2.29	0.57
7:W:163:TYR:O	7:W:163:TYR:CD1	2.57	0.57
7:W:217:ILE:HG22	7:W:242:VAL:HG22	1.87	0.57
7:W:319:ILE:CA	7:W:323:LYS:HE3	2.34	0.57
7:W:432:LYS:CG	7:W:435:GLY:C	2.68	0.57
8:Z:217:U:O2'	8:Z:218:C:H5'	2.05	0.57
7:W:319:ILE:O	7:W:319:ILE:CG2	2.52	0.57
7:W:364:ASN:CG	7:W:367:GLU:OE2	2.43	0.57
7:W:84:VAL:HG22	7:W:287:THR:O	2.05	0.57
7:W:234:LYS:HA	7:W:234:LYS:HZ1	1.69	0.57
7:W:285:PHE:HD1	7:W:285:PHE:HB2	1.63	0.57
7:W:335:GLN:CB	7:W:427:PHE:CZ	2.73	0.57
7:W:379:MET:HA	7:W:382:MET:HG3	1.87	0.57
7:W:364:ASN:CB	7:W:367:GLU:OE2	2.53	0.56
7:W:440:LEU:O	7:W:444:GLY:N	2.38	0.56
5:B:60:VAL:CG2	5:B:84:VAL:HG12	2.35	0.56
5:B:77:GLN:HG2	5:B:77:GLN:O	2.05	0.56
5:B:86:LEU:HD13	5:B:99:PRO:O	2.05	0.56
6:S:59:LEU:HG	7:W:352:ILE:CD1	2.34	0.56
7:W:84:VAL:O	7:W:260:LEU:HD21	2.03	0.56
7:W:89:PRO:CA	7:W:287:THR:CB	2.68	0.56
7:W:122:ALA:HB1	7:W:157:ILE:CD1	2.35	0.56
7:W:134:LEU:HB3	7:W:148:LEU:HD11	1.87	0.56
7:W:286:LYS:CB	7:W:286:LYS:HE3	2.35	0.56
7:W:391:ASP:HB3	7:W:394:LYS:HZ2	1.69	0.56
7:W:429:GLN:CA	7:W:432:LYS:HB2	2.33	0.56
8:Z:219:C:H2'	8:Z:220:A:H8	1.68	0.56
3:6:65:LYS:HD2	8:Z:64:C:HO2'	0.75	0.56
7:W:135:ILE:CD1	7:W:160:TYR:HB3	2.36	0.56
1:4:96:VAL:O	1:4:97:ASP:OD2	2.20	0.56
2:5:34:ARG:NH1	2:5:37:LYS:HZ3	2.02	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:127:A:C2'	4:A:128:U:C5'	2.79	0.56
7:W:104:ILE:HD11	7:W:188:ILE:HG12	1.87	0.56
7:W:250:LEU:HG	7:W:290:PHE:HZ	1.61	0.56
8:Z:202:C:H3'	8:Z:203:G:C8	2.40	0.56
8:Z:114:C:H4'	8:Z:115:C:OP2	2.06	0.56
8:Z:197:G:O2'	8:Z:198:G:H5'	2.05	0.56
2:5:44:LYS:HA	2:5:44:LYS:HZ2	1.70	0.56
7:W:8:ARG:HB2	7:W:253:HIS:NE2	2.21	0.56
7:W:83:LEU:HD13	7:W:294:LEU:N	2.21	0.56
7:W:444:GLY:CA	7:W:447:SER:O	2.52	0.56
1:4:125:ARG:NH2	1:4:131:LYS:HZ3	2.04	0.56
3:6:68:TRP:CH2	8:Z:47:U:C1'	2.89	0.56
7:W:56:VAL:HG13	7:W:57:LYS:N	2.21	0.56
7:W:84:VAL:O	7:W:88:ASP:CA	2.54	0.56
8:Z:226:G:O2'	8:Z:227:U:H5'	2.06	0.56
3:6:17:THR:HG22	3:6:82:ARG:HE	1.71	0.56
3:6:41:ILE:HD12	3:6:64:ASN:HD22	1.71	0.56
4:A:220:C:C3'	4:A:221:C:H5"	2.36	0.56
7:W:13:ALA:O	7:W:17:LEU:HA	2.06	0.56
7:W:96:PRO:HG2	7:W:130:TRP:HZ2	1.70	0.56
7:W:247:VAL:HG11	7:W:273:ILE:HD12	1.88	0.56
1:4:106:LYS:HG3	1:4:117:ALA:HB3	1.88	0.55
5:B:62:LEU:HD12	5:B:81:ARG:O	2.07	0.55
5:B:76:VAL:HG13	5:B:77:GLN:H	1.71	0.55
5:B:112:ILE:HG23	5:B:115:LEU:HD12	1.87	0.55
7:W:16:SER:H	7:W:17:LEU:HD22	1.71	0.55
7:W:151:ASN:HA	7:W:154:LYS:NZ	2.22	0.55
7:W:448:LYS:N	7:W:451:SER:CA	2.67	0.55
3:6:58:ARG:NH1	8:Z:49:G:OP2	2.37	0.55
7:W:84:VAL:C	7:W:260:LEU:HD11	2.26	0.55
1:4:109:VAL:HG22	1:4:115:ILE:HD11	1.89	0.55
4:A:171:U:C3'	4:A:172:A:H5"	2.36	0.55
7:W:90:GLY:HA3	7:W:286:LYS:CB	2.33	0.55
7:W:328:THR:O	7:W:328:THR:CG2	2.55	0.55
7:W:179:PHE:HD1	7:W:184:PHE:HD2	1.53	0.55
7:W:356:GLY:C	7:W:358:ASP:N	2.54	0.55
7:W:448:LYS:N	7:W:451:SER:H	2.04	0.55
2:5:36:GLN:C	2:5:40:SER:O	2.43	0.55
8:Z:196:G:O2'	8:Z:197:G:P	2.64	0.55
2:5:27:LYS:HE3	2:5:27:LYS:C	2.28	0.55
3:6:59:ILE:CB	8:Z:48:C:O3'	2.01	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:130:A:H2'	4:A:131:A:H8	1.72	0.55
6:S:62:THR:CG2	7:W:371:ARG:HH11	2.19	0.55
7:W:23:ILE:HG22	7:W:24:ASN:N	2.22	0.55
7:W:42:ALA:O	7:W:43:ASP:HB3	2.07	0.55
7:W:88:ASP:C	7:W:287:THR:HG1	2.10	0.55
7:W:118:CYS:SG	7:W:190:ASP:CG	2.85	0.55
7:W:332:MET:CG	7:W:424:TYR:HD1	2.20	0.55
5:B:64:LYS:HD3	5:B:64:LYS:H	1.71	0.55
6:S:57:LEU:HD23	7:W:430:MET:HE3	1.84	0.55
1:4:83:MET:O	1:4:86:ILE:HG22	2.07	0.54
7:W:225:ILE:CB	7:W:229:CYS:SG	2.94	0.54
7:W:306:LYS:O	7:W:310:LEU:HB2	2.07	0.54
7:W:430:MET:C	7:W:432:LYS:H	2.10	0.54
8:Z:135:A:H2'	8:Z:136:C:C6	2.43	0.54
7:W:23:ILE:CG2	7:W:26:GLU:CD	2.76	0.54
7:W:84:VAL:HG12	7:W:88:ASP:C	2.27	0.54
7:W:92:LYS:CE	7:W:269:PRO:HG2	2.36	0.54
7:W:135:ILE:HD13	7:W:160:TYR:HB3	1.89	0.54
8:Z:114:C:O2'	8:Z:158:A:H5'	2.07	0.54
1:4:145:VAL:O	7:W:68:GLY:CA	2.55	0.54
7:W:90:GLY:CA	7:W:286:LYS:CB	2.85	0.54
7:W:133:CYS:CB	7:W:179:PHE:HE1	2.19	0.54
8:Z:159:C:H2'	8:Z:160:G:C8	2.42	0.54
8:Z:160:G:H5'	8:Z:212:A:N3	2.15	0.54
5:B:73:ASN:HD21	5:B:75:ASP:N	2.05	0.54
5:B:116:LYS:HD2	5:B:116:LYS:N	2.23	0.54
1:4:125:ARG:HG3	1:4:129:LYS:O	2.08	0.54
5:B:60:VAL:HB	5:B:84:VAL:HG12	1.90	0.54
7:W:160:TYR:CE2	7:W:174:GLU:HB3	2.42	0.54
7:W:245:VAL:CG2	7:W:270:ILE:HG22	2.38	0.54
7:W:292:SER:O	7:W:295:LEU:N	2.37	0.54
7:W:450:VAL:C	7:W:454:GLN:H	2.03	0.54
7:W:460:GLN:N	7:W:461:GLN:N	2.55	0.54
3:6:65:LYS:CD	8:Z:64:C:HO2'	1.37	0.54
7:W:247:VAL:HG11	7:W:273:ILE:CD1	2.38	0.54
7:W:271:ILE:CD1	7:W:272:PHE:CZ	2.90	0.54
8:Z:243:A:H5'	8:Z:245:G:O4'	2.07	0.54
1:4:98:LEU:HG	1:4:100:ALA:H	1.73	0.54
7:W:32:LEU:O	7:W:35:VAL:HG12	2.08	0.54
7:W:84:VAL:O	7:W:88:ASP:N	2.39	0.54
7:W:130:TRP:CG	7:W:186:ILE:CD1	2.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:341:LYS:C	7:W:344:PRO:HB3	2.28	0.54
7:W:430:MET:C	7:W:433:LYS:CB	2.64	0.54
2:5:33:LEU:HD13	2:5:48:ILE:HG13	1.89	0.54
4:A:195:U:H4'	7:W:411:GLY:O	2.08	0.54
6:S:57:LEU:CB	7:W:430:MET:CE	2.85	0.54
7:W:448:LYS:H	7:W:451:SER:H	1.55	0.54
8:Z:159:C:O3'	8:Z:212:A:C1'	2.54	0.54
4:A:233:U:H3'	4:A:234:A:C5'	2.39	0.53
6:S:50:LEU:HD13	7:W:478:ALA:CA	2.24	0.53
7:W:314:ASP:OD1	7:W:315:ASN:N	2.41	0.53
8:Z:159:C:O2	8:Z:212:A:C2	2.61	0.53
8:Z:228:G:C6	8:Z:229:G:N1	2.77	0.53
1:4:75:TYR:CD1	2:5:34:ARG:C	2.79	0.53
1:4:123:LEU:HD23	8:Z:110:U:O2'	2.08	0.53
7:W:84:VAL:HG22	7:W:287:THR:HB	1.88	0.53
7:W:122:ALA:HB3	7:W:157:ILE:CD1	2.34	0.53
7:W:179:PHE:HZ	7:W:187:ILE:CG2	2.21	0.53
7:W:288:GLN:HB2	7:W:289:PRO:HD2	1.90	0.53
2:5:14:LYS:HA	2:5:14:LYS:NZ	2.23	0.53
1:4:72:ILE:O	1:4:97:ASP:OD2	2.25	0.53
7:W:179:PHE:CE1	7:W:187:ILE:HG12	2.35	0.53
2:5:34:ARG:HH11	2:5:37:LYS:HZ3	1.57	0.53
5:B:88:GLN:O	5:B:91:GLY:N	2.42	0.53
6:S:54:ILE:CG2	7:W:427:PHE:CZ	2.90	0.53
1:4:76:PRO:O	2:5:38:VAL:CG2	2.56	0.53
7:W:114:LYS:HG2	7:W:115:THR:H	1.74	0.53
7:W:260:LEU:HA	7:W:263:VAL:HG12	1.90	0.53
7:W:297:MET:CG	7:W:297:MET:CA	2.81	0.53
7:W:449:ASN:C	7:W:451:SER:N	2.61	0.53
4:A:208:A:H1'	7:W:380:ASP:O	2.08	0.53
7:W:42:ALA:CA	7:W:49:VAL:CG2	2.75	0.53
7:W:106:PHE:HZ	7:W:121:LEU:HD12	1.62	0.53
7:W:313:ASP:HA	7:W:319:ILE:CD1	2.19	0.53
8:Z:87:C:O2'	8:Z:88:A:H5'	2.08	0.53
6:S:60:TYR:CE2	7:W:358:ASP:OD2	2.61	0.53
7:W:88:ASP:OD2	7:W:259:ALA:CB	2.45	0.53
7:W:207:GLN:O	7:W:210:ASN:ND2	2.41	0.53
7:W:218:VAL:CG1	7:W:246:ILE:HG13	2.39	0.53
7:W:342:MET:HE3	7:W:347:GLN:HG3	1.88	0.53
7:W:365:GLU:N	7:W:366:GLN:N	2.56	0.53
8:Z:161:G:C4'	8:Z:267:G:C4'	2.86	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:231:A:H4'	8:Z:232:G:O5'	2.09	0.53
2:5:34:ARG:NH1	2:5:48:ILE:CG2	2.70	0.53
7:W:307:VAL:O	7:W:310:LEU:N	2.42	0.53
3:6:68:TRP:CZ2	8:Z:46:G:O2'	2.51	0.52
5:B:71:GLU:OE2	5:B:78:TYR:HD2	1.92	0.52
7:W:330:ARG:CZ	7:W:387:LEU:CD2	2.86	0.52
7:W:340:MET:HE2	7:W:369:MET:O	2.09	0.52
7:W:448:LYS:N	7:W:451:SER:N	2.58	0.52
8:Z:5:A:N1	8:Z:27:G:H4'	2.24	0.52
8:Z:229:G:H22	8:Z:245:G:H2'	1.73	0.52
6:S:62:THR:HG22	7:W:371:ARG:HH11	1.74	0.52
7:W:134:LEU:HD12	7:W:157:ILE:HG13	1.90	0.52
7:W:306:LYS:CB	7:W:347:GLN:CD	2.74	0.52
7:W:441:PHE:C	7:W:444:GLY:CA	2.77	0.52
3:6:61:VAL:CG1	8:Z:63:A:N3	2.69	0.52
7:W:293:LYS:C	7:W:294:LEU:C	2.69	0.52
7:W:442:LYS:C	7:W:444:GLY:H	2.10	0.52
1:4:85:LYS:HB3	1:4:91:THR:OG1	2.10	0.52
4:A:199:A:H8	4:A:199:A:OP1	1.93	0.52
5:B:116:LYS:O	5:B:120:GLN:HG2	2.09	0.52
7:W:122:ALA:CB	7:W:157:ILE:HD12	2.37	0.52
7:W:276:GLY:H	7:W:281:ASP:HB3	1.73	0.52
7:W:397:SER:HB3	8:Z:13:C:H5'	1.92	0.52
7:W:52:LEU:CD2	7:W:86:LEU:CD1	2.77	0.52
1:4:114:ASP:C	1:4:115:ILE:CG2	2.75	0.52
4:A:172:A:H2	4:A:225:C:H1'	1.73	0.52
4:A:175:G:H1	4:A:221:C:N4	2.08	0.52
5:B:15:PHE:CZ	5:B:85:GLN:HB2	2.45	0.52
7:W:194:ARG:NH2	7:W:202:PHE:CB	2.57	0.52
7:W:272:PHE:CB	7:W:282:PHE:HE1	2.19	0.52
8:Z:62:G:H2'	8:Z:63:A:C8	2.44	0.52
8:Z:256:A:H2'	8:Z:258:G:C8	2.46	0.52
1:4:96:VAL:CG1	1:4:97:ASP:N	2.73	0.51
1:4:123:LEU:CD1	8:Z:111:U:H5'	2.37	0.51
5:B:112:ILE:C	5:B:114:LYS:H	2.13	0.51
7:W:88:ASP:OD1	7:W:259:ALA:CA	2.59	0.51
7:W:92:LYS:HE3	7:W:269:PRO:CG	2.40	0.51
7:W:330:ARG:NH2	7:W:387:LEU:CD1	2.73	0.51
8:Z:24:G:H2'	8:Z:25:G:H8	1.75	0.51
4:A:136:G:N3	4:A:214:A:H2	2.09	0.51
7:W:40:LEU:HD23	7:W:41:GLU:HB3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4:119:LYS:CD	1:4:135:LYS:HZ3	2.13	0.51
4:A:164:G:OP2	4:A:164:G:H8	1.92	0.51
7:W:40:LEU:CB	7:W:40:LEU:CD2	2.82	0.51
7:W:56:VAL:HG13	7:W:57:LYS:H	1.75	0.51
7:W:134:LEU:HD13	7:W:148:LEU:HD11	1.93	0.51
7:W:284:PRO:O	7:W:286:LYS:HG2	2.03	0.51
5:B:56:VAL:HG21	5:B:107:TYR:CE2	2.45	0.51
5:B:93:LEU:HD23	5:B:93:LEU:H	1.75	0.51
7:W:134:LEU:CG	7:W:157:ILE:HD12	2.41	0.51
7:W:219:TYR:CE2	7:W:221:MET:HB3	2.45	0.51
1:4:75:TYR:CE1	2:5:35:ILE:CA	2.87	0.51
7:W:80:PHE:CD2	7:W:291:ILE:CG1	2.66	0.51
7:W:359:PHE:O	7:W:360:MET:CB	2.59	0.51
1:4:78:THR:HG23	2:5:38:VAL:CG1	2.40	0.51
3:6:59:ILE:HD13	8:Z:48:C:C3'	2.38	0.51
5:B:41:VAL:CG1	5:B:42:GLU:N	2.72	0.51
7:W:217:ILE:HG21	7:W:242:VAL:HG22	1.92	0.51
2:5:11:LEU:HD22	2:5:58:VAL:HG22	1.92	0.51
3:6:65:LYS:CB	8:Z:64:C:O2'	2.56	0.51
7:W:84:VAL:HG12	7:W:88:ASP:O	2.08	0.51
7:W:130:TRP:CB	7:W:186:ILE:CD1	2.88	0.51
7:W:329:LEU:C	7:W:331:ASP:H	2.14	0.51
7:W:354:GLY:O	7:W:355:PHE:CD1	2.64	0.51
7:W:450:VAL:O	7:W:454:GLN:CA	2.58	0.51
7:W:40:LEU:HD22	7:W:44:VAL:HG21	1.92	0.51
7:W:225:ILE:HB	7:W:229:CYS:SG	2.51	0.51
7:W:348:ILE:HG23	7:W:349:LEU:H	1.69	0.51
4:A:121:U:H2'	4:A:122:U:C6	2.46	0.50
7:W:21:THR:O	7:W:21:THR:CG2	2.54	0.50
1:4:125:ARG:CZ	1:4:131:LYS:CD	2.90	0.50
6:S:50:LEU:HG	7:W:479:GLY:HA3	1.93	0.50
6:S:54:ILE:HG23	7:W:427:PHE:CZ	2.43	0.50
7:W:106:PHE:HE2	7:W:121:LEU:HD11	1.74	0.50
7:W:245:VAL:HG21	7:W:270:ILE:HG22	1.93	0.50
1:4:98:LEU:HB2	1:4:130:LYS:CG	2.40	0.50
6:S:54:ILE:N	7:W:433:LYS:NZ	2.57	0.50
7:W:432:LYS:CB	7:W:432:LYS:HZ2	2.24	0.50
3:6:65:LYS:NZ	8:Z:64:C:O2'	2.41	0.50
7:W:239:LYS:CB	7:W:239:LYS:H	2.10	0.50
3:6:61:VAL:N	8:Z:48:C:H1'	2.26	0.50
7:W:130:TRP:CD2	7:W:186:ILE:HD11	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:179:PHE:CZ	7:W:187:ILE:HG23	2.46	0.50
1:4:123:LEU:CD2	8:Z:110:U:O2'	2.60	0.50
5:B:68:TYR:CE2	5:B:70:ARG:HB2	2.46	0.50
7:W:52:LEU:HD12	7:W:86:LEU:HD11	1.90	0.50
7:W:134:LEU:CD1	7:W:157:ILE:HD12	2.39	0.50
7:W:160:TYR:OH	7:W:174:GLU:CG	2.60	0.50
1:4:119:LYS:CE	1:4:135:LYS:HD3	2.41	0.50
2:5:29:GLU:O	2:5:33:LEU:HG	2.11	0.50
7:W:25:GLU:O	7:W:28:LEU:HB2	2.12	0.50
7:W:302:GLY:C	7:W:304:ILE:N	2.63	0.50
7:W:330:ARG:HH21	7:W:387:LEU:CD1	2.24	0.50
7:W:173:SER:O	7:W:176:VAL:CG1	2.56	0.50
8:Z:160:G:C1'	8:Z:266:A:H2	2.24	0.50
2:5:16:LYS:HE2	2:5:16:LYS:N	2.27	0.50
3:6:52:MET:CE	3:6:83:ILE:HD11	2.42	0.50
5:B:14:ARG:CZ	5:B:14:ARG:CB	2.88	0.50
1:4:98:LEU:CD1	1:4:130:LYS:HZ1	2.20	0.49
8:Z:6:A:O2'	8:Z:8:G:H5'	2.11	0.49
2:5:12:TRP:NE1	2:5:61:VAL:HG22	2.23	0.49
3:6:28:LEU:CD1	3:6:43:GLU:HG3	2.42	0.49
6:S:60:TYR:CE2	7:W:355:PHE:CA	2.95	0.49
7:W:340:MET:HE3	7:W:373:LYS:CB	2.41	0.49
7:W:430:MET:SD	7:W:433:LYS:HE3	2.52	0.49
7:W:431:VAL:O	7:W:436:GLY:C	2.50	0.49
8:Z:1:C:H3'	8:Z:2:U:H5"	1.94	0.49
1:4:125:ARG:CZ	1:4:131:LYS:HG3	2.42	0.49
7:W:162:SER:HB2	7:W:171:ILE:HG12	1.94	0.49
7:W:291:ILE:HD12	7:W:291:ILE:N	2.20	0.49
7:W:366:GLN:CG	7:W:367:GLU:CA	2.90	0.49
2:5:7:LYS:HA	2:5:7:LYS:NZ	2.27	0.49
7:W:89:PRO:C	7:W:287:THR:OG1	2.47	0.49
7:W:260:LEU:C	7:W:263:VAL:HG12	2.32	0.49
7:W:320:GLU:O	7:W:322:LEU:HG	2.12	0.49
7:W:365:GLU:O	7:W:368:SER:CA	2.53	0.49
5:B:64:LYS:NZ	5:B:65:ASN:H	2.06	0.49
7:W:74:MET:HA	7:W:77:HIS:ND1	2.28	0.49
7:W:91:VAL:HB	7:W:92:LYS:N	2.27	0.49
7:W:253:HIS:ND1	7:W:253:HIS:O	2.46	0.49
7:W:292:SER:O	7:W:295:LEU:O	2.30	0.49
7:W:69:LEU:HD23	7:W:70:ASN:O	2.13	0.49
7:W:92:LYS:HE3	7:W:269:PRO:HG2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:130:TRP:HB3	7:W:186:ILE:CD1	2.41	0.49
7:W:293:LYS:C	7:W:295:LEU:N	2.66	0.49
7:W:340:MET:HE1	7:W:373:LYS:CA	2.39	0.49
7:W:392:GLY:O	7:W:396:PHE:HD1	1.95	0.49
1:4:145:VAL:O	7:W:68:GLY:HA3	2.13	0.49
4:A:172:A:H2	4:A:225:C:C1'	2.26	0.49
7:W:285:PHE:CE1	7:W:304:ILE:HD13	2.46	0.49
7:W:339:ILE:HD11	7:W:427:PHE:CZ	2.47	0.49
8:Z:50:G:O2'	8:Z:51:G:H5'	2.11	0.49
6:S:61:VAL:CG1	7:W:423:GLN:HE21	2.24	0.49
7:W:75:ILE:O	7:W:78:ALA:HB3	2.13	0.49
7:W:133:CYS:SG	7:W:179:PHE:CE1	2.86	0.49
7:W:160:TYR:CE2	7:W:174:GLU:CB	2.95	0.49
7:W:373:LYS:O	7:W:377:THR:HG23	2.13	0.49
7:W:394:LYS:NZ	7:W:394:LYS:HB3	2.27	0.49
7:W:453:SER:O	7:W:456:ALA:CA	2.60	0.49
7:W:460:GLN:H	7:W:461:GLN:N	2.11	0.49
8:Z:127:A:H2'	8:Z:128:U:C6	2.48	0.49
6:S:57:LEU:O	6:S:61:VAL:HG23	2.13	0.49
2:5:30:LEU:O	2:5:37:LYS:HE3	2.12	0.48
6:S:56:PHE:CD1	7:W:351:MET:N	2.80	0.48
7:W:148:LEU:HD13	7:W:148:LEU:C	2.33	0.48
7:W:306:LYS:N	7:W:347:GLN:NE2	2.58	0.48
8:Z:44:U:O2	8:Z:44:U:C2'	2.60	0.48
8:Z:175:U:O2'	8:Z:176:G:H5'	2.13	0.48
4:A:160:A:H2'	4:A:161:C:C6	2.49	0.48
7:W:10:ILE:HG13	7:W:38:ALA:CB	2.43	0.48
7:W:221:MET:CE	7:W:247:VAL:HB	2.43	0.48
7:W:239:LYS:C	7:W:239:LYS:HB2	1.97	0.48
7:W:270:ILE:O	7:W:270:ILE:CG1	2.61	0.48
7:W:347:GLN:O	7:W:348:ILE:CG1	2.60	0.48
8:Z:17:G:H4'	8:Z:18:A:OP1	2.12	0.48
1:4:103:LYS:HE3	1:4:103:LYS:C	2.33	0.48
8:Z:208:G:O2'	8:Z:209:U:H5'	2.12	0.48
6:S:54:ILE:HG23	7:W:427:PHE:HE2	1.70	0.48
6:S:59:LEU:CD2	7:W:352:ILE:HD11	2.43	0.48
7:W:41:GLU:CA	7:W:41:GLU:H	2.06	0.48
7:W:449:ASN:C	7:W:451:SER:H	2.17	0.48
4:A:231:A:H5"	4:A:232:G:OP2	2.12	0.48
8:Z:29:A:H2'	8:Z:30:A:H5"	1.95	0.48
8:Z:89:G:O2'	8:Z:90:C:H5'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:264:A:O2'	8:Z:265:U:P	2.71	0.48
1:4:72:ILE:C	1:4:97:ASP:OD2	2.52	0.48
3:6:59:ILE:CD1	8:Z:49:G:P	2.88	0.48
7:W:303:LEU:HD21	7:W:348:ILE:HD12	1.96	0.48
8:Z:125:U:H2'	8:Z:126:C:C6	2.48	0.48
8:Z:160:G:O4'	8:Z:212:A:C2	2.66	0.48
1:4:119:LYS:HD2	1:4:120:VAL:N	2.29	0.48
3:6:58:ARG:HG3	8:Z:50:G:OP2	2.14	0.48
7:W:87:VAL:CA	7:W:259:ALA:HB3	2.39	0.48
7:W:206:LEU:HD23	7:W:206:LEU:C	2.34	0.48
8:Z:167:U:H2'	8:Z:168:A:O4'	2.13	0.48
1:4:78:THR:HG23	2:5:38:VAL:HG11	1.96	0.48
1:4:119:LYS:HZ3	1:4:135:LYS:HD3	1.78	0.48
7:W:134:LEU:HG	7:W:157:ILE:HD12	1.95	0.48
7:W:318:LEU:C	7:W:320:GLU:N	2.67	0.48
7:W:330:ARG:NH1	7:W:379:MET:CB	2.76	0.48
1:4:75:TYR:HE1	2:5:35:ILE:C	2.16	0.48
1:4:140:TYR:OH	1:4:145:VAL:HG11	2.14	0.48
2:5:16:LYS:HZ2	2:5:65:LYS:HE2	1.78	0.48
3:6:54:THR:CA	3:6:90:GLU:HB2	2.39	0.48
4:A:160:A:H2'	4:A:161:C:O4'	2.14	0.48
7:W:109:LEU:HD23	7:W:109:LEU:N	2.26	0.48
7:W:164:THR:OG1	7:W:170:ILE:CG2	2.62	0.48
7:W:358:ASP:CB	7:W:361:SER:HG	2.22	0.48
7:W:366:GLN:HA	7:W:367:GLU:N	2.28	0.48
4:A:125:G:H2'	4:A:126:C:C6	2.48	0.47
7:W:21:THR:HA	7:W:72:ARG:HH21	1.78	0.47
7:W:32:LEU:CD2	7:W:57:LYS:NZ	2.77	0.47
8:Z:159:C:O2	8:Z:212:A:H2	1.96	0.47
2:5:34:ARG:NH1	2:5:37:LYS:CE	2.72	0.47
6:S:59:LEU:HD23	7:W:352:ILE:HG12	1.95	0.47
7:W:16:SER:C	7:W:17:LEU:HB2	1.01	0.47
7:W:202:PHE:CD2	7:W:239:LYS:CD	2.73	0.47
8:Z:201:U:H2'	8:Z:202:C:C6	2.44	0.47
1:4:125:ARG:HH22	1:4:131:LYS:NZ	2.11	0.47
4:A:165:G:N7	4:A:176:A:C6	2.82	0.47
4:A:192:A:H2'	4:A:193:G:O4'	2.13	0.47
5:B:29:ILE:HG22	5:B:30:ALA:N	2.29	0.47
5:B:62:LEU:HD12	5:B:63:GLU:N	2.29	0.47
7:W:263:VAL:HG13	7:W:264:ALA:N	2.29	0.47
7:W:303:LEU:CD2	7:W:348:ILE:HD12	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6:68:TRP:CH2	8:Z:46:G:O2'	2.65	0.47
7:W:8:ARG:N	7:W:253:HIS:HE1	2.12	0.47
7:W:26:GLU:HG2	7:W:27:VAL:N	2.29	0.47
7:W:42:ALA:HB2	7:W:50:LYS:H	1.80	0.47
7:W:141:ARG:HH12	7:W:193:GLY:H	1.63	0.47
7:W:297:MET:HB3	7:W:300:ILE:CG1	2.45	0.47
7:W:297:MET:C	7:W:299:ASP:N	2.68	0.47
3:6:55:ASN:HD21	3:6:85:ARG:HB3	1.79	0.47
3:6:55:ASN:ND2	3:6:92:ASP:HB2	2.26	0.47
7:W:118:CYS:SG	7:W:190:ASP:OD1	2.72	0.47
7:W:430:MET:CG	7:W:430:MET:CB	2.92	0.47
1:4:125:ARG:CZ	1:4:125:ARG:HA	2.45	0.47
7:W:56:VAL:CG1	7:W:57:LYS:H	2.27	0.47
7:W:98:LYS:HA	7:W:98:LYS:HZ3	1.78	0.47
7:W:343:GLY:C	7:W:369:MET:HG2	2.35	0.47
4:A:224:G:H5'	4:A:224:G:H8	1.79	0.47
6:S:63:VAL:HG13	7:W:361:SER:CB	2.35	0.47
7:W:48:LEU:HD22	7:W:52:LEU:HD23	1.94	0.47
7:W:84:VAL:HG12	7:W:89:PRO:N	2.29	0.47
7:W:308:ASN:O	7:W:309:GLU:CB	2.62	0.47
8:Z:86:U:H2'	8:Z:87:C:C6	2.50	0.47
8:Z:193:G:H2'	8:Z:194:C:C6	2.50	0.47
4:A:116:C:H2'	4:A:117:U:C6	2.50	0.47
4:A:125:G:H1	4:A:225:C:N4	2.08	0.47
4:A:171:U:H3'	4:A:172:A:H5"	1.97	0.47
7:W:46:ILE:HG12	7:W:47:LYS:HB3	1.97	0.47
7:W:239:LYS:C	7:W:239:LYS:HB3	2.03	0.47
7:W:270:ILE:HD11	7:W:286:LYS:HA	1.97	0.47
8:Z:247:A:H2'	8:Z:248:G:O4'	2.15	0.47
1:4:91:THR:HG22	1:4:135:LYS:CG	2.44	0.47
7:W:157:ILE:O	7:W:157:ILE:HG13	2.15	0.47
8:Z:111:U:H3'	8:Z:170:U:O2	2.14	0.47
3:6:94:LYS:HZ2	3:6:94:LYS:HB3	1.80	0.47
5:B:75:ASP:OD1	5:B:76:VAL:N	2.47	0.47
7:W:133:CYS:CB	7:W:179:PHE:CE1	2.98	0.47
7:W:160:TYR:CZ	7:W:174:GLU:CB	2.98	0.47
7:W:196:LYS:O	7:W:239:LYS:HE2	2.15	0.47
7:W:249:LYS:CE	7:W:252:GLY:HA3	2.45	0.47
7:W:249:LYS:NZ	7:W:252:GLY:HA3	2.30	0.47
2:5:36:GLN:O	2:5:40:SER:C	2.50	0.46
4:A:167:U:H2'	4:A:168:G:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:218:VAL:HG11	7:W:246:ILE:CD1	2.44	0.46
3:6:59:ILE:HD13	8:Z:48:C:H3'	1.98	0.46
4:A:207:C:C4	4:A:208:A:N7	2.84	0.46
7:W:16:SER:CA	7:W:17:LEU:HD22	2.44	0.46
7:W:304:ILE:HG22	7:W:308:ASN:HB3	1.97	0.46
7:W:428:ALA:O	7:W:432:LYS:N	2.49	0.46
8:Z:185:U:O2'	8:Z:186:C:H5'	2.15	0.46
7:W:48:LEU:HD21	7:W:52:LEU:CD2	2.44	0.46
7:W:139:THR:HA	7:W:145:PHE:HE1	1.79	0.46
7:W:249:LYS:O	7:W:249:LYS:CD	2.51	0.46
8:Z:245:G:H5"	8:Z:245:G:C8	2.50	0.46
1:4:75:TYR:HH	2:5:39:ALA:H	1.60	0.46
3:6:40:ALA:HB2	3:6:75:VAL:HG21	1.98	0.46
7:W:219:TYR:HB2	7:W:242:VAL:HG11	1.96	0.46
7:W:477:MET:O	7:W:479:GLY:CA	2.61	0.46
8:Z:27:G:N2	8:Z:30:A:H5'	2.21	0.46
2:5:36:GLN:CA	2:5:40:SER:O	2.63	0.46
5:B:60:VAL:CG2	5:B:83:ARG:O	2.52	0.46
7:W:339:ILE:C	7:W:342:MET:CB	2.84	0.46
1:4:85:LYS:HE3	8:Z:111:U:O2	2.14	0.46
1:4:144:ASP:OD1	1:4:145:VAL:HG23	2.14	0.46
2:5:53:LYS:O	2:5:57:ARG:HD3	2.15	0.46
7:W:164:THR:OG1	7:W:170:ILE:HG22	2.15	0.46
7:W:207:GLN:HA	7:W:210:ASN:HD22	1.77	0.46
7:W:284:PRO:C	7:W:286:LYS:CG	2.79	0.46
7:W:297:MET:HB3	7:W:300:ILE:CB	2.46	0.46
7:W:442:LYS:CA	7:W:445:ASP:N	2.79	0.46
1:4:110:LYS:HZ2	1:4:115:ILE:N	2.14	0.46
2:5:5:LYS:NZ	2:5:47:ARG:HD2	2.31	0.46
3:6:52:MET:HE1	3:6:83:ILE:HD11	1.96	0.46
4:A:125:G:H2'	4:A:126:C:H6	1.81	0.46
5:B:24:ASN:ND2	5:B:27:LYS:HG3	2.22	0.46
7:W:40:LEU:HD23	7:W:41:GLU:CA	2.46	0.46
7:W:207:GLN:CA	7:W:210:ASN:HD21	2.23	0.46
7:W:311:LYS:O	7:W:312:LEU:C	2.54	0.46
8:Z:243:A:H4'	8:Z:244:G:OP2	2.14	0.46
1:4:125:ARG:HD3	1:4:127:ASP:CB	2.45	0.46
4:A:229:U:H2'	4:A:230:C:C6	2.51	0.46
5:B:73:ASN:HD21	5:B:75:ASP:HB3	1.80	0.46
6:S:52:PHE:CB	6:S:53:PRO:HD3	2.40	0.46
7:W:149:LYS:CG	7:W:159:PHE:CE1	2.95	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:202:PHE:CD1	7:W:239:LYS:CE	2.99	0.46
7:W:234:LYS:HA	7:W:234:LYS:HZ2	1.78	0.46
5:B:76:VAL:C	5:B:78:TYR:N	2.70	0.46
7:W:93:ALA:HA	7:W:271:ILE:HG12	1.98	0.46
7:W:234:LYS:HE3	7:W:237:LYS:NZ	2.31	0.46
7:W:287:THR:C	7:W:291:ILE:CD1	2.78	0.46
1:4:72:ILE:O	1:4:97:ASP:OD1	2.33	0.46
3:6:28:LEU:HD11	3:6:40:ALA:HA	1.97	0.46
4:A:146:G:C6	4:A:147:G:C5	3.03	0.46
4:A:223:U:H2'	4:A:224:G:H5"	1.98	0.46
7:W:306:LYS:CB	7:W:347:GLN:HE22	2.23	0.46
8:Z:161:G:O4'	8:Z:267:G:C4'	2.64	0.46
2:5:14:LYS:HB3	2:5:18:ASP:HB2	1.98	0.45
7:W:92:LYS:CD	7:W:269:PRO:HB2	2.45	0.45
7:W:134:LEU:HD11	7:W:157:ILE:HD12	1.88	0.45
7:W:330:ARG:NH2	7:W:387:LEU:HD13	2.30	0.45
7:W:48:LEU:HD23	7:W:48:LEU:C	2.36	0.45
7:W:251:ASP:HB2	7:W:275:THR:O	2.16	0.45
7:W:271:ILE:CG2	7:W:272:PHE:N	2.79	0.45
7:W:318:LEU:O	7:W:320:GLU:N	2.49	0.45
8:Z:226:G:H2'	8:Z:227:U:O4'	2.16	0.45
7:W:78:ALA:O	7:W:82:GLU:HG3	2.16	0.45
7:W:218:VAL:HG11	7:W:246:ILE:CG1	2.47	0.45
1:4:125:ARG:HB3	1:4:126:PRO:C	2.36	0.45
2:5:59:LEU:O	2:5:59:LEU:HD13	2.17	0.45
4:A:223:U:C2'	4:A:224:G:H5"	2.47	0.45
7:W:136:CYS:SG	7:W:148:LEU:CG	3.05	0.45
6:S:57:LEU:HD13	7:W:430:MET:HE1	1.99	0.45
7:W:139:THR:CG2	7:W:163:TYR:CE1	3.00	0.45
7:W:255:LYS:HA	7:W:255:LYS:HZ3	1.78	0.45
7:W:260:LEU:CA	7:W:263:VAL:HG12	2.46	0.45
7:W:340:MET:HE3	7:W:373:LYS:HB2	1.97	0.45
7:W:479:GLY:N	7:W:480:LEU:N	2.63	0.45
4:A:166:U:H2'	4:A:167:U:O4'	2.17	0.45
7:W:32:LEU:HD21	7:W:57:LYS:HZ3	1.80	0.45
7:W:90:GLY:C	7:W:286:LYS:CB	2.85	0.45
7:W:139:THR:HG23	7:W:163:TYR:CE1	2.52	0.45
7:W:289:PRO:CA	7:W:301:GLU:OE1	2.63	0.45
7:W:337:GLN:O	7:W:340:MET:O	2.35	0.45
7:W:351:MET:O	7:W:353:PRO:N	2.50	0.45
2:5:65:LYS:O	2:5:66:GLN:HB3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S:60:TYR:CE2	7:W:355:PHE:N	2.85	0.45
6:S:60:TYR:CE2	7:W:354:GLY:C	2.91	0.45
7:W:247:VAL:CG1	7:W:247:VAL:O	2.64	0.45
7:W:301:GLU:O	7:W:302:GLY:C	2.55	0.45
7:W:319:ILE:HA	7:W:323:LYS:HZ2	1.79	0.45
7:W:432:LYS:CB	7:W:436:GLY:HA3	2.47	0.45
8:Z:213:A:H2'	8:Z:214:C:O4'	2.16	0.45
4:A:168:G:H3'	4:A:169:C:H5'	1.99	0.45
7:W:336:PHE:CE2	7:W:379:MET:HE1	2.27	0.45
7:W:397:SER:CB	8:Z:13:C:H5'	2.46	0.45
8:Z:114:C:C4'	8:Z:115:C:OP2	2.64	0.45
4:A:162:C:H2'	4:A:163:A:C8	2.52	0.45
7:W:24:ASN:HB2	7:W:25:GLU:H	1.66	0.45
7:W:26:GLU:HG2	7:W:27:VAL:H	1.82	0.45
8:Z:70:A:H4'	8:Z:71:A:O5'	2.17	0.45
1:4:83:MET:CA	1:4:86:ILE:HG22	2.47	0.44
7:W:83:LEU:HD22	7:W:294:LEU:HD22	1.56	0.44
7:W:116:THR:HG22	7:W:120:LYS:HE3	2.00	0.44
4:A:186:C:O5'	4:A:186:C:H6	2.01	0.44
5:B:43:ASN:C	5:B:118:ARG:HH22	2.20	0.44
5:B:64:LYS:HZ3	5:B:65:ASN:HB2	1.82	0.44
7:W:160:TYR:OH	7:W:174:GLU:HB3	2.15	0.44
7:W:447:SER:CA	7:W:451:SER:N	2.81	0.44
3:6:25:HIS:CE1	3:6:79:VAL:CG1	2.99	0.44
6:S:57:LEU:HB3	7:W:430:MET:HE3	1.97	0.44
7:W:87:VAL:HA	7:W:260:LEU:N	2.27	0.44
8:Z:159:C:C2	8:Z:212:A:H2	2.36	0.44
1:4:85:LYS:HB3	1:4:91:THR:HG1	1.83	0.44
3:6:56:ASP:H	3:6:91:GLU:HA	1.83	0.44
5:B:35:ILE:HD11	5:B:40:ALA:HA	1.99	0.44
5:B:76:VAL:CG1	5:B:77:GLN:N	2.80	0.44
5:B:76:VAL:O	5:B:78:TYR:N	2.50	0.44
6:S:61:VAL:HG12	7:W:423:GLN:NE2	2.28	0.44
7:W:141:ARG:HB2	7:W:144:ALA:HB2	2.00	0.44
7:W:199:ASP:OD1	7:W:200:SER:N	2.51	0.44
8:Z:138:C:H5'	8:Z:138:C:C6	2.49	0.44
4:A:221:C:H2'	4:A:222:G:O4'	2.18	0.44
7:W:286:LYS:HD2	7:W:286:LYS:HB3	1.95	0.44
8:Z:97:G:O2'	8:Z:98:A:H5'	2.18	0.44
2:5:16:LYS:HG3	2:5:67:ARG:O	2.17	0.44
4:A:138:G:H2'	4:A:139:A:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:163:A:H2'	4:A:164:G:N9	2.32	0.44
7:W:35:VAL:O	7:W:39:LEU:HD13	2.18	0.44
7:W:70:ASN:HD22	7:W:73:LYS:NZ	2.15	0.44
8:Z:160:G:H2'	8:Z:161:G:C8	2.52	0.44
8:Z:209:U:H3'	8:Z:210:C:H5'	2.00	0.44
8:Z:227:U:C4	8:Z:228:G:C6	3.06	0.44
1:4:89:ASN:O	8:Z:172:C:OP1	2.36	0.44
2:5:66:GLN:O	2:5:66:GLN:HG2	2.18	0.44
5:B:93:LEU:N	5:B:93:LEU:CD2	2.78	0.44
5:B:116:LYS:N	5:B:116:LYS:CD	2.80	0.44
7:W:45:ASN:HB3	7:W:227:GLN:HG2	1.99	0.44
7:W:179:PHE:CD1	7:W:184:PHE:HD2	2.33	0.44
7:W:176:VAL:HG13	7:W:177:GLU:N	2.33	0.44
7:W:324:HIS:C	7:W:334:GLU:HG2	2.38	0.44
1:4:119:LYS:HE2	1:4:135:LYS:HD3	1.99	0.44
2:5:47:ARG:O	2:5:51:ILE:HG12	2.17	0.44
1:4:110:LYS:HE3	1:4:110:LYS:C	2.37	0.43
2:5:32:GLN:HE22	7:W:70:ASN:HB2	1.83	0.43
3:6:51:ALA:HB3	3:6:52:MET:HG3	1.99	0.43
5:B:88:GLN:HG3	5:B:92:SER:O	2.18	0.43
7:W:32:LEU:HD21	7:W:57:LYS:NZ	2.33	0.43
7:W:245:VAL:HG22	7:W:270:ILE:HA	1.99	0.43
8:Z:159:C:H2'	8:Z:160:G:H8	1.83	0.43
8:Z:160:G:H1'	8:Z:266:A:C2	2.53	0.43
1:4:74:LYS:NZ	1:4:74:LYS:HA	2.33	0.43
5:B:45:THR:O	5:B:46:ALA:C	2.56	0.43
7:W:90:GLY:C	7:W:286:LYS:HB3	2.38	0.43
7:W:141:ARG:O	7:W:144:ALA:HB3	2.18	0.43
7:W:271:ILE:HD11	7:W:272:PHE:CZ	2.52	0.43
7:W:282:PHE:O	7:W:283:GLU:OE2	2.36	0.43
8:Z:159:C:O4'	8:Z:213:A:N9	2.48	0.43
8:Z:234:C:O2'	8:Z:235:G:H5'	2.19	0.43
7:W:56:VAL:HA	7:W:82:GLU:CD	2.29	0.43
7:W:153:THR:HG23	7:W:156:ARG:NH2	2.33	0.43
7:W:306:LYS:CG	7:W:347:GLN:OE1	2.65	0.43
7:W:479:GLY:H	7:W:480:LEU:N	2.16	0.43
8:Z:159:C:O5'	8:Z:213:A:H4'	2.18	0.43
7:W:293:LYS:C	7:W:293:LYS:HG2	2.23	0.43
1:4:77:LEU:HD13	1:4:95:ILE:HD11	1.99	0.43
2:5:65:LYS:O	2:5:66:GLN:CB	2.66	0.43
5:B:96:VAL:HG23	5:B:97:GLN:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:10:ILE:HG21	7:W:35:VAL:HG23	2.01	0.43
7:W:45:ASN:C	7:W:227:GLN:CG	2.73	0.43
7:W:79:VAL:O	7:W:82:GLU:N	2.51	0.43
7:W:87:VAL:HG21	7:W:256:GLY:C	2.34	0.43
7:W:134:LEU:CD1	7:W:157:ILE:HG13	2.49	0.43
7:W:179:PHE:CD2	7:W:187:ILE:CD1	3.01	0.43
7:W:194:ARG:HH22	7:W:202:PHE:HB2	1.69	0.43
7:W:195:HIS:CE1	7:W:196:LYS:HD3	2.53	0.43
7:W:271:ILE:CG2	7:W:272:PHE:CD1	3.01	0.43
7:W:342:MET:CB	7:W:342:MET:CG	2.95	0.43
7:W:303:LEU:CD2	7:W:348:ILE:CD1	2.97	0.43
1:4:85:LYS:CD	8:Z:171:C:O2'	2.65	0.43
4:A:171:U:H3'	4:A:172:A:C5'	2.49	0.43
7:W:109:LEU:CG	7:W:112:SER:OG	2.66	0.43
7:W:153:THR:HG23	7:W:156:ARG:HH21	1.84	0.43
7:W:335:GLN:HG3	7:W:427:PHE:CE2	2.54	0.43
7:W:394:LYS:CA	8:Z:13:C:OP1	2.55	0.43
4:A:160:A:H2'	4:A:161:C:H6	1.84	0.43
6:S:52:PHE:CE2	7:W:351:MET:CE	3.00	0.43
6:S:57:LEU:HB2	7:W:430:MET:CE	2.48	0.43
7:W:29:ASN:O	7:W:32:LEU:HB2	2.18	0.43
7:W:329:LEU:C	7:W:331:ASP:N	2.72	0.43
1:4:110:LYS:HZ1	1:4:114:ASP:HA	1.83	0.43
1:4:118:LYS:HA	1:4:118:LYS:NZ	2.33	0.43
4:A:117:U:H2'	4:A:118:A:C8	2.53	0.43
4:A:127:A:H2'	4:A:128:U:H5'	1.99	0.43
6:S:54:ILE:CG2	7:W:427:PHE:HE2	2.23	0.43
6:S:57:LEU:CD1	7:W:430:MET:HE1	2.49	0.43
6:S:62:THR:HG22	7:W:371:ARG:CD	2.29	0.43
7:W:272:PHE:CZ	7:W:282:PHE:HE2	2.35	0.43
7:W:430:MET:O	7:W:431:VAL:C	2.58	0.43
8:Z:63:A:H2'	8:Z:64:C:C6	2.54	0.43
8:Z:161:G:O4'	8:Z:267:G:C1'	2.67	0.43
8:Z:161:G:O3'	8:Z:267:G:O3'	2.37	0.43
2:5:62:ILE:HG23	2:5:67:ARG:HA	2.01	0.43
4:A:117:U:H2'	4:A:118:A:H8	1.83	0.43
4:A:179:G:N2	4:A:180:G:H1'	2.33	0.43
5:B:15:PHE:O	5:B:83:ARG:NH2	2.52	0.43
5:B:23:LEU:HB2	5:B:44:PRO:HG3	2.01	0.43
7:W:16:SER:C	7:W:17:LEU:C	2.76	0.43
7:W:23:ILE:CG2	7:W:24:ASN:N	2.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:56:VAL:CG1	7:W:57:LYS:N	2.81	0.43
7:W:205:MET:O	7:W:208:VAL:CG1	2.62	0.43
7:W:205:MET:C	7:W:208:VAL:HG12	2.38	0.43
2:5:66:GLN:O	2:5:67:ARG:CB	2.67	0.42
7:W:42:ALA:HB2	7:W:50:LYS:N	2.34	0.42
7:W:194:ARG:C	7:W:194:ARG:HD3	2.39	0.42
8:Z:6:A:H1'	8:Z:7:A:H5'	2.00	0.42
1:4:119:LYS:C	1:4:119:LYS:CD	2.85	0.42
1:4:125:ARG:NE	1:4:131:LYS:HG3	2.34	0.42
2:5:54:SER:CA	2:5:57:ARG:HE	2.26	0.42
6:S:60:TYR:HE2	7:W:358:ASP:OD2	2.02	0.42
7:W:15:ARG:NE	7:W:15:ARG:O	2.52	0.42
7:W:92:LYS:NZ	7:W:269:PRO:HG2	2.34	0.42
7:W:285:PHE:CD1	7:W:285:PHE:HB2	2.37	0.42
7:W:289:PRO:O	7:W:292:SER:HB2	2.11	0.42
8:Z:160:G:H2'	8:Z:161:G:H8	1.83	0.42
6:S:59:LEU:CD2	7:W:352:ILE:CD1	2.97	0.42
7:W:106:PHE:HZ	7:W:121:LEU:CD1	2.25	0.42
7:W:225:ILE:HD12	7:W:225:ILE:HG23	1.79	0.42
7:W:237:LYS:NZ	7:W:237:LYS:HB3	2.34	0.42
7:W:455:MET:O	7:W:459:ASN:N	2.41	0.42
5:B:53:CYS:O	5:B:58:LEU:HB2	2.19	0.42
5:B:73:ASN:ND2	5:B:74:ARG:N	2.67	0.42
7:W:28:LEU:C	7:W:32:LEU:HD13	2.40	0.42
7:W:133:CYS:HB3	7:W:179:PHE:CE1	2.54	0.42
7:W:260:LEU:O	7:W:263:VAL:CG1	2.66	0.42
8:Z:121:U:O2'	8:Z:122:A:H5'	2.20	0.42
4:A:150:G:O2'	4:A:203:G:N3	2.49	0.42
4:A:223:U:H2'	4:A:224:G:C5'	2.49	0.42
5:B:116:LYS:HE3	5:B:116:LYS:H	1.83	0.42
7:W:32:LEU:C	7:W:36:CYS:HG	2.22	0.42
7:W:36:CYS:SG	7:W:53:ARG:NH1	2.93	0.42
8:Z:91:A:H61	8:Z:104:U:H1'	1.84	0.42
8:Z:160:G:C1'	8:Z:266:A:C2	3.02	0.42
8:Z:160:G:C4'	8:Z:212:A:C4	3.01	0.42
2:5:34:ARG:HG2	2:5:37:LYS:HZ3	0.62	0.42
7:W:11:THR:HA	7:W:14:LEU:CD2	2.39	0.42
8:Z:159:C:C4'	8:Z:213:A:C4	3.00	0.42
4:A:233:U:C3'	4:A:234:A:C5'	2.98	0.42
3:6:48:ALA:O	3:6:52:MET:HB2	2.19	0.42
3:6:83:ILE:HG22	3:6:94:LYS:CB	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:19:TYR:CE2	5:B:81:ARG:HD3	2.55	0.42
5:B:107:TYR:O	5:B:111:MET:HG2	2.19	0.42
6:S:56:PHE:HD1	7:W:350:GLY:C	2.12	0.42
7:W:33:LYS:HA	7:W:36:CYS:HB2	2.02	0.42
7:W:79:VAL:HG23	7:W:80:PHE:N	2.34	0.42
7:W:310:LEU:O	7:W:313:ASP:N	2.50	0.42
8:Z:249:C:H2'	8:Z:250:G:H8	1.83	0.42
5:B:42:GLU:HG3	5:B:43:ASN:N	2.34	0.42
5:B:60:VAL:CB	5:B:84:VAL:HG12	2.49	0.42
7:W:45:ASN:HB3	7:W:227:GLN:CG	2.50	0.42
7:W:260:LEU:HA	7:W:260:LEU:HD13	1.87	0.42
7:W:284:PRO:C	7:W:286:LYS:HG2	2.13	0.42
7:W:345:PHE:CE1	7:W:366:GLN:C	2.93	0.42
8:Z:43:A:O2'	8:Z:44:U:H5"	2.19	0.42
8:Z:55:G:H2'	8:Z:56:A:H5'	2.01	0.42
7:W:11:THR:C	7:W:14:LEU:HD23	2.40	0.42
7:W:42:ALA:HB2	7:W:49:VAL:HG23	2.02	0.42
7:W:323:LYS:CA	7:W:337:GLN:CD	2.84	0.42
4:A:195:U:C4'	7:W:411:GLY:HA3	2.49	0.41
7:W:10:ILE:C	7:W:12:SER:H	2.22	0.41
7:W:272:PHE:CZ	7:W:282:PHE:CE2	3.06	0.41
7:W:331:ASP:CG	7:W:331:ASP:CA	2.88	0.41
4:A:118:A:H2'	4:A:119:A:H5'	2.03	0.41
5:B:22:TYR:CD1	5:B:34:ARG:HG3	2.55	0.41
5:B:88:GLN:O	5:B:89:GLU:C	2.58	0.41
7:W:194:ARG:NH1	7:W:196:LYS:C	2.73	0.41
7:W:271:ILE:CD1	7:W:271:ILE:C	2.88	0.41
8:Z:186:C:H2'	8:Z:187:G:O4'	2.19	0.41
8:Z:266:A:H2'	8:Z:267:G:C5'	2.50	0.41
3:6:84:ALA:O	3:6:92:ASP:HA	2.19	0.41
5:B:41:VAL:HG12	5:B:42:GLU:N	2.34	0.41
7:W:95:THR:O	7:W:95:THR:CG2	2.66	0.41
7:W:180:LYS:HB3	7:W:180:LYS:NZ	2.36	0.41
7:W:319:ILE:O	7:W:323:LYS:HE3	2.20	0.41
7:W:479:GLY:HA2	7:W:482:SER:H	1.85	0.41
8:Z:126:C:H2'	8:Z:127:A:C8	2.55	0.41
4:A:182:G:H21	4:A:215:A:H62	1.67	0.41
7:W:114:LYS:HD3	7:W:114:LYS:N	2.31	0.41
7:W:341:LYS:C	7:W:344:PRO:CB	2.88	0.41
8:Z:125:U:H2'	8:Z:126:C:H6	1.86	0.41
1:4:125:ARG:HH22	1:4:131:LYS:CE	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6:59:ILE:HG22	3:6:94:LYS:HD2	2.01	0.41
5:B:56:VAL:O	5:B:56:VAL:HG12	2.20	0.41
7:W:205:MET:HG2	7:W:240:VAL:HG21	2.02	0.41
7:W:280:ASP:OD1	7:W:280:ASP:O	2.38	0.41
7:W:319:ILE:C	7:W:323:LYS:HE3	2.41	0.41
8:Z:158:A:O2'	8:Z:169:U:O2	2.29	0.41
1:4:88:ASP:O	8:Z:172:C:O3'	2.38	0.41
5:B:76:VAL:CG1	5:B:77:GLN:H	2.34	0.41
5:B:116:LYS:H	5:B:116:LYS:CE	2.34	0.41
7:W:9:LYS:O	7:W:10:ILE:HD13	2.21	0.41
7:W:339:ILE:HG22	7:W:372:LEU:HD11	2.03	0.41
2:5:5:LYS:HG3	2:5:6:VAL:HG23	2.03	0.41
7:W:250:LEU:CD1	7:W:290:PHE:CE1	2.83	0.41
8:Z:3:G:H4'	8:Z:29:A:N1	2.36	0.41
4:A:151:C:H2'	4:A:152:G:H8	1.86	0.41
5:B:16:ILE:HG12	5:B:84:VAL:HG22	2.01	0.41
5:B:112:ILE:C	5:B:114:LYS:N	2.74	0.41
7:W:33:LYS:O	7:W:37:THR:N	2.54	0.41
7:W:138:ASP:OD1	7:W:144:ALA:HB3	2.17	0.41
7:W:285:PHE:CD2	7:W:286:LYS:O	2.62	0.41
7:W:339:ILE:HD12	7:W:427:PHE:CE1	2.30	0.41
7:W:366:GLN:CG	7:W:367:GLU:C	2.84	0.41
8:Z:196:G:H4'	8:Z:270:A:H2	1.85	0.41
1:4:100:ALA:O	1:4:104:LYS:HG3	2.21	0.41
4:A:164:G:OP2	4:A:164:G:C8	2.73	0.41
7:W:40:LEU:HG	7:W:41:GLU:N	2.30	0.41
7:W:80:PHE:HZ	7:W:288:GLN:O	2.04	0.41
7:W:157:ILE:HD13	7:W:157:ILE:HG21	1.81	0.41
7:W:239:LYS:CG	7:W:239:LYS:CE	2.87	0.41
7:W:249:LYS:NZ	7:W:252:GLY:CA	2.84	0.41
7:W:260:LEU:HA	7:W:263:VAL:CG1	2.50	0.41
8:Z:196:G:O2'	8:Z:197:G:H8	2.03	0.41
8:Z:266:A:C2'	8:Z:267:G:H5'	2.50	0.41
3:6:51:ALA:HB3	3:6:52:MET:CG	2.51	0.41
7:W:134:LEU:CB	7:W:148:LEU:HD11	2.51	0.41
7:W:213:GLN:NE2	7:W:213:GLN:C	2.74	0.41
7:W:288:GLN:CA	7:W:289:PRO:CD	2.98	0.41
1:4:119:LYS:HE2	1:4:135:LYS:CB	2.52	0.40
1:4:124:ILE:HD12	1:4:124:ILE:O	2.20	0.40
4:A:171:U:H5'	4:A:172:A:OP2	2.20	0.40
7:W:42:ALA:O	7:W:43:ASP:CB	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:W:52:LEU:HB2	7:W:53:ARG:HE	1.85	0.40
7:W:249:LYS:HE3	7:W:252:GLY:HA3	2.02	0.40
7:W:412:VAL:HG22	7:W:416:ASP:OD2	2.20	0.40
8:Z:172:C:O2'	8:Z:173:C:H5'	2.21	0.40
5:B:18:ILE:HD12	5:B:105:MET:HG2	2.02	0.40
5:B:29:ILE:HD13	5:B:29:ILE:HA	1.78	0.40
5:B:99:PRO:HB2	5:B:100:SER:H	1.59	0.40
7:W:32:LEU:O	7:W:36:CYS:SG	2.80	0.40
7:W:365:GLU:O	7:W:368:SER:CB	2.70	0.40
7:W:442:LYS:O	7:W:443:GLY:C	2.52	0.40
8:Z:33:G:O3'	8:Z:34:A:H8	2.04	0.40
8:Z:181:G:O2'	8:Z:182:G:H5'	2.21	0.40
8:Z:196:G:C4'	8:Z:270:A:H2	2.35	0.40
1:4:106:LYS:O	1:4:109:VAL:HG12	2.20	0.40
3:6:54:THR:HA	3:6:90:GLU:CB	2.41	0.40
4:A:207:C:O2'	4:A:208:A:H5'	2.21	0.40
5:B:94:CYS:C	5:B:95:LEU:HD23	2.38	0.40
7:W:76:GLN:O	7:W:79:VAL:HG22	2.21	0.40
7:W:87:VAL:HG11	7:W:256:GLY:HA3	1.58	0.40
7:W:110:GLN:NE2	7:W:141:ARG:NH1	2.62	0.40
7:W:163:TYR:O	7:W:163:TYR:CG	2.74	0.40
7:W:297:MET:CG	7:W:300:ILE:HD12	2.52	0.40
8:Z:27:G:N2	8:Z:30:A:C5'	2.77	0.40
8:Z:117:G:H2'	8:Z:118:U:O4'	2.20	0.40
8:Z:168:A:O2'	8:Z:170:U:OP2	2.39	0.40
1:4:148:LYS:HA	7:W:69:LEU:HB2	1.06	0.40
3:6:20:TYR:CE1	3:6:52:MET:HE3	2.56	0.40
6:S:54:ILE:HG21	7:W:335:GLN:OE1	2.22	0.40
7:W:41:GLU:HA	7:W:41:GLU:H	1.70	0.40
7:W:52:LEU:HD22	7:W:86:LEU:HD21	1.81	0.40
7:W:131:LYS:CG	7:W:183:ASN:O	2.68	0.40
7:W:330:ARG:CD	7:W:333:TYR:CD1	2.92	0.40
7:W:272:PHE:CE1	7:W:282:PHE:HZ	2.35	0.40
7:W:360:MET:O	7:W:362:LYS:CG	2.54	0.40
8:Z:18:A:H2'	8:Z:19:A:H5'	2.03	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	4	75/152 (49%)	66 (88%)	4 (5%)	5 (7%)	1 15
2	5	62/124 (50%)	54 (87%)	3 (5%)	5 (8%)	1 12
3	6	79/123 (64%)	66 (84%)	10 (13%)	3 (4%)	3 24
5	B	105/108 (97%)	87 (83%)	12 (11%)	6 (6%)	1 18
6	S	15/17 (88%)	13 (87%)	2 (13%)	0	100 100
7	W	442/504 (88%)	338 (76%)	56 (13%)	48 (11%)	0 8
All	All	778/1028 (76%)	624 (80%)	87 (11%)	67 (9%)	2 12

All (67) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	4	101	ASP
1	4	125	ARG
2	5	35	ILE
2	5	36	GLN
2	5	40	SER
2	5	45	LEU
3	6	24	LEU
3	6	52	MET
3	6	90	GLU
5	B	42	GLU
5	B	75	ASP
7	W	41	GLU
7	W	46	ILE
7	W	48	LEU
7	W	49	VAL
7	W	88	ASP
7	W	89	PRO
7	W	162	SER
7	W	168	PRO
7	W	241	ASP

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Mol	Chain	Res	Type
7	W	244	SER
7	W	309	GLU
7	W	319	ILE
7	W	352	ILE
7	W	353	PRO
7	W	358	ASP
7	W	361	SER
7	W	442	LYS
7	W	443	GLY
7	W	448	LYS
7	W	478	ALA
1	4	97	ASP
1	4	127	ASP
1	4	141	ASP
2	5	66	GLN
5	B	99	PRO
7	W	10	ILE
7	W	19	ASN
7	W	32	LEU
7	W	47	LYS
7	W	56	VAL
7	W	60	ILE
7	W	67	SER
7	W	303	LEU
7	W	307	VAL
7	W	325	GLY
7	W	360	MET
7	W	431	VAL
7	W	450	VAL
7	W	28	LEU
7	W	62	LEU
7	W	69	LEU
7	W	73	LYS
7	W	74	MET
7	W	75	ILE
7	W	438	LYS
5	B	64	LYS
5	B	77	GLN
7	W	30	ALA
7	W	38	ALA
7	W	72	ARG
7	W	321	LYS

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Mol	Chain	Res	Type
7	W	79	VAL
7	W	291	ILE
7	W	308	ASN
7	W	14	LEU
5	B	56	VAL

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	4	72/128 (56%)	54 (75%)	18 (25%)	0	3
2	5	55/109 (50%)	45 (82%)	10 (18%)	1	10
3	6	72/108 (67%)	51 (71%)	21 (29%)	0	2
5	B	96/97 (99%)	92 (96%)	4 (4%)	30	54
6	S	16/16 (100%)	16 (100%)	0	100	100
7	W	360/420 (86%)	329 (91%)	31 (9%)	10	32
All	All	671/878 (76%)	587 (88%)	84 (12%)	8	19

All (84) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	4	70	TYR
1	4	74	LYS
1	4	80	GLU
1	4	87	GLU
1	4	90	ASN
1	4	99	LYS
1	4	101	ASP
1	4	103	LYS
1	4	104	LYS
1	4	110	LYS
1	4	115	ILE
1	4	118	LYS
1	4	119	LYS

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Mol	Chain	Res	Type
1	4	125	ARG
1	4	129	LYS
1	4	135	LYS
1	4	141	ASP
1	4	147	ASN
2	5	7	LYS
2	5	14	LYS
2	5	16	LYS
2	5	21	LYS
2	5	25	GLU
2	5	27	LYS
2	5	44	LYS
2	5	46	ASN
2	5	57	ARG
2	5	63	ASN
3	6	18	ARG
3	6	23	ASN
3	6	26	LYS
3	6	27	ARG
3	6	28	LEU
3	6	34	LYS
3	6	57	VAL
3	6	58	ARG
3	6	59	ILE
3	6	62	LYS
3	6	65	LYS
3	6	73	ARG
3	6	77	ARG
3	6	80	ARG
3	6	85	ARG
3	6	86	LYS
3	6	87	ARG
3	6	88	ASN
3	6	90	GLU
3	6	91	GLU
3	6	94	LYS
5	B	39	LYS
5	B	64	LYS
5	B	93	LEU
5	B	116	LYS
7	W	12	SER
7	W	15	ARG

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Mol	Chain	Res	Type
7	W	27	VAL
7	W	40	LEU
7	W	47	LYS
7	W	53	ARG
7	W	57	LYS
7	W	65	MET
7	W	98	LYS
7	W	114	LYS
7	W	131	LYS
7	W	180	LYS
7	W	194	ARG
7	W	196	LYS
7	W	197	GLN
7	W	213	GLN
7	W	234	LYS
7	W	237	LYS
7	W	255	LYS
7	W	267	LYS
7	W	271	ILE
7	W	284	PRO
7	W	285	PHE
7	W	286	LYS
7	W	294	LEU
7	W	331	ASP
7	W	340	MET
7	W	342	MET
7	W	383	ASN
7	W	412	VAL
7	W	427	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	4	71	GLN
1	4	89	ASN
1	4	116	GLN
2	5	22	GLN
2	5	32	GLN
2	5	36	GLN
2	5	63	ASN
2	5	66	GLN
3	6	23	ASN

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Mol	Chain	Res	Type
3	6	29	HIS
3	6	39	ASN
3	6	64	ASN
5	B	24	ASN
5	B	59	ASN
5	B	65	ASN
5	B	73	ASN
5	B	88	GLN
6	S	65	HIS
7	W	51	GLN
7	W	70	ASN
7	W	76	GLN
7	W	110	GLN
7	W	126	GLN
7	W	147	GLN
7	W	183	ASN
7	W	210	ASN
7	W	213	GLN
7	W	324	HIS
7	W	337	GLN
7	W	383	ASN
7	W	385	GLN
7	W	423	GLN
7	W	429	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	A	127/128 (99%)	22 (17%)	1 (0%)
8	Z	274/280 (97%)	35 (12%)	13 (4%)
All	All	401/408 (98%)	57 (14%)	14 (3%)

All (57) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	A	128	U
4	A	129	C
4	A	164	G
4	A	168	G
4	A	169	C
4	A	171	U

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Mol	Chain	Res	Type
4	A	172	A
4	A	173	A
4	A	174	G
4	A	176	A
4	A	177	G
4	A	187	G
4	A	191	C
4	A	213	A
4	A	214	A
4	A	215	A
4	A	219	C
4	A	221	C
4	A	224	G
4	A	227	G
4	A	232	G
4	A	234	A
8	Z	6	A
8	Z	7	A
8	Z	8	G
8	Z	18	A
8	Z	19	A
8	Z	31	U
8	Z	32	A
8	Z	33	G
8	Z	35	G
8	Z	36	C
8	Z	41	C
8	Z	44	U
8	Z	71	A
8	Z	73	G
8	Z	113	G
8	Z	115	C
8	Z	138	C
8	Z	149	A
8	Z	152	U
8	Z	156	A
8	Z	170	U
8	Z	171	C
8	Z	197	G
8	Z	203	G
8	Z	204	C
8	Z	232	G

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Mol	Chain	Res	Type
8	Z	233	C
8	Z	244	G
8	Z	245	G
8	Z	246	A
8	Z	264	A
8	Z	265	U
8	Z	266	A
8	Z	273	C
8	Z	274	G

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	A	212	C
8	Z	6	A
8	Z	17	G
8	Z	35	G
8	Z	43	A
8	Z	70	A
8	Z	72	U
8	Z	112	A
8	Z	114	C
8	Z	170	U
8	Z	231	A
8	Z	243	A
8	Z	245	G
8	Z	264	A

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
7	W	35
8	Z	5
1	4	2
2	5	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Z	37:A	O3'	38:C	P	52.59
1	Z	180:C	O3'	181:G	P	51.07
1	Z	200:A	O3'	201:U	P	4.54
1	W	432:LYS	C	433:LYS	N	3.98
1	4	98:LEU	C	99:LYS	N	3.96
1	W	366:GLN	C	367:GLU	N	3.94
1	Z	36:C	O3'	37:A	P	3.93
1	W	293:LYS	C	294:LEU	N	3.62
1	W	339:ILE	C	340:MET	N	3.60
1	W	344:PRO	C	345:PHE	N	3.57
1	Z	1:C	O3'	2:U	P	3.32
1	W	313:ASP	C	314:ASP	N	3.26
1	W	460:GLN	C	461:GLN	N	3.24
1	W	92:LYS	C	93:ALA	N	3.21
1	W	16:SER	C	17:LEU	N	3.13
1	W	429:GLN	C	430:MET	N	3.04
1	4	95:ILE	C	96:VAL	N	2.98
1	W	91:VAL	C	92:LYS	N	2.84
1	W	331:ASP	C	332:MET	N	2.78
1	W	343:GLY	C	344:PRO	N	2.77
1	W	444:GLY	C	445:ASP	N	2.55
1	W	475:GLY	C	476:GLY	N	2.22
1	W	283:GLU	C	284:PRO	N	2.13
1	W	479:GLY	C	480:LEU	N	2.07
1	W	314:ASP	C	315:ASN	N	2.05
1	W	365:GLU	C	366:GLN	N	1.78
1	W	298:GLY	C	299:ASP	N	1.73

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	W	40:LEU	C	41:GLU	N	1.66
1	W	303:LEU	C	304:ILE	N	1.61
1	W	442:LYS	C	443:GLY	N	1.19
1	W	451:SER	C	452:GLN	N	1.19
1	W	437:ILE	C	438:LYS	N	1.18
1	W	348:ILE	C	349:LEU	N	1.12
1	W	240:VAL	C	241:ASP	N	1.11
1	W	448:LYS	C	449:ASN	N	1.08
1	W	243:ALA	C	244:SER	N	1.07
1	W	363:GLY	C	364:ASN	N	1.04
1	5	39:ALA	C	40:SER	N	1.01
1	W	357:THR	C	358:ASP	N	0.97
1	W	360:MET	C	361:SER	N	0.93
1	W	354:GLY	C	355:PHE	N	0.92
1	W	351:MET	C	352:ILE	N	0.91
1	W	321:LYS	C	322:LEU	N	0.56

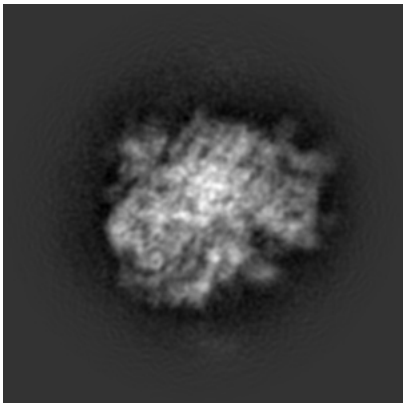
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-1264. These allow visual inspection of the internal detail of the map and identification of artifacts.

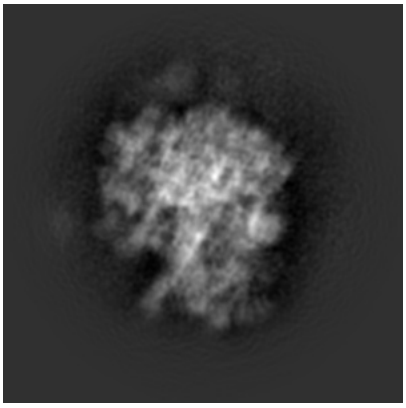
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

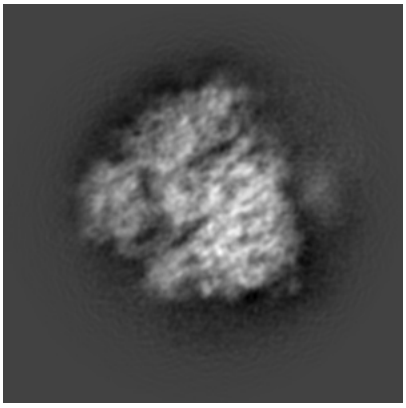
6.1.1 Primary map



X



Y

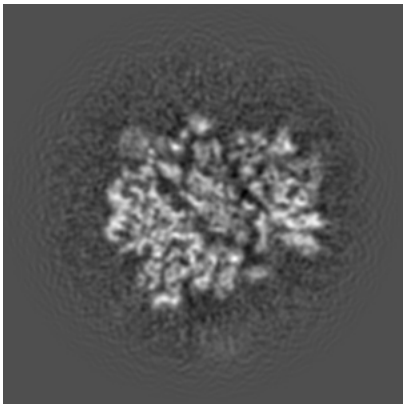


Z

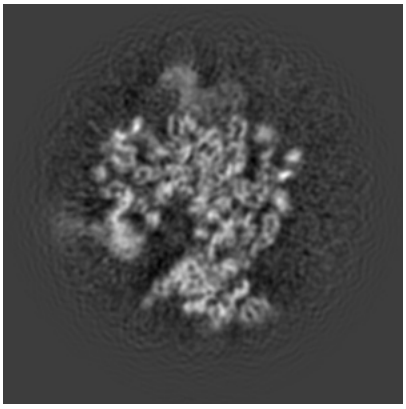
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

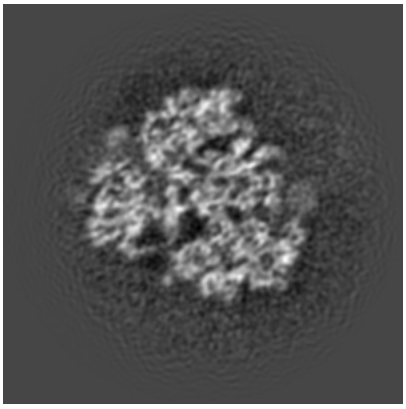
6.2.1 Primary map



X Index: 184



Y Index: 184

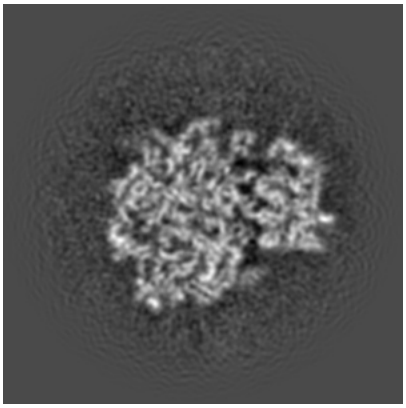


Z Index: 184

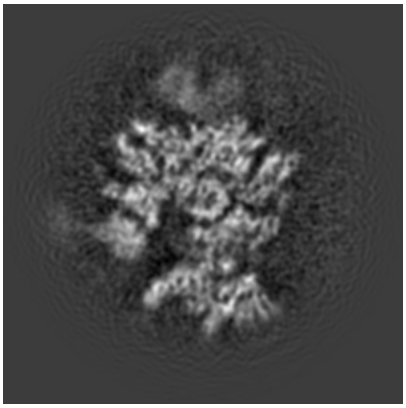
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

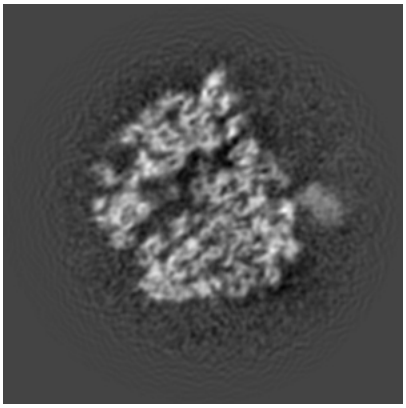
6.3.1 Primary map



X Index: 192



Y Index: 190

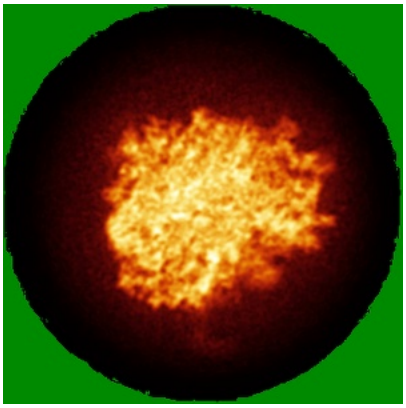


Z Index: 169

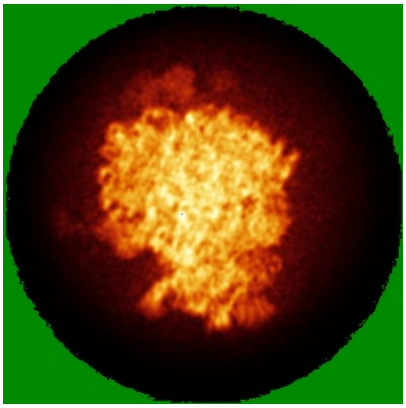
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

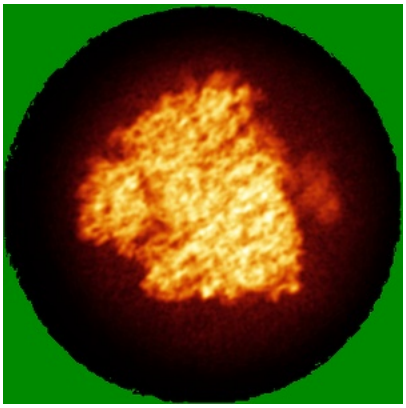
6.4.1 Primary map



X



Y

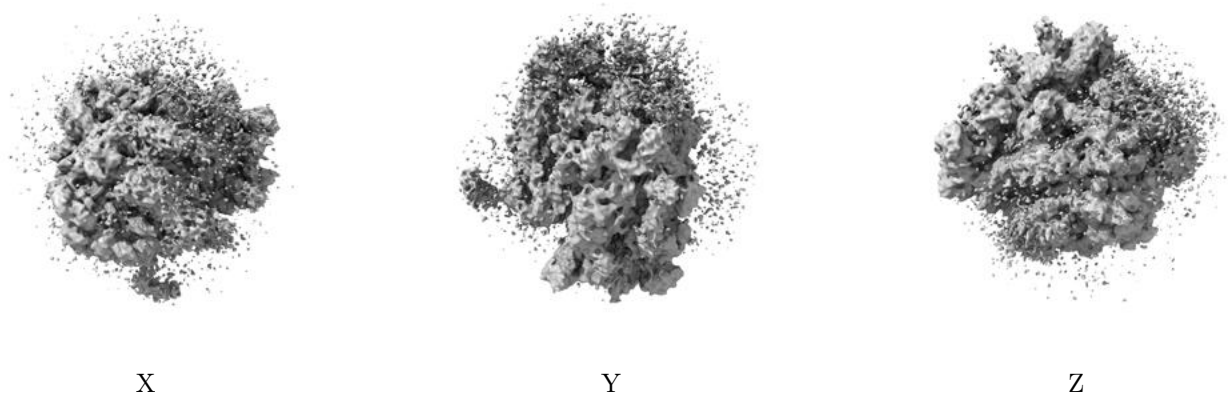


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0602. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

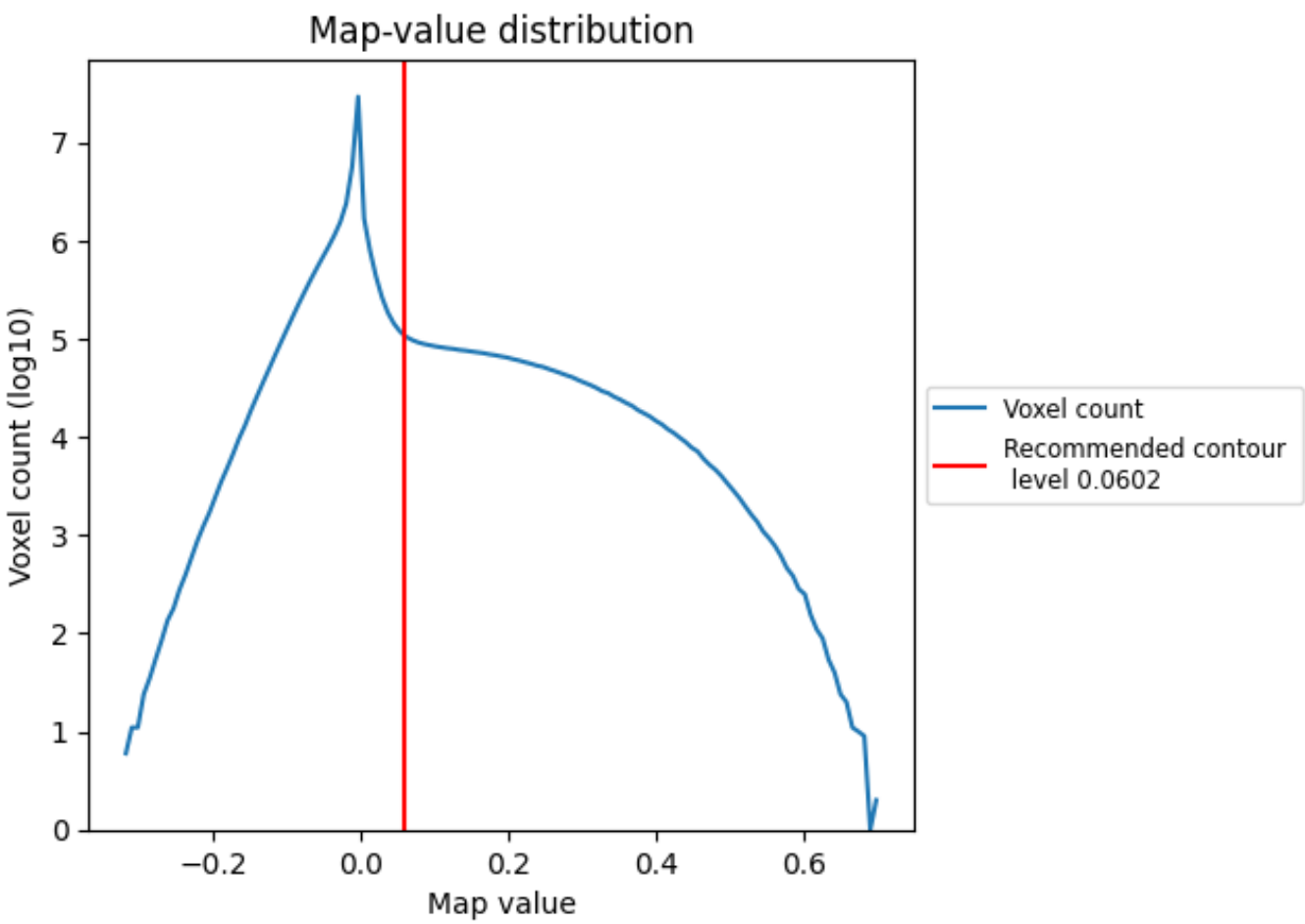
6.6 Mask visualisation (i)

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

7 Map analysis (i)

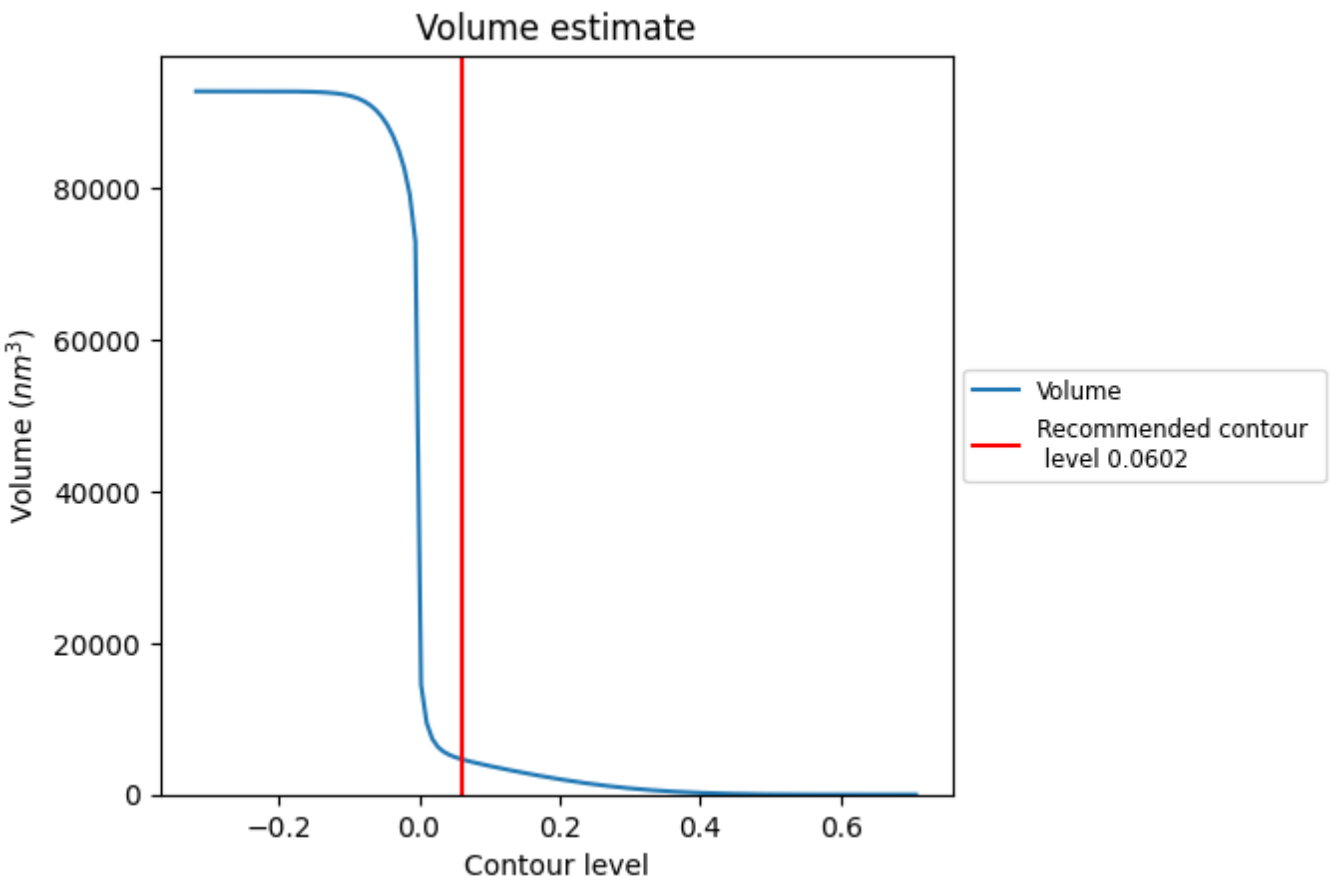
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

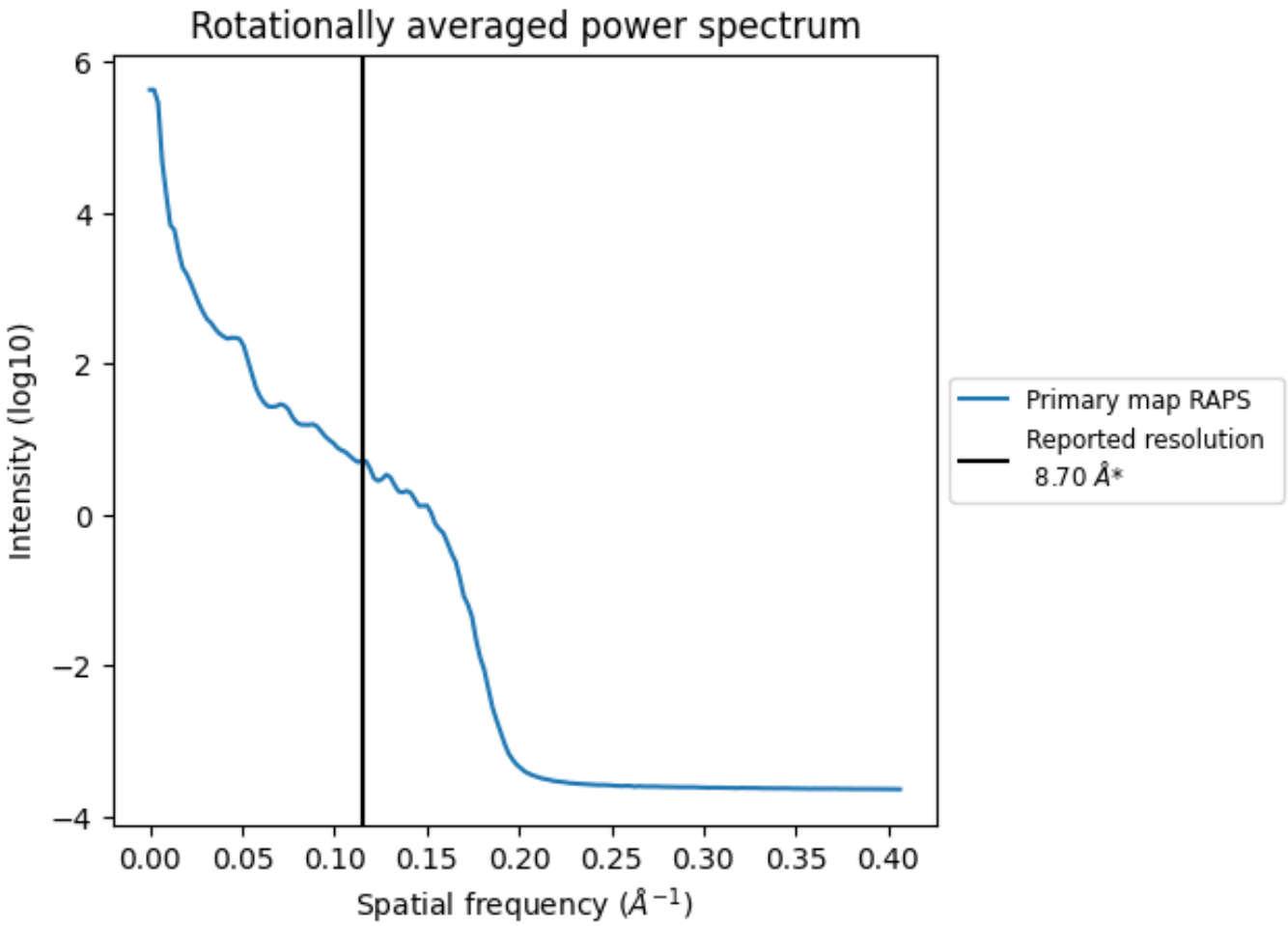
7.2 Volume estimate (i)



The volume at the recommended contour level is 4668 nm^3; this corresponds to an approximate mass of 4217 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.115 Å^{-1}

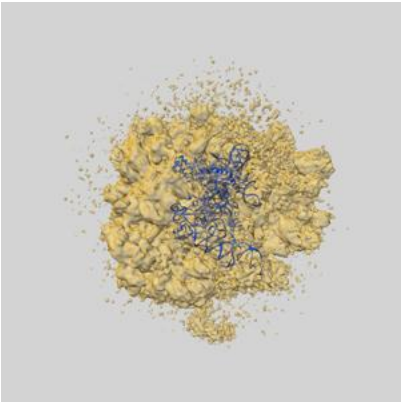
8 Fourier-Shell correlation (i)

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

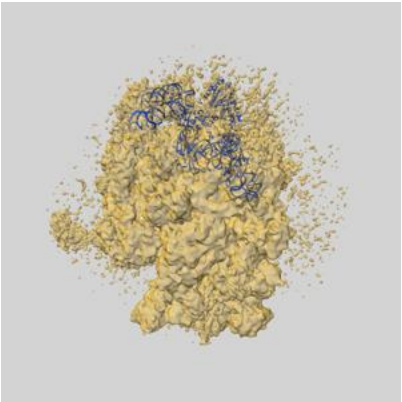
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-1264 and PDB model 2J37. Per-residue inclusion information can be found in section 3 on page 6.

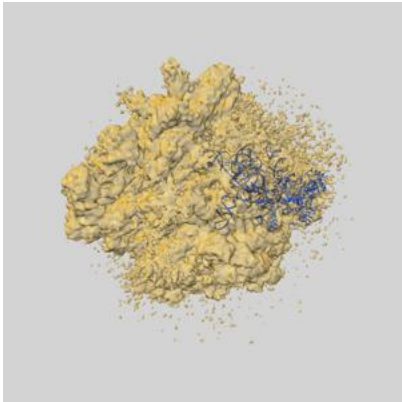
9.1 Map-model overlay (i)



X



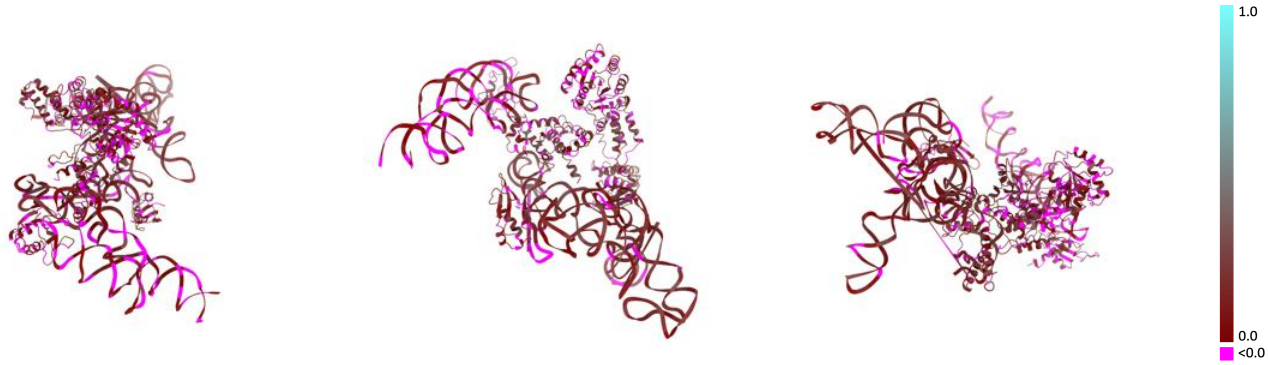
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0602 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.

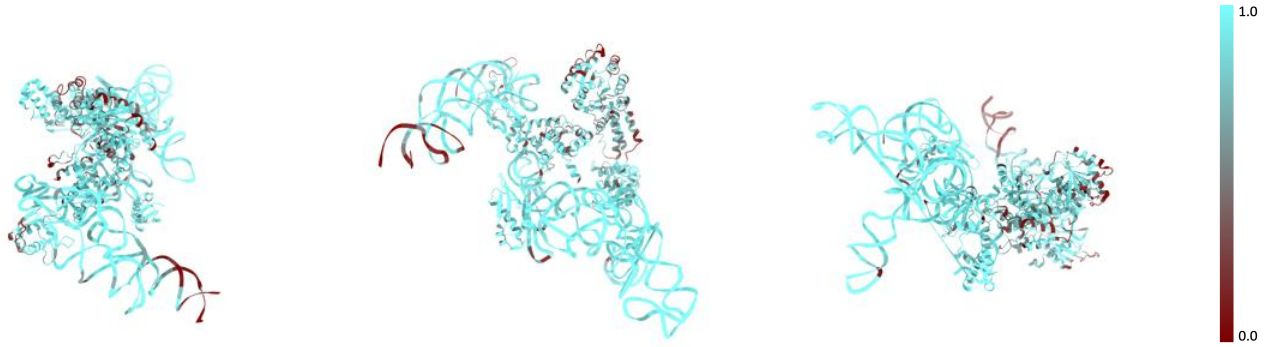
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

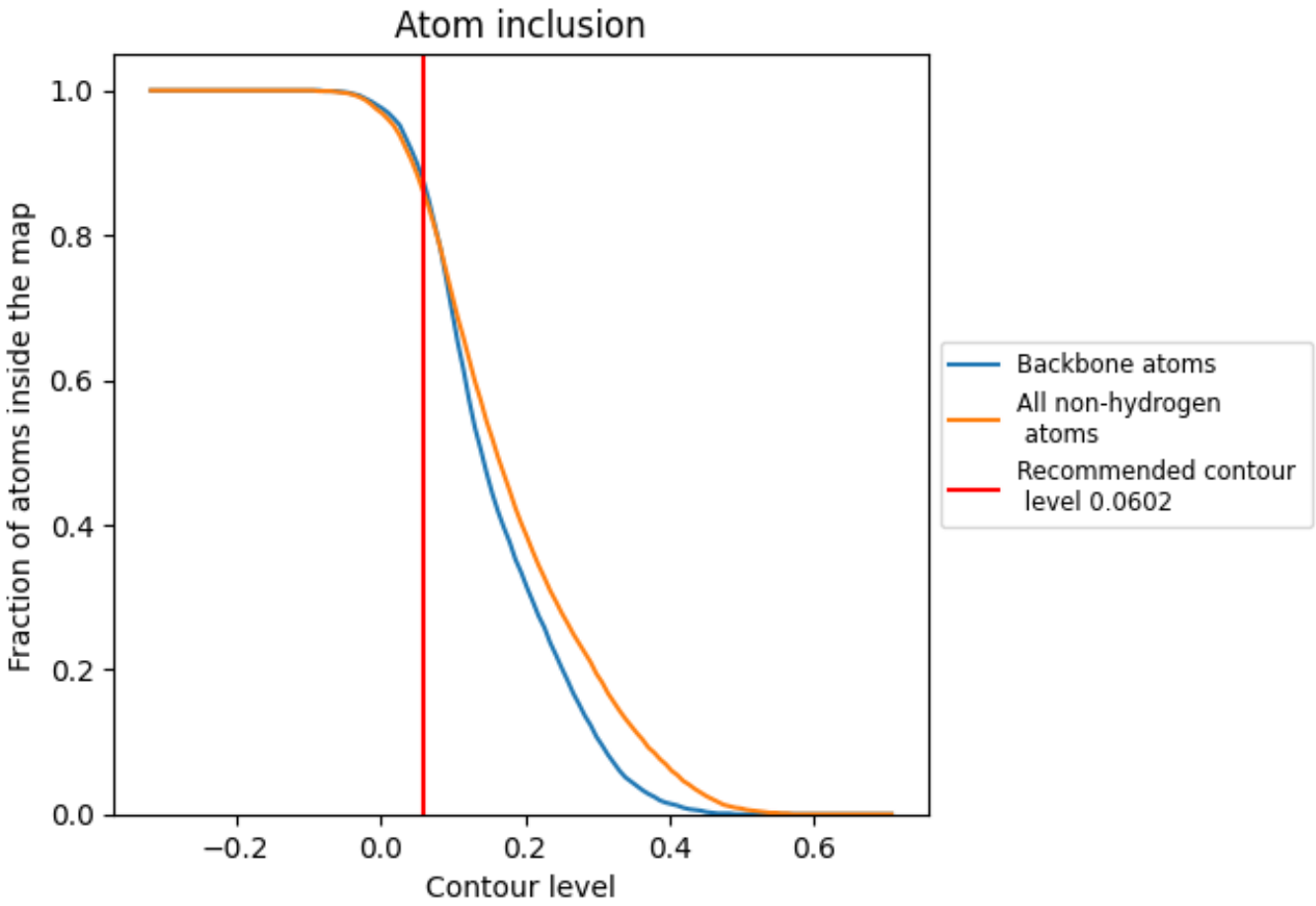
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.0602).

9.4 Atom inclusion (i)



At the recommended contour level, 87% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0602) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8570	0.0990
4	0.8930	0.1370
5	0.9270	0.1420
6	0.9400	0.1000
A	0.7990	0.0430
B	0.8200	0.0520
S	0.6210	0.0590
W	0.7140	0.0870
Z	0.9590	0.1320