



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 26, 2014 – 10:03 PM GMT

PDB ID : 4RCR
Title : STRUCTURE OF THE REACTION CENTER FROM RHODOBACTER SPHAEROIDES R-26 AND 2.4.1: PROTEIN-COFACTOR (BACTERIOCHLOROPHYLL, BACTERIOPHEOPHYTIN, AND CAROTENOID) INTERACTIONS
Authors : Komiya, H.; Yeates, T.O.; Chirino, A.J.; Rees, D.C.; Allen, J.P.; Feher, G.
Deposited on : 1991-09-09
Resolution : 2.80 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

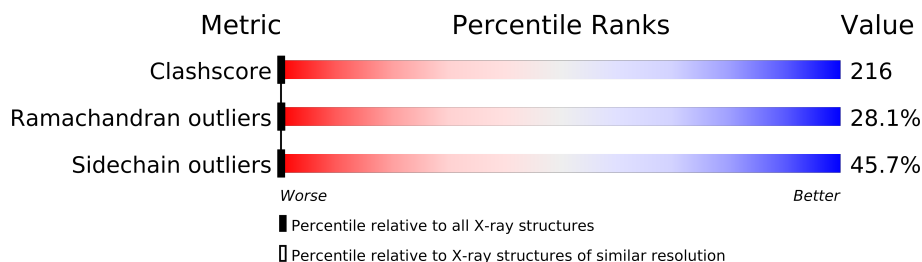
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : NOT EXECUTED
EDS : NOT EXECUTED
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.80 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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	L	281	
2	M	307	
3	H	260	

2 Entry composition i

There are 8 unique types of molecules in this entry. The entry contains 6764 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 PHOTOSYNTHETIC REACTION CENTER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	266	Total	C	N	O	S	0	0	0
			2120	1433	336	343	8			

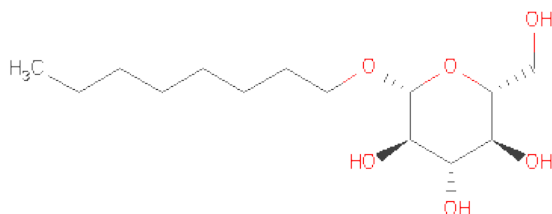
- Molecule 2 is a protein called PHOTOSYNTHETIC REACTION CENTER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	296	Total	C	N	O	S	0	0	0
			2361	1579	386	386	10			

- Molecule 3 is a protein called PHOTOSYNTHETIC REACTION CENTER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	237	Total	C	N	O	S	0	0	0
			1806	1156	310	331	9			

- Molecule 4 is SUGAR (B-OCTYLGLUCOSIDE) (three-letter code: BOG) (formula: C₁₄H₂₈O₆).

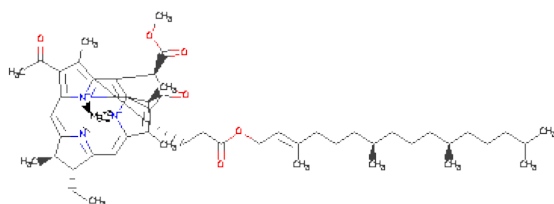


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	M	1	Total	C	O	0	0
			20	14	6		

- Molecule 5 is FE (III) ION (three-letter code: FE) (formula: Fe).

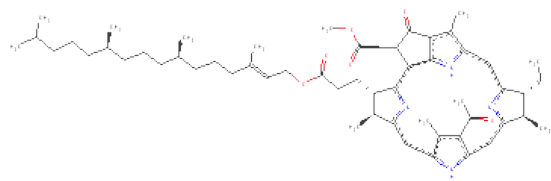
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	M	1	Total	Fe	0	0
			1	1		

- Molecule 6 is BACTERIOCHLOROPHYLL A (three-letter code: BCL) (formula: C₅₅H₇₄MgN₄O₆).



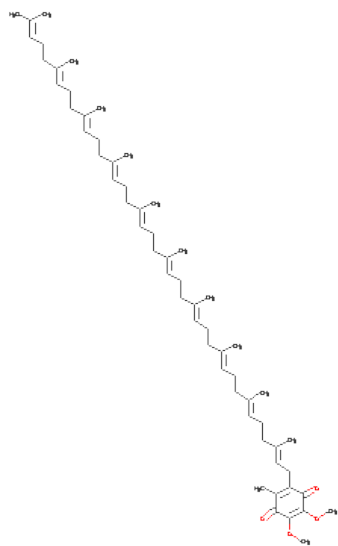
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	L	1	Total	C	Mg	N	O	0	0
			51	40	1	4	6		
6	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
6	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
6	M	1	Total	C	Mg	N	O	0	0
			51	40	1	4	6		

- Molecule 7 is BACTERIOPHEOPHYTIN A (three-letter code: BPH) (formula: C₅₅H₇₆N₄O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	M	1	Total	C	N	O	0	0
			65	55	4	6		
7	L	1	Total	C	N	O	0	0
			65	55	4	6		

- Molecule 8 is UBIQUINONE-10 (three-letter code: U10) (formula: C₅₉H₉₀O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	M	1	Total	C	O	0	0
			51	47	4		
8	L	1	Total	C	O	0	0
			41	37	4		

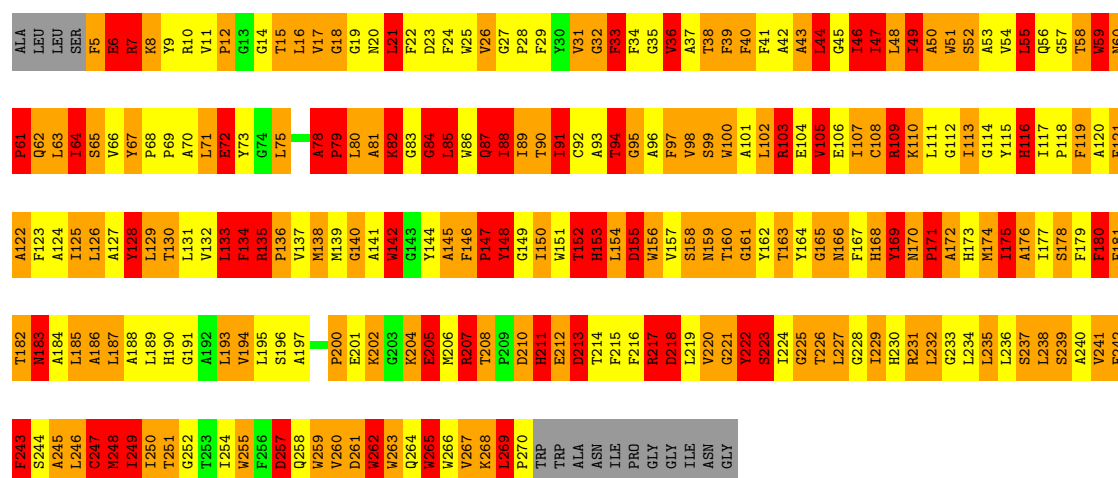
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

Note EDS was not executed.

• Molecule 1: PHOTOSYNTHETIC REACTION CENTER

Chain L: 



Chain H:



M242	E182	E122	P61	MET
Y243	L183	L123	K62	VAL
A244	K184	D124	T63	GLY
A245	D185	G125	F64	VAL
P246	G186	H126	I65	THR
K247	S187	G127	L66	ALA
R248	T188	H128	P67	PHE
VAL	L189	M129	H68	GLY
SER	L190	K130	G69	ASN
VAL	L191	I131	G70	PHE
VAL	P192	K132	R70	ASP
ALA	M193	P133	L73	L12
ALA	K194	M134	T74	A13
ALA	M195	K135	V75	S14
MET	L196	A136	P76	L15
LEU	A197	A137	G77	A16
ALA	L198	A138	P78	I17
GLU	V199	G139	E79	V18
THR	Q199	F140	S80	S19
ALA	S200	H141	E81	F20
	N201	V142	D82	W21
	R202	S143	R83	L22
	V203	A144	P84	F23
	H204	A145	I85	L24
	V205	K146	A86	A25
	N206	M147	L87	G26
	A207	P148	A88	L27
	L208	I149	R89	T28
	S209	G150	T90	V29
	S210	L151	A91	V30
	D211	P152	V92	L31
	L212	M153	S93	Q32
	F213	R154	E94	T33
	A214	G155	G95	E34
	G215	G156	F96	N35
	T216	D157	P97	N36
	P217	L158	H98	R37
	T218	E159	A99	E38
	L219	I160	P100	G39
	K220	A161	T101	V40
	S221	G162	G102	P41
	P222	K163	D103	L42
	T223	V164	P104	E43
	E224	V165	M105	N44
	V225	D166	K106	E45
	L226	I167	D107	D46
	T227	M168	G108	G47
	L228	V169	M109	T48
	E229	D170	G110	P49
	Z230	T171	P111	A50
	D231	P172	A112	A51
	K232	E173	S113	N52
	L233	O174	W114	N53
	C234	M175	V115	S54
	G235	A176	A116	P55
	V236	R177	R117	F56
	V237	F178	R118	P57
	A238	L179	D119	L58
	G239	V180	L120	P59
	G240	E181	P121	V60
	T241			

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	138.00Å 77.50Å 141.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.80	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.227 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6764	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: BCL, BPH, U10, FE, BOG

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	L	1.01	1/2203 (0.0%)	1.69	48/3014 (1.6%)
2	M	1.03	0/2452	1.71	52/3348 (1.6%)
3	H	1.16	4/1854 (0.2%)	1.95	48/2523 (1.9%)
All	All	1.06	5/6509 (0.1%)	1.78	148/8885 (1.7%)

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	L	0	36
2	M	0	29
3	H	2	39
All	All	2	104

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	53	GLN	C-N	17.61	1.64	1.33
3	H	56	PHE	C-N	-12.37	1.10	1.34
3	H	248	ARG	CD-NE	-6.33	1.35	1.46
3	H	248	ARG	NE-CZ	-5.38	1.26	1.33
1	L	94	THR	CA-CB	5.02	1.66	1.53

All (148) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	248	ARG	CD-NE-CZ	40.26	179.96	123.60
2	M	13	ARG	NE-CZ-NH1	14.66	127.63	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	13	ARG	NE-CZ-NH2	-11.69	114.46	120.30
3	H	177	ARG	NE-CZ-NH1	-10.41	115.10	120.30
3	H	248	ARG	NE-CZ-NH1	9.76	125.18	120.30
2	M	247	ARG	NE-CZ-NH1	9.65	125.13	120.30
2	M	30	SER	N-CA-CB	9.51	124.76	110.50
2	M	121	PHE	CB-CA-C	9.44	129.29	110.40
1	L	169	TYR	CB-CG-CD2	-9.15	115.51	121.00
3	H	227	LEU	CB-CA-C	8.94	127.19	110.20
2	M	205	SER	N-CA-CB	8.77	123.65	110.50
1	L	59	TRP	CB-CA-C	8.67	127.74	110.40
3	H	37	ARG	NE-CZ-NH1	8.66	124.63	120.30
3	H	42	LEU	CB-CA-C	8.59	126.52	110.20
1	L	169	TYR	CB-CG-CD1	8.49	126.09	121.00
1	L	211	HIS	CA-CB-CG	-8.26	99.55	113.60
3	H	23	PHE	N-CA-CB	8.25	125.45	110.60
1	L	168	HIS	N-CA-CB	8.15	125.28	110.60
1	L	109	ARG	NE-CZ-NH1	-8.14	116.23	120.30
3	H	238	ALA	CB-CA-C	8.01	122.11	110.10
1	L	135	ARG	NE-CZ-NH1	7.99	124.30	120.30
2	M	285	LEU	CB-CA-C	7.99	125.38	110.20
2	M	148	TRP	CA-CB-CG	7.97	128.84	113.70
2	M	21	THR	CA-CB-CG2	7.96	123.54	112.40
2	M	164	ARG	NE-CZ-NH1	7.92	124.26	120.30
2	M	38	LEU	CB-CA-C	7.78	124.98	110.20
1	L	158	SER	N-CA-CB	7.75	122.13	110.50
3	H	23	PHE	CA-CB-CG	7.71	132.41	113.90
1	L	231	ARG	NE-CZ-NH2	7.71	124.15	120.30
1	L	109	ARG	NE-CZ-NH2	7.67	124.13	120.30
3	H	211	ASP	CB-CA-C	7.65	125.70	110.40
2	M	184	ASP	CB-CG-OD1	-7.64	111.43	118.30
3	H	184	LYS	N-CA-CB	7.60	124.28	110.60
2	M	267	ARG	NE-CZ-NH2	7.49	124.05	120.30
2	M	121	PHE	CA-CB-CG	-7.48	95.94	113.90
2	M	21	THR	N-CA-CB	7.33	124.23	110.30
2	M	241	ARG	NE-CZ-NH1	7.20	123.90	120.30
1	L	217	ARG	NE-CZ-NH1	-7.18	116.71	120.30
3	H	70	ARG	NE-CZ-NH2	7.17	123.89	120.30
3	H	178	PHE	N-CA-CB	7.17	123.50	110.60
1	L	105	VAL	CA-CB-CG1	7.12	121.58	110.90
2	M	236	GLU	N-CA-CB	7.10	123.38	110.60
3	H	22	ILE	CB-CA-C	7.04	125.68	111.60
1	L	205	GLU	CA-CB-CG	6.99	128.77	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	207	ARG	NE-CZ-NH2	-6.96	116.82	120.30
2	M	148	TRP	CB-CA-C	6.94	124.28	110.40
1	L	82	LYS	N-CA-CB	6.88	122.98	110.60
2	M	243	THR	N-CA-CB	6.86	123.32	110.30
3	H	35	ASN	CB-CA-C	6.82	124.04	110.40
2	M	134	TYR	CB-CG-CD1	-6.73	116.96	121.00
2	M	155	TRP	CA-CB-CG	6.71	126.44	113.70
1	L	5	PHE	CA-CB-CG	6.69	129.96	113.90
3	H	20	PHE	N-CA-CB	6.67	122.60	110.60
2	M	132	ARG	NE-CZ-NH1	6.63	123.61	120.30
2	M	121	PHE	CB-CG-CD1	-6.62	116.16	120.80
2	M	247	ARG	CD-NE-CZ	6.57	132.80	123.60
1	L	155	ASP	CB-CA-C	6.56	123.53	110.40
3	H	204	HIS	N-CA-CB	6.54	122.37	110.60
1	L	5	PHE	N-CA-CB	6.48	122.26	110.60
3	H	171	ILE	N-CA-CB	6.46	125.65	110.80
2	M	142	MET	N-CA-CB	-6.40	99.08	110.60
1	L	254	ILE	CB-CA-C	6.39	124.37	111.60
1	L	180	PHE	CB-CG-CD1	-6.37	116.34	120.80
1	L	257	ASP	CB-CG-OD1	6.32	123.98	118.30
1	L	163	THR	N-CA-CB	6.32	122.30	110.30
1	L	78	ALA	CB-CA-C	6.28	119.52	110.10
2	M	95	GLU	CA-CB-CG	6.27	127.19	113.40
2	M	277	THR	N-CA-CB	6.25	122.18	110.30
1	L	213	ASP	CB-CG-OD1	6.25	123.92	118.30
1	L	142	TRP	CA-CB-CG	6.24	125.55	113.70
2	M	142	MET	CA-CB-CG	-6.18	102.80	113.30
2	M	218	MET	CG-SD-CE	6.18	110.09	100.20
3	H	33	THR	N-CA-CB	6.17	122.03	110.30
3	H	177	ARG	NE-CZ-NH2	6.16	123.38	120.30
2	M	88	ASP	CB-CA-C	6.15	122.71	110.40
1	L	220	VAL	CB-CA-C	6.08	122.96	111.40
1	L	222	TYR	CB-CG-CD2	-6.07	117.36	121.00
3	H	182	GLU	CG-CD-OE1	6.07	130.44	118.30
2	M	32	VAL	CB-CA-C	6.06	122.92	111.40
2	M	76	TYR	CB-CG-CD1	6.05	124.63	121.00
1	L	246	LEU	CB-CA-C	5.99	121.58	110.20
2	M	76	TYR	CB-CG-CD2	-5.97	117.42	121.00
3	H	204	HIS	N-CA-C	5.97	127.12	111.00
2	M	21	THR	OG1-CB-CG2	5.97	123.73	110.00
3	H	195	MET	CB-CA-C	5.92	122.24	110.40
3	H	212	LEU	CB-CA-C	5.86	121.32	110.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	142	TRP	N-CA-CB	5.84	121.12	110.60
2	M	236	GLU	OE1-CD-OE2	-5.83	116.30	123.30
3	H	168	TRP	CA-CB-CG	5.83	124.78	113.70
2	M	233	ARG	NE-CZ-NH1	-5.82	117.39	120.30
2	M	121	PHE	CB-CG-CD2	5.81	124.86	120.80
1	L	259	TRP	CA-CB-CG	5.77	124.66	113.70
1	L	36	VAL	CB-CA-C	5.73	122.29	111.40
1	L	116	HIS	N-CA-C	5.71	126.42	111.00
2	M	95	GLU	N-CA-CB	5.71	120.87	110.60
2	M	127	TRP	CB-CA-C	5.69	121.78	110.40
2	M	145	HIS	CB-CA-C	-5.68	99.03	110.40
3	H	43	GLU	N-CA-CB	5.67	120.80	110.60
3	H	177	ARG	N-CA-CB	5.64	120.76	110.60
1	L	130	THR	C-N-CA	5.63	135.76	121.70
3	H	66	LEU	CB-CA-C	5.62	120.89	110.20
1	L	213	ASP	OD1-CG-OD2	-5.60	112.66	123.30
1	L	218	ASP	CB-CG-OD1	-5.59	113.26	118.30
3	H	81	GLU	CA-CB-CG	5.54	125.59	113.40
1	L	105	VAL	CB-CA-C	5.54	121.92	111.40
3	H	248	ARG	NH1-CZ-NH2	-5.52	113.32	119.40
3	H	29	TYR	CB-CG-CD1	-5.52	117.69	121.00
3	H	115	VAL	CB-CA-C	5.51	121.87	111.40
1	L	103	ARG	NE-CZ-NH1	5.51	123.05	120.30
1	L	213	ASP	CA-CB-CG	5.49	125.47	113.40
2	M	70	ILE	CA-CB-CG2	5.49	121.87	110.90
2	M	262	MET	N-CA-CB	5.48	120.46	110.60
1	L	262	TRP	CB-CG-CD2	-5.40	119.58	126.60
2	M	274	VAL	CB-CA-C	5.39	121.63	111.40
2	M	100	GLU	CB-CG-CD	5.38	128.73	114.20
3	H	141	HIS	N-CA-CB	5.38	120.28	110.60
1	L	210	ASP	CB-CA-C	5.36	121.12	110.40
3	H	228	LEU	CB-CA-C	5.34	120.34	110.20
1	L	134	PHE	CB-CG-CD1	-5.34	117.06	120.80
3	H	75	VAL	CB-CA-C	5.31	121.49	111.40
1	L	210	ASP	CB-CG-OD2	5.29	123.06	118.30
3	H	206	ASN	CB-CA-C	5.26	120.92	110.40
2	M	226	VAL	CB-CA-C	5.25	121.39	111.40
3	H	210	SER	O-C-N	5.25	131.10	122.70
2	M	151	LEU	CB-CA-C	5.24	120.16	110.20
1	L	148	TYR	N-CA-CB	5.22	119.99	110.60
1	L	152	THR	CA-CB-CG2	5.21	119.70	112.40
3	H	18	TYR	CB-CG-CD1	-5.20	117.88	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	182	GLU	CA-CB-CG	5.20	124.84	113.40
3	H	194	GLN	N-CA-CB	5.18	119.92	110.60
3	H	166	ASP	C-N-CA	5.17	134.62	121.70
1	L	48	LEU	CA-CB-CG	5.16	127.17	115.30
3	H	166	ASP	CB-CG-OD2	5.16	122.94	118.30
2	M	89	LEU	CB-CA-C	5.15	119.99	110.20
2	M	272	MET	N-CA-CB	5.14	119.85	110.60
3	H	84	PRO	CA-N-CD	-5.14	104.30	111.50
2	M	295	TYR	CB-CG-CD1	-5.13	117.92	121.00
3	H	37	ARG	CD-NE-CZ	5.12	130.78	123.60
2	M	232	GLU	CG-CD-OE1	-5.12	108.06	118.30
3	H	243	TYR	CA-CB-CG	5.09	123.08	113.40
1	L	152	THR	N-CA-CB	5.08	119.95	110.30
1	L	221	GLY	C-N-CA	5.06	134.36	121.70
1	L	178	SER	N-CA-CB	5.05	118.08	110.50
3	H	208	LEU	N-CA-CB	-5.05	100.30	110.40
3	H	89	ARG	NE-CZ-NH2	5.04	122.82	120.30
2	M	193	HIS	CB-CA-C	5.04	120.47	110.40
2	M	180	PHE	CB-CG-CD1	-5.03	117.28	120.80
3	H	22	ILE	CA-CB-CG2	5.01	120.92	110.90

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	H	141	HIS	CA
3	H	204	HIS	CA

All (104) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	H	112	ALA	Mainchain
3	H	117	ARG	Sidechain
3	H	119	ASP	Mainchain
3	H	120	LEU	Mainchain
3	H	121	PRO	Mainchain
3	H	125	GLY	Mainchain
3	H	128	HIS	Mainchain
3	H	137	ALA	Mainchain
3	H	139	GLY	Mainchain
3	H	140	PHE	Mainchain
3	H	142	VAL	Mainchain
3	H	145	GLY	Mainchain

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Mol	Chain	Res	Type	Group
3	H	150	GLY	Mainchain
3	H	156	CYS	Mainchain
3	H	157	ASP	Mainchain
3	H	159	GLU	Mainchain
3	H	164	VAL	Mainchain
3	H	17	ILE	Mainchain
3	H	174	GLN	Mainchain
3	H	18	TYR	Sidechain
3	H	189	ARG	Sidechain
3	H	199	GLN	Mainchain
3	H	201	ASN	Mainchain
3	H	206	ASN	Mainchain
3	H	209	SER	Mainchain
3	H	218	THR	Mainchain
3	H	22	ILE	Mainchain
3	H	227	LEU	Mainchain
3	H	237	VAL	Mainchain
3	H	241	LEU	Mainchain
3	H	243	TYR	Mainchain
3	H	33	THR	Mainchain
3	H	40	TYR	Sidechain,Mainchain
3	H	41	PRO	Mainchain
3	H	42	LEU	Mainchain
3	H	48	THR	Mainchain
3	H	50	ALA	Mainchain
3	H	96	PHE	Sidechain
1	L	103	ARG	Mainchain
1	L	122	ALA	Mainchain
1	L	142	TRP	Mainchain
1	L	148	TYR	Sidechain
1	L	152	THR	Mainchain
1	L	154	LEU	Mainchain
1	L	155	ASP	Mainchain
1	L	160	THR	Mainchain
1	L	175	ILE	Mainchain
1	L	180	PHE	Sidechain
1	L	181	PHE	Sidechain,Mainchain
1	L	183	ASN	Sidechain
1	L	196	SER	Mainchain
1	L	204	LYS	Mainchain
1	L	211	HIS	Sidechain
1	L	218	ASP	Mainchain

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Mol	Chain	Res	Type	Group
1	L	222	TYR	Sidechain,Mainchain
1	L	248	MET	Mainchain
1	L	249	ILE	Mainchain
1	L	255	TRP	Mainchain
1	L	257	ASP	Mainchain
1	L	36	VAL	Mainchain
1	L	44	LEU	Mainchain
1	L	46	ILE	Mainchain
1	L	6	GLU	Mainchain
1	L	61	PRO	Mainchain
1	L	64	ILE	Mainchain
1	L	65	SER	Mainchain
1	L	7	ARG	Sidechain
1	L	75	LEU	Mainchain
1	L	84	GLY	Mainchain
1	L	85	LEU	Mainchain
1	L	88	ILE	Mainchain
1	L	97	PHE	Sidechain
2	M	100	GLU	Mainchain
2	M	13	ARG	Sidechain
2	M	131	GLY	Mainchain
2	M	134	TYR	Sidechain
2	M	136	ARG	Sidechain
2	M	142	MET	Mainchain
2	M	145	HIS	Mainchain
2	M	16	ALA	Mainchain
2	M	193	HIS	Sidechain,Mainchain
2	M	194	GLY	Mainchain
2	M	20	MET	Mainchain
2	M	208	PHE	Sidechain
2	M	21	THR	Mainchain
2	M	210	TYR	Sidechain
2	M	215	LEU	Mainchain
2	M	224	LEU	Mainchain
2	M	228	ARG	Mainchain
2	M	234	GLU	Mainchain
2	M	253	ARG	Mainchain
2	M	254	TRP	Mainchain
2	M	275	LEU	Mainchain
2	M	277	THR	Mainchain
2	M	291	VAL	Mainchain
2	M	30	SER	Mainchain

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Mol	Chain	Res	Type	Group
2	M	50	ILE	Mainchain
2	M	73	TRP	Mainchain
2	M	81	ASN	Mainchain
2	M	87	ARG	Mainchain

5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L	2120	0	2077	1093	0
2	M	2361	0	2279	1145	0
3	H	1806	0	1814	771	0
4	M	20	0	28	7	0
5	M	1	0	0	0	0
6	L	117	0	115	116	0
6	M	117	0	113	93	0
7	L	65	0	76	44	0
7	M	65	0	76	47	0
8	L	41	0	52	31	0
8	M	51	0	68	43	0
All	All	6764	0	6698	2900	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 216.

All (2900) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:73:TRP:CD1	2:M:114:LEU:HG	1.20	1.64
7:M:312:BPH:C11	7:M:312:BPH:C10	1.76	1.61
7:M:312:BPH:C6	7:M:312:BPH:C7	1.78	1.60
1:L:175:ILE:HG21	1:L:243:PHE:CD2	1.24	1.60
2:M:197:PHE:CZ	6:M:310:BCL:HBB2	1.33	1.57
1:L:208:THR:HG23	1:L:211:HIS:CD2	1.41	1.53
2:M:218:MET:HE2	2:M:252:TRP:CZ2	1.46	1.50
2:M:243:THR:CG2	2:M:247:ARG:HE	1.21	1.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:175:ILE:HD13	1:L:243:PHE:CE2	1.45	1.47
2:M:35:PHE:HD2	2:M:47:LEU:CD1	1.24	1.46
1:L:269:LEU:HD22	1:L:270:PRO:CD	1.47	1.44
3:H:132:LYS:NZ	3:H:223:THR:HG23	1.32	1.43
1:L:97:PHE:CE1	6:L:283:BCL:H142	1.51	1.43
7:L:284:BPH:C17	7:L:284:BPH:H143	1.46	1.43
2:M:197:PHE:HZ	6:M:310:BCL:CBB	1.32	1.43
1:L:175:ILE:HG21	1:L:243:PHE:CE2	1.54	1.42
1:L:33:PHE:O	1:L:33:PHE:CD1	1.69	1.41
3:H:27:LEU:HD12	3:H:28:ILE:N	1.26	1.41
3:H:56:PHE:HD1	3:H:57:PRO:N	1.10	1.40
1:L:185:LEU:HD23	1:L:186:ALA:N	1.31	1.40
1:L:97:PHE:HE1	6:L:283:BCL:C14	1.35	1.39
3:H:36:MET:H	3:H:36:MET:CE	1.35	1.38
2:M:249:ALA:HB2	8:M:313:U10:C4M	1.53	1.38
2:M:218:MET:CE	2:M:252:TRP:CZ2	2.04	1.37
8:L:285:U10:C11	8:L:285:U10:H152	1.54	1.37
1:L:175:ILE:CG2	1:L:243:PHE:HD2	1.36	1.36
7:L:284:BPH:C14	7:L:284:BPH:H171	1.50	1.36
8:L:285:U10:C15	8:L:285:U10:C11	2.02	1.36
3:H:191:LEU:CD1	3:H:205:VAL:HG11	1.55	1.36
2:M:187:ASN:HD22	2:M:188:ASN:N	1.20	1.36
2:M:243:THR:HG21	2:M:247:ARG:NE	1.37	1.35
8:L:285:U10:H111	8:L:285:U10:C15	1.42	1.34
1:L:51:TRP:HD1	1:L:51:TRP:O	1.06	1.33
3:H:36:MET:N	3:H:36:MET:HE2	1.37	1.33
2:M:218:MET:HE3	2:M:252:TRP:CH2	1.60	1.33
1:L:175:ILE:CG2	1:L:243:PHE:CD2	2.07	1.33
2:M:73:TRP:NE1	2:M:114:LEU:HG	1.40	1.33
3:H:151:LEU:O	3:H:164:VAL:HG23	1.25	1.33
3:H:56:PHE:CD1	3:H:57:PRO:HD2	1.62	1.32
3:H:56:PHE:CD1	3:H:57:PRO:CD	2.12	1.32
2:M:73:TRP:CD1	2:M:114:LEU:CG	2.13	1.31
1:L:185:LEU:CD2	1:L:186:ALA:H	1.43	1.31
1:L:248:MET:HE1	6:L:283:BCL:C3D	1.61	1.30
3:H:160:ILE:CD1	3:H:160:ILE:H	1.43	1.30
2:M:35:PHE:CD2	2:M:47:LEU:CD1	2.15	1.29
2:M:64:LEU:CD1	7:M:312:BPH:H7C1	1.63	1.28
3:H:213:PHE:O	3:H:216:ILE:HD12	1.21	1.28
1:L:208:THR:CG2	1:L:211:HIS:HD2	1.46	1.27
3:H:40:TYR:O	3:H:42:LEU:HD13	1.11	1.27
1:L:183:ASN:O	1:L:183:ASN:ND2	1.67	1.26

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:234:LEU:HD23	1:L:234:LEU:O	1.20	1.26
1:L:179:PHE:CB	1:L:240:ALA:HB2	1.63	1.26
1:L:232:LEU:HG	2:M:42:PHE:CE2	1.70	1.25
3:H:56:PHE:CD1	3:H:57:PRO:N	2.04	1.25
1:L:208:THR:CG2	1:L:211:HIS:CD2	2.20	1.24
1:L:7:ARG:O	3:H:87:LEU:HD23	1.36	1.24
2:M:51:TYR:O	2:M:51:TYR:HD1	1.22	1.23
1:L:53:ALA:HB2	1:L:64:ILE:CG1	1.68	1.23
1:L:269:LEU:CD2	1:L:270:PRO:HD3	1.69	1.23
2:M:70:ILE:HD12	4:M:308:BOG:O6	1.38	1.23
2:M:260:ALA:CA	3:H:36:MET:HG3	1.67	1.22
1:L:175:ILE:CD1	1:L:243:PHE:HE2	1.51	1.22
1:L:206:MET:N	3:H:65:ILE:HG22	1.53	1.22
1:L:185:LEU:HA	1:L:188:ALA:CB	1.70	1.21
2:M:260:ALA:HA	3:H:36:MET:CG	1.70	1.21
2:M:87:ARG:HD2	2:M:88:ASP:CG	1.61	1.21
2:M:109:LEU:HD22	2:M:110:LYS:N	1.55	1.20
2:M:20:MET:HG3	2:M:21:THR:N	1.39	1.20
1:L:73:TYR:CD2	1:L:82:LYS:HE3	1.75	1.20
3:H:20:PHE:CE1	3:H:24:LEU:HD12	1.75	1.20
2:M:187:ASN:ND2	2:M:188:ASN:N	1.85	1.20
1:L:175:ILE:CD1	1:L:243:PHE:CE2	2.24	1.20
2:M:185:TRP:O	2:M:185:TRP:CD2	1.95	1.20
3:H:40:TYR:O	3:H:42:LEU:CD1	1.88	1.20
3:H:27:LEU:HD13	3:H:32:GLN:OE1	1.41	1.19
3:H:27:LEU:HD22	3:H:32:GLN:HE22	1.03	1.19
2:M:249:ALA:CB	8:M:313:U10:C4M	2.19	1.19
2:M:87:ARG:CG	2:M:88:ASP:N	2.03	1.19
3:H:111:PRO:HG2	3:H:242:MET:CB	1.73	1.18
2:M:102:GLY:O	2:M:104:SER:N	1.75	1.18
1:L:216:PHE:CD2	8:L:285:U10:H71	1.77	1.18
3:H:27:LEU:CD2	3:H:32:GLN:HE22	1.55	1.17
1:L:51:TRP:CD1	1:L:51:TRP:O	1.96	1.17
1:L:177:ILE:HG22	1:L:181:PHE:CD2	1.79	1.17
2:M:88:ASP:HB2	2:M:92:PHE:CZ	1.79	1.17
2:M:87:ARG:HG3	2:M:88:ASP:N	1.22	1.17
3:H:27:LEU:HD13	3:H:32:GLN:CD	1.65	1.16
3:H:94:GLU:O	3:H:96:PHE:N	1.78	1.16
3:H:194:GLN:H	3:H:194:GLN:CD	1.43	1.16
1:L:185:LEU:O	1:L:188:ALA:N	1.77	1.16
1:L:149:GLY:O	1:L:151:TRP:N	1.76	1.16
2:M:46:GLN:NE2	2:M:49:PRO:HD2	1.61	1.16

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:179:LEU:O	3:H:179:LEU:HD23	1.44	1.16
3:H:20:PHE:CZ	3:H:24:LEU:HD12	1.80	1.16
2:M:242:GLY:HA2	3:H:115:VAL:HG11	1.28	1.15
1:L:222:TYR:CD1	1:L:223:SER:N	2.14	1.15
2:M:204:LEU:HA	2:M:207:ALA:CB	1.77	1.15
1:L:208:THR:O	1:L:211:HIS:HB2	1.43	1.15
1:L:269:LEU:HB3	1:L:270:PRO:HD2	1.25	1.15
2:M:289:THR:O	2:M:291:VAL:N	1.77	1.15
8:M:313:U10:C21	8:M:313:U10:H252	1.75	1.15
8:M:313:U10:H252	8:M:313:U10:H211	1.20	1.15
1:L:205:GLU:HA	3:H:65:ILE:CG2	1.76	1.15
2:M:21:THR:HB	2:M:139:ALA:HB1	1.20	1.15
1:L:269:LEU:CB	1:L:270:PRO:HD2	1.76	1.15
1:L:53:ALA:HB2	1:L:64:ILE:CD1	1.76	1.14
6:L:283:BCL:H143	7:L:284:BPH:HBA2	1.24	1.14
2:M:127:TRP:O	2:M:130:TRP:HB3	1.46	1.14
3:H:56:PHE:HD1	3:H:57:PRO:CD	1.56	1.14
2:M:187:ASN:ND2	2:M:188:ASN:H	1.41	1.14
2:M:88:ASP:C	2:M:92:PHE:CE2	2.21	1.14
1:L:133:LEU:O	1:L:137:VAL:HG23	1.47	1.14
3:H:124:ASP:OD1	3:H:125:GLY:N	1.78	1.14
3:H:151:LEU:O	3:H:164:VAL:CG2	1.96	1.14
1:L:224:ILE:O	1:L:225:GLY:O	1.63	1.14
2:M:131:GLY:O	2:M:134:TYR:N	1.81	1.14
2:M:204:LEU:HA	2:M:207:ALA:HB2	1.22	1.13
3:H:36:MET:N	3:H:36:MET:CE	2.01	1.13
2:M:196:LEU:HD13	2:M:294:TRP:CD1	1.84	1.13
3:H:56:PHE:HD1	3:H:56:PHE:C	1.51	1.13
1:L:206:MET:H	3:H:65:ILE:CG2	1.61	1.13
1:L:8:LYS:HA	3:H:87:LEU:CD2	1.79	1.13
6:L:283:BCL:H143	7:L:284:BPH:CBA	1.75	1.13
2:M:96:PRO:HB2	2:M:97:PRO:HD2	1.14	1.13
1:L:21:LEU:HD12	1:L:22:PHE:CE1	1.84	1.13
2:M:249:ALA:CB	8:M:313:U10:H4M3	1.79	1.13
1:L:10:ARG:NH2	3:H:95:GLY:HA2	1.63	1.12
8:M:313:U10:C21	8:M:313:U10:C25	2.25	1.12
3:H:27:LEU:CD1	3:H:28:ILE:N	2.11	1.12
2:M:17:ASP:C	2:M:18:LEU:HD12	1.68	1.12
1:L:227:LEU:HD23	1:L:231:ARG:HD2	1.21	1.12
2:M:261:THR:O	2:M:263:GLU:N	1.81	1.12
3:H:183:LEU:HD23	3:H:183:LEU:H	1.07	1.12
3:H:12:LEU:HD23	3:H:12:LEU:C	1.68	1.12

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:268:LYS:HG2	1:L:269:LEU:N	1.42	1.12
2:M:101:TYR:HD1	2:M:101:TYR:O	1.33	1.11
1:L:248:MET:HE1	6:L:283:BCL:C2D	1.79	1.11
3:H:191:LEU:HD13	3:H:205:VAL:HG11	1.16	1.11
3:H:148:PRO:O	3:H:151:LEU:HB2	1.50	1.11
2:M:186:THR:HG23	6:M:310:BCL:HMD2	1.13	1.10
1:L:234:LEU:CD2	1:L:234:LEU:O	1.98	1.10
7:M:312:BPH:HBC3	7:M:312:BPH:HHD	1.32	1.10
2:M:149:ALA:O	7:M:312:BPH:HMD3	1.48	1.10
1:L:94:THR:CG2	1:L:129:LEU:HD11	1.80	1.10
3:H:24:LEU:HD23	3:H:28:ILE:CD1	1.82	1.10
3:H:43:GLU:OE1	3:H:44:ASN:ND2	1.84	1.10
3:H:15:LEU:HA	3:H:18:TYR:CD2	1.87	1.10
2:M:114:LEU:O	2:M:117:ILE:HB	1.48	1.10
2:M:94:LEU:HD11	2:M:114:LEU:HD23	1.21	1.10
1:L:215:PHE:HE1	1:L:219:LEU:HD22	1.14	1.10
2:M:35:PHE:HD2	2:M:47:LEU:HD13	1.01	1.10
2:M:57:VAL:CG2	2:M:58:LEU:H	1.63	1.09
1:L:195:LEU:HB3	2:M:145:HIS:CD2	1.87	1.09
6:L:283:BCL:CMC	6:M:310:BCL:CBC	2.30	1.09
1:L:135:ARG:HB3	1:L:136:PRO:HD3	1.29	1.09
1:L:135:ARG:HG3	1:L:139:MET:HE1	1.24	1.09
1:L:86:TRP:CE3	1:L:87:GLN:N	2.20	1.09
2:M:243:THR:HG22	2:M:247:ARG:HG2	1.25	1.09
2:M:135:LEU:HD12	2:M:135:LEU:H	1.13	1.08
1:L:267:VAL:HG13	2:M:87:ARG:HD3	1.34	1.08
2:M:235:LEU:HD12	2:M:235:LEU:H	1.13	1.08
3:H:111:PRO:HD2	3:H:243:TYR:CE1	1.87	1.08
2:M:51:TYR:O	2:M:51:TYR:CD1	2.05	1.08
3:H:132:LYS:NZ	3:H:223:THR:CG2	2.17	1.08
2:M:164:ARG:HB3	2:M:165:PRO:HD3	1.16	1.08
2:M:218:MET:CE	2:M:252:TRP:CH2	2.32	1.08
1:L:107:ILE:HD12	2:M:255:THR:OG1	1.53	1.08
1:L:186:ALA:O	2:M:216:PHE:HE2	1.35	1.08
1:L:216:PHE:HD2	8:L:285:U10:H71	0.95	1.08
2:M:109:LEU:HD23	2:M:114:LEU:HD11	1.34	1.07
2:M:90:PHE:HA	2:M:179:ILE:HD12	1.31	1.07
2:M:54:SER:O	2:M:57:VAL:HG13	1.51	1.07
2:M:24:VAL:O	2:M:26:LEU:N	1.88	1.07
1:L:179:PHE:HB2	1:L:240:ALA:CB	1.84	1.07
1:L:215:PHE:CE1	1:L:219:LEU:HD22	1.87	1.07
1:L:231:ARG:NH2	2:M:7:PHE:HA	1.67	1.07

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:37:THR:HG22	2:M:38:LEU:HD12	1.34	1.07
3:H:24:LEU:HD23	3:H:28:ILE:HD11	1.14	1.07
1:L:93:ALA:O	1:L:95:GLY:N	1.86	1.07
1:L:205:GLU:HA	3:H:65:ILE:HG21	1.29	1.07
1:L:182:THR:O	1:L:185:LEU:CD2	2.03	1.06
1:L:20:ASN:O	1:L:22:PHE:N	1.87	1.06
3:H:14:SER:O	3:H:18:TYR:HB3	1.51	1.06
2:M:299:GLN:HA	2:M:299:GLN:HE21	1.13	1.06
3:H:37:ARG:NH2	3:H:41:PRO:O	1.87	1.06
1:L:232:LEU:HG	2:M:42:PHE:CZ	1.90	1.06
1:L:242:PHE:HD1	1:L:243:PHE:N	1.51	1.06
1:L:178:SER:HB2	6:L:282:BCL:O1A	1.50	1.06
2:M:206:ILE:HD11	6:M:310:BCL:C1B	1.85	1.06
3:H:191:LEU:CD1	3:H:205:VAL:CG1	2.32	1.06
3:H:210:SER:O	3:H:212:LEU:N	1.88	1.06
2:M:46:GLN:HG2	2:M:47:LEU:H	1.21	1.06
1:L:219:LEU:HD21	2:M:133:THR:HG23	1.34	1.06
2:M:218:MET:HE2	2:M:252:TRP:CE2	1.90	1.05
3:H:160:ILE:N	3:H:160:ILE:HD12	1.69	1.05
3:H:191:LEU:HD13	3:H:205:VAL:CG1	1.84	1.05
1:L:21:LEU:HD12	1:L:22:PHE:HE1	1.13	1.05
3:H:161:ALA:HB2	3:H:210:SER:HB2	1.31	1.05
3:H:157:ASP:OD2	3:H:211:ASP:HB2	1.56	1.05
1:L:5:PHE:HZ	3:H:40:TYR:CE2	1.73	1.05
3:H:27:LEU:HD22	3:H:32:GLN:NE2	1.70	1.05
2:M:218:MET:CE	2:M:252:TRP:CE2	2.39	1.05
3:H:189:ARG:HB2	3:H:216:ILE:HG21	1.30	1.05
2:M:64:LEU:HD11	7:M:312:BPH:H7C1	1.38	1.05
2:M:185:TRP:CE3	2:M:185:TRP:O	2.09	1.04
6:L:283:BCL:CMC	6:M:310:BCL:HBC1	1.87	1.04
6:L:283:BCL:H151	7:L:284:BPH:H3A	1.35	1.04
3:H:215:GLY:HA3	3:H:236:TYR:CZ	1.92	1.04
1:L:49:ILE:HG22	1:L:50:ALA:H	1.20	1.04
1:L:94:THR:OG1	1:L:129:LEU:CD1	2.03	1.04
8:L:285:U10:H1M1	8:L:285:U10:C8	1.87	1.04
2:M:35:PHE:CD2	2:M:47:LEU:HD11	1.91	1.04
2:M:135:LEU:HB3	2:M:138:GLN:OE1	1.57	1.04
6:L:283:BCL:HBD	6:M:311:BCL:HBC1	1.36	1.04
1:L:8:LYS:CA	3:H:87:LEU:HD22	1.88	1.03
1:L:177:ILE:CG2	1:L:181:PHE:CE2	2.41	1.03
1:L:79:PRO:O	1:L:81:ALA:N	1.89	1.03
1:L:183:ASN:ND2	1:L:183:ASN:C	2.10	1.03

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:185:LEU:HA	1:L:188:ALA:HB2	1.38	1.03
3:H:210:SER:OG	3:H:211:ASP:OD1	1.76	1.03
1:L:187:LEU:HD22	2:M:216:PHE:CG	1.92	1.03
1:L:269:LEU:CD2	1:L:270:PRO:CD	2.28	1.03
2:M:39:LEU:N	2:M:39:LEU:HD13	1.71	1.03
3:H:151:LEU:HD22	3:H:203:VAL:CG2	1.89	1.03
3:H:170:ASP:OD2	3:H:177:ARG:NH2	1.92	1.03
1:L:193:LEU:HD23	8:L:285:U10:C3	1.89	1.03
1:L:73:TYR:HB2	1:L:82:LYS:NZ	1.72	1.02
2:M:228:ARG:HH11	2:M:228:ARG:HG2	0.88	1.02
1:L:86:TRP:HE3	1:L:87:GLN:N	1.55	1.02
2:M:35:PHE:CD2	2:M:47:LEU:HD13	1.84	1.02
1:L:241:VAL:O	1:L:244:SER:HB2	1.57	1.02
1:L:73:TYR:HB2	1:L:82:LYS:HZ1	1.20	1.02
2:M:114:LEU:CD1	2:M:114:LEU:H	1.73	1.02
2:M:238:ILE:HG23	2:M:238:ILE:O	1.55	1.02
3:H:17:ILE:CD1	3:H:17:ILE:O	2.07	1.02
1:L:242:PHE:CD1	1:L:243:PHE:N	2.26	1.02
1:L:73:TYR:CD2	1:L:82:LYS:CE	2.41	1.02
2:M:65:MET:HG2	2:M:66:TRP:N	1.74	1.02
2:M:243:THR:CG2	2:M:247:ARG:NE	2.06	1.02
1:L:135:ARG:HH12	1:L:252:GLY:HA3	0.90	1.02
8:M:313:U10:H212	8:M:313:U10:C25	1.89	1.02
3:H:151:LEU:HD22	3:H:203:VAL:HG23	1.41	1.02
3:H:238:ALA:O	3:H:240:GLY:N	1.93	1.02
2:M:299:GLN:NE2	2:M:299:GLN:HA	1.64	1.02
3:H:195:MET:C	3:H:196:VAL:HG13	1.78	1.02
1:L:53:ALA:HB2	1:L:64:ILE:HG12	1.40	1.02
1:L:60:ASN:O	1:L:62:GLN:N	1.92	1.02
3:H:116:ALA:HA	3:H:228:LEU:CD1	1.90	1.02
1:L:135:ARG:NH1	1:L:252:GLY:HA3	1.75	1.01
3:H:160:ILE:N	3:H:160:ILE:CD1	2.16	1.01
2:M:228:ARG:NH1	2:M:228:ARG:HG2	1.72	1.01
2:M:64:LEU:HD12	7:M:312:BPH:H7C1	1.37	1.01
1:L:71:LEU:O	1:L:73:TYR:N	1.94	1.01
2:M:214:LEU:O	2:M:217:ALA:HB3	1.57	1.01
2:M:204:LEU:CA	2:M:207:ALA:HB2	1.90	1.01
2:M:257:GLY:O	2:M:258:PHE:HB3	1.56	1.01
2:M:205:SER:OG	2:M:279:THR:HG22	1.61	1.01
6:L:283:BCL:HMC1	6:M:310:BCL:HBC1	1.42	1.01
1:L:65:SER:OG	1:L:67:TYR:HE1	1.44	1.01
2:M:196:LEU:CD1	2:M:294:TRP:CD1	2.42	1.01

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:267:VAL:CG1	2:M:87:ARG:HD3	1.89	1.01
1:L:8:LYS:HA	3:H:87:LEU:HD22	1.01	1.01
1:L:179:PHE:HB2	1:L:240:ALA:HB2	1.01	1.01
2:M:54:SER:O	2:M:57:VAL:CG1	2.08	1.01
3:H:156:CYS:SG	3:H:209:SER:HA	2.01	1.01
2:M:218:MET:HE3	2:M:252:TRP:CZ3	1.96	1.01
1:L:5:PHE:CZ	3:H:40:TYR:CE2	2.49	1.00
2:M:228:ARG:CG	2:M:228:ARG:HH11	1.70	1.00
3:H:134:MET:HE2	3:H:167:ILE:HB	1.39	1.00
3:H:36:MET:H	3:H:36:MET:HE3	1.24	1.00
2:M:87:ARG:HD2	2:M:88:ASP:OD1	1.59	1.00
3:H:160:ILE:H	3:H:160:ILE:HD13	1.23	1.00
1:L:151:TRP:HH2	2:M:198:TYR:HA	1.24	1.00
2:M:249:ALA:CB	8:M:313:U10:H4M1	1.85	1.00
1:L:11:VAL:HG21	3:H:110:GLY:HA2	1.04	1.00
1:L:49:ILE:CG2	1:L:50:ALA:H	1.74	1.00
2:M:99:PRO:HB2	2:M:111:GLU:CG	1.92	1.00
2:M:96:PRO:CB	2:M:97:PRO:HD2	1.91	1.00
2:M:46:GLN:NE2	2:M:49:PRO:CD	2.24	1.00
1:L:17:VAL:HG13	1:L:18:GLY:H	1.27	1.00
1:L:224:ILE:HD12	1:L:232:LEU:HD12	1.42	0.99
2:M:299:GLN:CA	2:M:299:GLN:HE21	1.69	0.99
2:M:16:ALA:HB1	2:M:32:VAL:HG21	1.43	0.99
1:L:65:SER:OG	1:L:67:TYR:CE1	2.15	0.99
2:M:208:PHE:O	2:M:211:GLY:N	1.94	0.99
2:M:110:LYS:HE2	2:M:114:LEU:HD21	1.44	0.99
2:M:20:MET:CG	2:M:21:THR:N	2.25	0.99
2:M:46:GLN:HE22	2:M:49:PRO:HD2	1.26	0.99
1:L:51:TRP:C	1:L:51:TRP:HD1	1.65	0.99
1:L:97:PHE:CZ	6:L:283:BCL:H122	1.98	0.99
1:L:153:HIS:HD2	1:L:154:LEU:HD12	1.24	0.99
2:M:243:THR:HG21	2:M:247:ARG:CZ	1.91	0.99
1:L:237:SER:O	1:L:239:SER:N	1.96	0.98
2:M:37:THR:HG22	2:M:38:LEU:CD1	1.90	0.98
1:L:11:VAL:HG12	3:H:87:LEU:HD11	1.45	0.98
1:L:53:ALA:HB2	1:L:64:ILE:HD13	1.43	0.98
1:L:204:LYS:HB3	1:L:207:ARG:HH12	1.25	0.98
2:M:100:GLU:HA	2:M:172:SER:OG	1.63	0.98
2:M:119:SER:HA	2:M:177:TYR:OH	1.63	0.98
2:M:35:PHE:CD1	2:M:38:LEU:HB2	1.98	0.98
2:M:57:VAL:HG22	2:M:58:LEU:H	1.27	0.98
3:H:183:LEU:HD11	3:H:189:ARG:HE	1.23	0.98

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:11:VAL:HG21	3:H:110:GLY:CA	1.92	0.98
2:M:186:THR:CG2	6:M:310:BCL:HMD2	1.93	0.98
3:H:189:ARG:HH11	3:H:189:ARG:HB3	1.24	0.97
3:H:42:LEU:HD23	3:H:77:GLY:H	1.25	0.97
1:L:22:PHE:HE2	1:L:36:VAL:HG11	1.26	0.97
1:L:227:LEU:CD2	1:L:231:ARG:HD2	1.94	0.97
2:M:226:VAL:HG12	2:M:231:GLY:HA3	1.44	0.97
1:L:102:LEU:H	1:L:102:LEU:HD23	1.29	0.97
1:L:219:LEU:HA	2:M:132:ARG:HH21	1.26	0.97
3:H:116:ALA:HA	3:H:228:LEU:HG	1.46	0.97
2:M:94:LEU:HD21	2:M:114:LEU:HB3	1.45	0.97
1:L:154:LEU:HD23	2:M:197:PHE:HB3	1.42	0.97
1:L:231:ARG:CZ	2:M:7:PHE:HA	1.94	0.97
1:L:135:ARG:CG	1:L:139:MET:HE1	1.94	0.97
1:L:183:ASN:HB2	1:L:236:LEU:HB2	1.44	0.97
1:L:34:PHE:O	1:L:38:THR:N	1.97	0.97
1:L:208:THR:CB	1:L:211:HIS:HD2	1.76	0.97
2:M:238:ILE:CG2	2:M:238:ILE:O	2.13	0.97
1:L:180:PHE:HE1	2:M:213:ALA:HB2	1.29	0.96
2:M:164:ARG:NH2	2:M:168:MET:HE1	1.80	0.96
2:M:241:ARG:HH11	2:M:241:ARG:HB3	1.29	0.96
2:M:152:SER:C	2:M:277:THR:HG21	1.85	0.96
2:M:27:ALA:O	2:M:28:ASN:OD1	1.83	0.96
2:M:46:GLN:CG	2:M:47:LEU:H	1.69	0.96
2:M:203:GLY:O	2:M:207:ALA:N	1.97	0.96
2:M:237:GLN:OE1	2:M:244:ALA:HB3	1.65	0.96
1:L:268:LYS:HG2	1:L:269:LEU:H	0.88	0.96
1:L:177:ILE:HG22	1:L:181:PHE:CE2	2.00	0.96
2:M:21:THR:OG1	2:M:23:ASP:O	1.83	0.96
3:H:210:SER:OG	3:H:211:ASP:N	1.93	0.96
1:L:156:TRP:C	1:L:156:TRP:CE3	2.39	0.96
2:M:108:PRO:HG2	2:M:111:GLU:HB3	1.48	0.96
2:M:209:LEU:O	2:M:209:LEU:HD13	1.65	0.96
6:L:283:BCL:C4	7:L:284:BPH:CAB	2.43	0.96
1:L:215:PHE:O	1:L:218:ASP:HB2	1.63	0.96
2:M:204:LEU:O	2:M:207:ALA:N	1.98	0.96
1:L:135:ARG:HH12	1:L:252:GLY:CA	1.79	0.95
1:L:49:ILE:CG2	1:L:50:ALA:N	2.26	0.95
2:M:59:SER:OG	2:M:129:TRP:HB2	1.66	0.95
1:L:128:TYR:O	1:L:130:THR:N	1.99	0.95
1:L:185:LEU:HA	1:L:188:ALA:HB3	1.46	0.95
3:H:111:PRO:HG3	3:H:242:MET:HG3	1.44	0.95

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:96:PRO:HB2	2:M:97:PRO:CD	1.96	0.95
3:H:151:LEU:HB3	3:H:203:VAL:HG21	1.45	0.95
2:M:109:LEU:C	2:M:109:LEU:HD22	1.85	0.95
1:L:48:LEU:HD11	1:L:89:ILE:HG13	1.48	0.95
3:H:189:ARG:HD3	3:H:216:ILE:HB	1.48	0.95
2:M:253:ARG:HG2	2:M:259:ASN:OD1	1.67	0.95
2:M:15:PRO:HD2	3:H:140:PHE:CE1	2.00	0.95
2:M:122:MET:HG2	2:M:122:MET:O	1.65	0.95
2:M:268:TRP:CD1	8:M:313:U10:H111	2.02	0.95
2:M:197:PHE:CZ	6:M:310:BCL:CBB	2.19	0.94
2:M:249:ALA:HB2	8:M:313:U10:H4M1	0.98	0.94
2:M:73:TRP:NE1	2:M:114:LEU:CG	2.23	0.94
3:H:17:ILE:HD12	3:H:17:ILE:O	1.65	0.94
3:H:183:LEU:CD2	3:H:183:LEU:H	1.79	0.94
1:L:232:LEU:HG	2:M:42:PHE:HE2	1.31	0.94
8:L:285:U10:H261	8:L:285:U10:H303	1.48	0.94
1:L:24:PHE:CE2	1:L:31:VAL:HG21	2.02	0.94
1:L:186:ALA:O	2:M:216:PHE:CE2	2.20	0.94
3:H:195:MET:O	3:H:196:VAL:HG22	1.67	0.94
1:L:232:LEU:HA	2:M:42:PHE:HZ	1.32	0.94
2:M:164:ARG:NH2	2:M:168:MET:CE	2.30	0.94
1:L:241:VAL:HG12	1:L:242:PHE:N	1.81	0.94
3:H:160:ILE:HD12	3:H:160:ILE:H	1.26	0.94
1:L:135:ARG:HH11	1:L:139:MET:HE1	1.31	0.94
2:M:209:LEU:N	2:M:276:VAL:HG22	1.82	0.94
3:H:24:LEU:CD2	3:H:28:ILE:HD11	1.96	0.94
2:M:135:LEU:HD12	2:M:135:LEU:N	1.81	0.93
1:L:133:LEU:HD12	1:L:133:LEU:C	1.88	0.93
2:M:101:TYR:CD1	2:M:101:TYR:O	2.20	0.93
3:H:19:SER:O	3:H:22:ILE:N	2.02	0.93
2:M:67:PHE:CD1	2:M:67:PHE:C	2.39	0.93
1:L:156:TRP:CE3	1:L:156:TRP:O	2.20	0.93
1:L:168:HIS:O	1:L:169:TYR:HD1	1.52	0.93
1:L:97:PHE:CE1	6:L:283:BCL:C14	2.25	0.93
2:M:227:SER:HB3	3:H:194:GLN:HG2	1.50	0.93
2:M:16:ALA:CB	2:M:32:VAL:HG21	1.99	0.93
3:H:133:PRO:HD2	3:H:136:ALA:HB3	1.49	0.93
6:L:283:BCL:CMC	6:M:310:BCL:HBC2	1.98	0.93
2:M:46:GLN:NE2	2:M:48:GLY:O	2.02	0.93
1:L:97:PHE:HE1	6:L:283:BCL:H142	0.83	0.93
2:M:138:GLN:O	2:M:141:GLY:N	2.00	0.93
2:M:164:ARG:O	2:M:167:LEU:N	2.02	0.93

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:268:LYS:CG	1:L:269:LEU:H	1.81	0.93
1:L:60:ASN:HB3	1:L:63:LEU:HD12	1.51	0.93
3:H:247:LYS:C	3:H:248:ARG:HG3	1.89	0.93
1:L:6:GLU:OE2	1:L:10:ARG:HD3	1.69	0.93
2:M:290:VAL:O	2:M:291:VAL:HG23	1.69	0.93
1:L:237:SER:OG	1:L:238:LEU:N	1.99	0.92
1:L:93:ALA:HB1	1:L:97:PHE:CE2	2.03	0.92
3:H:179:LEU:O	3:H:179:LEU:CD2	2.17	0.92
3:H:210:SER:C	3:H:212:LEU:H	1.71	0.92
1:L:154:LEU:H	1:L:154:LEU:HD12	1.30	0.92
2:M:73:TRP:CG	2:M:114:LEU:HG	2.03	0.92
2:M:264:GLY:HA2	2:M:267:ARG:HB2	1.51	0.92
1:L:12:PRO:HD2	3:H:98:HIS:O	1.70	0.92
1:L:153:HIS:CD2	1:L:154:LEU:HD12	2.05	0.92
2:M:170:SER:OG	2:M:172:SER:CB	2.17	0.92
3:H:154:ARG:NE	3:H:160:ILE:HG13	1.84	0.92
1:L:175:ILE:HG22	1:L:243:PHE:HD2	1.33	0.92
2:M:26:LEU:HD23	2:M:27:ALA:H	1.34	0.92
2:M:170:SER:OG	2:M:172:SER:HB2	1.69	0.92
2:M:67:PHE:HD1	2:M:67:PHE:C	1.70	0.92
3:H:190:LEU:H	3:H:190:LEU:HD23	1.30	0.92
2:M:164:ARG:CB	2:M:165:PRO:HD3	1.99	0.92
3:H:148:PRO:O	3:H:164:VAL:HG21	1.67	0.92
1:L:146:PHE:HB2	1:L:147:PRO:HD2	1.49	0.92
2:M:164:ARG:HB3	2:M:165:PRO:CD	2.00	0.92
2:M:17:ASP:CA	2:M:18:LEU:HD12	2.00	0.92
3:H:194:GLN:N	3:H:194:GLN:CD	2.19	0.92
1:L:43:ALA:O	1:L:45:GLY:N	2.01	0.92
2:M:90:PHE:CD2	2:M:180:PHE:CE1	2.57	0.92
3:H:183:LEU:CD1	3:H:189:ARG:HE	1.82	0.91
3:H:213:PHE:O	3:H:216:ILE:CD1	2.14	0.91
3:H:228:LEU:CD2	3:H:232:LYS:HD2	2.00	0.91
1:L:214:THR:HG22	2:M:140:LEU:HD21	1.52	0.91
1:L:151:TRP:CH2	2:M:198:TYR:HA	2.05	0.91
3:H:124:ASP:C	3:H:124:ASP:OD1	2.09	0.91
3:H:61:PRO:HA	3:H:76:PRO:HG2	1.52	0.91
1:L:113:ILE:HD11	2:M:226:VAL:HG22	1.49	0.91
1:L:39:PHE:O	1:L:41:PHE:N	2.02	0.91
1:L:86:TRP:HE3	1:L:87:GLN:H	1.08	0.91
3:H:183:LEU:N	3:H:183:LEU:HD23	1.84	0.91
3:H:111:PRO:HG2	3:H:242:MET:HB3	1.51	0.91
3:H:20:PHE:O	3:H:22:ILE:N	2.03	0.91

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:161:ALA:HB2	3:H:210:SER:CB	1.99	0.91
3:H:94:GLU:C	3:H:96:PHE:H	1.68	0.91
1:L:133:LEU:CD1	1:L:137:VAL:HG21	2.00	0.91
2:M:87:ARG:CD	2:M:88:ASP:CG	2.38	0.91
1:L:167:PHE:HD2	6:L:283:BCL:CHD	1.82	0.91
1:L:6:GLU:O	1:L:9:TYR:N	2.04	0.91
2:M:204:LEU:CA	2:M:207:ALA:CB	2.47	0.91
3:H:211:ASP:O	3:H:212:LEU:HD12	1.71	0.91
3:H:27:LEU:CD1	3:H:32:GLN:OE1	2.19	0.91
1:L:97:PHE:CE1	6:L:283:BCL:H111	2.06	0.91
2:M:159:VAL:O	2:M:161:GLY:N	2.02	0.91
3:H:27:LEU:CD1	3:H:28:ILE:H	1.73	0.91
1:L:173:HIS:CE1	1:L:177:ILE:HD11	2.06	0.91
1:L:49:ILE:O	1:L:52:SER:N	2.03	0.91
2:M:94:LEU:CD1	2:M:114:LEU:HD23	2.00	0.91
2:M:284:ILE:HD12	6:M:310:BCL:O2D	1.72	0.90
3:H:110:GLY:O	3:H:113:SER:OG	1.86	0.90
3:H:155:GLY:O	3:H:204:HIS:HD2	1.55	0.90
1:L:135:ARG:HG3	1:L:139:MET:CE	2.02	0.90
1:L:269:LEU:CG	1:L:270:PRO:HD2	2.00	0.90
1:L:94:THR:OG1	1:L:129:LEU:HD11	1.72	0.90
1:L:171:PRO:O	1:L:173:HIS:N	2.04	0.90
1:L:156:TRP:HE3	1:L:157:VAL:N	1.70	0.90
6:L:283:BCL:HMC2	6:M:310:BCL:CBC	2.02	0.90
2:M:243:THR:HG22	2:M:247:ARG:CG	2.01	0.90
2:M:249:ALA:HA	8:M:313:U10:H4M3	1.53	0.90
2:M:87:ARG:CG	2:M:88:ASP:H	1.84	0.90
1:L:33:PHE:HD1	1:L:33:PHE:O	1.44	0.90
1:L:232:LEU:O	1:L:235:LEU:HB2	1.70	0.90
1:L:187:LEU:HD22	2:M:216:PHE:CD2	2.07	0.90
6:M:311:BCL:CBB	6:M:311:BCL:HMB1	2.02	0.90
3:H:173:GLU:HB3	3:H:175:MET:HG3	1.52	0.90
3:H:20:PHE:CE1	3:H:24:LEU:CD1	2.55	0.90
2:M:105:PHE:CD1	2:M:106:ALA:N	2.39	0.90
3:H:116:ALA:HA	3:H:228:LEU:CG	2.02	0.90
3:H:39:GLY:HA2	3:H:42:LEU:HD21	1.51	0.90
1:L:147:PRO:HG2	1:L:152:THR:HG22	1.52	0.90
1:L:152:THR:O	1:L:155:ASP:N	2.05	0.90
1:L:156:TRP:CE3	1:L:157:VAL:HA	2.07	0.90
2:M:243:THR:HG22	2:M:247:ARG:HE	1.34	0.90
2:M:35:PHE:CG	2:M:39:LEU:CD2	2.55	0.90
2:M:57:VAL:CG2	2:M:58:LEU:N	2.27	0.90

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:13:ARG:HA	3:H:174:GLN:HG2	1.52	0.89
2:M:99:PRO:HB2	2:M:111:GLU:CD	1.93	0.89
3:H:97:PRO:O	3:H:98:HIS:CD2	2.26	0.89
1:L:10:ARG:HH22	3:H:95:GLY:HA2	1.34	0.89
1:L:248:MET:O	1:L:251:THR:N	2.04	0.89
8:L:285:U10:H112	8:L:285:U10:C15	2.02	0.89
3:H:27:LEU:CD1	3:H:28:ILE:HG13	2.02	0.89
1:L:64:ILE:HD12	1:L:65:SER:N	1.87	0.89
2:M:114:LEU:HD12	2:M:114:LEU:H	1.37	0.89
2:M:208:PHE:HB3	2:M:276:VAL:HG23	1.52	0.89
2:M:105:PHE:HD1	2:M:106:ALA:N	1.69	0.89
3:H:63:THR:HG23	3:H:74:THR:HG23	1.55	0.89
3:H:191:LEU:HD11	3:H:205:VAL:HG11	1.54	0.89
3:H:161:ALA:CB	3:H:210:SER:HB2	2.02	0.89
2:M:60:LEU:HD12	7:M:312:BPH:H6C1	1.54	0.89
3:H:204:HIS:ND1	3:H:205:VAL:N	2.20	0.89
4:M:308:BOG:H5	4:M:308:BOG:O2	1.71	0.89
3:H:179:LEU:C	3:H:179:LEU:HD23	1.92	0.89
1:L:255:TRP:CD1	1:L:259:TRP:CE3	2.61	0.89
2:M:39:LEU:H	2:M:39:LEU:HD13	1.32	0.89
2:M:57:VAL:HG23	2:M:58:LEU:N	1.85	0.89
3:H:151:LEU:HB3	3:H:203:VAL:CG2	2.01	0.89
2:M:90:PHE:CE2	2:M:180:PHE:CE1	2.61	0.89
1:L:17:VAL:HG13	1:L:18:GLY:N	1.85	0.89
1:L:9:TYR:OH	2:M:246:GLU:OE1	1.90	0.88
2:M:24:VAL:HG12	2:M:26:LEU:HD22	1.54	0.88
1:L:234:LEU:HD12	2:M:221:ALA:HA	1.54	0.88
1:L:248:MET:O	1:L:250:ILE:N	2.07	0.88
2:M:88:ASP:CB	2:M:92:PHE:CZ	2.56	0.88
2:M:233:ARG:NH2	3:H:122:GLU:OE1	2.05	0.88
8:L:285:U10:H153	8:L:285:U10:C11	2.02	0.88
1:L:51:TRP:CD1	1:L:51:TRP:C	2.33	0.88
3:H:56:PHE:CD1	3:H:56:PHE:C	2.25	0.88
3:H:114:TRP:HD1	3:H:115:VAL:O	1.57	0.88
1:L:177:ILE:HG22	1:L:181:PHE:HD2	1.37	0.88
2:M:65:MET:SD	2:M:121:PHE:HB3	2.11	0.88
1:L:94:THR:HG23	1:L:129:LEU:HD11	1.56	0.88
2:M:275:LEU:HD12	2:M:278:LEU:HD23	1.54	0.88
1:L:17:VAL:CG1	1:L:18:GLY:H	1.87	0.88
3:H:140:PHE:CD2	3:H:169:VAL:HG11	2.09	0.88
3:H:183:LEU:HD11	3:H:189:ARG:NE	1.88	0.88
3:H:40:TYR:H	3:H:42:LEU:CD1	1.86	0.88

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:103:ARG:HH11	1:L:103:ARG:HG2	1.39	0.88
2:M:249:ALA:CA	8:M:313:U10:H4M3	2.04	0.88
2:M:87:ARG:HG3	2:M:88:ASP:H	1.39	0.88
3:H:191:LEU:HD23	3:H:213:PHE:HE1	1.39	0.88
3:H:132:LYS:HZ1	3:H:223:THR:HG23	1.34	0.88
1:L:171:PRO:HA	1:L:174:MET:HG3	1.54	0.88
1:L:20:ASN:C	1:L:22:PHE:H	1.74	0.88
2:M:171:TRP:C	2:M:173:GLU:H	1.74	0.88
2:M:241:ARG:HH11	2:M:241:ARG:CB	1.86	0.88
3:H:134:MET:SD	3:H:141:HIS:CE1	2.68	0.87
2:M:149:ALA:O	7:M:312:BPH:HMD1	1.74	0.87
2:M:87:ARG:HG3	2:M:88:ASP:CA	2.04	0.87
2:M:88:ASP:HB2	2:M:92:PHE:CE1	2.09	0.87
3:H:132:LYS:HZ1	3:H:223:THR:CG2	1.83	0.87
1:L:170:ASN:O	1:L:173:HIS:HB3	1.73	0.87
2:M:33:GLY:O	2:M:34:PRO:O	1.91	0.87
1:L:269:LEU:CB	1:L:270:PRO:CD	2.53	0.87
1:L:227:LEU:HD23	1:L:231:ARG:CD	2.03	0.87
2:M:163:ILE:O	2:M:166:ILE:HB	1.72	0.87
2:M:291:VAL:O	2:M:291:VAL:HG12	1.74	0.87
2:M:65:MET:CE	2:M:121:PHE:HB3	2.05	0.87
3:H:15:LEU:HA	3:H:18:TYR:CE2	2.08	0.87
1:L:133:LEU:CD1	1:L:137:VAL:CG2	2.53	0.87
2:M:152:SER:O	2:M:154:ILE:N	2.08	0.87
3:H:97:PRO:O	3:H:98:HIS:HD2	1.58	0.87
1:L:232:LEU:CG	2:M:42:PHE:CE2	2.58	0.87
1:L:268:LYS:CG	1:L:269:LEU:N	2.30	0.87
3:H:156:CYS:SG	3:H:209:SER:CA	2.62	0.87
2:M:155:TRP:O	2:M:159:VAL:HG23	1.75	0.87
2:M:94:LEU:HD11	2:M:114:LEU:CD2	2.02	0.87
2:M:81:ASN:OD1	2:M:84:VAL:HG23	1.75	0.87
3:H:12:LEU:C	3:H:12:LEU:CD2	2.41	0.86
1:L:185:LEU:C	1:L:188:ALA:H	1.76	0.86
1:L:73:TYR:HD2	1:L:82:LYS:HE3	1.36	0.86
1:L:73:TYR:CB	1:L:82:LYS:HZ1	1.87	0.86
2:M:197:PHE:HE1	6:M:311:BCL:CMD	1.87	0.86
2:M:63:GLY:HA3	7:M:312:BPH:H5C1	1.57	0.86
3:H:111:PRO:CG	3:H:242:MET:HG3	2.04	0.86
1:L:60:ASN:O	1:L:61:PRO:C	2.13	0.86
3:H:191:LEU:CD2	3:H:213:PHE:CE1	2.59	0.86
1:L:222:TYR:CG	1:L:223:SER:N	2.32	0.86
2:M:99:PRO:HB2	2:M:111:GLU:HG3	1.57	0.86

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:296:VAL:O	2:M:298:GLY:N	2.09	0.86
2:M:204:LEU:O	2:M:207:ALA:HB3	1.75	0.86
2:M:148:TRP:O	2:M:150:PHE:N	2.09	0.86
2:M:241:ARG:HH12	2:M:246:GLU:HG2	1.40	0.86
2:M:65:MET:O	2:M:69:THR:N	2.08	0.86
3:H:132:LYS:HD2	3:H:133:PRO:HD3	1.57	0.86
3:H:40:TYR:O	3:H:42:LEU:N	2.07	0.86
1:L:185:LEU:C	1:L:187:LEU:H	1.79	0.86
1:L:53:ALA:CB	1:L:64:ILE:CG1	2.53	0.86
1:L:151:TRP:CZ3	1:L:154:LEU:HD22	2.11	0.86
1:L:73:TYR:CD2	1:L:82:LYS:NZ	2.44	0.85
6:L:283:BCL:H2C	6:M:310:BCL:HBC2	1.58	0.85
2:M:89:LEU:N	2:M:92:PHE:CE2	2.43	0.85
2:M:136:ARG:HA	2:M:136:ARG:HE	1.41	0.85
2:M:271:TRP:CZ3	3:H:31:LEU:HD23	2.10	0.85
6:L:283:BCL:HMC1	6:M:310:BCL:CBC	2.01	0.85
2:M:126:VAL:CG1	2:M:154:ILE:HD11	2.05	0.85
3:H:111:PRO:CG	3:H:242:MET:CB	2.55	0.85
3:H:191:LEU:HD11	3:H:205:VAL:CG1	2.05	0.85
1:L:177:ILE:CG2	1:L:181:PHE:CD2	2.57	0.85
2:M:199:ASN:ND2	2:M:294:TRP:CE2	2.44	0.85
2:M:81:ASN:CG	2:M:84:VAL:HG23	1.96	0.85
2:M:185:TRP:CE3	2:M:185:TRP:C	2.50	0.85
2:M:187:ASN:O	2:M:190:SER:N	2.10	0.85
3:H:115:VAL:CG1	3:H:116:ALA:H	1.90	0.85
3:H:189:ARG:HB2	3:H:216:ILE:CG2	2.05	0.85
3:H:229:GLU:O	3:H:233:ILE:HG12	1.77	0.85
1:L:53:ALA:CB	1:L:64:ILE:HD13	2.06	0.85
2:M:131:GLY:O	2:M:134:TYR:CB	2.23	0.85
2:M:280:GLY:O	6:M:310:BCL:HED3	1.76	0.85
2:M:37:THR:HA	2:M:41:TRP:CD1	2.12	0.85
2:M:17:ASP:C	2:M:18:LEU:CD1	2.45	0.85
3:H:132:LYS:HZ2	3:H:223:THR:HG23	0.96	0.85
3:H:42:LEU:CD2	3:H:76:PRO:HA	2.05	0.85
2:M:226:VAL:CG1	2:M:231:GLY:HA3	2.05	0.85
3:H:219:ILE:CG2	3:H:229:GLU:HG2	2.07	0.85
1:L:121:PHE:O	1:L:124:ALA:N	2.10	0.85
2:M:103:LEU:HD11	2:M:166:ILE:HG12	1.58	0.85
2:M:226:VAL:HG21	2:M:248:ALA:HB2	1.58	0.85
3:H:175:MET:SD	3:H:177:ARG:NH1	2.50	0.85
2:M:70:ILE:CD1	4:M:308:BOG:O6	2.25	0.85
6:M:311:BCL:H43	6:M:311:BCL:O1A	1.76	0.85

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:M:313:U10:H212	8:M:313:U10:H253	1.55	0.85
1:L:248:MET:C	1:L:250:ILE:N	2.30	0.84
2:M:99:PRO:CB	2:M:111:GLU:HG3	2.07	0.84
3:H:157:ASP:OD2	3:H:211:ASP:CB	2.25	0.84
8:L:285:U10:H1M1	8:L:285:U10:H8	1.57	0.84
2:M:94:LEU:HD21	2:M:114:LEU:CB	2.06	0.84
3:H:42:LEU:HD23	3:H:77:GLY:N	1.91	0.84
1:L:185:LEU:CA	1:L:188:ALA:HB3	2.07	0.84
3:H:228:LEU:HD23	3:H:232:LYS:HD2	1.58	0.84
1:L:133:LEU:O	1:L:133:LEU:HD12	1.78	0.84
1:L:10:ARG:NH2	1:L:25:TRP:HB2	1.90	0.84
2:M:212:SER:O	2:M:214:LEU:N	2.10	0.84
2:M:50:ILE:HG23	2:M:51:TYR:N	1.92	0.84
3:H:103:ASP:OD1	3:H:106:LYS:NZ	2.09	0.84
3:H:183:LEU:N	3:H:183:LEU:CD2	2.37	0.84
1:L:10:ARG:NH2	3:H:95:GLY:CA	2.41	0.84
2:M:235:LEU:HD12	2:M:235:LEU:N	1.91	0.84
8:L:285:U10:C1M	8:L:285:U10:H8	2.07	0.84
2:M:243:THR:HG21	2:M:247:ARG:HE	0.68	0.84
3:H:196:VAL:HA	3:H:204:HIS:O	1.77	0.84
1:L:48:LEU:CD1	1:L:89:ILE:HG13	2.07	0.84
1:L:191:GLY:O	1:L:195:LEU:HD12	1.78	0.84
1:L:68:PRO:HB3	1:L:86:TRP:CE2	2.13	0.84
1:L:11:VAL:CG2	3:H:110:GLY:HA2	2.00	0.84
1:L:248:MET:CE	6:L:283:BCL:C3D	2.53	0.84
2:M:21:THR:HB	2:M:139:ALA:CB	2.06	0.84
3:H:134:MET:O	3:H:137:ALA:HB3	1.78	0.83
2:M:64:LEU:HD11	7:M:312:BPH:C7	2.08	0.83
1:L:154:LEU:CD1	1:L:154:LEU:H	1.92	0.83
3:H:233:ILE:O	3:H:237:VAL:HG22	1.78	0.83
1:L:146:PHE:CB	1:L:156:TRP:CD1	2.61	0.83
2:M:275:LEU:O	2:M:277:THR:N	2.10	0.83
3:H:191:LEU:CD2	3:H:213:PHE:HE1	1.92	0.83
2:M:85:PHE:CE1	2:M:89:LEU:HD12	2.12	0.83
3:H:213:PHE:C	3:H:216:ILE:HD12	1.98	0.83
1:L:53:ALA:HB1	1:L:64:ILE:HB	1.58	0.83
2:M:89:LEU:HA	2:M:92:PHE:CD2	2.12	0.83
3:H:204:HIS:CG	3:H:205:VAL:N	2.47	0.83
6:L:282:BCL:HHC	6:L:282:BCL:HBB2	1.60	0.83
1:L:79:PRO:HD2	1:L:83:GLY:N	1.93	0.83
3:H:140:PHE:HD2	3:H:169:VAL:HG11	1.41	0.83
1:L:113:ILE:CG2	1:L:114:GLY:H	1.90	0.83

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:54:VAL:O	1:L:57:GLY:N	2.11	0.83
1:L:168:HIS:O	1:L:169:TYR:CD1	2.30	0.83
1:L:97:PHE:HZ	6:L:283:BCL:H122	1.39	0.83
1:L:73:TYR:HD2	1:L:82:LYS:CE	1.87	0.83
2:M:18:LEU:N	2:M:18:LEU:HD12	1.93	0.83
1:L:79:PRO:HD2	1:L:83:GLY:H	1.43	0.83
2:M:238:ILE:HD11	2:M:263:GLU:CA	2.08	0.83
2:M:235:LEU:CD1	2:M:235:LEU:H	1.90	0.83
1:L:170:ASN:HB2	1:L:259:TRP:NE1	1.93	0.82
1:L:84:GLY:O	1:L:86:TRP:N	2.10	0.82
2:M:109:LEU:O	2:M:114:LEU:HD13	1.78	0.82
2:M:87:ARG:HD2	2:M:88:ASP:OD2	1.76	0.82
1:L:205:GLU:CA	3:H:65:ILE:CG2	2.57	0.82
3:H:27:LEU:HD13	3:H:32:GLN:NE2	1.93	0.82
1:L:186:ALA:C	2:M:216:PHE:HE2	1.83	0.82
3:H:37:ARG:O	3:H:42:LEU:HD11	1.80	0.82
1:L:214:THR:HG22	2:M:140:LEU:CD2	2.08	0.82
1:L:175:ILE:CG2	1:L:243:PHE:CE2	2.48	0.82
7:L:284:BPH:H171	7:L:284:BPH:H143	0.83	0.82
2:M:154:ILE:HG23	2:M:157:TRP:HE3	1.44	0.82
2:M:277:THR:HG23	2:M:277:THR:O	1.78	0.82
3:H:151:LEU:CD2	3:H:203:VAL:HG23	2.10	0.82
2:M:20:MET:HG3	2:M:21:THR:CA	2.10	0.82
3:H:123:LEU:CD2	3:H:127:GLY:HA2	2.09	0.82
3:H:143:SER:O	3:H:144:ALA:HB3	1.80	0.82
1:L:124:ALA:C	1:L:126:LEU:H	1.81	0.82
1:L:156:TRP:CZ3	1:L:157:VAL:HA	2.15	0.82
1:L:195:LEU:HB3	2:M:145:HIS:HD2	1.41	0.82
2:M:171:TRP:C	2:M:173:GLU:N	2.32	0.82
2:M:90:PHE:HD2	2:M:180:PHE:CD1	1.96	0.82
1:L:107:ILE:CD1	2:M:255:THR:OG1	2.27	0.82
1:L:234:LEU:HD12	2:M:221:ALA:CA	2.10	0.82
1:L:24:PHE:O	1:L:31:VAL:HG23	1.78	0.82
2:M:227:SER:O	2:M:230:GLY:N	2.06	0.82
3:H:147:ASN:O	3:H:151:LEU:HD12	1.79	0.82
3:H:130:LYS:O	3:H:171:ILE:HD13	1.79	0.82
2:M:175:VAL:HG22	2:M:185:TRP:CZ2	2.14	0.82
1:L:33:PHE:C	1:L:33:PHE:CD1	2.50	0.82
3:H:15:LEU:HA	3:H:18:TYR:HD2	1.45	0.82
3:H:134:MET:HE1	3:H:167:ILE:HD12	1.61	0.82
2:M:186:THR:O	2:M:189:PHE:HB3	1.80	0.82
2:M:131:GLY:O	2:M:134:TYR:CA	2.28	0.82

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:124:ALA:HB2	7:L:284:BPH:HBC2	1.62	0.81
6:M:310:BCL:HHC	6:M:310:BCL:CBB	2.09	0.81
6:M:310:BCL:HHC	6:M:310:BCL:HBB3	1.62	0.81
3:H:17:ILE:HD13	3:H:17:ILE:O	1.81	0.81
3:H:14:SER:O	3:H:18:TYR:CB	2.27	0.81
1:L:156:TRP:HE3	1:L:157:VAL:CA	1.94	0.81
1:L:185:LEU:O	1:L:187:LEU:N	2.12	0.81
1:L:156:TRP:O	1:L:156:TRP:CD2	2.34	0.81
1:L:242:PHE:C	1:L:242:PHE:CD1	2.52	0.81
7:M:312:BPH:C6	7:M:312:BPH:C8	2.58	0.81
1:L:54:VAL:O	1:L:56:GLN:N	2.13	0.81
1:L:181:PHE:O	1:L:184:ALA:HB3	1.80	0.81
2:M:99:PRO:HG2	2:M:111:GLU:HG3	1.61	0.81
3:H:134:MET:SD	3:H:141:HIS:ND1	2.54	0.81
3:H:156:CYS:O	3:H:157:ASP:C	2.19	0.81
2:M:26:LEU:HD23	2:M:27:ALA:N	1.94	0.81
3:H:185:ASP:O	3:H:187:SER:N	2.14	0.81
1:L:232:LEU:CA	2:M:42:PHE:HZ	1.94	0.81
2:M:102:GLY:C	2:M:104:SER:H	1.84	0.81
1:L:119:PHE:CE1	1:L:238:LEU:HD11	2.16	0.81
1:L:212:GLU:O	1:L:214:THR:N	2.12	0.81
2:M:156:LEU:HD23	2:M:156:LEU:O	1.81	0.81
3:H:56:PHE:O	3:H:58:LEU:N	2.14	0.81
1:L:135:ARG:CG	1:L:139:MET:CE	2.57	0.81
2:M:186:THR:HG23	6:M:310:BCL:CMD	2.04	0.81
2:M:271:TRP:HZ3	3:H:31:LEU:HD23	1.45	0.81
2:M:64:LEU:O	2:M:68:PHE:N	2.14	0.81
2:M:65:MET:CG	2:M:66:TRP:N	2.38	0.81
1:L:260:VAL:HG12	1:L:260:VAL:O	1.81	0.81
1:L:219:LEU:CA	2:M:132:ARG:HH21	1.93	0.81
1:L:75:LEU:HG	1:L:140:GLY:O	1.81	0.81
1:L:127:ALA:CB	6:L:283:BCL:H2	2.10	0.81
8:L:285:U10:H112	8:L:285:U10:H153	1.62	0.81
2:M:90:PHE:CA	2:M:179:ILE:HD12	2.09	0.81
2:M:17:ASP:O	2:M:18:LEU:HG	1.81	0.81
1:L:22:PHE:HB3	1:L:32:GLY:HA2	1.63	0.80
1:L:219:LEU:O	2:M:132:ARG:NH2	2.14	0.80
6:L:283:BCL:H143	7:L:284:BPH:CGA	2.11	0.80
1:L:69:PRO:HB3	1:L:78:ALA:CB	2.11	0.80
3:H:194:GLN:H	3:H:194:GLN:NE2	1.78	0.80
1:L:123:PHE:O	1:L:126:LEU:HB3	1.79	0.80
6:L:282:BCL:H11	7:M:312:BPH:OBB	1.81	0.80

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:130:LYS:HB3	3:H:130:LYS:HZ3	1.44	0.80
3:H:246:PRO:O	3:H:248:ARG:HG3	1.82	0.80
1:L:195:LEU:HD21	2:M:267:ARG:HD3	1.64	0.80
3:H:60:LYS:O	3:H:60:LYS:HG3	1.81	0.80
1:L:132:VAL:HG12	1:L:132:VAL:O	1.80	0.80
1:L:133:LEU:HD12	1:L:137:VAL:HG23	1.64	0.80
1:L:219:LEU:HD21	2:M:133:THR:CG2	2.11	0.80
1:L:224:ILE:CD1	1:L:232:LEU:HD12	2.11	0.80
1:L:204:LYS:HD2	1:L:207:ARG:HH22	1.47	0.80
3:H:238:ALA:O	3:H:241:LEU:N	2.14	0.80
1:L:156:TRP:CE3	1:L:157:VAL:CA	2.64	0.80
1:L:262:TRP:O	1:L:264:GLN:N	2.15	0.80
3:H:111:PRO:HD2	3:H:243:TYR:HE1	1.46	0.80
3:H:154:ARG:HE	3:H:160:ILE:HG13	1.45	0.80
2:M:108:PRO:CG	2:M:111:GLU:HB3	2.12	0.80
1:L:42:ALA:O	1:L:46:ILE:HG23	1.81	0.80
2:M:120:PHE:CD1	2:M:162:PHE:HE2	1.99	0.80
6:L:283:BCL:H43	7:L:284:BPH:CAB	2.11	0.79
2:M:206:ILE:HD13	6:M:311:BCL:HMD1	1.62	0.79
3:H:196:VAL:HA	3:H:204:HIS:C	2.02	0.79
1:L:49:ILE:HG23	1:L:50:ALA:N	1.97	0.79
2:M:35:PHE:CD2	2:M:39:LEU:CD2	2.65	0.79
3:H:117:ARG:HB2	3:H:227:LEU:CB	2.13	0.79
3:H:155:GLY:O	3:H:204:HIS:CD2	2.33	0.79
2:M:196:LEU:HD12	2:M:199:ASN:HB2	1.63	0.79
2:M:134:TYR:HD1	2:M:134:TYR:O	1.64	0.79
2:M:205:SER:O	6:M:310:BCL:CMA	2.29	0.79
3:H:90:THR:O	3:H:91:ALA:CB	2.30	0.79
1:L:58:THR:O	1:L:59:TRP:HB3	1.81	0.79
2:M:90:PHE:CD2	2:M:180:PHE:CD1	2.71	0.79
3:H:124:ASP:OD1	3:H:125:GLY:CA	2.29	0.79
1:L:232:LEU:CG	2:M:42:PHE:HE2	1.96	0.79
2:M:120:PHE:O	2:M:121:PHE:CD1	2.36	0.79
2:M:264:GLY:O	2:M:268:TRP:N	2.16	0.79
2:M:227:SER:HB3	3:H:194:GLN:CG	2.12	0.79
3:H:238:ALA:HA	3:H:241:LEU:HD12	1.63	0.79
7:L:284:BPH:H172	7:L:284:BPH:H143	1.62	0.79
1:L:47:ILE:HG22	1:L:48:LEU:H	1.45	0.79
2:M:218:MET:CE	8:M:313:U10:H1M3	2.12	0.79
1:L:102:LEU:CD2	1:L:102:LEU:N	2.46	0.79
2:M:253:ARG:O	2:M:257:GLY:HA2	1.82	0.79
2:M:20:MET:HG3	2:M:21:THR:H	1.48	0.79

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:27:ALA:HB1	2:M:51:TYR:HA	1.65	0.79
3:H:111:PRO:HG2	3:H:242:MET:HB2	1.62	0.79
2:M:73:TRP:CG	2:M:114:LEU:CD2	2.65	0.78
1:L:11:VAL:CG1	3:H:87:LEU:HD11	2.13	0.78
1:L:132:VAL:O	1:L:132:VAL:CG1	2.28	0.78
1:L:179:PHE:HB3	1:L:240:ALA:HB2	1.64	0.78
1:L:226:THR:HG22	2:M:232:GLU:HB3	1.65	0.78
3:H:127:GLY:O	3:H:129:ASN:N	2.17	0.78
1:L:149:GLY:C	1:L:151:TRP:H	1.84	0.78
1:L:242:PHE:HD1	1:L:243:PHE:H	1.29	0.78
2:M:208:PHE:C	2:M:210:TYR:H	1.86	0.78
2:M:64:LEU:CD1	7:M:312:BPH:C7	2.55	0.78
2:M:99:PRO:CG	2:M:111:GLU:HG3	2.14	0.78
3:H:13:ALA:O	3:H:16:ALA:HB3	1.83	0.78
3:H:201:ASN:OD1	3:H:202:ARG:N	2.17	0.78
1:L:101:ALA:O	1:L:104:GLU:HB2	1.83	0.78
1:L:116:HIS:HE1	2:M:225:ALA:HA	1.48	0.78
2:M:114:LEU:CD1	2:M:114:LEU:N	2.41	0.78
2:M:212:SER:O	2:M:213:ALA:C	2.20	0.78
2:M:222:THR:O	2:M:225:ALA:N	2.14	0.78
2:M:290:VAL:HG12	2:M:290:VAL:O	1.84	0.78
2:M:38:LEU:O	2:M:40:GLY:N	2.16	0.78
1:L:205:GLU:CA	3:H:65:ILE:HG21	2.13	0.78
1:L:183:ASN:C	1:L:183:ASN:HD22	1.85	0.78
1:L:225:GLY:HA3	3:H:173:GLU:OE2	1.84	0.78
1:L:173:HIS:HB2	1:L:247:CYS:SG	2.23	0.78
1:L:69:PRO:HG3	1:L:83:GLY:CA	2.13	0.78
2:M:284:ILE:HG13	6:M:310:BCL:HED1	1.64	0.78
3:H:111:PRO:HG2	3:H:242:MET:CG	2.12	0.78
3:H:234:CYS:O	3:H:237:VAL:HG23	1.83	0.78
1:L:93:ALA:HB3	1:L:128:TYR:OH	1.84	0.78
1:L:135:ARG:HB3	1:L:136:PRO:CD	2.09	0.78
1:L:185:LEU:C	1:L:187:LEU:N	2.33	0.78
2:M:241:ARG:NH1	2:M:241:ARG:CB	2.47	0.78
2:M:89:LEU:HA	2:M:92:PHE:HD2	1.46	0.78
2:M:17:ASP:HA	2:M:18:LEU:HD12	1.65	0.78
2:M:296:VAL:O	2:M:297:TRP:C	2.22	0.78
3:H:184:LYS:CE	3:H:184:LYS:HA	2.14	0.78
3:H:207:ALA:O	3:H:247:LYS:NZ	2.14	0.78
1:L:53:ALA:CB	1:L:64:ILE:HG12	2.13	0.78
1:L:92:CYS:O	1:L:96:ALA:HB2	1.83	0.78
1:L:25:TRP:CH2	1:L:110:LYS:NZ	2.51	0.78

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:177:ILE:HD13	6:L:283:BCL:HHB	1.65	0.78
2:M:126:VAL:CG1	2:M:154:ILE:CD1	2.62	0.78
2:M:119:SER:HB2	2:M:177:TYR:OH	1.84	0.78
3:H:182:GLU:HA	3:H:187:SER:O	1.84	0.78
3:H:42:LEU:CD2	3:H:77:GLY:H	1.97	0.78
6:L:283:BCL:CB	6:M:311:BCL:HBC1	2.14	0.78
1:L:127:ALA:HB1	6:L:283:BCL:H2	1.67	0.78
6:L:283:BCL:C2C	6:M:310:BCL:HBC2	2.13	0.78
3:H:103:ASP:HB3	3:H:106:LYS:HE3	1.66	0.78
3:H:12:LEU:HD23	3:H:12:LEU:O	1.83	0.77
3:H:148:PRO:O	3:H:151:LEU:CB	2.32	0.77
3:H:183:LEU:HD21	3:H:189:ARG:HG2	1.66	0.77
3:H:117:ARG:HB2	3:H:227:LEU:HB3	1.65	0.77
1:L:180:PHE:HE1	2:M:213:ALA:CB	1.97	0.77
1:L:24:PHE:CZ	1:L:31:VAL:HG21	2.19	0.77
1:L:48:LEU:HD11	1:L:89:ILE:CG1	2.14	0.77
1:L:224:ILE:HG22	1:L:224:ILE:O	1.84	0.77
3:H:191:LEU:HD23	3:H:213:PHE:CE1	2.20	0.77
1:L:182:THR:C	1:L:184:ALA:H	1.87	0.77
1:L:263:TRP:CD1	2:M:180:PHE:HE2	2.01	0.77
2:M:243:THR:HG21	2:M:247:ARG:NH2	1.99	0.77
3:H:132:LYS:HZ2	3:H:223:THR:CG2	1.85	0.77
1:L:156:TRP:CE3	1:L:157:VAL:N	2.51	0.77
1:L:182:THR:O	1:L:185:LEU:HD21	1.83	0.77
1:L:48:LEU:HD12	1:L:89:ILE:CD1	2.14	0.77
1:L:269:LEU:HB3	1:L:270:PRO:CD	2.11	0.77
1:L:269:LEU:CG	1:L:270:PRO:CD	2.62	0.77
3:H:157:ASP:OD1	3:H:210:SER:N	2.18	0.77
1:L:153:HIS:HD2	1:L:154:LEU:CD1	1.98	0.77
1:L:175:ILE:HD13	1:L:243:PHE:HE2	0.65	0.77
1:L:25:TRP:O	1:L:27:GLY:N	2.18	0.77
1:L:31:VAL:HG12	1:L:36:VAL:CG2	2.15	0.77
1:L:46:ILE:HA	1:L:49:ILE:CG2	2.14	0.77
2:M:197:PHE:HE1	6:M:311:BCL:HMD1	1.50	0.77
2:M:204:LEU:O	2:M:207:ALA:CB	2.33	0.77
3:H:111:PRO:CG	3:H:242:MET:CG	2.63	0.77
1:L:111:LEU:CD2	2:M:251:PHE:HB2	2.14	0.77
7:M:312:BPH:CB	7:M:312:BPH:HHD	2.12	0.77
3:H:44:ASN:ND2	3:H:44:ASN:N	2.29	0.76
2:M:93:SER:HB2	2:M:178:GLY:HA3	1.67	0.76
2:M:209:LEU:N	2:M:276:VAL:CG2	2.47	0.76
2:M:98:ALA:HA	2:M:99:PRO:C	2.04	0.76

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:52:ASN:O	3:H:53:GLN:HB2	1.83	0.76
3:H:108:GLY:HA3	3:H:114:TRP:CZ3	2.20	0.76
7:L:284:BPH:H141	7:L:284:BPH:H171	1.61	0.76
2:M:119:SER:CA	2:M:177:TYR:OH	2.33	0.76
3:H:12:LEU:CD2	3:H:13:ALA:N	2.48	0.76
1:L:21:LEU:CD1	1:L:22:PHE:HE1	1.95	0.76
2:M:11:GLN:HB3	3:H:143:SER:O	1.85	0.76
1:L:73:TYR:CE2	1:L:82:LYS:HE3	2.20	0.76
2:M:196:LEU:HD11	2:M:199:ASN:ND2	2.01	0.76
3:H:195:MET:C	3:H:196:VAL:CG1	2.51	0.76
1:L:73:TYR:CB	1:L:82:LYS:NZ	2.46	0.76
3:H:215:GLY:HA3	3:H:236:TYR:OH	1.84	0.76
1:L:133:LEU:HD12	1:L:137:VAL:CG2	2.15	0.76
1:L:151:TRP:CE3	1:L:154:LEU:HD22	2.20	0.76
1:L:154:LEU:N	1:L:154:LEU:HD12	2.00	0.76
1:L:46:ILE:O	1:L:46:ILE:HG13	1.85	0.76
1:L:69:PRO:CG	1:L:78:ALA:HB3	2.16	0.76
1:L:5:PHE:HZ	3:H:40:TYR:CZ	2.02	0.76
2:M:205:SER:O	6:M:310:BCL:HMA2	1.85	0.76
2:M:236:GLU:CG	3:H:122:GLU:HG3	2.16	0.76
3:H:124:ASP:O	3:H:126:HIS:N	2.18	0.76
3:H:90:THR:O	3:H:91:ALA:HB2	1.86	0.76
1:L:7:ARG:O	3:H:87:LEU:CD2	2.28	0.76
2:M:118:ALA:O	2:M:121:PHE:N	2.19	0.76
1:L:263:TRP:CD1	2:M:180:PHE:CE2	2.74	0.76
7:L:284:BPH:H141	7:L:284:BPH:C17	2.15	0.76
1:L:22:PHE:CE2	1:L:36:VAL:HG11	2.17	0.76
1:L:60:ASN:C	1:L:62:GLN:N	2.35	0.76
1:L:49:ILE:CA	1:L:89:ILE:HD11	2.16	0.76
1:L:12:PRO:HD3	3:H:97:PRO:HB2	1.66	0.76
1:L:108:CYS:O	1:L:109:ARG:C	2.25	0.76
1:L:185:LEU:CD2	1:L:186:ALA:N	2.18	0.75
1:L:248:MET:O	1:L:249:ILE:C	2.23	0.75
2:M:264:GLY:O	2:M:267:ARG:HB2	1.86	0.75
8:L:285:U10:C26	8:L:285:U10:H303	2.15	0.75
1:L:43:ALA:C	1:L:45:GLY:H	1.89	0.75
1:L:208:THR:H	1:L:211:HIS:CG	2.04	0.75
1:L:180:PHE:CE1	2:M:213:ALA:HB2	2.19	0.75
6:L:283:BCL:H141	7:L:284:BPH:O2A	1.86	0.75
2:M:163:ILE:HG21	2:M:285:LEU:HD13	1.68	0.75
2:M:196:LEU:CD1	2:M:199:ASN:HB2	2.16	0.75
2:M:20:MET:SD	2:M:22:GLU:N	2.59	0.75

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:148:PRO:C	3:H:151:LEU:HB2	2.06	0.75
1:L:94:THR:CB	1:L:129:LEU:HD11	2.15	0.75
1:L:175:ILE:HG22	1:L:176:ALA:N	2.00	0.75
6:L:283:BCL:C14	7:L:284:BPH:CBA	2.60	0.75
1:L:8:LYS:CA	3:H:87:LEU:CD2	2.54	0.75
1:L:219:LEU:CD2	2:M:133:THR:HG23	2.14	0.75
2:M:264:GLY:CA	2:M:267:ARG:HB2	2.17	0.75
2:M:194:GLY:O	2:M:195:ASN:C	2.24	0.75
3:H:142:VAL:O	3:H:142:VAL:HG12	1.87	0.75
1:L:112:GLY:O	1:L:113:ILE:O	2.05	0.75
1:L:117:ILE:HB	1:L:118:PRO:HD3	1.68	0.75
1:L:197:ALA:HB1	2:M:235:LEU:HD21	1.69	0.75
1:L:113:ILE:CD1	2:M:226:VAL:HG22	2.16	0.75
6:L:283:BCL:H112	7:L:284:BPH:HBA2	1.69	0.75
2:M:25:ASN:O	2:M:27:ALA:O	2.05	0.75
1:L:15:THR:HG21	1:L:19:GLY:CA	2.16	0.75
1:L:226:THR:HG23	2:M:232:GLU:O	1.86	0.75
2:M:81:ASN:O	2:M:84:VAL:HB	1.85	0.75
1:L:206:MET:H	3:H:65:ILE:HG22	0.69	0.75
8:L:285:U10:O4	8:L:285:U10:C3M	2.33	0.75
2:M:46:GLN:CG	2:M:47:LEU:N	2.46	0.75
2:M:71:GLY:O	2:M:74:PHE:CB	2.35	0.75
3:H:219:ILE:HG23	3:H:229:GLU:HG2	1.66	0.75
1:L:133:LEU:O	1:L:137:VAL:CG2	2.32	0.75
1:L:60:ASN:O	1:L:63:LEU:N	2.18	0.75
2:M:78:ALA:O	2:M:84:VAL:HG11	1.86	0.75
1:L:171:PRO:O	1:L:174:MET:N	2.19	0.74
1:L:177:ILE:HD13	6:L:283:BCL:CHB	2.16	0.74
1:L:182:THR:O	1:L:184:ALA:N	2.20	0.74
2:M:21:THR:CB	2:M:139:ALA:HB1	2.10	0.74
3:H:27:LEU:HD11	3:H:28:ILE:HG13	1.68	0.74
3:H:92:VAL:CG1	3:H:93:SER:H	2.01	0.74
2:M:20:MET:HG3	2:M:22:GLU:H	1.52	0.74
2:M:88:ASP:CA	2:M:92:PHE:CZ	2.70	0.74
1:L:151:TRP:CZ3	1:L:154:LEU:CD2	2.70	0.74
2:M:291:VAL:HG13	2:M:293:ASN:O	1.87	0.74
2:M:13:ARG:NH1	2:M:34:PRO:HB3	2.01	0.74
3:H:120:LEU:HD23	3:H:121:PRO:O	1.88	0.74
2:M:12:VAL:C	2:M:13:ARG:HG2	2.07	0.74
2:M:289:THR:C	2:M:291:VAL:H	1.89	0.74
6:M:311:BCL:HBB2	6:M:311:BCL:HMB1	1.69	0.74
3:H:134:MET:CE	3:H:167:ILE:HB	2.15	0.74

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:36:MET:CA	3:H:36:MET:CE	2.61	0.74
1:L:94:THR:OG1	1:L:129:LEU:HD12	1.86	0.74
2:M:135:LEU:CB	2:M:138:GLN:OE1	2.36	0.74
1:L:146:PHE:HB3	1:L:156:TRP:NE1	2.02	0.74
1:L:39:PHE:C	1:L:41:PHE:H	1.91	0.74
1:L:226:THR:HG22	2:M:232:GLU:CB	2.17	0.74
2:M:25:ASN:O	2:M:26:LEU:C	2.24	0.74
1:L:146:PHE:HB3	1:L:156:TRP:CD1	2.21	0.74
1:L:170:ASN:HB2	1:L:259:TRP:CE2	2.22	0.74
1:L:51:TRP:CH2	1:L:80:LEU:HD13	2.23	0.74
2:M:114:LEU:O	2:M:117:ILE:CB	2.32	0.74
2:M:205:SER:CB	2:M:279:THR:HG22	2.16	0.74
3:H:133:PRO:HA	3:H:168:TRP:HA	1.68	0.74
3:H:228:LEU:O	3:H:232:LYS:HB2	1.87	0.74
1:L:123:PHE:CG	1:L:238:LEU:HD21	2.22	0.74
2:M:208:PHE:O	2:M:210:TYR:N	2.21	0.74
2:M:284:ILE:HD12	6:M:310:BCL:CED	2.17	0.74
2:M:46:GLN:HE21	2:M:49:PRO:HD2	1.53	0.74
3:H:14:SER:O	3:H:18:TYR:CD2	2.41	0.74
8:L:285:U10:O4	8:L:285:U10:H3M3	1.87	0.74
1:L:6:GLU:HG2	1:L:10:ARG:HG2	1.68	0.74
1:L:95:GLY:O	1:L:99:SER:HB3	1.87	0.74
3:H:116:ALA:CA	3:H:228:LEU:CD1	2.65	0.73
3:H:124:ASP:OD1	3:H:126:HIS:N	2.19	0.73
3:H:130:LYS:NZ	3:H:130:LYS:HB3	1.99	0.73
3:H:148:PRO:HA	3:H:151:LEU:CD1	2.17	0.73
1:L:255:TRP:HZ2	1:L:262:TRP:N	1.86	0.73
2:M:206:ILE:CD1	6:M:310:BCL:C1B	2.64	0.73
2:M:85:PHE:CE1	2:M:89:LEU:CD1	2.71	0.73
1:L:135:ARG:NH1	1:L:139:MET:HE1	2.01	0.73
1:L:197:ALA:HB1	2:M:235:LEU:CD2	2.16	0.73
1:L:222:TYR:O	1:L:223:SER:CB	2.36	0.73
2:M:114:LEU:H	2:M:114:LEU:HD13	1.50	0.73
3:H:82:ASP:O	3:H:84:PRO:CD	2.36	0.73
3:H:198:VAL:HG12	3:H:198:VAL:O	1.86	0.73
1:L:102:LEU:HD23	1:L:102:LEU:N	2.00	0.73
1:L:113:ILE:CG2	1:L:114:GLY:N	2.51	0.73
1:L:171:PRO:O	1:L:174:MET:HB2	1.88	0.73
2:M:146:THR:O	2:M:150:PHE:HB2	1.87	0.73
2:M:35:PHE:HD1	2:M:38:LEU:HB2	1.47	0.73
1:L:232:LEU:O	1:L:235:LEU:CB	2.37	0.73
2:M:128:SER:O	2:M:131:GLY:N	2.21	0.73

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:58:LEU:HA	2:M:61:PHE:HB3	1.70	0.73
3:H:226:THR:HG22	3:H:229:GLU:CD	2.09	0.73
3:H:92:VAL:HG12	3:H:93:SER:H	1.54	0.73
1:L:241:VAL:CG1	1:L:242:PHE:N	2.51	0.73
2:M:284:ILE:CD1	6:M:310:BCL:O2D	2.36	0.73
2:M:46:GLN:HG2	2:M:48:GLY:O	1.88	0.73
2:M:75:TRP:O	2:M:78:ALA:N	2.20	0.73
1:L:269:LEU:HD22	1:L:270:PRO:HD3	0.78	0.73
3:H:19:SER:O	3:H:20:PHE:C	2.27	0.73
2:M:215:LEU:HD12	2:M:215:LEU:O	1.88	0.73
3:H:114:TRP:CD1	3:H:115:VAL:O	2.42	0.73
1:L:123:PHE:O	1:L:126:LEU:CB	2.36	0.73
1:L:225:GLY:HA2	8:L:285:U10:C4M	2.17	0.73
1:L:244:SER:HB3	6:L:283:BCL:HED3	1.71	0.73
2:M:185:TRP:CG	2:M:185:TRP:O	2.41	0.73
2:M:271:TRP:O	2:M:274:VAL:N	2.22	0.73
2:M:152:SER:CB	2:M:277:THR:HG22	2.19	0.73
1:L:259:TRP:O	1:L:261:ASP:N	2.22	0.72
2:M:113:GLY:O	2:M:114:LEU:C	2.26	0.72
2:M:37:THR:CG2	2:M:38:LEU:N	2.51	0.72
2:M:67:PHE:HD1	2:M:68:PHE:N	1.87	0.72
1:L:133:LEU:N	1:L:136:PRO:HG2	2.04	0.72
2:M:268:TRP:NE1	8:M:313:U10:H111	2.05	0.72
1:L:204:LYS:HB3	1:L:207:ARG:NH1	2.01	0.72
1:L:205:GLU:O	1:L:207:ARG:NH1	2.21	0.72
2:M:237:GLN:HG2	2:M:240:ASP:O	1.89	0.72
2:M:87:ARG:CD	2:M:88:ASP:OD2	2.34	0.72
3:H:134:MET:CE	3:H:141:HIS:CE1	2.73	0.72
3:H:168:TRP:N	3:H:178:PHE:O	2.22	0.72
1:L:151:TRP:CZ3	2:M:198:TYR:HD1	2.08	0.72
6:M:311:BCL:HBB3	6:M:311:BCL:HMB1	1.68	0.72
3:H:37:ARG:O	3:H:42:LEU:CD1	2.36	0.72
2:M:109:LEU:C	2:M:109:LEU:CD2	2.57	0.72
2:M:28:ASN:C	2:M:29:ARG:O	2.24	0.72
1:L:266:TRP:HE1	2:M:87:ARG:HA	1.52	0.72
2:M:90:PHE:CG	2:M:179:ILE:HD12	2.24	0.72
2:M:96:PRO:CB	2:M:97:PRO:CD	2.58	0.72
3:H:30:TYR:O	3:H:34:GLU:HB2	1.90	0.72
1:L:84:GLY:C	1:L:86:TRP:N	2.41	0.72
1:L:97:PHE:CE1	6:L:283:BCL:C11	2.73	0.72
2:M:241:ARG:HH12	2:M:246:GLU:CG	2.02	0.72
2:M:54:SER:C	2:M:57:VAL:HG13	2.07	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:111:PRO:HD2	3:H:243:TYR:CZ	2.25	0.72
1:L:48:LEU:HD12	1:L:89:ILE:HD12	1.69	0.72
2:M:126:VAL:HG12	2:M:154:ILE:HD11	1.72	0.72
2:M:20:MET:CG	2:M:22:GLU:H	2.02	0.72
2:M:266:HIS:O	2:M:270:ILE:HG22	1.90	0.72
3:H:194:GLN:N	3:H:194:GLN:OE1	2.22	0.72
1:L:113:ILE:CD1	2:M:226:VAL:CG2	2.68	0.72
1:L:114:GLY:H	2:M:225:ALA:HB1	1.55	0.72
1:L:167:PHE:CZ	1:L:251:THR:HG21	2.25	0.72
2:M:245:ALA:O	2:M:247:ARG:N	2.23	0.72
4:M:308:BOG:C5	4:M:308:BOG:O2	2.37	0.72
3:H:40:TYR:N	3:H:42:LEU:CD1	2.53	0.72
1:L:185:LEU:HB3	7:M:312:BPH:H3C	1.71	0.72
7:M:312:BPH:CHD	7:M:312:BPH:HBC3	2.16	0.72
2:M:260:ALA:HA	3:H:36:MET:HG3	0.81	0.72
1:L:113:ILE:HG23	1:L:114:GLY:H	1.55	0.72
2:M:73:TRP:CE2	2:M:114:LEU:HG	2.24	0.72
8:M:313:U10:C8	8:M:313:U10:H1M1	2.20	0.72
3:H:133:PRO:HD2	3:H:136:ALA:CB	2.20	0.71
3:H:14:SER:O	3:H:18:TYR:HD2	1.73	0.71
2:M:9:GLN:HE22	3:H:197:LYS:HD2	1.54	0.71
1:L:113:ILE:HD12	2:M:226:VAL:HG23	1.71	0.71
1:L:187:LEU:CD2	2:M:216:PHE:CG	2.73	0.71
6:L:283:BCL:C14	7:L:284:BPH:CGA	2.68	0.71
1:L:53:ALA:CA	1:L:64:ILE:HD13	2.20	0.71
1:L:6:GLU:HG2	1:L:10:ARG:CG	2.19	0.71
1:L:116:HIS:HE1	2:M:225:ALA:CA	2.04	0.71
2:M:25:ASN:O	2:M:27:ALA:N	2.23	0.71
2:M:291:VAL:HG21	2:M:294:TRP:CH2	2.25	0.71
2:M:71:GLY:O	2:M:74:PHE:HB3	1.90	0.71
3:H:204:HIS:NE2	3:H:205:VAL:O	2.23	0.71
1:L:102:LEU:H	1:L:102:LEU:CD2	1.99	0.71
6:L:283:BCL:H151	7:L:284:BPH:C3A	2.17	0.71
2:M:154:ILE:HG23	2:M:157:TRP:CE3	2.23	0.71
2:M:170:SER:OG	2:M:172:SER:HB3	1.91	0.71
2:M:136:ARG:NE	2:M:136:ARG:CA	2.53	0.71
1:L:119:PHE:O	1:L:122:ALA:HB3	1.90	0.71
1:L:146:PHE:HB2	1:L:147:PRO:CD	2.20	0.71
1:L:193:LEU:HG	1:L:212:GLU:OE1	1.90	0.71
1:L:75:LEU:HD21	1:L:141:ALA:C	2.11	0.71
2:M:205:SER:N	2:M:279:THR:HG21	2.05	0.71
2:M:136:ARG:NE	2:M:136:ARG:HA	2.04	0.71

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:40:TYR:N	3:H:42:LEU:HD13	2.05	0.71
2:M:39:LEU:H	2:M:39:LEU:HD22	1.55	0.71
3:H:246:PRO:O	3:H:248:ARG:CG	2.38	0.71
3:H:26:GLY:O	3:H:30:TYR:HB2	1.90	0.71
3:H:116:ALA:CB	3:H:228:LEU:HD11	2.21	0.71
3:H:59:PRO:O	3:H:61:PRO:HD3	1.89	0.71
2:M:21:THR:HG22	2:M:140:LEU:CD1	2.21	0.71
2:M:186:THR:O	2:M:189:PHE:CB	2.38	0.71
3:H:128:HIS:C	3:H:130:LYS:H	1.94	0.71
2:M:35:PHE:CG	2:M:39:LEU:HD22	2.26	0.71
3:H:157:ASP:O	3:H:158:LEU:HB2	1.88	0.71
3:H:20:PHE:CZ	3:H:24:LEU:CD1	2.68	0.71
1:L:16:LEU:HB3	1:L:106:GLU:OE2	1.91	0.71
1:L:146:PHE:O	1:L:147:PRO:O	2.07	0.71
3:H:124:ASP:CG	3:H:125:GLY:N	2.42	0.71
3:H:148:PRO:O	3:H:164:VAL:CG2	2.39	0.71
3:H:218:THR:HG22	3:H:219:ILE:O	1.91	0.71
8:L:285:U10:H111	8:L:285:U10:H152	0.73	0.70
1:L:47:ILE:HG22	1:L:48:LEU:N	2.06	0.70
1:L:171:PRO:HA	1:L:174:MET:CG	2.21	0.70
1:L:72:GLU:OE2	1:L:73:TYR:N	2.23	0.70
2:M:35:PHE:CE1	2:M:38:LEU:HD13	2.25	0.70
2:M:218:MET:HE2	8:M:313:U10:H1M3	1.73	0.70
3:H:92:VAL:CG1	3:H:93:SER:N	2.54	0.70
2:M:206:ILE:HD11	6:M:310:BCL:C2B	2.21	0.70
2:M:153:ALA:O	6:M:310:BCL:H71	1.91	0.70
2:M:37:THR:HG22	2:M:38:LEU:N	2.07	0.70
2:M:73:TRP:CE2	2:M:114:LEU:CD1	2.75	0.70
3:H:12:LEU:O	3:H:14:SER:N	2.24	0.70
2:M:139:ALA:HB3	2:M:140:LEU:CD1	2.21	0.70
2:M:149:ALA:HB2	2:M:270:ILE:HD12	1.74	0.70
2:M:64:LEU:O	2:M:67:PHE:N	2.24	0.70
3:H:82:ASP:O	3:H:84:PRO:HD2	1.92	0.70
3:H:146:LYS:NZ	3:H:198:VAL:HG12	2.06	0.70
1:L:177:ILE:CD1	6:L:283:BCL:C1B	2.70	0.70
1:L:231:ARG:O	1:L:235:LEU:HD23	1.92	0.70
2:M:156:LEU:HG	2:M:160:LEU:HD22	1.73	0.70
1:L:147:PRO:O	1:L:148:TYR:CD1	2.43	0.70
1:L:224:ILE:HD12	1:L:232:LEU:CD1	2.19	0.70
2:M:196:LEU:HD13	2:M:294:TRP:HD1	1.52	0.70
2:M:206:ILE:HD13	6:M:311:BCL:CMD	2.21	0.70
3:H:183:LEU:HD21	3:H:189:ARG:CG	2.21	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:128:TYR:O	1:L:129:LEU:C	2.29	0.70
2:M:156:LEU:HD21	2:M:160:LEU:HD23	1.72	0.70
3:H:229:GLU:C	3:H:233:ILE:HG12	2.11	0.70
3:H:22:ILE:O	3:H:24:LEU:N	2.24	0.70
1:L:149:GLY:C	1:L:151:TRP:N	2.39	0.70
2:M:156:LEU:O	2:M:160:LEU:HB2	1.92	0.70
2:M:203:GLY:HA2	6:M:311:BCL:OBD	1.92	0.70
2:M:51:TYR:CD1	2:M:51:TYR:C	2.63	0.70
2:M:73:TRP:CE2	2:M:114:LEU:HD11	2.25	0.70
2:M:73:TRP:CG	2:M:114:LEU:CG	2.71	0.70
3:H:134:MET:CE	3:H:141:HIS:HE1	2.05	0.70
1:L:97:PHE:CE1	6:L:283:BCL:C12	2.75	0.70
6:L:283:BCL:HMC2	6:M:310:BCL:HBC1	1.66	0.70
2:M:109:LEU:HA	2:M:113:GLY:HA3	1.73	0.70
2:M:33:GLY:O	2:M:34:PRO:C	2.28	0.70
3:H:93:SER:O	3:H:96:PHE:HB2	1.92	0.69
1:L:248:MET:HE1	6:L:283:BCL:CAD	2.21	0.69
1:L:248:MET:HE1	6:L:283:BCL:CMD	2.22	0.69
1:L:53:ALA:CB	1:L:64:ILE:HB	2.22	0.69
1:L:69:PRO:HG3	1:L:83:GLY:HA2	1.74	0.69
2:M:109:LEU:HD22	2:M:110:LYS:CA	2.22	0.69
2:M:39:LEU:N	2:M:39:LEU:CD1	2.45	0.69
1:L:183:ASN:HB2	1:L:236:LEU:CB	2.20	0.69
2:M:46:GLN:HE22	2:M:49:PRO:CD	1.95	0.69
3:H:168:TRP:CE2	3:H:190:LEU:HD13	2.27	0.69
1:L:69:PRO:CG	1:L:87:GLN:OE1	2.39	0.69
2:M:139:ALA:HB3	2:M:140:LEU:HD13	1.74	0.69
1:L:208:THR:H	1:L:211:HIS:CD2	2.10	0.69
2:M:299:GLN:NE2	2:M:299:GLN:CA	2.37	0.69
3:H:226:THR:HG22	3:H:229:GLU:OE1	1.92	0.69
1:L:11:VAL:HG13	3:H:87:LEU:HD21	1.73	0.69
1:L:69:PRO:HG3	1:L:83:GLY:HA3	1.74	0.69
2:M:241:ARG:HB2	2:M:241:ARG:NH1	2.07	0.69
2:M:48:GLY:HA2	2:M:49:PRO:O	1.91	0.69
1:L:269:LEU:CD1	1:L:270:PRO:HD2	2.23	0.69
3:H:48:THR:HG23	3:H:51:ALA:O	1.92	0.69
1:L:108:CYS:O	1:L:111:LEU:N	2.24	0.69
2:M:97:PRO:CA	2:M:111:GLU:OE2	2.40	0.69
3:H:111:PRO:CG	3:H:242:MET:HB2	2.20	0.69
3:H:191:LEU:CD2	3:H:205:VAL:HG11	2.21	0.69
3:H:210:SER:HA	3:H:213:PHE:HD2	1.57	0.69
3:H:215:GLY:HA3	3:H:236:TYR:CE2	2.26	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:197:PHE:HE1	6:M:311:BCL:HMD3	1.57	0.69
1:L:165:GLY:HA3	1:L:258:GLN:HG2	1.74	0.69
1:L:25:TRP:HZ2	1:L:110:LYS:HE3	1.57	0.69
2:M:206:ILE:CG1	6:M:310:BCL:CHB	2.71	0.69
1:L:231:ARG:NH2	2:M:7:PHE:CA	2.50	0.69
1:L:195:LEU:CB	2:M:145:HIS:HD2	2.04	0.69
1:L:177:ILE:HD12	6:L:283:BCL:C2B	2.23	0.69
1:L:35:GLY:HA2	1:L:38:THR:HB	1.75	0.69
1:L:71:LEU:C	1:L:73:TYR:H	1.96	0.69
2:M:135:LEU:H	2:M:135:LEU:CD1	1.96	0.69
2:M:208:PHE:CB	2:M:276:VAL:HG23	2.23	0.69
2:M:121:PHE:O	2:M:123:PHE:N	2.26	0.69
2:M:94:LEU:N	2:M:177:TYR:O	2.22	0.69
2:M:197:PHE:CE1	6:M:311:BCL:HMD3	2.28	0.69
1:L:208:THR:OG1	1:L:211:HIS:CD2	2.46	0.69
3:H:238:ALA:O	3:H:239:GLY:C	2.31	0.69
3:H:111:PRO:HB2	3:H:239:GLY:HA2	1.74	0.69
3:H:27:LEU:C	3:H:27:LEU:HD12	2.09	0.69
3:H:179:LEU:CD2	3:H:181:VAL:CG2	2.71	0.68
6:L:283:BCL:HMC2	6:M:310:BCL:HBC2	1.69	0.68
3:H:151:LEU:HD22	3:H:203:VAL:HG22	1.73	0.68
3:H:190:LEU:H	3:H:190:LEU:CD2	2.04	0.68
3:H:85:ILE:C	3:H:87:LEU:H	1.93	0.68
1:L:156:TRP:C	1:L:156:TRP:CD2	2.64	0.68
3:H:156:CYS:O	3:H:158:LEU:HD22	1.94	0.68
2:M:88:ASP:C	2:M:92:PHE:CD2	2.67	0.68
3:H:63:THR:HG23	3:H:74:THR:CG2	2.23	0.68
3:H:12:LEU:C	3:H:14:SER:H	1.95	0.68
3:H:27:LEU:CD1	3:H:32:GLN:NE2	2.56	0.68
1:L:45:GLY:O	1:L:49:ILE:HB	1.93	0.68
2:M:21:THR:O	2:M:21:THR:OG1	2.09	0.68
6:M:310:BCL:C4	7:M:312:BPH:HBB2	2.24	0.68
1:L:10:ARG:HH22	1:L:25:TRP:HB2	1.56	0.68
3:H:156:CYS:O	3:H:158:LEU:N	2.27	0.68
3:H:207:ALA:C	3:H:247:LYS:HZ1	1.96	0.68
3:H:35:ASN:HD22	3:H:35:ASN:N	1.92	0.68
2:M:20:MET:HG3	2:M:22:GLU:N	2.08	0.68
2:M:291:VAL:HG11	2:M:294:TRP:CE2	2.28	0.68
2:M:73:TRP:NE1	2:M:114:LEU:CD1	2.57	0.68
2:M:126:VAL:HG12	2:M:154:ILE:CD1	2.23	0.68
2:M:164:ARG:NH2	2:M:168:MET:HE2	2.09	0.68
2:M:247:ARG:HA	2:M:250:LEU:HB2	1.75	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:73:TYR:HD2	1:L:82:LYS:NZ	1.91	0.68
1:L:86:TRP:O	1:L:87:GLN:C	2.31	0.68
2:M:204:LEU:HA	2:M:207:ALA:HB3	1.75	0.68
1:L:173:HIS:O	1:L:174:MET:C	2.33	0.68
2:M:185:TRP:C	2:M:185:TRP:CD2	2.64	0.68
2:M:214:LEU:O	2:M:217:ALA:CB	2.37	0.68
2:M:73:TRP:CD1	2:M:114:LEU:CD2	2.77	0.68
2:M:81:ASN:CG	2:M:84:VAL:CG2	2.63	0.68
2:M:98:ALA:HB2	2:M:172:SER:HA	1.75	0.68
1:L:101:ALA:HB2	1:L:121:PHE:HE1	1.59	0.67
1:L:153:HIS:CD2	1:L:154:LEU:CD1	2.75	0.67
1:L:171:PRO:O	1:L:172:ALA:C	2.33	0.67
1:L:232:LEU:HA	2:M:42:PHE:CZ	2.23	0.67
1:L:167:PHE:CD2	6:L:283:BCL:CHD	2.73	0.67
1:L:107:ILE:HG22	2:M:254:TRP:HE3	1.59	0.67
1:L:269:LEU:HD13	1:L:270:PRO:HD2	1.76	0.67
3:H:12:LEU:HD23	3:H:13:ALA:N	2.08	0.67
2:M:192:VAL:HG12	2:M:193:HIS:NE2	2.09	0.67
2:M:38:LEU:C	2:M:40:GLY:H	1.96	0.67
7:L:284:BPH:C14	7:L:284:BPH:C17	2.11	0.67
2:M:122:MET:O	2:M:122:MET:CG	2.40	0.67
2:M:164:ARG:O	2:M:167:LEU:HB2	1.94	0.67
1:L:208:THR:O	1:L:211:HIS:CB	2.31	0.67
3:H:206:ASN:O	3:H:208:LEU:N	2.28	0.67
1:L:103:ARG:NH1	1:L:103:ARG:HG2	2.02	0.67
1:L:182:THR:HG22	1:L:183:ASN:N	2.10	0.67
2:M:132:ARG:O	2:M:134:TYR:N	2.28	0.67
2:M:35:PHE:CE2	2:M:47:LEU:HD11	2.29	0.67
1:L:144:TYR:C	1:L:145:ALA:O	2.27	0.67
2:M:90:PHE:HA	2:M:179:ILE:CD1	2.18	0.67
2:M:187:ASN:C	2:M:190:SER:H	1.97	0.67
1:L:17:VAL:O	1:L:19:GLY:N	2.28	0.67
3:H:219:ILE:HG22	3:H:229:GLU:OE2	1.92	0.67
2:M:171:TRP:O	2:M:173:GLU:N	2.28	0.67
1:L:233:GLY:C	1:L:235:LEU:H	1.96	0.67
2:M:152:SER:CA	2:M:277:THR:CG2	2.72	0.67
3:H:103:ASP:C	3:H:106:LYS:HZ1	1.98	0.67
1:L:248:MET:CE	6:L:283:BCL:CMD	2.73	0.67
2:M:284:ILE:CG1	6:M:310:BCL:HED1	2.25	0.67
1:L:35:GLY:HA3	8:M:313:U10:H402	1.77	0.67
1:L:202:LYS:O	1:L:202:LYS:HG2	1.94	0.67
1:L:174:MET:CE	2:M:180:PHE:CZ	2.78	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:119:SER:CB	2:M:177:TYR:OH	2.43	0.67
2:M:264:GLY:HA2	2:M:267:ARG:CB	2.25	0.67
2:M:89:LEU:N	2:M:92:PHE:HE2	1.93	0.67
3:H:80:SER:O	3:H:81:GLU:HG3	1.95	0.67
3:H:44:ASN:H	3:H:44:ASN:HD22	1.42	0.66
8:M:313:U10:H8	8:M:313:U10:H1M1	1.77	0.66
2:M:39:LEU:H	2:M:39:LEU:CD1	1.97	0.66
3:H:146:LYS:NZ	3:H:198:VAL:O	2.28	0.66
1:L:181:PHE:O	1:L:184:ALA:CB	2.43	0.66
2:M:98:ALA:HA	2:M:100:GLU:N	2.10	0.66
2:M:54:SER:O	2:M:57:VAL:HG11	1.94	0.66
3:H:170:ASP:OD2	3:H:177:ARG:CZ	2.43	0.66
3:H:34:GLU:OE2	3:H:59:PRO:HB3	1.95	0.66
1:L:241:VAL:O	1:L:244:SER:CB	2.41	0.66
1:L:248:MET:CE	6:L:283:BCL:HMD1	2.25	0.66
2:M:72:ILE:C	2:M:74:PHE:N	2.49	0.66
3:H:156:CYS:SG	3:H:209:SER:N	2.68	0.66
3:H:37:ARG:O	3:H:39:GLY:N	2.29	0.66
3:H:64:PHE:N	3:H:73:LEU:O	2.22	0.66
1:L:69:PRO:HB3	1:L:78:ALA:HB2	1.75	0.66
2:M:85:PHE:O	2:M:89:LEU:HB2	1.95	0.66
3:H:155:GLY:O	3:H:206:ASN:HA	1.96	0.66
3:H:40:TYR:H	3:H:42:LEU:HD11	1.57	0.66
1:L:182:THR:O	1:L:185:LEU:HD23	1.94	0.66
1:L:49:ILE:HA	1:L:89:ILE:HD11	1.75	0.66
2:M:154:ILE:O	2:M:158:MET:N	2.28	0.66
2:M:159:VAL:O	2:M:162:PHE:N	2.27	0.66
2:M:46:GLN:HE21	2:M:48:GLY:C	1.98	0.66
2:M:87:ARG:CG	2:M:88:ASP:CG	2.63	0.66
3:H:184:LYS:HE3	3:H:184:LYS:HA	1.76	0.66
1:L:222:TYR:HD1	1:L:223:SER:N	1.87	0.66
1:L:60:ASN:CB	1:L:63:LEU:HD12	2.24	0.66
2:M:131:GLY:O	2:M:134:TYR:HB2	1.93	0.66
3:H:140:PHE:HZ	3:H:171:ILE:HG23	1.61	0.66
3:H:27:LEU:HD12	3:H:28:ILE:HG13	1.66	0.66
1:L:212:GLU:O	1:L:215:PHE:N	2.27	0.66
1:L:242:PHE:HE1	1:L:243:PHE:HD1	1.44	0.66
1:L:244:SER:OG	6:L:283:BCL:HMA2	1.95	0.66
1:L:51:TRP:CH2	1:L:80:LEU:CD1	2.79	0.66
2:M:238:ILE:HD11	2:M:263:GLU:N	2.10	0.66
2:M:157:TRP:HB2	6:M:310:BCL:H92	1.77	0.66
2:M:82:PRO:O	2:M:83:ALA:C	2.33	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:135:ARG:CB	1:L:136:PRO:HD3	2.15	0.66
1:L:119:PHE:HE1	1:L:238:LEU:CD1	2.09	0.66
2:M:50:ILE:CG2	2:M:51:TYR:N	2.59	0.66
3:H:103:ASP:C	3:H:106:LYS:NZ	2.49	0.66
1:L:119:PHE:CE1	1:L:238:LEU:CD1	2.78	0.66
1:L:53:ALA:O	1:L:59:TRP:HB3	1.95	0.66
2:M:152:SER:CA	2:M:277:THR:HG21	2.24	0.66
1:L:232:LEU:C	1:L:235:LEU:HB2	2.15	0.66
2:M:228:ARG:HH12	3:H:241:LEU:HD11	1.61	0.66
2:M:237:GLN:OE1	2:M:244:ALA:CB	2.42	0.66
2:M:275:LEU:HA	2:M:278:LEU:HB3	1.77	0.66
1:L:33:PHE:CG	1:L:33:PHE:O	2.39	0.66
3:H:105:MET:N	3:H:106:LYS:NZ	2.44	0.66
3:H:206:ASN:O	3:H:207:ALA:C	2.35	0.65
3:H:104:PRO:HG3	3:H:243:TYR:CE2	2.31	0.65
1:L:86:TRP:O	1:L:87:GLN:O	2.14	0.65
2:M:228:ARG:CG	2:M:228:ARG:NH1	2.40	0.65
2:M:72:ILE:C	2:M:74:PHE:H	1.97	0.65
3:H:124:ASP:O	3:H:125:GLY:C	2.33	0.65
1:L:85:LEU:HA	1:L:88:ILE:HD12	1.78	0.65
2:M:109:LEU:CD2	2:M:110:LYS:N	2.47	0.65
2:M:201:PHE:CG	2:M:282:ILE:HG22	2.32	0.65
1:L:113:ILE:HG22	1:L:114:GLY:N	2.11	0.65
2:M:275:LEU:CD1	2:M:278:LEU:HD23	2.25	0.65
3:H:187:SER:OG	3:H:188:THR:N	2.30	0.65
1:L:48:LEU:CD1	1:L:89:ILE:CG1	2.73	0.65
1:L:47:ILE:CG2	1:L:48:LEU:N	2.59	0.65
2:M:214:LEU:HD12	2:M:214:LEU:C	2.16	0.65
1:L:226:THR:CG2	2:M:232:GLU:HB2	2.25	0.65
1:L:208:THR:CB	1:L:211:HIS:CD2	2.69	0.65
3:H:235:GLY:O	3:H:238:ALA:N	2.29	0.65
3:H:30:TYR:O	3:H:31:LEU:C	2.35	0.65
2:M:120:PHE:O	2:M:121:PHE:HD1	1.75	0.65
3:H:191:LEU:HD21	3:H:213:PHE:CE1	2.32	0.65
1:L:10:ARG:HH21	3:H:95:GLY:C	2.00	0.65
1:L:175:ILE:HG23	1:L:179:PHE:HE1	1.62	0.65
1:L:248:MET:CE	6:L:283:BCL:C2D	2.69	0.65
2:M:204:LEU:CA	2:M:207:ALA:HB3	2.25	0.65
2:M:209:LEU:HD23	2:M:276:VAL:HG11	1.78	0.65
2:M:21:THR:HG22	2:M:140:LEU:HD11	1.79	0.65
3:H:20:PHE:C	3:H:20:PHE:CD1	2.70	0.65
1:L:139:MET:O	1:L:141:ALA:N	2.30	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:128:SER:OG	2:M:129:TRP:N	2.25	0.65
2:M:233:ARG:HH21	3:H:122:GLU:CD	1.98	0.65
1:L:20:ASN:O	1:L:23:ASP:N	2.30	0.65
1:L:208:THR:HG23	1:L:211:HIS:NE2	2.08	0.65
2:M:236:GLU:OE2	3:H:122:GLU:HA	1.97	0.65
3:H:75:VAL:HB	3:H:76:PRO:HD3	1.77	0.65
1:L:11:VAL:CG1	3:H:87:LEU:HD21	2.27	0.65
1:L:97:PHE:HE1	6:L:283:BCL:H143	1.54	0.65
2:M:128:SER:C	2:M:130:TRP:N	2.48	0.65
3:H:115:VAL:CG1	3:H:116:ALA:N	2.58	0.64
3:H:171:ILE:N	3:H:171:ILE:HD12	2.12	0.64
3:H:215:GLY:O	3:H:216:ILE:C	2.36	0.64
3:H:42:LEU:HD21	3:H:76:PRO:HA	1.77	0.64
1:L:124:ALA:C	1:L:126:LEU:N	2.50	0.64
1:L:187:LEU:HD12	1:L:187:LEU:O	1.97	0.64
2:M:242:GLY:HA2	3:H:115:VAL:CG1	2.18	0.64
3:H:116:ALA:HA	3:H:228:LEU:HD12	1.76	0.64
1:L:185:LEU:N	1:L:185:LEU:CD2	2.59	0.64
1:L:215:PHE:HZ	2:M:133:THR:HG22	1.60	0.64
1:L:248:MET:C	1:L:250:ILE:H	1.97	0.64
3:H:193:MET:O	3:H:195:MET:O	2.16	0.64
3:H:204:HIS:CE1	3:H:205:VAL:HG13	2.33	0.64
1:L:86:TRP:CE3	1:L:87:GLN:CA	2.79	0.64
2:M:88:ASP:O	2:M:92:PHE:CD2	2.50	0.64
1:L:123:PHE:CD1	1:L:238:LEU:HD21	2.32	0.64
1:L:171:PRO:HG3	1:L:263:TRP:CZ2	2.32	0.64
2:M:152:SER:CB	2:M:277:THR:CG2	2.75	0.64
2:M:57:VAL:HG23	2:M:58:LEU:H	1.47	0.64
3:H:182:GLU:CA	3:H:187:SER:O	2.45	0.64
1:L:94:THR:HG23	1:L:129:LEU:CD1	2.27	0.64
1:L:159:ASN:O	1:L:160:THR:C	2.36	0.64
1:L:16:LEU:CB	1:L:106:GLU:OE2	2.45	0.64
1:L:171:PRO:C	1:L:173:HIS:N	2.50	0.64
1:L:173:HIS:HA	1:L:247:CYS:SG	2.37	0.64
1:L:25:TRP:CZ2	1:L:110:LYS:HE3	2.33	0.64
2:M:119:SER:OG	2:M:120:PHE:N	2.25	0.64
2:M:275:LEU:O	2:M:278:LEU:N	2.30	0.64
3:H:105:MET:N	3:H:106:LYS:HZ1	1.95	0.64
1:L:48:LEU:HD13	1:L:85:LEU:HD12	1.79	0.64
2:M:164:ARG:CZ	2:M:168:MET:CE	2.76	0.64
2:M:208:PHE:C	2:M:276:VAL:CG2	2.65	0.64
1:L:67:TYR:HD1	1:L:67:TYR:N	1.95	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:187:ASN:ND2	2:M:187:ASN:C	2.51	0.64
3:H:39:GLY:HA2	3:H:42:LEU:CD2	2.27	0.64
1:L:215:PHE:HE1	1:L:219:LEU:CD2	2.03	0.64
2:M:117:ILE:HG22	2:M:118:ALA:N	2.11	0.64
2:M:35:PHE:CD2	2:M:39:LEU:HD23	2.33	0.64
2:M:66:TRP:HZ2	4:M:308:BOG:H1'1	1.62	0.64
3:H:44:ASN:N	3:H:44:ASN:HD22	1.96	0.64
1:L:241:VAL:HG21	7:L:284:BPH:HBC3	1.80	0.64
1:L:85:LEU:O	1:L:89:ILE:HB	1.98	0.64
1:L:205:GLU:HA	3:H:65:ILE:HG23	1.75	0.64
3:H:196:VAL:HG12	3:H:205:VAL:HB	1.79	0.64
1:L:175:ILE:O	1:L:178:SER:N	2.31	0.64
1:L:97:PHE:CZ	6:L:283:BCL:C12	2.78	0.64
2:M:12:VAL:HG13	2:M:13:ARG:N	2.13	0.64
2:M:175:VAL:HG22	2:M:185:TRP:CE2	2.33	0.64
1:L:75:LEU:HG	1:L:140:GLY:C	2.18	0.63
2:M:138:GLN:O	2:M:139:ALA:C	2.36	0.63
2:M:298:GLY:O	2:M:301:HIS:N	2.29	0.63
3:H:31:LEU:O	3:H:32:GLN:O	2.16	0.63
1:L:135:ARG:O	1:L:139:MET:HE2	1.98	0.63
1:L:226:THR:CG2	2:M:232:GLU:CB	2.76	0.63
2:M:150:PHE:CE1	7:M:312:BPH:C4D	2.81	0.63
3:H:208:LEU:O	3:H:209:SER:C	2.36	0.63
1:L:93:ALA:HB1	1:L:97:PHE:CD2	2.33	0.63
3:H:168:TRP:NE1	3:H:190:LEU:HD13	2.13	0.63
1:L:123:PHE:CD2	1:L:238:LEU:CD2	2.81	0.63
3:H:175:MET:O	3:H:177:ARG:N	2.30	0.63
1:L:67:TYR:CD1	1:L:67:TYR:N	2.66	0.63
2:M:197:PHE:HZ	6:M:310:BCL:HBB1	1.52	0.63
2:M:208:PHE:CB	2:M:276:VAL:CG2	2.77	0.63
2:M:34:PRO:HA	2:M:45:ALA:O	1.99	0.63
1:L:206:MET:CB	3:H:65:ILE:O	2.46	0.63
1:L:241:VAL:HG12	1:L:242:PHE:H	1.58	0.63
7:L:284:BPH:HHC	7:L:284:BPH:OBB	1.97	0.63
3:H:151:LEU:CD2	3:H:203:VAL:CG2	2.73	0.63
1:L:108:CYS:O	1:L:110:LYS:N	2.32	0.63
1:L:109:ARG:CA	1:L:109:ARG:HE	2.10	0.63
1:L:135:ARG:HG2	1:L:139:MET:CE	2.29	0.63
1:L:226:THR:CG2	2:M:232:GLU:O	2.47	0.63
1:L:244:SER:O	1:L:247:CYS:HB2	1.98	0.63
2:M:114:LEU:HD12	2:M:114:LEU:N	2.06	0.63
3:H:12:LEU:HD22	3:H:13:ALA:N	2.14	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:42:LEU:HD23	3:H:76:PRO:HA	1.80	0.63
2:M:156:LEU:HD23	2:M:156:LEU:C	2.19	0.63
2:M:197:PHE:CE2	6:M:310:BCL:HMC2	2.34	0.63
3:H:203:VAL:O	3:H:204:HIS:HB2	1.99	0.63
1:L:109:ARG:HE	1:L:109:ARG:HA	1.63	0.63
1:L:133:LEU:HD13	1:L:137:VAL:HG21	1.76	0.63
1:L:147:PRO:CD	1:L:156:TRP:HB2	2.27	0.63
1:L:193:LEU:CD2	8:L:285:U10:C3	2.73	0.63
1:L:48:LEU:CD1	1:L:89:ILE:CD1	2.77	0.63
2:M:152:SER:HB3	2:M:277:THR:CG2	2.29	0.63
2:M:25:ASN:HD22	2:M:26:LEU:N	1.97	0.63
2:M:157:TRP:O	2:M:159:VAL:N	2.32	0.62
1:L:177:ILE:CD1	6:L:283:BCL:C2B	2.76	0.62
2:M:164:ARG:CZ	2:M:168:MET:HE1	2.30	0.62
2:M:243:THR:HG21	2:M:247:ARG:HH21	1.64	0.62
1:L:181:PHE:HE1	6:M:310:BCL:HBA2	1.63	0.62
2:M:38:LEU:HD12	2:M:38:LEU:H	1.64	0.62
1:L:54:VAL:HG12	1:L:55:LEU:H	1.64	0.62
3:H:27:LEU:HB2	3:H:32:GLN:OE1	1.99	0.62
1:L:185:LEU:CA	1:L:188:ALA:CB	2.59	0.62
1:L:219:LEU:CA	2:M:132:ARG:NH2	2.60	0.62
2:M:35:PHE:CD1	2:M:39:LEU:HD22	2.34	0.62
2:M:51:TYR:HE1	2:M:53:GLY:HA3	1.64	0.62
1:L:113:ILE:HD12	2:M:226:VAL:CG2	2.27	0.62
1:L:21:LEU:HD12	1:L:22:PHE:CD1	2.33	0.62
2:M:96:PRO:C	2:M:98:ALA:H	2.02	0.62
3:H:177:ARG:NH1	3:H:177:ARG:HG3	2.14	0.62
3:H:20:PHE:HD1	3:H:21:TRP:N	1.98	0.62
1:L:152:THR:O	1:L:154:LEU:N	2.32	0.62
1:L:181:PHE:CE1	6:M:310:BCL:H11	2.34	0.62
1:L:188:ALA:HB2	7:M:312:BPH:HBC2	1.81	0.62
1:L:227:LEU:CD2	1:L:231:ARG:HH11	2.13	0.62
2:M:73:TRP:CG	2:M:114:LEU:HD21	2.35	0.62
2:M:76:TYR:O	2:M:76:TYR:HD1	1.83	0.62
3:H:132:LYS:HB3	3:H:133:PRO:CD	2.28	0.62
1:L:232:LEU:CG	2:M:42:PHE:CZ	2.77	0.62
2:M:88:ASP:CA	2:M:92:PHE:CE2	2.83	0.62
3:H:183:LEU:HD11	3:H:189:ARG:CD	2.28	0.62
3:H:39:GLY:CA	3:H:42:LEU:HD11	2.28	0.62
1:L:113:ILE:HD12	2:M:225:ALA:O	2.00	0.62
1:L:159:ASN:O	1:L:163:THR:N	2.33	0.62
2:M:215:LEU:HA	2:M:218:MET:HB2	1.81	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:242:GLY:O	2:M:243:THR:C	2.37	0.62
3:H:56:PHE:CE1	3:H:57:PRO:HD2	2.32	0.62
1:L:54:VAL:HG12	1:L:55:LEU:N	2.13	0.62
1:L:64:ILE:HD12	1:L:64:ILE:C	2.20	0.62
2:M:103:LEU:CD1	2:M:166:ILE:HA	2.30	0.62
2:M:277:THR:CG2	2:M:277:THR:O	2.48	0.62
3:H:27:LEU:CD2	3:H:32:GLN:NE2	2.39	0.62
3:H:44:ASN:H	3:H:44:ASN:ND2	1.97	0.62
1:L:133:LEU:CD1	1:L:137:VAL:HG23	2.25	0.62
1:L:155:ASP:O	1:L:157:VAL:N	2.33	0.62
1:L:222:TYR:O	1:L:223:SER:HB3	1.99	0.62
1:L:111:LEU:HD21	2:M:251:PHE:HB2	1.81	0.62
1:L:206:MET:HB3	3:H:65:ILE:O	1.98	0.62
3:H:115:VAL:HG12	3:H:116:ALA:H	1.62	0.62
1:L:193:LEU:HD23	8:L:285:U10:C2	2.30	0.62
1:L:15:THR:HG21	1:L:19:GLY:N	2.15	0.62
1:L:10:ARG:NH1	1:L:25:TRP:CD1	2.68	0.61
1:L:79:PRO:C	1:L:81:ALA:H	1.99	0.61
2:M:193:HIS:ND1	2:M:287:SER:O	2.33	0.61
2:M:60:LEU:CD1	7:M:312:BPH:H6C1	2.27	0.61
3:H:27:LEU:C	3:H:32:GLN:OE1	2.39	0.61
3:H:123:LEU:HD23	3:H:126:HIS:O	2.00	0.61
3:H:148:PRO:HA	3:H:151:LEU:HD13	1.81	0.61
3:H:27:LEU:CB	3:H:32:GLN:OE1	2.47	0.61
1:L:32:GLY:O	1:L:34:PHE:N	2.29	0.61
2:M:135:LEU:HA	2:M:138:GLN:HB2	1.83	0.61
2:M:140:LEU:HD12	2:M:140:LEU:N	2.15	0.61
1:L:208:THR:OG1	1:L:211:HIS:HD2	1.82	0.61
1:L:219:LEU:HA	2:M:132:ARG:NH2	2.06	0.61
6:L:282:BCL:C1	7:M:312:BPH:OBB	2.48	0.61
1:L:248:MET:CE	6:L:283:BCL:CAD	2.78	0.61
2:M:100:GLU:O	2:M:101:TYR:HB2	1.99	0.61
2:M:204:LEU:C	2:M:207:ALA:HB3	2.19	0.61
2:M:37:THR:CG2	2:M:38:LEU:HG	2.30	0.61
3:H:115:VAL:HG13	3:H:116:ALA:H	1.65	0.61
1:L:78:ALA:HB1	1:L:79:PRO:CD	2.30	0.61
1:L:195:LEU:CB	2:M:145:HIS:CD2	2.72	0.61
2:M:92:PHE:O	2:M:93:SER:HB3	1.99	0.61
3:H:205:VAL:HG22	3:H:205:VAL:O	2.01	0.61
1:L:146:PHE:HB2	1:L:156:TRP:CD1	2.35	0.61
1:L:264:GLN:C	1:L:266:TRP:N	2.50	0.61
1:L:62:GLN:HB3	1:L:63:LEU:HG	1.81	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:230:GLY:O	2:M:232:GLU:N	2.33	0.61
3:H:189:ARG:CB	3:H:189:ARG:HH11	2.07	0.61
1:L:222:TYR:HE1	2:M:44:ASN:HB3	1.64	0.61
6:L:283:BCL:C14	7:L:284:BPH:O2A	2.47	0.61
2:M:290:VAL:CG1	2:M:290:VAL:O	2.47	0.61
2:M:199:ASN:ND2	2:M:294:TRP:CZ2	2.68	0.61
2:M:284:ILE:CD1	6:M:310:BCL:CED	2.78	0.61
2:M:78:ALA:HB1	2:M:84:VAL:HG12	1.81	0.61
1:L:10:ARG:HH21	3:H:95:GLY:CA	2.12	0.61
1:L:255:TRP:CD1	1:L:259:TRP:CZ3	2.88	0.61
2:M:105:PHE:O	2:M:107:ALA:N	2.33	0.61
2:M:186:THR:O	2:M:189:PHE:N	2.34	0.61
1:L:206:MET:N	3:H:65:ILE:CG2	2.34	0.61
3:H:106:LYS:NZ	3:H:106:LYS:H	1.98	0.61
2:M:109:LEU:HD23	2:M:114:LEU:CD1	2.21	0.61
2:M:185:TRP:CE3	2:M:186:THR:HA	2.36	0.61
2:M:35:PHE:N	2:M:45:ALA:O	2.23	0.61
2:M:97:PRO:HA	2:M:111:GLU:OE2	2.01	0.61
2:M:102:GLY:C	2:M:104:SER:N	2.48	0.61
3:H:199:GLN:HE21	3:H:200:SER:N	1.99	0.61
2:M:261:THR:HB	3:H:36:MET:HA	1.82	0.61
6:L:283:BCL:H102	7:L:284:BPH:CHB	2.30	0.61
2:M:120:PHE:CD1	2:M:162:PHE:CE2	2.86	0.61
2:M:238:ILE:HD11	2:M:263:GLU:HA	1.82	0.61
2:M:206:ILE:HG12	6:M:310:BCL:CHB	2.31	0.61
2:M:70:ILE:HD11	2:M:74:PHE:CE2	2.35	0.61
1:L:204:LYS:CB	1:L:207:ARG:HH12	2.09	0.61
3:H:213:PHE:CD1	3:H:216:ILE:CD1	2.84	0.60
1:L:175:ILE:HG23	1:L:179:PHE:CE1	2.36	0.60
1:L:75:LEU:CD2	1:L:141:ALA:CA	2.79	0.60
1:L:73:TYR:HD2	1:L:82:LYS:HZ1	1.41	0.60
1:L:174:MET:HE3	2:M:180:PHE:CZ	2.36	0.60
2:M:264:GLY:O	2:M:267:ARG:N	2.34	0.60
2:M:37:THR:O	2:M:41:TRP:HD1	1.83	0.60
1:L:6:GLU:CD	1:L:10:ARG:HD3	2.20	0.60
3:H:179:LEU:HD23	3:H:181:VAL:CG2	2.31	0.60
3:H:190:LEU:HD23	3:H:190:LEU:N	2.06	0.60
3:H:20:PHE:C	3:H:22:ILE:H	2.05	0.60
6:L:283:BCL:H41	6:L:283:BCL:H71	1.83	0.60
8:L:285:U10:C26	8:L:285:U10:C30	2.79	0.60
2:M:282:ILE:O	2:M:283:GLY:C	2.38	0.60
3:H:123:LEU:HD21	3:H:127:GLY:HA2	1.82	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:132:LYS:O	3:H:168:TRP:HB3	2.01	0.60
3:H:204:HIS:HB3	3:H:206:ASN:ND2	2.17	0.60
1:L:133:LEU:HD13	1:L:137:VAL:CG2	2.29	0.60
1:L:215:PHE:CZ	2:M:133:THR:HG22	2.36	0.60
2:M:100:GLU:CA	2:M:172:SER:OG	2.46	0.60
2:M:271:TRP:O	2:M:272:MET:C	2.38	0.60
3:H:129:ASN:O	3:H:131:ILE:N	2.34	0.60
3:H:219:ILE:HA	3:H:229:GLU:CG	2.31	0.60
2:M:260:ALA:CB	3:H:36:MET:HG3	2.28	0.60
1:L:234:LEU:HD21	1:L:238:LEU:HD12	1.84	0.60
2:M:168:MET:HG3	2:M:173:GLU:HG3	1.82	0.60
3:H:191:LEU:CG	3:H:205:VAL:HG11	2.29	0.60
1:L:124:ALA:O	1:L:126:LEU:N	2.34	0.60
1:L:267:VAL:CG1	2:M:87:ARG:CD	2.73	0.60
2:M:13:ARG:NH1	2:M:34:PRO:CB	2.64	0.60
2:M:197:PHE:C	2:M:199:ASN:H	2.03	0.60
2:M:35:PHE:CD2	2:M:39:LEU:HD21	2.35	0.60
3:H:123:LEU:HD23	3:H:127:GLY:HA2	1.84	0.60
2:M:13:ARG:CD	3:H:143:SER:OG	2.49	0.60
1:L:154:LEU:O	1:L:158:SER:N	2.34	0.60
1:L:262:TRP:HD1	1:L:263:TRP:CE3	2.18	0.60
8:L:285:U10:H261	8:L:285:U10:C30	2.27	0.60
2:M:114:LEU:O	2:M:118:ALA:N	2.35	0.60
3:H:94:GLU:OE1	3:H:94:GLU:N	2.34	0.60
1:L:244:SER:O	1:L:246:LEU:N	2.34	0.60
2:M:222:THR:O	2:M:224:LEU:N	2.34	0.60
2:M:235:LEU:C	2:M:237:GLN:H	2.02	0.60
1:L:28:PRO:O	2:M:254:TRP:HA	2.01	0.60
3:H:135:LYS:O	3:H:137:ALA:N	2.35	0.60
3:H:180:GLU:C	3:H:181:VAL:CG2	2.70	0.60
1:L:101:ALA:O	1:L:104:GLU:N	2.35	0.60
1:L:107:ILE:HD12	2:M:255:THR:HG1	1.65	0.60
1:L:60:ASN:ND2	1:L:63:LEU:CD1	2.64	0.60
2:M:150:PHE:HE1	7:M:312:BPH:C4D	2.13	0.60
2:M:85:PHE:CD1	2:M:89:LEU:HD12	2.36	0.60
3:H:134:MET:N	3:H:166:ASP:OD2	2.35	0.60
3:H:185:ASP:C	3:H:187:SER:N	2.54	0.60
1:L:123:PHE:CD2	1:L:238:LEU:HD21	2.37	0.60
1:L:25:TRP:O	1:L:26:VAL:C	2.40	0.60
1:L:24:PHE:CD2	1:L:31:VAL:HG21	2.37	0.60
1:L:75:LEU:HD21	1:L:141:ALA:CA	2.32	0.60
2:M:129:TRP:HA	2:M:132:ARG:HB2	1.84	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:M:313:U10:H361	8:M:313:U10:H402	1.83	0.60
2:M:17:ASP:C	2:M:18:LEU:CG	2.70	0.60
1:L:169:TYR:O	1:L:170:ASN:C	2.40	0.59
1:L:49:ILE:HG12	1:L:89:ILE:HD13	1.84	0.59
1:L:53:ALA:CB	1:L:64:ILE:CB	2.80	0.59
2:M:140:LEU:CD1	2:M:140:LEU:H	2.15	0.59
2:M:208:PHE:C	2:M:210:TYR:N	2.54	0.59
2:M:238:ILE:HG23	3:H:64:PHE:CE2	2.37	0.59
2:M:27:ALA:CB	2:M:51:TYR:HA	2.32	0.59
2:M:291:VAL:HG21	2:M:294:TRP:CZ3	2.37	0.59
3:H:60:LYS:O	3:H:60:LYS:CG	2.48	0.59
3:H:31:LEU:O	3:H:34:GLU:CB	2.50	0.59
1:L:144:TYR:HE1	1:L:160:THR:OG1	1.85	0.59
2:M:197:PHE:CE1	6:M:311:BCL:CMD	2.77	0.59
7:M:312:BPH:H4C1	7:M:312:BPH:H8	1.84	0.59
1:L:84:GLY:C	1:L:86:TRP:H	2.04	0.59
1:L:113:ILE:HD13	2:M:229:PHE:HE1	1.68	0.59
2:M:164:ARG:HH11	2:M:164:ARG:HG2	1.67	0.59
1:L:5:PHE:CZ	2:M:246:GLU:HA	2.38	0.59
3:H:134:MET:O	3:H:137:ALA:CB	2.48	0.59
3:H:34:GLU:CD	3:H:59:PRO:HB3	2.22	0.59
2:M:271:TRP:O	2:M:273:ALA:N	2.36	0.59
6:M:310:BCL:HBB3	6:M:310:BCL:CHC	2.32	0.59
2:M:35:PHE:HE1	2:M:38:LEU:HD13	1.67	0.59
2:M:37:THR:HG22	2:M:38:LEU:CG	2.31	0.59
2:M:95:GLU:OE1	2:M:176:PRO:HB2	2.03	0.59
3:H:204:HIS:HE1	3:H:213:PHE:CZ	2.20	0.59
1:L:8:LYS:O	1:L:11:VAL:CG1	2.50	0.59
1:L:135:ARG:O	1:L:139:MET:CE	2.51	0.59
1:L:73:TYR:CG	1:L:82:LYS:NZ	2.68	0.59
2:M:205:SER:CA	2:M:279:THR:HG21	2.31	0.59
2:M:24:VAL:C	2:M:26:LEU:H	2.05	0.59
3:H:103:ASP:O	3:H:106:LYS:CE	2.50	0.59
1:L:171:PRO:O	1:L:174:MET:CB	2.49	0.59
2:M:137:ALA:HA	2:M:142:MET:HG3	1.83	0.59
2:M:82:PRO:O	2:M:84:VAL:N	2.36	0.59
3:H:179:LEU:O	3:H:181:VAL:HG23	2.02	0.59
1:L:25:TRP:CZ2	1:L:110:LYS:CE	2.86	0.59
1:L:62:GLN:C	1:L:63:LEU:HG	2.23	0.59
1:L:80:LEU:HD12	1:L:80:LEU:O	2.03	0.59
1:L:90:THR:C	1:L:92:CYS:H	2.05	0.59
2:M:201:PHE:CD2	2:M:282:ILE:HG22	2.38	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:11:GLN:NE2	3:H:144:ALA:HB3	2.18	0.59
3:H:204:HIS:CD2	3:H:205:VAL:C	2.76	0.59
1:L:100:TRP:O	1:L:104:GLU:N	2.36	0.59
1:L:10:ARG:NH2	1:L:25:TRP:CB	2.63	0.59
1:L:237:SER:O	1:L:238:LEU:C	2.41	0.59
1:L:167:PHE:HZ	1:L:251:THR:HG21	1.68	0.59
1:L:67:TYR:HB3	1:L:68:PRO:HD2	1.85	0.59
1:L:227:LEU:HD12	2:M:232:GLU:CD	2.23	0.59
1:L:268:LYS:HD2	1:L:269:LEU:HB2	1.84	0.59
3:H:183:LEU:N	3:H:187:SER:O	2.36	0.58
1:L:92:CYS:O	1:L:96:ALA:CB	2.51	0.58
1:L:147:PRO:HD2	1:L:156:TRP:CB	2.32	0.58
1:L:162:TYR:CE1	6:L:283:BCL:HBC3	2.38	0.58
1:L:75:LEU:HD23	1:L:142:TRP:N	2.18	0.58
2:M:135:LEU:O	2:M:138:GLN:HB2	2.03	0.58
2:M:193:HIS:O	2:M:293:ASN:HA	2.02	0.58
2:M:249:ALA:HB1	8:M:313:U10:C4M	2.27	0.58
3:H:117:ARG:HB2	3:H:227:LEU:HB2	1.85	0.58
3:H:41:PRO:O	3:H:43:GLU:N	2.37	0.58
1:L:248:MET:CE	6:L:283:BCL:OBD	2.51	0.58
2:M:103:LEU:HD13	2:M:166:ILE:HA	1.85	0.58
2:M:224:LEU:C	2:M:226:VAL:H	2.06	0.58
2:M:36:SER:OG	2:M:37:THR:N	2.36	0.58
3:H:191:LEU:HD21	3:H:213:PHE:CZ	2.36	0.58
3:H:239:GLY:O	3:H:243:TYR:N	2.26	0.58
3:H:238:ALA:C	3:H:240:GLY:N	2.53	0.58
1:L:177:ILE:CD1	6:L:283:BCL:CHB	2.81	0.58
2:M:120:PHE:CE1	2:M:162:PHE:HE2	2.22	0.58
2:M:46:GLN:HG2	2:M:47:LEU:N	2.05	0.58
2:M:187:ASN:HD22	2:M:188:ASN:H	0.61	0.58
3:H:20:PHE:C	3:H:22:ILE:N	2.56	0.58
2:M:243:THR:O	2:M:244:ALA:C	2.42	0.58
1:L:31:VAL:HA	8:M:313:U10:H403	1.83	0.58
2:M:37:THR:HG22	2:M:38:LEU:H	1.69	0.58
2:M:71:GLY:O	2:M:74:PHE:HB2	2.04	0.58
2:M:68:PHE:O	2:M:72:ILE:N	2.36	0.58
3:H:116:ALA:CB	3:H:228:LEU:CD1	2.82	0.58
2:M:114:LEU:O	2:M:117:ILE:N	2.35	0.58
1:L:226:THR:HG21	2:M:232:GLU:HB2	1.85	0.58
2:M:25:ASN:HD22	2:M:25:ASN:C	2.06	0.58
2:M:201:PHE:CE1	2:M:282:ILE:HG21	2.38	0.58
1:L:269:LEU:HD13	1:L:270:PRO:CD	2.34	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:57:PRO:O	3:H:58:LEU:HB2	2.02	0.58
1:L:151:TRP:O	1:L:154:LEU:HD13	2.03	0.58
1:L:85:LEU:O	1:L:89:ILE:HD12	2.04	0.58
2:M:35:PHE:CD1	2:M:39:LEU:CD2	2.86	0.58
3:H:195:MET:O	3:H:196:VAL:CG2	2.48	0.58
3:H:20:PHE:HE1	3:H:24:LEU:CD1	2.14	0.58
1:L:101:ALA:O	1:L:104:GLU:CB	2.51	0.58
1:L:127:ALA:CB	6:L:283:BCL:C2	2.81	0.58
1:L:146:PHE:HB2	1:L:156:TRP:CG	2.38	0.58
1:L:127:ALA:HB3	6:L:283:BCL:H2	1.86	0.58
1:L:190:HIS:HA	8:L:285:U10:O2	2.03	0.58
3:H:134:MET:SD	3:H:140:PHE:O	2.61	0.58
3:H:140:PHE:CZ	3:H:171:ILE:HG23	2.38	0.58
3:H:212:LEU:C	3:H:214:ALA:H	2.07	0.58
3:H:213:PHE:HD1	3:H:216:ILE:HD13	1.69	0.58
3:H:39:GLY:N	3:H:42:LEU:HD11	2.18	0.58
3:H:96:PHE:C	3:H:97:PRO:O	2.42	0.58
2:M:204:LEU:C	2:M:207:ALA:CB	2.73	0.58
2:M:155:TRP:NE1	2:M:278:LEU:O	2.36	0.58
3:H:56:PHE:CE1	3:H:57:PRO:CD	2.85	0.58
3:H:183:LEU:HD11	3:H:189:ARG:HD2	1.86	0.58
3:H:116:ALA:CA	3:H:228:LEU:HD12	2.31	0.58
1:L:262:TRP:CD1	1:L:263:TRP:CE3	2.92	0.58
1:L:33:PHE:HD1	1:L:33:PHE:C	1.99	0.58
1:L:15:THR:HG22	1:L:15:THR:O	2.04	0.58
3:H:219:ILE:HG22	3:H:229:GLU:HG2	1.84	0.57
6:L:282:BCL:HMD2	6:L:283:BCL:CBB	2.34	0.57
1:L:6:GLU:O	1:L:8:LYS:N	2.37	0.57
2:M:39:LEU:H	2:M:39:LEU:CD2	2.13	0.57
1:L:98:VAL:CG2	1:L:125:ILE:HD11	2.35	0.57
1:L:179:PHE:CB	1:L:240:ALA:CB	2.58	0.57
1:L:78:ALA:HB1	1:L:83:GLY:HA3	1.86	0.57
2:M:205:SER:CB	2:M:279:THR:CG2	2.82	0.57
2:M:281:GLY:O	2:M:285:LEU:HD23	2.04	0.57
2:M:82:PRO:O	2:M:85:PHE:N	2.37	0.57
3:H:123:LEU:O	3:H:130:LYS:HG3	2.03	0.57
3:H:154:ARG:HA	3:H:160:ILE:HG23	1.86	0.57
3:H:229:GLU:O	3:H:233:ILE:CG1	2.52	0.57
2:M:73:TRP:CE2	2:M:114:LEU:CG	2.85	0.57
3:H:146:LYS:HZ3	3:H:198:VAL:HG12	1.67	0.57
1:L:133:LEU:CD1	1:L:133:LEU:C	2.65	0.57
1:L:216:PHE:C	1:L:218:ASP:H	2.06	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:182:HIS:CE1	2:M:183:LEU:HD12	2.40	0.57
1:L:60:ASN:ND2	1:L:63:LEU:HD11	2.19	0.57
2:M:21:THR:CG2	2:M:139:ALA:HB1	2.34	0.57
7:M:312:BPH:C11	7:M:312:BPH:H102	2.18	0.57
3:H:48:THR:CG2	3:H:51:ALA:C	2.73	0.57
3:H:143:SER:O	3:H:144:ALA:CB	2.51	0.57
3:H:27:LEU:O	3:H:30:TYR:N	2.37	0.57
1:L:10:ARG:HH21	3:H:95:GLY:HA2	1.61	0.57
1:L:103:ARG:O	1:L:107:ILE:HG12	2.03	0.57
1:L:182:THR:CG2	1:L:236:LEU:HD13	2.34	0.57
1:L:237:SER:C	1:L:239:SER:N	2.58	0.57
1:L:264:GLN:O	1:L:266:TRP:N	2.38	0.57
2:M:126:VAL:HG11	2:M:154:ILE:HD12	1.87	0.57
1:L:174:MET:HE1	2:M:180:PHE:CZ	2.40	0.57
1:L:146:PHE:CE2	6:M:311:BCL:HMC2	2.39	0.57
8:M:313:U10:H8	8:M:313:U10:C1M	2.34	0.57
2:M:58:LEU:O	2:M:61:PHE:N	2.38	0.57
3:H:201:ASN:C	3:H:201:ASN:OD1	2.41	0.57
3:H:32:GLN:O	3:H:36:MET:HE1	2.05	0.57
1:L:84:GLY:O	1:L:85:LEU:C	2.42	0.57
2:M:149:ALA:HB2	2:M:270:ILE:CD1	2.34	0.57
1:L:69:PRO:CB	1:L:78:ALA:CB	2.81	0.57
1:L:75:LEU:CD2	1:L:141:ALA:C	2.73	0.57
2:M:171:TRP:O	2:M:174:ALA:N	2.28	0.57
1:L:174:MET:HE1	2:M:180:PHE:CE1	2.39	0.57
2:M:260:ALA:CB	3:H:36:MET:CG	2.83	0.57
3:H:15:LEU:CA	3:H:18:TYR:HD2	2.15	0.57
1:L:155:ASP:O	1:L:158:SER:N	2.38	0.57
2:M:284:ILE:CD1	6:M:310:BCL:HED1	2.35	0.57
3:H:17:ILE:CD1	3:H:21:TRP:CD1	2.88	0.56
1:L:98:VAL:O	1:L:102:LEU:HD23	2.05	0.56
1:L:135:ARG:HG2	1:L:139:MET:HE3	1.87	0.56
1:L:121:PHE:HB2	7:L:284:BPH:C2D	2.35	0.56
1:L:263:TRP:CE3	1:L:263:TRP:HA	2.38	0.56
2:M:135:LEU:O	2:M:138:GLN:N	2.39	0.56
2:M:204:LEU:C	2:M:207:ALA:H	2.08	0.56
2:M:237:GLN:C	2:M:239:ALA:H	2.07	0.56
2:M:28:ASN:O	2:M:29:ARG:O	2.22	0.56
2:M:17:ASP:O	2:M:18:LEU:CG	2.52	0.56
3:H:49:PRO:HD2	3:H:50:ALA:O	2.04	0.56
3:H:104:PRO:CG	3:H:243:TYR:CE2	2.88	0.56
1:L:108:CYS:SG	2:M:251:PHE:CE2	2.99	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:153:HIS:O	1:L:157:VAL:HB	2.06	0.56
1:L:114:GLY:N	2:M:225:ALA:HB1	2.20	0.56
2:M:70:ILE:O	2:M:74:PHE:HB2	2.04	0.56
3:H:15:LEU:CA	3:H:18:TYR:CD2	2.76	0.56
1:L:12:PRO:HD3	3:H:97:PRO:CB	2.35	0.56
1:L:255:TRP:NE1	1:L:259:TRP:CE3	2.73	0.56
2:M:13:ARG:HE	3:H:143:SER:CB	2.18	0.56
2:M:64:LEU:O	2:M:67:PHE:CA	2.54	0.56
3:H:12:LEU:C	3:H:14:SER:N	2.54	0.56
3:H:35:ASN:O	3:H:37:ARG:N	2.39	0.56
3:H:92:VAL:HG13	3:H:93:SER:N	2.20	0.56
1:L:111:LEU:HD23	2:M:251:PHE:HB2	1.86	0.56
2:M:132:ARG:C	2:M:134:TYR:N	2.56	0.56
2:M:206:ILE:CD1	6:M:310:BCL:C2B	2.83	0.56
2:M:187:ASN:O	2:M:188:ASN:C	2.43	0.56
3:H:96:PHE:O	3:H:97:PRO:O	2.23	0.56
1:L:219:LEU:C	2:M:132:ARG:NH2	2.58	0.56
1:L:227:LEU:HD22	1:L:231:ARG:HH11	1.69	0.56
1:L:58:THR:O	1:L:59:TRP:CB	2.50	0.56
1:L:8:LYS:O	1:L:11:VAL:HG13	2.05	0.56
2:M:132:ARG:C	2:M:134:TYR:H	2.07	0.56
2:M:14:GLY:O	2:M:15:PRO:O	2.24	0.56
2:M:205:SER:OG	2:M:279:THR:CG2	2.47	0.56
3:H:134:MET:HE3	3:H:141:HIS:HE1	1.70	0.56
3:H:171:ILE:N	3:H:171:ILE:CD1	2.68	0.56
3:H:177:ARG:CG	3:H:177:ARG:HH11	2.17	0.56
1:L:155:ASP:O	1:L:156:TRP:C	2.43	0.56
1:L:182:THR:O	1:L:186:ALA:HB2	2.05	0.56
1:L:60:ASN:C	1:L:62:GLN:H	2.08	0.56
2:M:126:VAL:HG11	2:M:154:ILE:CD1	2.35	0.56
2:M:264:GLY:C	2:M:267:ARG:HB2	2.26	0.56
2:M:26:LEU:CD2	2:M:27:ALA:N	2.67	0.56
3:H:148:PRO:HB2	3:H:164:VAL:HG11	1.88	0.56
3:H:177:ARG:HH11	3:H:177:ARG:HG3	1.70	0.56
1:L:14:GLY:HA3	1:L:110:LYS:HB3	1.88	0.56
1:L:212:GLU:C	1:L:214:THR:N	2.58	0.56
1:L:36:VAL:HG22	8:M:313:U10:H412	1.88	0.56
2:M:110:LYS:HE2	2:M:114:LEU:CD2	2.27	0.56
2:M:21:THR:OG1	2:M:23:ASP:C	2.44	0.56
2:M:271:TRP:CZ3	3:H:31:LEU:CD2	2.87	0.56
3:H:103:ASP:CG	3:H:106:LYS:HZ2	2.04	0.56
1:L:147:PRO:HG2	1:L:152:THR:CG2	2.31	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:L:283:BCL:C15	7:L:284:BPH:H3A	2.23	0.56
1:L:40:PHE:HD1	1:L:41:PHE:CD1	2.22	0.56
2:M:90:PHE:CG	2:M:179:ILE:CD1	2.88	0.56
3:H:212:LEU:O	3:H:213:PHE:HB2	2.05	0.56
2:M:140:LEU:N	2:M:140:LEU:CD1	2.68	0.56
2:M:37:THR:CA	2:M:41:TRP:CD1	2.88	0.56
2:M:35:PHE:CE1	2:M:38:LEU:HB2	2.41	0.56
2:M:58:LEU:O	2:M:59:SER:C	2.44	0.56
2:M:18:LEU:N	2:M:18:LEU:CD1	2.64	0.56
3:H:149:ILE:C	3:H:151:LEU:H	2.08	0.56
1:L:175:ILE:HD12	1:L:243:PHE:CE2	2.33	0.56
2:M:218:MET:CE	8:M:313:U10:C1M	2.84	0.56
6:M:310:BCL:H42	7:M:312:BPH:CBB	2.37	0.56
2:M:238:ILE:HG23	3:H:64:PHE:CZ	2.40	0.55
1:L:173:HIS:CB	1:L:247:CYS:SG	2.92	0.55
2:M:241:ARG:HB2	2:M:241:ARG:CZ	2.36	0.55
2:M:291:VAL:HG11	2:M:294:TRP:CD2	2.40	0.55
6:L:283:BCL:C11	7:L:284:BPH:HBA2	2.35	0.55
2:M:70:ILE:HD11	2:M:74:PHE:CD2	2.41	0.55
1:L:208:THR:N	1:L:211:HIS:CD2	2.73	0.55
3:H:151:LEU:C	3:H:164:VAL:HG23	2.18	0.55
1:L:101:ALA:O	1:L:104:GLU:CA	2.54	0.55
1:L:173:HIS:CA	1:L:247:CYS:SG	2.95	0.55
2:M:107:ALA:HB1	2:M:108:PRO:HD2	1.89	0.55
3:H:112:ALA:O	3:H:113:SER:C	2.45	0.55
3:H:183:LEU:CG	3:H:189:ARG:HE	2.20	0.55
1:L:244:SER:O	1:L:245:ALA:C	2.45	0.55
6:L:283:BCL:CBB	6:L:283:BCL:HMB1	2.36	0.55
2:M:90:PHE:CD2	2:M:179:ILE:HB	2.42	0.55
3:H:119:ASP:OD1	3:H:226:THR:HG21	2.05	0.55
3:H:27:LEU:CD1	3:H:32:GLN:CD	2.58	0.55
1:L:185:LEU:CG	1:L:186:ALA:N	2.69	0.55
6:L:283:BCL:H42	7:L:284:BPH:CAB	2.33	0.55
1:L:53:ALA:HA	1:L:64:ILE:HD13	1.87	0.55
2:M:102:GLY:O	2:M:104:SER:HB2	2.07	0.55
2:M:242:GLY:CA	3:H:115:VAL:HG11	2.18	0.55
3:H:148:PRO:HA	3:H:151:LEU:HD12	1.88	0.55
1:L:121:PHE:O	1:L:123:PHE:N	2.40	0.55
1:L:216:PHE:HB3	1:L:223:SER:HB2	1.87	0.55
1:L:39:PHE:C	1:L:41:PHE:N	2.53	0.55
2:M:114:LEU:HD13	2:M:114:LEU:N	2.15	0.55
2:M:23:ASP:O	2:M:25:ASN:N	2.40	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:37:THR:CG2	2:M:38:LEU:CD1	2.76	0.55
3:H:103:ASP:O	3:H:106:LYS:NZ	2.39	0.55
1:L:147:PRO:CG	1:L:152:THR:HG22	2.31	0.55
1:L:175:ILE:CG2	1:L:176:ALA:N	2.66	0.55
1:L:177:ILE:CG2	1:L:181:PHE:HE2	2.12	0.55
1:L:47:ILE:O	1:L:48:LEU:C	2.43	0.55
3:H:132:LYS:HZ1	3:H:223:THR:HG21	1.66	0.55
3:H:190:LEU:CD2	3:H:190:LEU:N	2.68	0.55
1:L:189:LEU:HD11	7:M:312:BPH:HED3	1.89	0.55
1:L:53:ALA:HB2	1:L:64:ILE:CB	2.37	0.55
1:L:260:VAL:O	1:L:260:VAL:CG1	2.53	0.55
1:L:232:LEU:CA	2:M:42:PHE:CZ	2.83	0.55
2:M:37:THR:O	2:M:41:TRP:CD1	2.59	0.55
2:M:13:ARG:HD2	2:M:45:ALA:HB1	1.87	0.55
3:H:205:VAL:CG2	3:H:205:VAL:O	2.55	0.55
3:H:235:GLY:O	3:H:236:TYR:C	2.46	0.55
2:M:105:PHE:O	2:M:106:ALA:C	2.45	0.55
2:M:134:TYR:C	2:M:134:TYR:HD1	2.09	0.55
2:M:204:LEU:O	2:M:207:ALA:CA	2.55	0.55
1:L:113:ILE:HG23	2:M:225:ALA:HB1	1.88	0.55
2:M:270:ILE:O	2:M:270:ILE:HG13	2.05	0.55
2:M:93:SER:HA	2:M:177:TYR:O	2.07	0.55
1:L:205:GLU:OE1	3:H:68:HIS:HA	2.06	0.55
3:H:115:VAL:O	3:H:116:ALA:HB2	2.07	0.54
3:H:197:LYS:N	3:H:204:HIS:O	2.40	0.54
3:H:27:LEU:CG	3:H:32:GLN:HE22	2.17	0.54
1:L:144:TYR:HE1	1:L:160:THR:HG1	1.46	0.54
3:H:119:ASP:HA	3:H:226:THR:OG1	2.07	0.54
3:H:234:CYS:C	3:H:237:VAL:HG23	2.27	0.54
2:M:300:ASN:O	2:M:301:HIS:CD2	2.59	0.54
1:L:104:GLU:HB3	1:L:118:PRO:HG3	1.89	0.54
1:L:131:LEU:HD13	1:L:146:PHE:CE2	2.42	0.54
1:L:48:LEU:O	1:L:51:TRP:HB3	2.07	0.54
2:M:129:TRP:C	2:M:129:TRP:CD1	2.80	0.54
2:M:13:ARG:CZ	2:M:34:PRO:HB3	2.37	0.54
2:M:14:GLY:HA3	3:H:140:PHE:CE1	2.42	0.54
2:M:218:MET:CE	2:M:252:TRP:CD2	2.89	0.54
3:H:27:LEU:HD12	3:H:28:ILE:H	0.77	0.54
1:L:25:TRP:HA	1:L:29:PHE:O	2.07	0.54
7:L:284:BPH:H162	6:M:311:BCL:HBB3	1.87	0.54
1:L:48:LEU:CD1	1:L:85:LEU:HD12	2.38	0.54
1:L:64:ILE:HD12	1:L:65:SER:H	1.72	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:152:SER:O	2:M:153:ALA:C	2.46	0.54
2:M:295:TYR:O	2:M:298:GLY:N	2.39	0.54
3:H:154:ARG:CD	3:H:160:ILE:HG13	2.37	0.54
3:H:218:THR:HG22	3:H:219:ILE:N	2.22	0.54
3:H:27:LEU:C	3:H:27:LEU:CD1	2.69	0.54
1:L:174:MET:HE3	2:M:180:PHE:HZ	1.71	0.54
2:M:266:HIS:HA	2:M:269:ALA:HB3	1.89	0.54
2:M:249:ALA:HB1	8:M:313:U10:H4M3	1.83	0.54
1:L:102:LEU:O	1:L:103:ARG:C	2.46	0.54
1:L:255:TRP:CZ2	1:L:262:TRP:CA	2.90	0.54
1:L:69:PRO:CG	1:L:78:ALA:CB	2.86	0.54
1:L:93:ALA:O	1:L:96:ALA:N	2.41	0.54
1:L:8:LYS:NZ	1:L:9:TYR:CE1	2.73	0.54
2:M:127:TRP:CE3	2:M:127:TRP:HA	2.42	0.54
2:M:12:VAL:C	2:M:13:ARG:CG	2.76	0.54
2:M:260:ALA:HB1	3:H:36:MET:SD	2.47	0.54
3:H:168:TRP:CZ3	3:H:223:THR:C	2.81	0.54
1:L:234:LEU:C	1:L:234:LEU:CD2	2.76	0.54
3:H:173:GLU:O	3:H:174:GLN:CB	2.55	0.54
1:L:230:HIS:CG	2:M:223:ILE:HG21	2.42	0.54
2:M:262:MET:C	2:M:265:ILE:HG22	2.28	0.54
2:M:88:ASP:HB3	2:M:91:PHE:HB2	1.89	0.54
3:H:32:GLN:O	3:H:36:MET:CE	2.56	0.54
1:L:135:ARG:HG3	1:L:135:ARG:HH11	1.70	0.54
1:L:215:PHE:O	1:L:218:ASP:CB	2.48	0.54
2:M:192:VAL:HG12	2:M:193:HIS:CD2	2.42	0.54
2:M:230:GLY:O	2:M:231:GLY:C	2.46	0.54
2:M:279:THR:HG22	2:M:280:GLY:N	2.22	0.54
1:L:54:VAL:CG1	1:L:55:LEU:N	2.71	0.54
3:H:167:ILE:HA	3:H:178:PHE:O	2.08	0.54
3:H:180:GLU:C	3:H:181:VAL:HG23	2.28	0.54
1:L:181:PHE:CE1	6:M:310:BCL:HBA2	2.43	0.54
2:M:209:LEU:O	2:M:209:LEU:CD1	2.47	0.54
3:H:105:MET:HB3	3:H:106:LYS:HZ3	1.73	0.54
3:H:211:ASP:N	3:H:211:ASP:OD1	2.41	0.53
2:M:116:LEU:O	2:M:120:PHE:HB2	2.07	0.53
2:M:284:ILE:O	2:M:284:ILE:CG2	2.56	0.53
3:H:15:LEU:O	3:H:16:ALA:O	2.26	0.53
3:H:201:ASN:OD1	3:H:202:ARG:HB2	2.07	0.53
3:H:32:GLN:O	3:H:35:ASN:N	2.36	0.53
1:L:10:ARG:HH22	1:L:25:TRP:CB	2.21	0.53
1:L:86:TRP:CD2	1:L:87:GLN:N	2.75	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:122:MET:O	2:M:126:VAL:HG23	2.08	0.53
3:H:131:ILE:HD11	3:H:225:VAL:HG21	1.90	0.53
2:M:238:ILE:CG2	3:H:64:PHE:CZ	2.91	0.53
1:L:121:PHE:C	1:L:123:PHE:N	2.61	0.53
1:L:197:ALA:CB	2:M:235:LEU:HD21	2.38	0.53
1:L:26:VAL:O	1:L:29:PHE:N	2.39	0.53
1:L:31:VAL:HG12	1:L:36:VAL:HG23	1.90	0.53
2:M:136:ARG:NE	2:M:136:ARG:N	2.57	0.53
1:L:184:ALA:O	1:L:187:LEU:N	2.40	0.53
1:L:249:ILE:HG23	1:L:250:ILE:HD12	1.90	0.53
2:M:196:LEU:O	2:M:199:ASN:HB2	2.07	0.53
2:M:259:ASN:C	2:M:259:ASN:HD22	2.12	0.53
3:H:150:GLY:O	3:H:152:PRO:HD3	2.08	0.53
1:L:130:THR:HA	1:L:134:PHE:HD2	1.72	0.53
1:L:79:PRO:O	1:L:79:PRO:HG2	2.06	0.53
2:M:128:SER:O	2:M:130:TRP:N	2.42	0.53
2:M:126:VAL:CG1	2:M:154:ILE:HD12	2.38	0.53
2:M:205:SER:HA	2:M:279:THR:HG21	1.89	0.53
2:M:150:PHE:HD1	7:M:312:BPH:C2D	2.21	0.53
2:M:237:GLN:HA	2:M:240:ASP:O	2.08	0.53
2:M:261:THR:C	2:M:263:GLU:H	2.11	0.53
3:H:191:LEU:CD1	3:H:205:VAL:HG12	2.35	0.53
1:L:110:LYS:C	1:L:112:GLY:H	2.11	0.53
1:L:244:SER:O	1:L:247:CYS:N	2.41	0.53
6:L:283:BCL:H2C	6:M:310:BCL:CBC	2.35	0.53
1:L:5:PHE:CZ	3:H:40:TYR:HE2	2.20	0.53
8:M:313:U10:C8	8:M:313:U10:C1M	2.87	0.53
2:M:13:ARG:HD2	2:M:45:ALA:CB	2.39	0.53
3:H:127:GLY:O	3:H:128:HIS:C	2.45	0.53
3:H:17:ILE:HG23	3:H:17:ILE:O	2.07	0.53
3:H:219:ILE:HA	3:H:229:GLU:HG2	1.90	0.53
3:H:228:LEU:HD22	3:H:232:LYS:HD2	1.88	0.53
1:L:186:ALA:C	2:M:216:PHE:CE2	2.74	0.53
1:L:197:ALA:HB1	2:M:235:LEU:HD23	1.90	0.53
2:M:6:ILE:HG22	2:M:7:PHE:HB3	1.91	0.53
2:M:187:ASN:O	2:M:190:SER:HB3	2.08	0.53
3:H:63:THR:HA	3:H:74:THR:HA	1.91	0.53
2:M:80:TRP:O	2:M:80:TRP:CG	2.61	0.53
3:H:185:ASP:C	3:H:187:SER:H	2.12	0.53
3:H:194:GLN:N	3:H:194:GLN:NE2	2.52	0.53
3:H:213:PHE:HD1	3:H:216:ILE:CD1	2.22	0.53
1:L:233:GLY:C	1:L:235:LEU:N	2.62	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:152:SER:C	2:M:154:ILE:N	2.61	0.53
2:M:206:ILE:HG12	6:M:310:BCL:HHB	1.90	0.53
2:M:289:THR:C	2:M:291:VAL:N	2.53	0.53
3:H:199:GLN:NE2	3:H:200:SER:OG	2.41	0.53
3:H:19:SER:HA	3:H:22:ILE:HD12	1.91	0.53
1:L:94:THR:HG21	1:L:129:LEU:HD11	1.79	0.53
3:H:65:ILE:HG22	3:H:65:ILE:O	2.09	0.53
1:L:16:LEU:HB2	1:L:106:GLU:HG2	1.90	0.52
1:L:160:THR:O	1:L:164:TYR:HD1	1.92	0.52
1:L:173:HIS:O	1:L:175:ILE:N	2.42	0.52
1:L:73:TYR:CD1	1:L:78:ALA:HB2	2.44	0.52
2:M:115:TRP:HE3	2:M:116:LEU:N	2.07	0.52
3:H:247:LYS:O	3:H:248:ARG:HG3	2.08	0.52
1:L:114:GLY:CA	2:M:225:ALA:HB1	2.39	0.52
1:L:131:LEU:O	1:L:145:ALA:HA	2.09	0.52
1:L:264:GLN:O	1:L:267:VAL:N	2.42	0.52
2:M:15:PRO:HD2	3:H:140:PHE:HE1	1.65	0.52
2:M:257:GLY:O	2:M:258:PHE:CB	2.44	0.52
2:M:268:TRP:CG	8:M:313:U10:H111	2.44	0.52
3:H:115:VAL:HG13	3:H:116:ALA:N	2.22	0.52
1:L:123:PHE:O	1:L:126:LEU:N	2.42	0.52
1:L:130:THR:HA	1:L:134:PHE:CD2	2.45	0.52
1:L:177:ILE:HG23	1:L:181:PHE:CE2	2.43	0.52
2:M:238:ILE:HD11	2:M:263:GLU:CB	2.38	0.52
2:M:281:GLY:O	2:M:285:LEU:CD2	2.58	0.52
8:M:313:U10:C4M	8:M:313:U10:O5	2.57	0.52
2:M:97:PRO:O	2:M:99:PRO:O	2.27	0.52
3:H:63:THR:HG23	3:H:74:THR:CB	2.38	0.52
3:H:121:PRO:HB3	3:H:225:VAL:O	2.09	0.52
3:H:128:HIS:C	3:H:130:LYS:N	2.63	0.52
3:H:191:LEU:HD11	3:H:205:VAL:HG12	1.89	0.52
3:H:196:VAL:O	3:H:196:VAL:CG2	2.57	0.52
1:L:185:LEU:O	1:L:189:LEU:N	2.40	0.52
8:M:313:U10:C36	8:M:313:U10:C40	2.88	0.52
2:M:65:MET:CE	2:M:121:PHE:CB	2.83	0.52
2:M:81:ASN:O	2:M:82:PRO:O	2.27	0.52
3:H:106:LYS:H	3:H:106:LYS:CE	2.23	0.52
3:H:108:GLY:CA	3:H:114:TRP:CZ3	2.89	0.52
2:M:9:GLN:HE22	3:H:197:LYS:CD	2.21	0.52
3:H:212:LEU:O	3:H:213:PHE:CB	2.57	0.52
3:H:191:LEU:CD2	3:H:213:PHE:CZ	2.92	0.52
2:M:162:PHE:O	2:M:163:ILE:O	2.28	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:33:PHE:CE1	1:L:33:PHE:O	2.50	0.52
1:L:15:THR:HG21	1:L:19:GLY:O	2.10	0.52
1:L:216:PHE:C	1:L:218:ASP:N	2.63	0.52
2:M:261:THR:O	2:M:262:MET:C	2.46	0.52
1:L:15:THR:CG2	1:L:19:GLY:N	2.72	0.52
2:M:200:PRO:HG3	2:M:297:TRP:CZ3	2.45	0.52
3:H:142:VAL:CG1	3:H:142:VAL:O	2.57	0.52
1:L:193:LEU:O	1:L:195:LEU:N	2.42	0.52
1:L:255:TRP:CZ2	1:L:262:TRP:HA	2.44	0.52
1:L:255:TRP:HZ2	1:L:262:TRP:CA	2.22	0.52
2:M:139:ALA:CB	2:M:140:LEU:HD12	2.40	0.52
3:H:214:ALA:O	3:H:215:GLY:C	2.48	0.52
1:L:11:VAL:HA	3:H:98:HIS:O	2.09	0.52
1:L:177:ILE:HG13	6:L:282:BCL:OBD	2.10	0.52
1:L:187:LEU:CD2	2:M:216:PHE:CD2	2.87	0.52
8:M:313:U10:C36	8:M:313:U10:H402	2.40	0.52
1:L:232:LEU:CD1	2:M:42:PHE:HE2	2.22	0.52
3:H:151:LEU:HB3	3:H:203:VAL:HG23	1.89	0.52
3:H:31:LEU:O	3:H:34:GLU:HB2	2.10	0.52
3:H:31:LEU:O	3:H:34:GLU:N	2.43	0.52
2:M:261:THR:OG1	3:H:40:TYR:CD1	2.63	0.52
1:L:129:LEU:O	1:L:133:LEU:HB3	2.10	0.52
1:L:133:LEU:O	1:L:137:VAL:N	2.33	0.52
1:L:217:ARG:HA	1:L:221:GLY:HA2	1.92	0.52
6:L:283:BCL:C4	7:L:284:BPH:C3B	2.88	0.52
1:L:97:PHE:HE1	6:L:283:BCL:C13	2.16	0.52
2:M:186:THR:O	2:M:189:PHE:CA	2.57	0.52
2:M:35:PHE:O	2:M:45:ALA:HA	2.10	0.52
3:H:204:HIS:CD2	3:H:205:VAL:O	2.63	0.51
3:H:94:GLU:C	3:H:96:PHE:N	2.34	0.51
1:L:60:ASN:HD22	1:L:63:LEU:CD1	2.20	0.51
1:L:51:TRP:CZ2	1:L:80:LEU:CD1	2.93	0.51
2:M:162:PHE:O	2:M:163:ILE:C	2.47	0.51
6:M:310:BCL:C4	7:M:312:BPH:CBB	2.88	0.51
3:H:178:PHE:CD2	3:H:192:PRO:HA	2.45	0.51
1:L:228:GLY:HA2	1:L:231:ARG:HD3	1.92	0.51
1:L:53:ALA:HB1	1:L:59:TRP:HB2	1.92	0.51
2:M:115:TRP:O	2:M:119:SER:HB3	2.11	0.51
2:M:203:GLY:CA	6:M:311:BCL:OBD	2.57	0.51
1:L:188:ALA:CB	7:M:312:BPH:HBC2	2.41	0.51
3:H:131:ILE:HG13	3:H:131:ILE:O	2.08	0.51
3:H:38:GLU:O	3:H:76:PRO:CA	2.59	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:10:ARG:HH22	3:H:95:GLY:CA	2.15	0.51
1:L:75:LEU:CD2	1:L:141:ALA:HA	2.41	0.51
1:L:75:LEU:CD2	1:L:142:TRP:N	2.73	0.51
1:L:195:LEU:HB3	2:M:145:HIS:NE2	2.25	0.51
2:M:71:GLY:C	2:M:74:PHE:HB2	2.30	0.51
3:H:184:LYS:HD3	3:H:184:LYS:C	2.30	0.51
3:H:226:THR:CG2	3:H:229:GLU:OE1	2.59	0.51
3:H:233:ILE:O	3:H:237:VAL:CG2	2.56	0.51
1:L:116:HIS:CE1	2:M:225:ALA:CA	2.89	0.51
1:L:237:SER:C	1:L:239:SER:H	2.14	0.51
1:L:46:ILE:HA	1:L:49:ILE:HG22	1.90	0.51
1:L:117:ILE:HG21	2:M:252:TRP:CH2	2.45	0.51
2:M:236:GLU:CB	3:H:122:GLU:HG3	2.40	0.51
2:M:295:TYR:O	2:M:296:VAL:O	2.28	0.51
3:H:31:LEU:O	3:H:32:GLN:C	2.48	0.51
3:H:85:ILE:C	3:H:87:LEU:N	2.64	0.51
1:L:181:PHE:HE1	6:M:310:BCL:CBA	2.24	0.51
1:L:249:ILE:CG2	1:L:250:ILE:HD12	2.41	0.51
2:M:24:VAL:O	2:M:24:VAL:HG12	2.10	0.51
2:M:209:LEU:H	2:M:276:VAL:HG22	1.70	0.51
2:M:50:ILE:CG2	2:M:52:LEU:HG	2.40	0.51
1:L:119:PHE:CD1	1:L:120:ALA:N	2.79	0.51
1:L:85:LEU:CA	1:L:88:ILE:HD12	2.41	0.51
2:M:109:LEU:HD13	2:M:110:LYS:H	1.75	0.51
2:M:65:MET:HE1	2:M:121:PHE:HB3	1.91	0.51
6:M:310:BCL:HBB2	6:M:310:BCL:HHC	1.90	0.51
3:H:116:ALA:HA	3:H:228:LEU:HD11	1.87	0.51
1:L:232:LEU:HG	2:M:42:PHE:HZ	1.69	0.51
1:L:238:LEU:HD23	1:L:238:LEU:O	2.11	0.51
2:M:134:TYR:C	2:M:134:TYR:CD1	2.84	0.51
2:M:204:LEU:O	2:M:205:SER:C	2.48	0.51
1:L:113:ILE:HG23	2:M:225:ALA:CB	2.40	0.51
8:M:313:U10:H4M2	8:M:313:U10:O5	2.11	0.51
2:M:70:ILE:HD13	2:M:71:GLY:N	2.26	0.51
1:L:208:THR:C	1:L:211:HIS:HB2	2.26	0.51
2:M:16:ALA:HB1	2:M:32:VAL:CG2	2.29	0.51
3:H:196:VAL:CA	3:H:204:HIS:O	2.54	0.51
1:L:135:ARG:CG	1:L:139:MET:HE3	2.41	0.51
1:L:262:TRP:HD1	1:L:263:TRP:CD2	2.27	0.51
1:L:26:VAL:HG12	1:L:26:VAL:O	2.10	0.51
1:L:75:LEU:HD23	1:L:142:TRP:H	1.75	0.51
1:L:69:PRO:HG2	1:L:87:GLN:OE1	2.08	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:114:LEU:O	2:M:117:ILE:CA	2.58	0.51
2:M:239:ALA:O	3:H:73:LEU:HD12	2.11	0.51
1:L:185:LEU:HB3	7:M:312:BPH:C3C	2.38	0.51
2:M:35:PHE:CG	2:M:39:LEU:HD23	2.44	0.51
3:H:111:PRO:CB	3:H:242:MET:HB2	2.40	0.51
1:L:12:PRO:HD2	3:H:98:HIS:C	2.30	0.51
1:L:187:LEU:HD22	2:M:216:PHE:CD1	2.41	0.51
1:L:264:GLN:C	1:L:266:TRP:H	2.14	0.51
2:M:12:VAL:CG1	2:M:13:ARG:N	2.74	0.51
2:M:193:HIS:N	2:M:193:HIS:CD2	2.79	0.51
1:L:234:LEU:HD12	2:M:221:ALA:CB	2.40	0.51
2:M:236:GLU:HG2	3:H:122:GLU:HG3	1.91	0.51
2:M:13:ARG:NE	3:H:143:SER:OG	2.44	0.51
3:H:239:GLY:O	3:H:240:GLY:C	2.48	0.51
2:M:264:GLY:O	2:M:267:ARG:CB	2.58	0.51
1:L:212:GLU:O	1:L:213:ASP:C	2.49	0.50
2:M:241:ARG:NH1	2:M:241:ARG:HB3	2.09	0.50
2:M:23:ASP:OD1	2:M:24:VAL:HG23	2.11	0.50
2:M:268:TRP:CE2	8:M:313:U10:H111	2.46	0.50
3:H:132:LYS:CB	3:H:133:PRO:CD	2.89	0.50
3:H:27:LEU:CD1	3:H:32:GLN:HE22	2.20	0.50
1:L:189:LEU:HD21	7:M:312:BPH:CAD	2.41	0.50
6:L:282:BCL:HMD2	6:L:283:BCL:CAB	2.41	0.50
3:H:183:LEU:HD21	3:H:189:ARG:CD	2.41	0.50
3:H:35:ASN:O	3:H:36:MET:C	2.48	0.50
1:L:11:VAL:HG12	3:H:87:LEU:CD1	2.32	0.50
1:L:11:VAL:O	1:L:12:PRO:O	2.29	0.50
1:L:135:ARG:N	1:L:136:PRO:CD	2.74	0.50
1:L:255:TRP:CD1	1:L:259:TRP:CD2	2.99	0.50
1:L:94:THR:O	1:L:94:THR:HG22	2.11	0.50
1:L:6:GLU:HA	1:L:9:TYR:HD1	1.75	0.50
2:M:133:THR:HG21	2:M:146:THR:CG2	2.41	0.50
3:H:215:GLY:O	3:H:217:PRO:N	2.43	0.50
3:H:40:TYR:O	3:H:41:PRO:C	2.49	0.50
1:L:128:TYR:HB3	6:L:283:BCL:H61	1.92	0.50
1:L:86:TRP:HE3	1:L:87:GLN:CA	2.21	0.50
2:M:208:PHE:HB3	2:M:276:VAL:CG2	2.31	0.50
2:M:214:LEU:HG	2:M:215:LEU:N	2.25	0.50
1:L:146:PHE:HB3	1:L:156:TRP:CE2	2.47	0.50
1:L:160:THR:O	1:L:161:GLY:O	2.29	0.50
1:L:46:ILE:O	1:L:49:ILE:HG22	2.11	0.50
6:M:310:BCL:H172	7:M:312:BPH:HMB1	1.93	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:205:GLU:O	1:L:207:ARG:HD3	2.12	0.50
3:H:154:ARG:HD2	3:H:160:ILE:HG23	1.94	0.50
1:L:40:PHE:HD1	1:L:41:PHE:HD1	1.59	0.50
2:M:155:TRP:CD1	2:M:278:LEU:O	2.65	0.50
2:M:236:GLU:CD	3:H:122:GLU:HG3	2.32	0.50
1:L:5:PHE:O	1:L:7:ARG:N	2.45	0.50
3:H:153:VAL:O	3:H:160:ILE:HG22	2.12	0.50
3:H:179:LEU:CD2	3:H:181:VAL:HG22	2.42	0.50
3:H:245:ALA:O	3:H:246:PRO:O	2.30	0.50
1:L:160:THR:HA	1:L:163:THR:OG1	2.11	0.50
6:L:283:BCL:HBB3	6:L:283:BCL:HMB1	1.94	0.50
2:M:164:ARG:CZ	2:M:168:MET:HE2	2.41	0.50
2:M:290:VAL:O	2:M:291:VAL:CG2	2.52	0.50
2:M:78:ALA:HB1	2:M:84:VAL:CG1	2.41	0.50
3:H:193:MET:C	3:H:195:MET:H	2.15	0.50
3:H:204:HIS:HD2	3:H:206:ASN:HA	1.76	0.50
3:H:112:ALA:O	3:H:235:GLY:HA3	2.12	0.50
1:L:87:GLN:NE2	1:L:142:TRP:HE1	2.10	0.50
1:L:261:ASP:O	1:L:262:TRP:C	2.49	0.50
1:L:262:TRP:CE3	1:L:262:TRP:HA	2.46	0.50
1:L:48:LEU:CD1	1:L:89:ILE:HD12	2.39	0.50
2:M:13:ARG:NE	3:H:143:SER:CB	2.75	0.50
2:M:213:ALA:O	2:M:217:ALA:HB2	2.12	0.50
2:M:52:LEU:O	2:M:53:GLY:O	2.30	0.50
2:M:87:ARG:HG3	2:M:88:ASP:CB	2.41	0.50
3:H:199:GLN:NE2	3:H:200:SER:N	2.59	0.50
3:H:233:ILE:N	3:H:233:ILE:HD13	2.27	0.49
1:L:119:PHE:CD1	1:L:119:PHE:C	2.85	0.49
2:M:154:ILE:O	2:M:157:TRP:HB3	2.12	0.49
2:M:196:LEU:HG	2:M:196:LEU:O	2.12	0.49
2:M:196:LEU:HD12	2:M:294:TRP:CD1	2.41	0.49
4:M:308:BOG:H1'2	4:M:308:BOG:O2	2.12	0.49
3:H:207:ALA:C	3:H:247:LYS:NZ	2.62	0.49
1:L:12:PRO:HG2	3:H:99:ALA:HA	1.93	0.49
1:L:8:LYS:HB3	3:H:85:ILE:CG2	2.42	0.49
2:M:204:LEU:O	2:M:206:ILE:N	2.45	0.49
2:M:28:ASN:O	2:M:29:ARG:C	2.51	0.49
2:M:35:PHE:CD1	2:M:38:LEU:HD13	2.47	0.49
3:H:82:ASP:O	3:H:84:PRO:HD3	2.11	0.49
3:H:210:SER:C	3:H:212:LEU:N	2.43	0.49
3:H:111:PRO:CD	3:H:243:TYR:CE1	2.78	0.49
3:H:40:TYR:O	3:H:42:LEU:HD12	2.01	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:108:CYS:SG	2:M:251:PHE:HE2	2.36	0.49
1:L:121:PHE:C	1:L:123:PHE:H	2.14	0.49
1:L:134:PHE:O	1:L:135:ARG:C	2.50	0.49
2:M:261:THR:O	2:M:264:GLY:N	2.44	0.49
2:M:89:LEU:CA	2:M:92:PHE:CD2	2.91	0.49
1:L:54:VAL:C	1:L:56:GLN:N	2.64	0.49
1:L:25:TRP:HZ2	2:M:254:TRP:CH2	2.31	0.49
1:L:49:ILE:HA	1:L:89:ILE:CD1	2.42	0.49
1:L:79:PRO:O	1:L:79:PRO:CG	2.61	0.49
2:M:208:PHE:CE2	2:M:275:LEU:HB3	2.47	0.49
2:M:230:GLY:C	2:M:232:GLU:N	2.66	0.49
2:M:50:ILE:HG23	2:M:52:LEU:HG	1.95	0.49
3:H:198:VAL:CG1	3:H:198:VAL:O	2.58	0.49
3:H:219:ILE:CG2	3:H:225:VAL:HG12	2.43	0.49
3:H:227:LEU:O	3:H:229:GLU:N	2.46	0.49
1:L:173:HIS:HE1	1:L:177:ILE:HD11	1.72	0.49
1:L:97:PHE:CE1	6:L:283:BCL:H122	2.38	0.49
1:L:46:ILE:CA	1:L:49:ILE:HG22	2.43	0.49
2:M:107:ALA:HB1	2:M:112:GLY:HA3	1.95	0.49
2:M:129:TRP:CD1	2:M:129:TRP:O	2.66	0.49
2:M:164:ARG:HH21	2:M:168:MET:HE1	1.73	0.49
1:L:174:MET:CE	2:M:180:PHE:CE1	2.96	0.49
1:L:234:LEU:CD1	2:M:221:ALA:HB2	2.42	0.49
2:M:25:ASN:C	2:M:27:ALA:N	2.63	0.49
3:H:27:LEU:O	3:H:28:ILE:C	2.51	0.49
1:L:10:ARG:NH2	3:H:95:GLY:C	2.64	0.49
1:L:123:PHE:O	1:L:126:LEU:CA	2.60	0.49
1:L:167:PHE:CD2	6:L:283:BCL:C1D	2.96	0.49
1:L:241:VAL:HG21	7:L:284:BPH:H2C	1.95	0.49
1:L:225:GLY:HA2	8:L:285:U10:H4M1	1.94	0.49
1:L:36:VAL:O	1:L:39:PHE:HB3	2.13	0.49
2:M:206:ILE:HD11	6:M:310:BCL:NB	2.25	0.49
1:L:113:ILE:CD1	2:M:229:PHE:HE1	2.26	0.49
2:M:64:LEU:HD12	7:M:312:BPH:C7	2.24	0.49
3:H:146:LYS:HZ2	3:H:198:VAL:HG12	1.75	0.49
2:M:191:LEU:H	2:M:191:LEU:HD13	1.76	0.49
3:H:124:ASP:C	3:H:126:HIS:N	2.64	0.49
1:L:98:VAL:HG23	1:L:125:ILE:HD11	1.95	0.49
1:L:149:GLY:O	1:L:150:ILE:C	2.47	0.49
1:L:48:LEU:HB2	1:L:85:LEU:HD12	1.94	0.49
2:M:125:ALA:O	2:M:126:VAL:C	2.50	0.49
2:M:206:ILE:HG12	6:M:310:BCL:HMB3	1.95	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:48:THR:HG23	3:H:51:ALA:C	2.33	0.49
3:H:87:LEU:HD13	3:H:109:VAL:CG1	2.43	0.49
3:H:204:HIS:CD2	3:H:206:ASN:HA	2.48	0.49
1:L:181:PHE:HE1	6:M:310:BCL:CGA	2.25	0.49
2:M:256:MET:O	2:M:257:GLY:O	2.30	0.49
2:M:228:ARG:HH12	3:H:241:LEU:CD1	2.24	0.49
1:L:158:SER:O	1:L:162:TYR:HD1	1.96	0.49
1:L:261:ASP:O	1:L:262:TRP:O	2.30	0.49
7:L:284:BPH:HMC3	2:M:213:ALA:HB1	1.95	0.49
1:L:66:VAL:O	1:L:147:PRO:HA	2.13	0.49
2:M:108:PRO:HG2	2:M:111:GLU:CB	2.31	0.49
2:M:114:LEU:C	2:M:117:ILE:HB	2.30	0.49
2:M:102:GLY:O	2:M:104:SER:CA	2.59	0.49
3:H:189:ARG:CB	3:H:216:ILE:CG2	2.85	0.49
1:L:151:TRP:CZ3	2:M:198:TYR:CD1	2.95	0.49
1:L:46:ILE:HA	1:L:49:ILE:HG21	1.92	0.49
2:M:243:THR:HG22	2:M:247:ARG:CD	2.42	0.49
3:H:135:LYS:C	3:H:137:ALA:N	2.64	0.48
1:L:187:LEU:HA	2:M:216:PHE:CE2	2.48	0.48
6:L:283:BCL:H162	7:L:284:BPH:HBA1	1.95	0.48
2:M:128:SER:C	2:M:130:TRP:H	2.15	0.48
3:H:196:VAL:H	3:H:205:VAL:HA	1.77	0.48
1:L:135:ARG:NH1	1:L:139:MET:CE	2.76	0.48
1:L:20:ASN:C	1:L:22:PHE:N	2.43	0.48
1:L:46:ILE:C	1:L:49:ILE:HG22	2.34	0.48
2:M:120:PHE:HD1	2:M:162:PHE:CE2	2.30	0.48
2:M:89:LEU:HA	2:M:92:PHE:CE2	2.47	0.48
1:L:15:THR:HG21	1:L:19:GLY:HA2	1.93	0.48
2:M:296:VAL:C	2:M:298:GLY:N	2.67	0.48
1:L:144:TYR:CE1	1:L:160:THR:OG1	2.59	0.48
1:L:183:ASN:OD1	1:L:237:SER:HB3	2.13	0.48
2:M:46:GLN:CG	2:M:48:GLY:O	2.58	0.48
1:L:231:ARG:NH1	2:M:7:PHE:HA	2.29	0.48
1:L:269:LEU:HD22	1:L:270:PRO:N	2.20	0.48
3:H:56:PHE:CD1	3:H:57:PRO:CA	2.92	0.48
3:H:52:ASN:O	3:H:53:GLN:CB	2.59	0.48
3:H:170:ASP:O	3:H:174:GLN:HA	2.13	0.48
3:H:41:PRO:C	3:H:43:GLU:N	2.66	0.48
1:L:147:PRO:CD	1:L:156:TRP:CB	2.91	0.48
1:L:212:GLU:C	1:L:214:THR:H	2.16	0.48
6:L:282:BCL:HMD2	6:L:283:BCL:HBB3	1.96	0.48
1:L:34:PHE:HB3	1:L:99:SER:O	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:73:TYR:CE1	1:L:78:ALA:HA	2.48	0.48
2:M:205:SER:CA	2:M:279:THR:CG2	2.91	0.48
2:M:98:ALA:CA	2:M:99:PRO:C	2.80	0.48
3:H:157:ASP:OD2	3:H:211:ASP:CG	2.51	0.48
1:L:182:THR:O	1:L:185:LEU:HD22	2.03	0.48
7:L:284:BPH:H2C	7:L:284:BPH:HBC3	1.34	0.48
2:M:119:SER:HB2	2:M:177:TYR:CZ	2.48	0.48
2:M:154:ILE:HD12	2:M:157:TRP:CE3	2.49	0.48
2:M:222:THR:O	2:M:223:ILE:C	2.51	0.48
2:M:88:ASP:HB2	2:M:92:PHE:HZ	1.64	0.48
3:H:80:SER:O	3:H:81:GLU:CG	2.61	0.48
3:H:135:LYS:O	3:H:136:ALA:C	2.51	0.48
1:L:119:PHE:HD1	1:L:120:ALA:N	2.12	0.48
1:L:147:PRO:HD3	1:L:156:TRP:CD1	2.49	0.48
1:L:167:PHE:HE2	6:L:283:BCL:C2D	2.26	0.48
1:L:265:TRP:CH2	1:L:266:TRP:HE3	2.31	0.48
2:M:123:PHE:CE1	2:M:127:TRP:CD1	3.02	0.48
2:M:152:SER:C	2:M:154:ILE:H	2.16	0.48
2:M:158:MET:O	2:M:162:PHE:HB2	2.14	0.48
2:M:206:ILE:HA	6:M:310:BCL:HMA1	1.95	0.48
6:M:311:BCL:HBB2	6:M:311:BCL:CMB	2.42	0.48
2:M:72:ILE:O	2:M:72:ILE:CD1	2.62	0.48
2:M:97:PRO:HB3	2:M:112:GLY:HA2	1.94	0.48
3:H:30:TYR:O	3:H:31:LEU:O	2.30	0.48
1:L:177:ILE:HG21	1:L:181:PHE:CE2	2.41	0.48
1:L:242:PHE:CE1	1:L:243:PHE:HD1	2.29	0.48
1:L:15:THR:CG2	1:L:15:THR:O	2.61	0.48
3:H:82:ASP:CG	3:H:82:ASP:O	2.52	0.48
3:H:208:LEU:HD12	3:H:208:LEU:C	2.30	0.48
3:H:219:ILE:HG22	3:H:229:GLU:CG	2.43	0.48
1:L:113:ILE:HD11	2:M:226:VAL:CG2	2.27	0.48
1:L:147:PRO:HD2	1:L:156:TRP:CG	2.48	0.48
1:L:153:HIS:HD2	1:L:154:LEU:H	1.60	0.48
1:L:265:TRP:C	1:L:265:TRP:CE3	2.87	0.48
1:L:65:SER:C	1:L:66:VAL:CG2	2.82	0.48
1:L:73:TYR:CE1	1:L:78:ALA:HB2	2.49	0.48
2:M:206:ILE:CG1	6:M:310:BCL:C1B	2.92	0.48
2:M:78:ALA:CB	2:M:84:VAL:HG12	2.44	0.48
2:M:295:TYR:HB3	2:M:296:VAL:H	1.24	0.48
3:H:153:VAL:HG21	3:H:181:VAL:CG1	2.44	0.48
6:L:282:BCL:HED1	2:M:179:ILE:CG2	2.43	0.48
2:M:121:PHE:C	2:M:123:PHE:H	2.17	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:201:PHE:CD2	2:M:282:ILE:CG2	2.97	0.48
1:L:116:HIS:NE2	2:M:224:LEU:HB3	2.28	0.48
6:M:310:BCL:H3A	6:M:310:BCL:HBA1	1.56	0.48
2:M:38:LEU:C	2:M:40:GLY:N	2.65	0.48
2:M:62:SER:C	2:M:64:LEU:H	2.16	0.48
1:L:15:THR:CG2	1:L:19:GLY:H	2.26	0.48
3:H:120:LEU:CD2	3:H:121:PRO:O	2.59	0.48
1:L:225:GLY:CA	3:H:173:GLU:OE2	2.60	0.48
3:H:210:SER:HA	3:H:213:PHE:CD2	2.44	0.48
3:H:110:GLY:HA3	3:H:243:TYR:OH	2.13	0.48
3:H:36:MET:CA	3:H:36:MET:HE2	2.27	0.48
1:L:25:TRP:CZ2	1:L:110:LYS:NZ	2.79	0.48
2:M:94:LEU:CD2	2:M:114:LEU:HB3	2.31	0.48
1:L:224:ILE:HA	2:M:44:ASN:HB2	1.96	0.48
2:M:89:LEU:CA	2:M:92:PHE:CE2	2.97	0.48
3:H:210:SER:O	3:H:212:LEU:C	2.53	0.47
3:H:240:GLY:O	3:H:241:LEU:O	2.31	0.47
1:L:169:TYR:O	1:L:171:PRO:N	2.47	0.47
1:L:255:TRP:CG	1:L:259:TRP:CZ3	3.02	0.47
2:M:116:LEU:O	2:M:120:PHE:CB	2.62	0.47
1:L:208:THR:H	1:L:211:HIS:CB	2.26	0.47
3:H:56:PHE:CG	3:H:57:PRO:HD2	2.37	0.47
3:H:38:GLU:O	3:H:76:PRO:HA	2.14	0.47
1:L:151:TRP:CE3	1:L:154:LEU:CD2	2.93	0.47
6:L:283:BCL:H102	7:L:284:BPH:C1B	2.43	0.47
2:M:208:PHE:HB2	2:M:276:VAL:HG22	1.97	0.47
2:M:51:TYR:CE1	2:M:53:GLY:HA3	2.47	0.47
1:L:146:PHE:CE2	6:M:311:BCL:CMC	2.97	0.47
1:L:49:ILE:CG1	1:L:89:ILE:HD13	2.44	0.47
2:M:132:ARG:O	2:M:133:THR:C	2.52	0.47
2:M:203:GLY:O	2:M:206:ILE:N	2.47	0.47
1:L:35:GLY:CA	8:M:313:U10:H402	2.43	0.47
1:L:232:LEU:CB	2:M:42:PHE:CZ	2.97	0.47
2:M:67:PHE:CD1	2:M:67:PHE:O	2.67	0.47
3:H:199:GLN:HE21	3:H:200:SER:H	1.62	0.47
1:L:113:ILE:CD1	2:M:226:VAL:HG23	2.37	0.47
1:L:132:VAL:C	1:L:136:PRO:HG2	2.34	0.47
6:L:283:BCL:H42	7:L:284:BPH:OBB	2.13	0.47
2:M:157:TRP:CB	6:M:310:BCL:H92	2.44	0.47
2:M:245:ALA:O	2:M:248:ALA:N	2.43	0.47
2:M:24:VAL:C	2:M:26:LEU:N	2.56	0.47
2:M:66:TRP:C	2:M:66:TRP:CD1	2.86	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:88:ASP:OD1	2:M:91:PHE:HD2	1.97	0.47
3:H:69:GLY:O	3:H:70:ARG:HB2	2.14	0.47
1:L:93:ALA:C	1:L:95:GLY:N	2.62	0.47
2:M:167:LEU:HD23	2:M:167:LEU:HA	1.54	0.47
6:L:283:BCL:H72	6:M:311:BCL:CAB	2.44	0.47
2:M:53:GLY:O	2:M:57:VAL:HG12	2.14	0.47
3:H:123:LEU:CD2	3:H:126:HIS:O	2.62	0.47
3:H:22:ILE:C	3:H:24:LEU:H	2.17	0.47
3:H:38:GLU:HG3	3:H:76:PRO:HD3	1.96	0.47
1:L:25:TRP:HB2	3:H:95:GLY:O	2.15	0.47
1:L:216:PHE:CE1	1:L:219:LEU:HD23	2.50	0.47
1:L:241:VAL:O	1:L:244:SER:N	2.47	0.47
2:M:121:PHE:C	2:M:123:PHE:N	2.67	0.47
2:M:21:THR:HG22	2:M:139:ALA:HB1	1.95	0.47
2:M:214:LEU:CG	2:M:215:LEU:N	2.74	0.47
2:M:208:PHE:CD2	2:M:275:LEU:HB3	2.50	0.47
2:M:39:LEU:N	2:M:39:LEU:HD22	2.27	0.47
1:L:17:VAL:CG1	1:L:18:GLY:N	2.51	0.47
2:M:13:ARG:HD3	3:H:143:SER:OG	2.15	0.47
3:H:153:VAL:HG23	3:H:164:VAL:HG22	1.97	0.47
3:H:19:SER:O	3:H:20:PHE:O	2.32	0.47
3:H:24:LEU:CD2	3:H:28:ILE:CD1	2.69	0.47
3:H:34:GLU:HB3	3:H:35:ASN:HD22	1.79	0.47
1:L:152:THR:O	1:L:153:HIS:C	2.53	0.47
1:L:239:SER:O	1:L:242:PHE:N	2.48	0.47
6:L:282:BCL:CHC	6:L:282:BCL:HBB2	2.38	0.47
1:L:177:ILE:HD12	6:L:283:BCL:CMB	2.44	0.47
1:L:78:ALA:CB	1:L:79:PRO:HD3	2.45	0.47
2:M:192:VAL:CG1	2:M:192:VAL:O	2.63	0.47
2:M:196:LEU:O	2:M:199:ASN:CB	2.63	0.47
2:M:242:GLY:O	2:M:243:THR:O	2.33	0.47
6:M:310:BCL:H42	7:M:312:BPH:HBB1	1.96	0.47
2:M:97:PRO:CB	2:M:111:GLU:OE2	2.62	0.47
3:H:213:PHE:CD1	3:H:216:ILE:HD13	2.49	0.47
3:H:241:LEU:O	3:H:242:MET:C	2.52	0.47
3:H:36:MET:HE3	3:H:36:MET:N	1.98	0.47
2:M:70:ILE:HG12	2:M:74:PHE:HD2	1.79	0.47
3:H:147:ASN:OD1	3:H:148:PRO:HD2	2.15	0.47
3:H:153:VAL:O	3:H:160:ILE:CG2	2.62	0.47
3:H:191:LEU:HD22	3:H:205:VAL:HG11	1.96	0.47
3:H:36:MET:H	3:H:36:MET:HE2	0.99	0.47
1:L:110:LYS:HG3	1:L:111:LEU:N	2.29	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:21:LEU:CD1	1:L:22:PHE:CE1	2.76	0.47
2:M:130:TRP:CZ3	2:M:151:LEU:HG	2.50	0.47
2:M:170:SER:HG	2:M:172:SER:HB3	1.78	0.47
2:M:264:GLY:O	2:M:267:ARG:CA	2.63	0.47
2:M:206:ILE:CD1	6:M:311:BCL:HMD1	2.38	0.47
7:M:312:BPH:C11	7:M:312:BPH:H101	2.18	0.47
2:M:88:ASP:C	2:M:92:PHE:CZ	2.79	0.47
3:H:156:CYS:O	3:H:157:ASP:O	2.32	0.47
1:L:78:ALA:CB	1:L:79:PRO:CD	2.93	0.47
2:M:139:ALA:CB	2:M:140:LEU:CD1	2.92	0.47
2:M:168:MET:HG3	2:M:173:GLU:CG	2.45	0.47
2:M:189:PHE:CD1	2:M:189:PHE:O	2.68	0.47
2:M:196:LEU:HD11	2:M:199:ASN:HD22	1.75	0.47
2:M:245:ALA:O	2:M:246:GLU:C	2.54	0.47
3:H:14:SER:C	3:H:18:TYR:HD2	2.18	0.47
1:L:133:LEU:C	1:L:136:PRO:HD2	2.35	0.47
1:L:170:ASN:O	1:L:173:HIS:CB	2.57	0.47
6:L:282:BCL:H3A	6:L:282:BCL:HBA2	1.46	0.47
6:L:283:BCL:H2C	6:L:283:BCL:HBC2	1.68	0.47
6:L:283:BCL:H41	7:L:284:BPH:C3B	2.45	0.47
1:L:98:VAL:HG22	1:L:125:ILE:HD11	1.97	0.47
2:M:139:ALA:HB3	2:M:140:LEU:HD12	1.94	0.47
2:M:206:ILE:HG13	6:M:310:BCL:CHB	2.43	0.47
2:M:300:ASN:C	2:M:301:HIS:CD2	2.88	0.47
1:L:202:LYS:O	1:L:202:LYS:CG	2.63	0.47
2:M:95:GLU:OE1	2:M:176:PRO:CB	2.62	0.47
3:H:14:SER:O	3:H:18:TYR:CG	2.68	0.46
1:L:105:VAL:O	1:L:106:GLU:C	2.53	0.46
1:L:182:THR:C	1:L:184:ALA:N	2.50	0.46
1:L:228:GLY:O	1:L:232:LEU:HB2	2.15	0.46
2:M:13:ARG:HH11	2:M:13:ARG:HB2	1.80	0.46
2:M:222:THR:HG22	2:M:223:ILE:N	2.30	0.46
6:L:282:BCL:HAC1	6:M:310:BCL:C3D	2.45	0.46
2:M:46:GLN:NE2	2:M:49:PRO:HD3	2.26	0.46
3:H:161:ALA:CB	3:H:210:SER:CB	2.80	0.46
3:H:118:ARG:HH11	3:H:227:LEU:CD1	2.28	0.46
1:L:266:TRP:HD1	1:L:267:VAL:HG22	1.81	0.46
1:L:49:ILE:N	1:L:89:ILE:HD11	2.30	0.46
2:M:182:HIS:ND1	2:M:183:LEU:HD12	2.30	0.46
2:M:212:SER:C	2:M:214:LEU:N	2.68	0.46
2:M:24:VAL:O	2:M:25:ASN:C	2.49	0.46
1:L:110:LYS:HE2	2:M:254:TRP:CZ3	2.49	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:217:ARG:O	2:M:50:ILE:HA	2.15	0.46
3:H:100:PRO:HB3	3:H:109:VAL:CG1	2.45	0.46
2:M:111:GLU:O	2:M:112:GLY:O	2.33	0.46
2:M:185:TRP:HE3	2:M:185:TRP:C	2.15	0.46
2:M:35:PHE:HE1	2:M:38:LEU:HD22	1.80	0.46
2:M:295:TYR:O	2:M:296:VAL:C	2.53	0.46
3:H:219:ILE:HG22	3:H:229:GLU:CD	2.36	0.46
8:L:285:U10:C32	2:M:60:LEU:HD21	2.45	0.46
2:M:131:GLY:O	2:M:132:ARG:C	2.54	0.46
2:M:157:TRP:CE3	2:M:158:MET:HG2	2.51	0.46
2:M:238:ILE:HG12	2:M:263:GLU:HG3	1.96	0.46
2:M:50:ILE:HG23	2:M:51:TYR:H	1.78	0.46
1:L:264:GLN:O	1:L:265:TRP:C	2.53	0.46
6:L:282:BCL:HED1	2:M:179:ILE:HG22	1.96	0.46
2:M:197:PHE:C	2:M:199:ASN:N	2.68	0.46
2:M:230:GLY:HA2	2:M:232:GLU:OE2	2.16	0.46
3:H:83:ARG:HA	3:H:83:ARG:HE	1.80	0.46
3:H:151:LEU:HA	3:H:152:PRO:HD2	1.75	0.46
1:L:100:TRP:O	1:L:103:ARG:N	2.49	0.46
1:L:110:LYS:HE2	2:M:254:TRP:HZ3	1.81	0.46
1:L:8:LYS:O	1:L:11:VAL:HG11	2.14	0.46
1:L:127:ALA:HB3	6:L:283:BCL:H52	1.96	0.46
1:L:171:PRO:C	1:L:173:HIS:H	2.18	0.46
1:L:69:PRO:HA	1:L:82:LYS:HD3	1.97	0.46
1:L:69:PRO:CB	1:L:78:ALA:HB3	2.46	0.46
1:L:70:ALA:H	1:L:82:LYS:HD3	1.80	0.46
2:M:204:LEU:C	2:M:206:ILE:N	2.66	0.46
2:M:209:LEU:HA	2:M:276:VAL:HG21	1.97	0.46
2:M:72:ILE:HD13	2:M:72:ILE:HA	1.63	0.46
1:L:146:PHE:CB	1:L:156:TRP:CG	2.96	0.46
2:M:168:MET:CG	2:M:173:GLU:HG3	2.45	0.46
2:M:206:ILE:HG21	6:M:311:BCL:C2D	2.45	0.46
2:M:70:ILE:CD1	2:M:74:PHE:CD2	2.99	0.46
1:L:185:LEU:CA	1:L:188:ALA:H	2.28	0.46
1:L:193:LEU:O	1:L:194:VAL:C	2.54	0.46
1:L:249:ILE:HG22	1:L:250:ILE:N	2.31	0.46
6:L:282:BCL:C2	7:M:312:BPH:HMB2	2.46	0.46
1:L:124:ALA:CB	7:L:284:BPH:HBC2	2.42	0.46
7:L:284:BPH:CHC	7:L:284:BPH:OBB	2.64	0.46
2:M:165:PRO:CB	2:M:173:GLU:HB2	2.46	0.46
2:M:278:LEU:C	2:M:278:LEU:HD12	2.36	0.46
2:M:168:MET:HE1	2:M:288:GLY:HA3	1.96	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:186:THR:HG22	6:M:310:BCL:HHD	1.97	0.46
2:M:7:PHE:CD1	2:M:7:PHE:O	2.69	0.46
3:H:118:ARG:HH11	3:H:227:LEU:HD12	1.79	0.46
1:L:128:TYR:CD1	1:L:129:LEU:N	2.84	0.46
1:L:226:THR:HG22	2:M:232:GLU:HB2	1.91	0.46
1:L:249:ILE:HG23	1:L:249:ILE:O	2.15	0.46
1:L:97:PHE:CE1	6:L:283:BCL:C13	2.96	0.46
2:M:164:ARG:NH1	2:M:164:ARG:HG2	2.28	0.46
2:M:150:PHE:CD1	7:M:312:BPH:C3D	2.99	0.46
2:M:37:THR:HA	2:M:41:TRP:NE1	2.31	0.46
3:H:157:ASP:CG	3:H:211:ASP:OD1	2.53	0.45
3:H:204:HIS:CE1	3:H:213:PHE:CE2	3.04	0.45
3:H:40:TYR:N	3:H:42:LEU:HD11	2.24	0.45
1:L:194:VAL:HG21	2:M:234:GLU:OE1	2.16	0.45
6:L:283:BCL:H8	6:M:311:BCL:CBB	2.46	0.45
2:M:24:VAL:O	2:M:26:LEU:HB3	2.16	0.45
6:M:311:BCL:HBB3	6:M:311:BCL:CMB	2.42	0.45
1:L:68:PRO:HB2	1:L:69:PRO:CD	2.46	0.45
2:M:155:TRP:C	2:M:157:TRP:N	2.68	0.45
2:M:273:ALA:O	2:M:276:VAL:HB	2.16	0.45
2:M:201:PHE:CE2	2:M:282:ILE:CG2	2.99	0.45
2:M:28:ASN:O	2:M:30:SER:O	2.34	0.45
3:H:191:LEU:HD22	3:H:205:VAL:HG21	1.98	0.45
3:H:117:ARG:NH1	3:H:231:ASP:OD1	2.49	0.45
3:H:27:LEU:O	3:H:28:ILE:O	2.35	0.45
3:H:94:GLU:O	3:H:96:PHE:CA	2.62	0.45
3:H:96:PHE:CD1	3:H:97:PRO:HD2	2.52	0.45
1:L:154:LEU:O	1:L:158:SER:HB2	2.16	0.45
1:L:248:MET:HE2	6:L:283:BCL:OBD	2.16	0.45
1:L:48:LEU:CG	1:L:89:ILE:HG13	2.46	0.45
1:L:9:TYR:CE2	2:M:243:THR:HG23	2.52	0.45
2:M:256:MET:CE	8:M:313:U10:H102	2.45	0.45
2:M:65:MET:CG	2:M:66:TRP:H	2.26	0.45
3:H:17:ILE:HD11	3:H:21:TRP:HE1	1.80	0.45
3:H:204:HIS:CD2	3:H:206:ASN:N	2.84	0.45
3:H:204:HIS:HE1	3:H:213:PHE:HZ	1.63	0.45
3:H:32:GLN:O	3:H:34:GLU:N	2.49	0.45
1:L:128:TYR:C	1:L:130:THR:N	2.69	0.45
1:L:216:PHE:HD1	1:L:216:PHE:HA	1.54	0.45
2:M:218:MET:HE1	8:M:313:U10:C1M	2.47	0.45
2:M:259:ASN:C	2:M:259:ASN:ND2	2.70	0.45
2:M:264:GLY:HA2	2:M:267:ARG:CG	2.45	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:46:GLN:HE21	2:M:49:PRO:CD	2.08	0.45
2:M:62:SER:C	2:M:64:LEU:N	2.70	0.45
2:M:87:ARG:C	2:M:89:LEU:H	2.19	0.45
1:L:204:LYS:CD	1:L:207:ARG:HH22	2.23	0.45
3:H:37:ARG:NH2	3:H:44:ASN:OD1	2.48	0.45
1:L:8:LYS:C	3:H:87:LEU:CD2	2.85	0.45
1:L:193:LEU:C	1:L:195:LEU:N	2.68	0.45
1:L:249:ILE:CG2	1:L:250:ILE:N	2.78	0.45
1:L:84:GLY:CA	1:L:87:GLN:HB2	2.47	0.45
2:M:109:LEU:O	2:M:113:GLY:HA3	2.17	0.45
2:M:90:PHE:CB	2:M:179:ILE:HD12	2.47	0.45
2:M:185:TRP:CZ3	2:M:186:THR:HA	2.52	0.45
1:L:86:TRP:CE3	1:L:87:GLN:HA	2.50	0.45
1:L:124:ALA:O	1:L:127:ALA:N	2.50	0.45
1:L:11:VAL:O	1:L:12:PRO:C	2.55	0.45
1:L:170:ASN:OD1	1:L:170:ASN:C	2.55	0.45
1:L:182:THR:O	1:L:186:ALA:CB	2.65	0.45
2:M:72:ILE:O	2:M:72:ILE:HD12	2.16	0.45
3:H:168:TRP:CH2	3:H:223:THR:C	2.91	0.45
1:L:170:ASN:ND2	1:L:247:CYS:O	2.49	0.45
1:L:193:LEU:HD23	8:L:285:U10:O3	2.14	0.45
6:L:283:BCL:C4	7:L:284:BPH:OBB	2.64	0.45
2:M:192:VAL:O	2:M:192:VAL:HG12	2.16	0.45
2:M:152:SER:CA	2:M:277:THR:HG22	2.42	0.45
2:M:252:TRP:CD1	8:M:313:U10:C6	2.99	0.45
2:M:218:MET:HE1	8:M:313:U10:H1M3	1.98	0.45
3:H:130:LYS:O	3:H:171:ILE:CD1	2.57	0.45
3:H:179:LEU:HD21	3:H:181:VAL:CG2	2.46	0.45
1:L:177:ILE:HD12	6:L:283:BCL:HMB3	1.99	0.45
1:L:90:THR:C	1:L:92:CYS:N	2.70	0.45
2:M:237:GLN:O	2:M:239:ALA:N	2.50	0.45
2:M:208:PHE:C	2:M:276:VAL:HG22	2.30	0.45
2:M:62:SER:O	2:M:64:LEU:N	2.50	0.45
1:L:54:VAL:C	1:L:56:GLN:H	2.20	0.45
3:H:131:ILE:HD11	3:H:225:VAL:CG2	2.47	0.45
1:L:109:ARG:NE	1:L:109:ARG:HA	2.31	0.45
1:L:93:ALA:HB1	1:L:97:PHE:HE2	1.75	0.45
2:M:152:SER:HA	2:M:277:THR:CG2	2.46	0.45
2:M:44:ASN:HD22	2:M:44:ASN:HA	1.42	0.45
3:H:24:LEU:HD23	3:H:28:ILE:HD12	1.87	0.44
1:L:147:PRO:CG	1:L:152:THR:CG2	2.92	0.44
1:L:156:TRP:HZ3	1:L:157:VAL:HA	1.75	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:185:LEU:O	1:L:188:ALA:CA	2.61	0.44
1:L:241:VAL:HG21	7:L:284:BPH:CB	2.46	0.44
2:M:133:THR:HG21	2:M:146:THR:HG21	2.00	0.44
2:M:258:PHE:C	2:M:258:PHE:CD1	2.89	0.44
2:M:284:ILE:HG23	2:M:284:ILE:O	2.17	0.44
2:M:55:LEU:O	2:M:57:VAL:N	2.50	0.44
2:M:92:PHE:O	2:M:93:SER:CB	2.62	0.44
1:L:268:LYS:HB3	1:L:268:LYS:HE2	1.43	0.44
2:M:191:LEU:N	2:M:191:LEU:CD1	2.80	0.44
3:H:130:LYS:HZ3	3:H:131:ILE:HG22	1.83	0.44
1:L:102:LEU:O	1:L:104:GLU:N	2.51	0.44
1:L:146:PHE:HA	1:L:156:TRP:CD1	2.53	0.44
6:M:310:BCL:H41	7:M:312:BPH:HBB2	1.98	0.44
3:H:213:PHE:CD1	3:H:216:ILE:HD11	2.52	0.44
1:L:16:LEU:HB2	1:L:106:GLU:OE2	2.17	0.44
1:L:123:PHE:CG	1:L:238:LEU:CD2	2.96	0.44
1:L:147:PRO:CG	1:L:156:TRP:HB2	2.47	0.44
1:L:183:ASN:HA	1:L:186:ALA:HB3	1.98	0.44
1:L:47:ILE:O	1:L:49:ILE:N	2.50	0.44
2:M:212:SER:O	2:M:215:LEU:N	2.51	0.44
2:M:297:TRP:O	2:M:301:HIS:HD2	2.01	0.44
2:M:11:GLN:NE2	3:H:144:ALA:CB	2.79	0.44
1:L:244:SER:HB3	6:L:283:BCL:HBA2	1.99	0.44
8:L:285:U10:H3M3	8:L:285:U10:C4M	2.47	0.44
2:M:105:PHE:CD1	2:M:106:ALA:CB	3.01	0.44
2:M:109:LEU:HD22	2:M:110:LYS:HA	1.98	0.44
2:M:35:PHE:CD2	2:M:47:LEU:HD12	2.39	0.44
2:M:58:LEU:O	2:M:62:SER:N	2.51	0.44
3:H:100:PRO:HB3	3:H:109:VAL:HG11	1.99	0.44
3:H:135:LYS:C	3:H:137:ALA:H	2.20	0.44
3:H:143:SER:O	3:H:144:ALA:O	2.35	0.44
1:L:5:PHE:CZ	3:H:40:TYR:CZ	2.91	0.44
1:L:102:LEU:C	1:L:104:GLU:N	2.68	0.44
2:M:148:TRP:C	2:M:150:PHE:H	2.12	0.44
6:M:310:BCL:H42	7:M:312:BPH:HBB2	1.98	0.44
2:M:93:SER:HB2	2:M:178:GLY:CA	2.44	0.44
1:L:17:VAL:C	1:L:19:GLY:H	2.20	0.44
3:H:83:ARG:HA	3:H:84:PRO:HD2	1.78	0.44
2:M:77:GLN:HE21	2:M:77:GLN:HB2	1.54	0.44
1:L:150:ILE:HG22	1:L:151:TRP:CD1	2.53	0.44
1:L:69:PRO:HG2	1:L:78:ALA:HB3	1.96	0.44
1:L:87:GLN:O	1:L:90:THR:HB	2.18	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:35:PHE:CB	2:M:39:LEU:CD2	2.95	0.44
1:L:232:LEU:CB	2:M:42:PHE:HZ	2.30	0.44
1:L:200:PRO:HB2	1:L:201:GLU:H	1.63	0.44
3:H:18:TYR:CD1	3:H:18:TYR:C	2.90	0.44
3:H:36:MET:HB2	3:H:36:MET:HE3	1.56	0.44
1:L:175:ILE:CG2	1:L:179:PHE:CE1	3.00	0.44
1:L:177:ILE:HG21	1:L:181:PHE:HE2	1.80	0.44
1:L:6:GLU:C	1:L:8:LYS:N	2.70	0.44
8:M:313:U10:H33	8:M:313:U10:H372	1.74	0.44
2:M:51:TYR:CE1	2:M:53:GLY:CA	3.00	0.44
8:L:285:U10:H321	2:M:60:LEU:HD21	1.99	0.44
2:M:81:ASN:O	2:M:82:PRO:C	2.56	0.44
3:H:57:PRO:C	3:H:58:LEU:HD12	2.37	0.44
1:L:102:LEU:N	1:L:102:LEU:HD22	2.30	0.44
1:L:190:HIS:CE1	1:L:229:ILE:HG21	2.52	0.44
1:L:84:GLY:O	1:L:86:TRP:C	2.56	0.44
2:M:58:LEU:O	2:M:60:LEU:N	2.51	0.44
3:H:27:LEU:HD12	3:H:28:ILE:CA	2.33	0.44
1:L:10:ARG:CZ	1:L:25:TRP:CG	3.01	0.44
1:L:10:ARG:NH2	3:H:95:GLY:O	2.51	0.44
1:L:112:GLY:HA3	2:M:247:ARG:HH11	1.82	0.44
1:L:98:VAL:HG23	1:L:125:ILE:CD1	2.47	0.44
1:L:131:LEU:HD13	1:L:146:PHE:HE2	1.83	0.44
1:L:161:GLY:O	1:L:163:THR:N	2.51	0.44
2:M:244:ALA:O	2:M:245:ALA:O	2.36	0.44
2:M:265:ILE:O	2:M:268:TRP:HB2	2.18	0.44
2:M:282:ILE:HG22	2:M:283:GLY:N	2.32	0.44
7:M:312:BPH:H2A	7:M:312:BPH:O2D	2.17	0.44
3:H:219:ILE:HG21	3:H:225:VAL:HG12	1.99	0.43
1:L:242:PHE:C	1:L:244:SER:N	2.71	0.43
2:M:124:VAL:O	2:M:125:ALA:O	2.36	0.43
3:H:105:MET:CB	3:H:106:LYS:HZ3	2.30	0.43
3:H:158:LEU:HD12	3:H:158:LEU:HA	1.77	0.43
3:H:227:LEU:O	3:H:228:LEU:C	2.56	0.43
1:L:105:VAL:O	1:L:107:ILE:N	2.51	0.43
2:M:163:ILE:HG21	2:M:285:LEU:CD1	2.44	0.43
2:M:222:THR:C	2:M:224:LEU:N	2.71	0.43
2:M:35:PHE:CE1	2:M:38:LEU:HD22	2.54	0.43
2:M:41:TRP:HA	2:M:41:TRP:CE3	2.53	0.43
3:H:140:PHE:CE2	3:H:169:VAL:HG11	2.50	0.43
1:L:110:LYS:C	1:L:112:GLY:N	2.70	0.43
1:L:225:GLY:HA2	8:L:285:U10:H4M2	1.97	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:177:ILE:HD11	6:L:283:BCL:C1B	2.47	0.43
1:L:68:PRO:HB3	1:L:86:TRP:CZ2	2.52	0.43
1:L:48:LEU:HD13	1:L:85:LEU:HA	2.00	0.43
2:M:165:PRO:HG3	2:M:173:GLU:CB	2.48	0.43
2:M:205:SER:N	2:M:279:THR:CG2	2.80	0.43
7:L:284:BPH:CMC	2:M:213:ALA:HB1	2.49	0.43
1:L:113:ILE:CD1	2:M:225:ALA:O	2.64	0.43
3:H:102:GLY:O	3:H:103:ASP:C	2.57	0.43
3:H:88:ALA:C	3:H:89:ARG:HG2	2.38	0.43
3:H:171:ILE:CD1	3:H:171:ILE:H	2.30	0.43
3:H:85:ILE:HG12	3:H:85:ILE:H	1.49	0.43
1:L:123:PHE:CD2	1:L:238:LEU:HD23	2.53	0.43
1:L:79:PRO:HG2	1:L:82:LYS:H	1.84	0.43
1:L:6:GLU:C	1:L:8:LYS:H	2.22	0.43
2:M:150:PHE:CD1	7:M:312:BPH:C2D	3.01	0.43
2:M:201:PHE:CZ	2:M:282:ILE:HG21	2.53	0.43
2:M:60:LEU:O	2:M:61:PHE:C	2.56	0.43
2:M:73:TRP:CH2	2:M:109:LEU:CD2	3.00	0.43
3:H:149:ILE:C	3:H:151:LEU:N	2.72	0.43
3:H:170:ASP:OD2	3:H:177:ARG:NE	2.52	0.43
1:L:159:ASN:O	1:L:162:TYR:N	2.52	0.43
1:L:178:SER:O	1:L:182:THR:HB	2.18	0.43
1:L:8:LYS:NZ	1:L:9:TYR:HE1	2.14	0.43
2:M:113:GLY:O	2:M:116:LEU:N	2.52	0.43
2:M:119:SER:CB	2:M:177:TYR:CE2	3.02	0.43
1:L:116:HIS:CE1	2:M:225:ALA:N	2.86	0.43
2:M:268:TRP:HA	2:M:268:TRP:CE3	2.54	0.43
2:M:69:THR:CG2	2:M:118:ALA:HB2	2.49	0.43
2:M:87:ARG:HG3	2:M:88:ASP:CG	2.38	0.43
3:H:116:ALA:HB1	3:H:228:LEU:CD1	2.48	0.43
3:H:148:PRO:O	3:H:151:LEU:N	2.48	0.43
3:H:190:LEU:HD22	3:H:219:ILE:HD11	2.00	0.43
1:L:135:ARG:N	1:L:136:PRO:HD2	2.33	0.43
1:L:147:PRO:CD	1:L:156:TRP:CD1	3.01	0.43
1:L:182:THR:HG22	1:L:236:LEU:HD13	1.99	0.43
1:L:237:SER:HB2	2:M:213:ALA:O	2.18	0.43
1:L:69:PRO:HA	1:L:82:LYS:CD	2.48	0.43
2:M:122:MET:O	2:M:126:VAL:CG2	2.66	0.43
2:M:69:THR:O	2:M:72:ILE:HG22	2.18	0.43
1:L:231:ARG:NH2	2:M:7:PHE:CB	2.82	0.43
2:M:12:VAL:HG22	3:H:141:HIS:O	2.18	0.43
3:H:210:SER:O	3:H:212:LEU:CA	2.63	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:11:VAL:HA	1:L:12:PRO:HD2	1.62	0.43
1:L:138:MET:SD	1:L:249:ILE:HD11	2.59	0.43
2:M:36:SER:O	2:M:40:GLY:HA3	2.18	0.43
2:M:58:LEU:C	2:M:60:LEU:N	2.71	0.43
1:L:54:VAL:O	1:L:55:LEU:C	2.56	0.43
3:H:20:PHE:CD1	3:H:21:TRP:N	2.81	0.43
3:H:168:TRP:CH2	3:H:224:GLU:N	2.87	0.43
1:L:178:SER:CB	6:L:282:BCL:O1A	2.42	0.43
1:L:72:GLU:OE2	1:L:72:GLU:C	2.56	0.43
2:M:119:SER:HA	2:M:177:TYR:CZ	2.50	0.43
2:M:237:GLN:C	2:M:239:ALA:N	2.71	0.43
2:M:26:LEU:CG	2:M:27:ALA:N	2.81	0.43
2:M:76:TYR:CD1	2:M:76:TYR:C	2.93	0.43
3:H:134:MET:SD	3:H:141:HIS:HE1	2.34	0.43
3:H:196:VAL:HA	3:H:205:VAL:N	2.32	0.43
3:H:242:MET:HE3	3:H:243:TYR:CZ	2.54	0.43
1:L:111:LEU:CD2	2:M:251:PHE:CB	2.93	0.43
1:L:167:PHE:CE2	6:L:283:BCL:C2D	3.01	0.43
1:L:9:TYR:O	1:L:11:VAL:HG22	2.19	0.43
1:L:31:VAL:HG13	8:M:313:U10:C40	2.49	0.43
2:M:96:PRO:O	2:M:98:ALA:N	2.50	0.43
1:L:219:LEU:HA	1:L:219:LEU:HD12	1.82	0.43
1:L:26:VAL:O	1:L:27:GLY:C	2.57	0.43
6:L:282:BCL:H2C	6:L:282:BCL:HBC3	1.50	0.43
2:M:264:GLY:C	2:M:267:ARG:H	2.21	0.43
3:H:58:LEU:N	3:H:58:LEU:HD12	2.34	0.43
3:H:65:ILE:CG2	3:H:65:ILE:O	2.66	0.43
3:H:106:LYS:HB2	3:H:106:LYS:HE2	1.43	0.43
1:L:101:ALA:HB2	1:L:121:PHE:CE1	2.47	0.42
1:L:11:VAL:HG23	1:L:11:VAL:O	2.18	0.42
1:L:135:ARG:C	1:L:139:MET:HE3	2.39	0.42
1:L:185:LEU:HD23	1:L:186:ALA:H	0.48	0.42
1:L:248:MET:HA	1:L:251:THR:HG22	2.00	0.42
2:M:116:LEU:HD23	2:M:116:LEU:HA	1.78	0.42
2:M:214:LEU:O	2:M:217:ALA:CA	2.67	0.42
2:M:24:VAL:O	2:M:24:VAL:CG1	2.67	0.42
3:H:39:GLY:HA2	3:H:42:LEU:HD11	2.00	0.42
1:L:148:TYR:HD1	1:L:148:TYR:HA	1.69	0.42
1:L:147:PRO:HD3	1:L:156:TRP:HD1	1.83	0.42
1:L:262:TRP:C	1:L:264:GLN:H	2.19	0.42
7:L:284:BPH:H3A	7:L:284:BPH:HBA1	1.73	0.42
2:M:209:LEU:HG	6:M:310:BCL:O1A	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:285:LEU:H	2:M:285:LEU:HD23	1.85	0.42
7:M:312:BPH:C6	7:M:312:BPH:H8	2.46	0.42
3:H:151:LEU:HD22	3:H:202:ARG:C	2.39	0.42
3:H:229:GLU:O	3:H:233:ILE:CD1	2.67	0.42
1:L:210:ASP:OD1	1:L:213:ASP:HB2	2.19	0.42
1:L:249:ILE:HD13	1:L:249:ILE:O	2.19	0.42
7:L:284:BPH:HMD1	7:L:284:BPH:HHD	1.86	0.42
1:L:51:TRP:HH2	1:L:80:LEU:CD1	2.32	0.42
2:M:208:PHE:CB	2:M:276:VAL:HG22	2.47	0.42
2:M:87:ARG:NH1	2:M:87:ARG:HB2	2.34	0.42
1:L:166:ASN:OD1	1:L:166:ASN:C	2.57	0.42
3:H:196:VAL:N	3:H:205:VAL:HA	2.35	0.42
1:L:167:PHE:HD2	6:L:283:BCL:HHD	1.76	0.42
6:L:283:BCL:HHC	6:L:283:BCL:OBB	2.19	0.42
1:L:49:ILE:CB	1:L:89:ILE:HD11	2.49	0.42
2:M:157:TRP:O	2:M:158:MET:C	2.58	0.42
2:M:242:GLY:HA3	3:H:117:ARG:HD3	2.01	0.42
2:M:279:THR:O	2:M:282:ILE:HB	2.20	0.42
4:M:308:BOG:H2'2	4:M:308:BOG:H5'1	1.22	0.42
2:M:160:LEU:HD21	6:M:310:BCL:OBD	2.20	0.42
3:H:116:ALA:CA	3:H:228:LEU:HD11	2.43	0.42
1:L:139:MET:C	1:L:141:ALA:N	2.72	0.42
1:L:75:LEU:HD23	1:L:141:ALA:HA	2.01	0.42
1:L:246:LEU:O	1:L:247:CYS:C	2.57	0.42
6:L:282:BCL:HHC	6:L:282:BCL:CBB	2.41	0.42
1:L:97:PHE:CE1	6:L:283:BCL:H143	2.38	0.42
2:M:110:LYS:HA	2:M:110:LYS:HD3	1.32	0.42
2:M:56:GLY:CA	2:M:132:ARG:HD2	2.49	0.42
2:M:137:ALA:O	2:M:141:GLY:N	2.52	0.42
3:H:105:MET:H	3:H:106:LYS:NZ	2.14	0.42
1:L:91:ILE:O	1:L:91:ILE:HG22	2.19	0.42
2:M:290:VAL:HG21	3:H:12:LEU:HD13	2.01	0.42
3:H:153:VAL:O	3:H:153:VAL:HG12	2.19	0.42
1:L:157:VAL:HG12	1:L:158:SER:N	2.35	0.42
1:L:123:PHE:CE2	1:L:238:LEU:CD2	3.03	0.42
2:M:115:TRP:CE3	2:M:116:LEU:N	2.87	0.42
2:M:224:LEU:C	2:M:226:VAL:N	2.69	0.42
1:L:9:TYR:CD1	2:M:250:LEU:HD11	2.55	0.42
2:M:271:TRP:CH2	3:H:31:LEU:CD2	3.02	0.42
6:L:283:BCL:H72	6:M:311:BCL:CBB	2.50	0.42
2:M:60:LEU:O	2:M:64:LEU:HD13	2.18	0.42
3:H:184:LYS:HE2	3:H:186:GLY:HA2	2.01	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:193:MET:C	3:H:195:MET:N	2.72	0.42
3:H:26:GLY:O	3:H:30:TYR:CB	2.64	0.42
1:L:135:ARG:NH1	1:L:139:MET:SD	2.92	0.42
1:L:150:ILE:CD1	1:L:150:ILE:H	2.33	0.42
8:L:285:U10:H251	8:L:285:U10:H271	1.67	0.42
2:M:73:TRP:CZ2	2:M:114:LEU:HD11	2.55	0.42
2:M:130:TRP:HZ3	2:M:147:ALA:O	2.02	0.42
2:M:163:ILE:HG22	2:M:164:ARG:N	2.35	0.42
2:M:266:HIS:HA	2:M:269:ALA:CB	2.50	0.42
2:M:208:PHE:HB2	2:M:276:VAL:CG2	2.50	0.42
2:M:35:PHE:CB	2:M:39:LEU:HD22	2.49	0.42
3:H:60:LYS:HD2	3:H:62:LYS:HG2	2.00	0.42
3:H:111:PRO:CD	3:H:243:TYR:CZ	2.97	0.42
1:L:6:GLU:HG2	1:L:10:ARG:CD	2.50	0.42
1:L:177:ILE:O	1:L:181:PHE:N	2.52	0.42
6:L:282:BCL:H2	7:M:312:BPH:C2B	2.50	0.42
1:L:111:LEU:HD22	2:M:251:PHE:HA	2.01	0.42
3:H:64:PHE:HB2	3:H:73:LEU:O	2.19	0.42
1:L:127:ALA:HB3	6:L:283:BCL:C2	2.46	0.42
1:L:179:PHE:HB3	1:L:236:LEU:O	2.20	0.42
1:L:255:TRP:CZ2	1:L:262:TRP:HE3	2.38	0.42
1:L:174:MET:SD	6:L:282:BCL:O1D	2.78	0.42
1:L:60:ASN:O	1:L:62:GLN:CA	2.67	0.42
1:L:8:LYS:O	3:H:87:LEU:HD21	2.20	0.42
1:L:263:TRP:CG	2:M:180:PHE:HE2	2.34	0.42
1:L:5:PHE:CE1	2:M:246:GLU:HA	2.54	0.42
2:M:279:THR:CG2	2:M:280:GLY:N	2.82	0.42
6:M:310:BCL:H172	7:M:312:BPH:CMB	2.50	0.42
2:M:59:SER:O	2:M:63:GLY:N	2.47	0.42
1:L:231:ARG:HH22	2:M:7:PHE:HA	1.69	0.42
3:H:83:ARG:HA	3:H:83:ARG:NE	2.35	0.42
3:H:182:GLU:HA	3:H:188:THR:HA	2.02	0.42
3:H:195:MET:O	3:H:196:VAL:O	2.38	0.42
3:H:43:GLU:CD	3:H:44:ASN:HD21	2.23	0.42
3:H:143:SER:OG	3:H:143:SER:O	2.35	0.41
3:H:201:ASN:OD1	3:H:202:ARG:CB	2.68	0.41
1:L:185:LEU:N	1:L:185:LEU:HD22	2.35	0.41
1:L:189:LEU:HD22	1:L:216:PHE:HZ	1.85	0.41
2:M:35:PHE:CE2	2:M:39:LEU:HD21	2.55	0.41
2:M:73:TRP:CD2	2:M:114:LEU:HD21	2.55	0.41
1:L:240:ALA:O	1:L:241:VAL:C	2.58	0.41
1:L:121:PHE:HB2	7:L:284:BPH:C3D	2.50	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:15:PRO:HD2	3:H:140:PHE:CD1	2.52	0.41
1:L:113:ILE:CG2	2:M:225:ALA:HB1	2.49	0.41
2:M:238:ILE:CD1	2:M:263:GLU:HG3	2.50	0.41
3:H:17:ILE:O	3:H:21:TRP:HD1	2.03	0.41
3:H:190:LEU:HD11	3:H:225:VAL:HG11	2.02	0.41
3:H:37:ARG:O	3:H:42:LEU:HD12	2.19	0.41
1:L:109:ARG:N	1:L:109:ARG:HE	2.19	0.41
2:M:152:SER:OG	2:M:277:THR:HG22	2.20	0.41
1:L:123:PHE:O	1:L:127:ALA:N	2.53	0.41
2:M:211:GLY:O	2:M:214:LEU:HB3	2.20	0.41
2:M:279:THR:O	2:M:281:GLY:N	2.53	0.41
1:L:205:GLU:HG3	3:H:67:PRO:HA	2.01	0.41
2:M:191:LEU:N	2:M:191:LEU:HD13	2.35	0.41
3:H:130:LYS:HG2	3:H:172:PRO:HG2	2.02	0.41
3:H:17:ILE:HD11	3:H:21:TRP:NE1	2.35	0.41
3:H:121:PRO:HG3	3:H:224:GLU:HG2	2.02	0.41
3:H:90:THR:OG1	3:H:97:PRO:O	2.38	0.41
1:L:146:PHE:HE1	1:L:148:TYR:HE1	1.68	0.41
1:L:168:HIS:HE1	2:M:183:LEU:O	2.04	0.41
1:L:221:GLY:HA3	2:M:50:ILE:HG13	2.01	0.41
2:M:130:TRP:CZ3	2:M:147:ALA:O	2.73	0.41
1:L:9:TYR:HE2	2:M:243:THR:HG23	1.85	0.41
3:H:234:CYS:O	3:H:237:VAL:CG2	2.61	0.41
1:L:86:TRP:HZ2	1:L:145:ALA:CB	2.33	0.41
2:M:164:ARG:CB	2:M:165:PRO:CD	2.69	0.41
2:M:228:ARG:HH22	3:H:241:LEU:HD21	1.84	0.41
2:M:152:SER:OG	2:M:274:VAL:HG22	2.20	0.41
2:M:27:ALA:HB1	2:M:52:LEU:H	1.86	0.41
2:M:35:PHE:HB3	2:M:39:LEU:HD22	2.02	0.41
2:M:16:ALA:HB2	2:M:32:VAL:HG21	1.96	0.41
3:H:134:MET:HB3	3:H:166:ASP:OD2	2.21	0.41
3:H:155:GLY:CA	3:H:204:HIS:CD2	3.04	0.41
3:H:168:TRP:CZ3	3:H:223:THR:O	2.74	0.41
3:H:234:CYS:C	3:H:237:VAL:CG2	2.89	0.41
1:L:126:LEU:O	1:L:126:LEU:HD13	2.21	0.41
1:L:146:PHE:HD1	1:L:146:PHE:C	2.23	0.41
1:L:244:SER:CB	6:L:283:BCL:HBA2	2.51	0.41
1:L:193:LEU:CD2	8:L:285:U10:C2	2.98	0.41
1:L:37:ALA:C	1:L:39:PHE:N	2.72	0.41
2:M:290:VAL:HG12	3:H:13:ALA:HB2	2.03	0.41
2:M:64:LEU:O	2:M:65:MET:C	2.58	0.41
2:M:94:LEU:HD11	2:M:114:LEU:CB	2.50	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:160:THR:O	1:L:164:TYR:CD1	2.72	0.41
1:L:173:HIS:CE1	1:L:177:ILE:CD1	2.90	0.41
1:L:29:PHE:CD1	1:L:29:PHE:N	2.89	0.41
1:L:73:TYR:CB	1:L:82:LYS:HZ2	2.32	0.41
2:M:113:GLY:O	2:M:114:LEU:O	2.39	0.41
2:M:159:VAL:C	2:M:161:GLY:H	2.21	0.41
3:H:218:THR:CG2	3:H:219:ILE:N	2.83	0.41
3:H:117:ARG:CB	3:H:227:LEU:HB3	2.43	0.41
1:L:111:LEU:CD2	2:M:251:PHE:HA	2.51	0.41
1:L:127:ALA:O	1:L:130:THR:HB	2.20	0.41
1:L:146:PHE:CD1	1:L:146:PHE:C	2.93	0.41
1:L:187:LEU:HA	1:L:187:LEU:HD13	1.88	0.41
1:L:60:ASN:CG	1:L:63:LEU:HD12	2.41	0.41
1:L:69:PRO:HG3	1:L:78:ALA:HB3	1.98	0.41
1:L:87:GLN:O	1:L:88:ILE:C	2.60	0.41
2:M:252:TRP:CD1	8:M:313:U10:C1	3.04	0.41
1:L:159:ASN:O	1:L:161:GLY:N	2.54	0.41
1:L:215:PHE:HD1	1:L:216:PHE:CD1	2.39	0.41
2:M:14:GLY:HA3	3:H:140:PHE:CD1	2.55	0.41
2:M:201:PHE:HB2	2:M:283:GLY:HA2	2.03	0.41
1:L:187:LEU:CA	2:M:216:PHE:CE2	3.04	0.41
2:M:256:MET:HE1	8:M:313:U10:H102	2.02	0.41
2:M:263:GLU:O	2:M:266:HIS:N	2.49	0.41
6:L:283:BCL:C2C	6:M:310:BCL:CBC	2.85	0.41
1:L:269:LEU:CD1	1:L:270:PRO:CD	2.90	0.41
3:H:155:GLY:HA3	3:H:210:SER:H	1.86	0.41
1:L:32:GLY:C	1:L:34:PHE:H	2.20	0.41
1:L:61:PRO:O	1:L:64:ILE:HG23	2.21	0.41
2:M:165:PRO:HB3	2:M:173:GLU:HB2	2.02	0.41
2:M:21:THR:OG1	2:M:23:ASP:CA	2.69	0.41
2:M:20:MET:CG	2:M:22:GLU:N	2.70	0.41
1:L:15:THR:HG21	1:L:19:GLY:C	2.40	0.41
3:H:109:VAL:O	3:H:112:ALA:HB3	2.20	0.40
3:H:166:ASP:O	3:H:179:LEU:HA	2.22	0.40
1:L:149:GLY:O	1:L:152:THR:N	2.54	0.40
2:M:152:SER:HB3	2:M:277:THR:HG21	2.03	0.40
8:M:313:U10:H212	8:M:313:U10:H252	1.64	0.40
3:H:108:GLY:HA3	3:H:114:TRP:CE3	2.54	0.40
3:H:189:ARG:HB3	3:H:189:ARG:NH1	2.09	0.40
2:M:260:ALA:CB	3:H:36:MET:SD	3.08	0.40
1:L:170:ASN:HB2	1:L:259:TRP:CD1	2.53	0.40
2:M:275:LEU:O	2:M:276:VAL:C	2.59	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:M:279:THR:HG22	2:M:280:GLY:H	1.86	0.40
2:M:65:MET:O	2:M:66:TRP:C	2.59	0.40
3:H:179:LEU:CD2	3:H:181:VAL:HG21	2.50	0.40
3:H:226:THR:O	3:H:229:GLU:HB2	2.21	0.40
1:L:110:LYS:HE3	2:M:254:TRP:CH2	2.56	0.40
1:L:235:LEU:HA	1:L:235:LEU:HD22	1.87	0.40
1:L:176:ALA:HB2	1:L:243:PHE:HB3	2.02	0.40
2:M:168:MET:HG3	2:M:173:GLU:CD	2.42	0.40
1:L:206:MET:HB2	3:H:65:ILE:O	2.19	0.40
1:L:55:LEU:HA	1:L:55:LEU:HD23	1.56	0.40
3:H:147:ASN:HA	3:H:148:PRO:HD2	1.86	0.40
3:H:183:LEU:CG	3:H:189:ARG:NE	2.83	0.40
3:H:185:ASP:O	3:H:186:GLY:C	2.60	0.40
1:L:122:ALA:O	1:L:126:LEU:HB2	2.21	0.40
1:L:185:LEU:HD23	1:L:185:LEU:N	2.26	0.40
1:L:49:ILE:C	1:L:51:TRP:N	2.74	0.40
1:L:84:GLY:HA2	1:L:87:GLN:HB2	2.03	0.40
2:M:105:PHE:N	2:M:105:PHE:CD1	2.86	0.40
2:M:130:TRP:HE3	2:M:150:PHE:HD2	1.68	0.40
2:M:152:SER:CB	2:M:277:THR:HG21	2.50	0.40
2:M:164:ARG:O	2:M:167:LEU:CB	2.65	0.40
2:M:170:SER:O	2:M:173:GLU:HB2	2.21	0.40
6:M:310:BCL:H61	7:M:312:BPH:HBB2	2.03	0.40
7:M:312:BPH:C12	7:M:312:BPH:C10	2.83	0.40
2:M:37:THR:O	2:M:38:LEU:O	2.39	0.40
2:M:233:ARG:HD3	2:M:233:ARG:HH11	1.65	0.40
3:H:117:ARG:HG2	3:H:117:ARG:H	1.52	0.40
3:H:130:LYS:NZ	3:H:130:LYS:CB	2.77	0.40
3:H:37:ARG:O	3:H:38:GLU:C	2.59	0.40
1:L:101:ALA:C	1:L:104:GLU:H	2.25	0.40
1:L:146:PHE:CE1	1:L:148:TYR:HE1	2.39	0.40
1:L:84:GLY:HA2	1:L:87:GLN:CB	2.51	0.40
1:L:5:PHE:HB2	1:L:8:LYS:HZ1	1.87	0.40
2:M:130:TRP:CH2	2:M:151:LEU:HD11	2.56	0.40
2:M:21:THR:HG22	2:M:140:LEU:HD12	2.00	0.40
2:M:94:LEU:HD21	2:M:115:TRP:N	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. 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	L	264/281 (94%)	118 (45%)	65 (25%)	81 (31%)	0	0
2	M	294/307 (96%)	141 (48%)	74 (25%)	79 (27%)	0	0
3	H	235/260 (90%)	107 (46%)	65 (28%)	63 (27%)	0	0
All	All	793/848 (94%)	366 (46%)	204 (26%)	223 (28%)	0	0

All (223) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	6	GLU
1	L	7	ARG
1	L	18	GLY
1	L	21	LEU
1	L	31	VAL
1	L	32	GLY
1	L	33	PHE
1	L	40	PHE
1	L	44	LEU
1	L	55	LEU
1	L	61	PRO
1	L	72	GLU
1	L	79	PRO
1	L	80	LEU
1	L	85	LEU
1	L	87	GLN
1	L	94	THR
1	L	108	CYS
1	L	109	ARG
1	L	113	ILE
1	L	128	TYR
1	L	129	LEU
1	L	147	PRO
1	L	150	ILE
1	L	171	PRO

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Mol	Chain	Res	Type
1	L	172	ALA
1	L	186	ALA
1	L	213	ASP
1	L	223	SER
1	L	225	GLY
1	L	226	THR
1	L	237	SER
1	L	238	LEU
1	L	249	ILE
1	L	260	VAL
1	L	263	TRP
1	L	265	TRP
2	M	8	SER
2	M	15	PRO
2	M	20	MET
2	M	22	GLU
2	M	24	VAL
2	M	25	ASN
2	M	29	ARG
2	M	34	PRO
2	M	38	LEU
2	M	39	LEU
2	M	46	GLN
2	M	47	LEU
2	M	82	PRO
2	M	99	PRO
2	M	103	LEU
2	M	105	PHE
2	M	106	ALA
2	M	114	LEU
2	M	122	MET
2	M	129	TRP
2	M	138	GLN
2	M	139	ALA
2	M	153	ALA
2	M	155	TRP
2	M	159	VAL
2	M	160	LEU
2	M	163	ILE
2	M	172	SER
2	M	209	LEU
2	M	213	ALA

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Mol	Chain	Res	Type
2	M	228	ARG
2	M	244	ALA
2	M	245	ALA
2	M	246	GLU
2	M	258	PHE
2	M	262	MET
2	M	276	VAL
2	M	290	VAL
2	M	291	VAL
2	M	296	VAL
3	H	13	ALA
3	H	16	ALA
3	H	21	TRP
3	H	28	ILE
3	H	31	LEU
3	H	32	GLN
3	H	38	GLU
3	H	41	PRO
3	H	49	PRO
3	H	51	ALA
3	H	53	GLN
3	H	80	SER
3	H	83	ARG
3	H	84	PRO
3	H	91	ALA
3	H	95	GLY
3	H	97	PRO
3	H	113	SER
3	H	116	ALA
3	H	130	LYS
3	H	176	ALA
3	H	200	SER
3	H	211	ASP
3	H	247	LYS
1	L	12	PRO
1	L	26	VAL
1	L	39	PHE
1	L	43	ALA
1	L	58	THR
1	L	59	TRP
1	L	71	LEU
1	L	84	GLY

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Mol	Chain	Res	Type
1	L	140	GLY
1	L	145	ALA
1	L	148	TYR
1	L	153	HIS
1	L	161	GLY
1	L	174	MET
1	L	175	ILE
1	L	176	ALA
1	L	183	ASN
1	L	194	VAL
1	L	269	LEU
2	M	28	ASN
2	M	32	VAL
2	M	53	GLY
2	M	59	SER
2	M	63	GLY
2	M	101	TYR
2	M	111	GLU
2	M	112	GLY
2	M	125	ALA
2	M	126	VAL
2	M	158	MET
2	M	191	LEU
2	M	195	ASN
2	M	223	ILE
2	M	257	GLY
2	M	295	TYR
3	H	23	PHE
3	H	42	LEU
3	H	55	PRO
3	H	92	VAL
3	H	115	VAL
3	H	118	ARG
3	H	123	LEU
3	H	125	GLY
3	H	128	HIS
3	H	129	ASN
3	H	136	ALA
3	H	144	ALA
3	H	157	ASP
3	H	158	LEU
3	H	172	PRO

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Mol	Chain	Res	Type
3	H	186	GLY
3	H	196	VAL
3	H	209	SER
3	H	239	GLY
3	H	246	PRO
1	L	50	ALA
1	L	91	ILE
1	L	95	GLY
1	L	169	TYR
1	L	200	PRO
1	L	212	GLU
1	L	239	SER
1	L	245	ALA
1	L	262	TRP
2	M	26	LEU
2	M	30	SER
2	M	96	PRO
2	M	118	ALA
2	M	152	SER
2	M	164	ARG
2	M	214	LEU
2	M	272	MET
2	M	279	THR
2	M	297	TRP
3	H	67	PRO
3	H	81	GLU
3	H	86	ALA
3	H	94	GLU
3	H	138	ALA
3	H	236	TYR
1	L	17	VAL
1	L	81	ALA
1	L	133	LEU
1	L	134	PHE
1	L	247	CYS
1	L	248	MET
2	M	149	ALA
2	M	288	GLY
3	H	46	ASP
3	H	58	LEU
3	H	59	PRO
3	H	112	ALA

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Mol	Chain	Res	Type
3	H	156	CYS
3	H	207	ALA
3	H	212	LEU
3	H	241	LEU
1	L	49	ILE
1	L	78	ALA
1	L	165	GLY
1	L	193	LEU
1	L	243	PHE
2	M	13	ARG
2	M	84	VAL
2	M	93	SER
3	H	78	PRO
1	L	47	ILE
1	L	105	VAL
1	L	136	PRO
2	M	58	LEU
2	M	222	THR
2	M	231	GLY
3	H	30	TYR
3	H	135	LYS
1	L	241	VAL
2	M	72	ILE
1	L	60	ASN
2	M	283	GLY
2	M	56	GLY
3	H	133	PRO
3	H	132	LYS
2	M	57	VAL
2	M	49	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. 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	L	210/220 (96%)	124 (59%)	86 (41%)	0	0
2	M	232/240 (97%)	128 (55%)	104 (45%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	H	192/208 (92%)	92 (48%)	100 (52%)	0	0
All	All	634/668 (95%)	344 (54%)	290 (46%)	0	0

All (290) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	7	ARG
1	L	8	LYS
1	L	15	THR
1	L	16	LEU
1	L	21	LEU
1	L	33	PHE
1	L	38	THR
1	L	44	LEU
1	L	46	ILE
1	L	47	ILE
1	L	49	ILE
1	L	51	TRP
1	L	52	SER
1	L	55	LEU
1	L	59	TRP
1	L	62	GLN
1	L	63	LEU
1	L	64	ILE
1	L	67	TYR
1	L	72	GLU
1	L	79	PRO
1	L	82	LYS
1	L	85	LEU
1	L	87	GLN
1	L	88	ILE
1	L	89	ILE
1	L	90	THR
1	L	91	ILE
1	L	98	VAL
1	L	99	SER
1	L	100	TRP
1	L	102	LEU
1	L	103	ARG
1	L	107	ILE
1	L	109	ARG
1	L	110	LYS

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Mol	Chain	Res	Type
1	L	115	TYR
1	L	116	HIS
1	L	119	PHE
1	L	121	PHE
1	L	125	ILE
1	L	126	LEU
1	L	128	TYR
1	L	133	LEU
1	L	135	ARG
1	L	138	MET
1	L	142	TRP
1	L	146	PHE
1	L	147	PRO
1	L	153	HIS
1	L	156	TRP
1	L	159	ASN
1	L	166	ASN
1	L	170	ASN
1	L	171	PRO
1	L	180	PHE
1	L	182	THR
1	L	183	ASN
1	L	185	LEU
1	L	187	LEU
1	L	202	LYS
1	L	205	GLU
1	L	207	ARG
1	L	208	THR
1	L	211	HIS
1	L	217	ARG
1	L	220	VAL
1	L	222	TYR
1	L	223	SER
1	L	227	LEU
1	L	229	ILE
1	L	232	LEU
1	L	235	LEU
1	L	242	PHE
1	L	243	PHE
1	L	247	CYS
1	L	248	MET
1	L	249	ILE

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Mol	Chain	Res	Type
1	L	250	ILE
1	L	251	THR
1	L	257	ASP
1	L	261	ASP
1	L	265	TRP
1	L	267	VAL
1	L	268	LYS
1	L	269	LEU
2	M	7	PHE
2	M	11	GLN
2	M	13	ARG
2	M	18	LEU
2	M	20	MET
2	M	22	GLU
2	M	23	ASP
2	M	25	ASN
2	M	26	LEU
2	M	29	ARG
2	M	30	SER
2	M	32	VAL
2	M	34	PRO
2	M	35	PHE
2	M	37	THR
2	M	39	LEU
2	M	44	ASN
2	M	47	LEU
2	M	50	ILE
2	M	51	TYR
2	M	52	LEU
2	M	55	LEU
2	M	57	VAL
2	M	58	LEU
2	M	59	SER
2	M	60	LEU
2	M	65	MET
2	M	67	PHE
2	M	70	ILE
2	M	72	ILE
2	M	74	PHE
2	M	76	TYR
2	M	77	GLN
2	M	82	PRO

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Mol	Chain	Res	Type
2	M	87	ARG
2	M	93	SER
2	M	95	GLU
2	M	100	GLU
2	M	101	TYR
2	M	103	LEU
2	M	104	SER
2	M	105	PHE
2	M	109	LEU
2	M	110	LYS
2	M	114	LEU
2	M	119	SER
2	M	120	PHE
2	M	121	PHE
2	M	122	MET
2	M	126	VAL
2	M	133	THR
2	M	134	TYR
2	M	135	LEU
2	M	136	ARG
2	M	144	LYS
2	M	145	HIS
2	M	148	TRP
2	M	152	SER
2	M	155	TRP
2	M	160	LEU
2	M	164	ARG
2	M	165	PRO
2	M	166	ILE
2	M	168	MET
2	M	172	SER
2	M	179	ILE
2	M	182	HIS
2	M	185	TRP
2	M	187	ASN
2	M	190	SER
2	M	191	LEU
2	M	205	SER
2	M	209	LEU
2	M	214	LEU
2	M	216	PHE
2	M	218	MET

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Mol	Chain	Res	Type
2	M	227	SER
2	M	228	ARG
2	M	229	PHE
2	M	232	GLU
2	M	233	ARG
2	M	235	LEU
2	M	236	GLU
2	M	238	ILE
2	M	240	ASP
2	M	241	ARG
2	M	243	THR
2	M	250	LEU
2	M	253	ARG
2	M	258	PHE
2	M	259	ASN
2	M	261	THR
2	M	263	GLU
2	M	267	ARG
2	M	268	TRP
2	M	270	ILE
2	M	271	TRP
2	M	274	VAL
2	M	275	LEU
2	M	277	THR
2	M	278	LEU
2	M	279	THR
2	M	299	GLN
2	M	300	ASN
3	H	12	LEU
3	H	14	SER
3	H	15	LEU
3	H	17	ILE
3	H	18	TYR
3	H	20	PHE
3	H	23	PHE
3	H	24	LEU
3	H	27	LEU
3	H	29	TYR
3	H	30	TYR
3	H	33	THR
3	H	34	GLU
3	H	35	ASN

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Mol	Chain	Res	Type
3	H	36	MET
3	H	37	ARG
3	H	38	GLU
3	H	40	TYR
3	H	42	LEU
3	H	44	ASN
3	H	46	ASP
3	H	53	GLN
3	H	56	PHE
3	H	60	LYS
3	H	62	LYS
3	H	63	THR
3	H	64	PHE
3	H	65	ILE
3	H	66	LEU
3	H	68	HIS
3	H	74	THR
3	H	79	GLU
3	H	82	ASP
3	H	83	ARG
3	H	85	ILE
3	H	92	VAL
3	H	93	SER
3	H	94	GLU
3	H	105	MET
3	H	106	LYS
3	H	107	ASP
3	H	109	VAL
3	H	113	SER
3	H	115	VAL
3	H	117	ARG
3	H	118	ARG
3	H	119	ASP
3	H	123	LEU
3	H	124	ASP
3	H	126	HIS
3	H	128	HIS
3	H	129	ASN
3	H	131	ILE
3	H	134	MET
3	H	135	LYS
3	H	141	HIS

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Mol	Chain	Res	Type
3	H	151	LEU
3	H	156	CYS
3	H	158	LEU
3	H	159	GLU
3	H	160	ILE
3	H	163	LYS
3	H	166	ASP
3	H	171	ILE
3	H	174	GLN
3	H	178	PHE
3	H	179	LEU
3	H	182	GLU
3	H	183	LEU
3	H	184	LYS
3	H	185	ASP
3	H	188	THR
3	H	189	ARG
3	H	194	GLN
3	H	195	MET
3	H	196	VAL
3	H	197	LYS
3	H	199	GLN
3	H	204	HIS
3	H	205	VAL
3	H	209	SER
3	H	210	SER
3	H	211	ASP
3	H	212	LEU
3	H	213	PHE
3	H	219	ILE
3	H	220	LYS
3	H	221	SER
3	H	223	THR
3	H	228	LEU
3	H	229	GLU
3	H	231	ASP
3	H	232	LYS
3	H	234	CYS
3	H	237	VAL
3	H	241	LEU
3	H	242	MET
3	H	243	TYR

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Mol	Chain	Res	Type
3	H	247	LYS
3	H	248	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	60	ASN
1	L	62	GLN
1	L	116	HIS
1	L	153	HIS
1	L	168	HIS
1	L	211	HIS
2	M	9	GLN
2	M	25	ASN
2	M	28	ASN
2	M	44	ASN
2	M	46	GLN
2	M	77	GLN
2	M	145	HIS
2	M	187	ASN
2	M	299	GLN
2	M	301	HIS
3	H	35	ASN
3	H	98	HIS
3	H	199	GLN
3	H	204	HIS
3	H	206	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	BCL	L	282	2	59,59,74	1.89	12 (20%)	77,97,115	2.50	21 (27%)
6	BCL	L	283	1	74,74,74	1.92	16 (21%)	97,115,115	2.43	31 (31%)
7	BPH	L	284	-	70,70,70	1.71	12 (17%)	94,101,101	2.20	21 (22%)
8	U10	L	285	-	40,41,63	0.98	1 (2%)	51,52,79	2.01	15 (29%)
4	BOG	M	308	-	20,20,20	0.65	0	25,25,25	1.38	3 (12%)
6	BCL	M	310	2	74,74,74	1.89	15 (20%)	97,115,115	2.41	25 (25%)
6	BCL	M	311	-	59,59,74	3.11	22 (37%)	77,97,115	3.20	29 (37%)
7	BPH	M	312	2	70,70,70	1.69	10 (14%)	94,101,101	2.23	20 (21%)
8	U10	M	313	-	50,51,63	0.93	1 (2%)	63,64,79	2.10	21 (33%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	BCL	L	282	2	-	0/23/119/137	0/0/9/9
6	BCL	L	283	1	-	0/41/137/137	0/0/9/9
7	BPH	L	284	-	2/2/18/22	0/49/105/105	0/0/6/6
8	U10	L	285	-	-	0/37/61/87	0/1/1/1
4	BOG	M	308	-	1/1/5/5	0/11/31/31	0/1/1/1
6	BCL	M	310	2	-	0/41/137/137	0/0/9/9
6	BCL	M	311	-	-	0/23/119/137	0/0/9/9
7	BPH	M	312	2	2/2/18/22	0/49/105/105	0/0/6/6
8	U10	M	313	-	-	0/49/73/87	0/1/1/1

All (89) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	M	311	BCL	MG-ND	14.99	2.38	2.05
6	M	311	BCL	CHB-C4A	-7.56	1.19	1.36
6	M	311	BCL	MG-NB	-7.07	1.89	2.05
7	L	284	BPH	C1D-CHD	6.70	1.42	1.35
6	L	282	BCL	O1D-CGD	5.66	1.35	1.21
6	L	283	BCL	MG-NB	5.57	2.17	2.05
7	M	312	BPH	C6-C7	5.45	1.78	1.52
6	M	310	BCL	MG-ND	5.33	2.16	2.05
6	M	310	BCL	O1D-CGD	5.30	1.34	1.21
6	L	283	BCL	O1D-CGD	5.24	1.34	1.21
6	L	282	BCL	C1B-C2B	5.15	1.46	1.40
6	L	283	BCL	MG-ND	5.08	2.16	2.05
6	M	311	BCL	O1D-CGD	5.03	1.33	1.21
6	M	311	BCL	CAA-C2A	4.98	1.63	1.54
6	M	310	BCL	MG-NB	4.98	2.16	2.05
7	M	312	BPH	O1D-CGD	4.97	1.33	1.21
7	M	312	BPH	C11-C10	4.91	1.76	1.52
6	M	310	BCL	C1B-C2B	4.90	1.46	1.40
6	L	283	BCL	C1B-C2B	4.89	1.46	1.40
7	L	284	BPH	C3B-C4B	4.57	1.47	1.40
7	L	284	BPH	O2D-CGD	-4.47	1.21	1.33
6	M	311	BCL	C1B-C2B	4.43	1.45	1.40
6	L	283	BCL	C3B-C4B	4.41	1.47	1.40
7	M	312	BPH	O2D-CGD	-4.41	1.21	1.33
6	M	310	BCL	C4B-NB	4.36	1.40	1.34
7	L	284	BPH	O1D-CGD	4.25	1.31	1.21
6	L	282	BCL	C4B-NB	4.13	1.39	1.34
6	M	310	BCL	C1B-NB	4.10	1.39	1.34
6	L	282	BCL	C1B-NB	4.04	1.39	1.34
6	M	311	BCL	C4B-NB	3.97	1.39	1.34
6	L	283	BCL	C1B-NB	3.94	1.39	1.34
7	M	312	BPH	C3B-C4B	3.94	1.46	1.40
6	L	282	BCL	C3B-C4B	3.90	1.46	1.40
7	L	284	BPH	C1B-CHB	3.88	1.62	1.46
6	M	310	BCL	O2D-CGD	-3.77	1.23	1.33
6	L	283	BCL	C4B-NB	3.67	1.39	1.34
7	M	312	BPH	C1D-CHD	3.66	1.39	1.35
6	L	283	BCL	C4C-NC	3.64	1.40	1.32
6	M	310	BCL	C3B-C4B	3.62	1.45	1.40
6	L	283	BCL	MG-NC	3.56	2.17	2.07
6	M	311	BCL	CMA-C3A	-3.52	1.45	1.53
6	M	310	BCL	C4C-NC	3.41	1.39	1.32
6	M	310	BCL	C1A-NA	3.40	1.39	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	L	284	BPH	C4B-CHC	3.36	1.60	1.46
6	L	282	BCL	C1A-NA	3.33	1.39	1.32
6	M	311	BCL	C3B-C4B	3.30	1.45	1.40
6	L	282	BCL	MG-ND	3.30	2.12	2.05
6	M	311	BCL	C4D-C3D	3.26	1.45	1.41
6	M	311	BCL	C1A-NA	3.23	1.39	1.32
7	L	284	BPH	C4D-ND	3.22	1.42	1.38
7	M	312	BPH	C4D-ND	3.17	1.42	1.38
6	M	311	BCL	C1B-NB	3.16	1.38	1.34
6	L	282	BCL	CAC-C3C	-3.15	1.47	1.54
6	L	282	BCL	C4C-NC	3.13	1.39	1.32
6	L	282	BCL	O2D-CGD	-3.11	1.24	1.33
6	L	283	BCL	C1A-NA	3.08	1.39	1.32
6	M	311	BCL	C4C-NC	3.08	1.39	1.32
6	M	311	BCL	C1A-CHA	3.07	1.56	1.43
6	L	283	BCL	MG-NA	3.05	2.16	2.07
6	L	283	BCL	O2D-CGD	-3.04	1.25	1.33
7	M	312	BPH	CAC-C3C	-3.02	1.47	1.54
6	M	310	BCL	MG-NA	3.02	2.16	2.07
6	M	310	BCL	MG-NC	2.91	2.15	2.07
6	M	311	BCL	CAC-C3C	-2.79	1.48	1.54
6	L	283	BCL	CAC-C3C	-2.77	1.48	1.54
6	M	311	BCL	CBD-CAD	-2.71	1.44	1.56
6	M	311	BCL	O2D-CGD	-2.62	1.26	1.33
7	L	284	BPH	C1B-C2B	2.53	1.48	1.42
7	M	312	BPH	C4D-C3D	2.52	1.44	1.41
6	M	311	BCL	O2D-CED	2.52	1.51	1.45
6	M	311	BCL	CHC-C1C	2.48	1.42	1.36
7	L	284	BPH	C3B-C2B	-2.48	1.32	1.40
6	M	311	BCL	MG-NC	2.46	2.14	2.07
6	M	310	BCL	C4D-C3D	2.46	1.44	1.41
7	M	312	BPH	CAA-C2A	2.45	1.58	1.54
7	L	284	BPH	CAA-C2A	2.34	1.58	1.54
6	L	283	BCL	C4D-C3D	2.33	1.44	1.41
6	M	310	BCL	CAC-C3C	-2.23	1.49	1.54
7	L	284	BPH	C1B-NB	2.21	1.38	1.36
6	L	282	BCL	C4D-ND	2.16	1.43	1.36
6	L	283	BCL	CHB-C4A	2.15	1.41	1.36
7	L	284	BPH	CAC-C3C	-2.11	1.49	1.54
6	M	311	BCL	C4D-CHA	2.11	1.47	1.39
6	L	282	BCL	CAA-C2A	2.10	1.57	1.54
6	L	283	BCL	C2-C3	2.09	1.37	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	L	285	U10	C12-C13	2.07	1.56	1.50
6	M	311	BCL	C5-C3	2.07	1.51	1.40
6	M	310	BCL	C4D-ND	2.06	1.43	1.36
8	M	313	U10	C16-C14	2.04	1.56	1.51

All (186) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	M	311	BCL	CBD-CHA-C1A	13.16	145.97	128.77
6	M	310	BCL	C4D-C3D-CAD	-12.77	92.36	108.05
6	M	311	BCL	C4D-C3D-CAD	-12.37	92.84	108.05
6	L	282	BCL	C4D-C3D-CAD	-11.90	93.42	108.05
6	L	283	BCL	C4D-C3D-CAD	-11.73	93.63	108.05
7	M	312	BPH	C11-C10-C8	7.85	137.75	115.14
6	M	311	BCL	C4D-CHA-CBD	-7.71	91.20	109.37
7	L	284	BPH	C2B-C1B-CHB	7.54	147.13	125.72
7	M	312	BPH	C7-C6-C5	6.91	133.38	113.01
6	L	283	BCL	C4-C3-C5	6.59	125.41	115.39
6	L	283	BCL	CMB-C2B-C1B	-6.41	118.76	128.62
6	L	282	BCL	C3D-CAD-CBD	6.19	116.35	107.60
7	L	284	BPH	CMD-C2D-C3D	6.19	134.72	124.97
6	M	311	BCL	CMD-C2D-C3D	6.14	134.64	124.97
8	L	285	U10	C12-C13-C14	-6.08	114.68	127.80
6	M	310	BCL	CMD-C2D-C3D	6.03	134.47	124.97
6	L	282	BCL	CMD-C2D-C3D	6.00	134.41	124.97
6	M	311	BCL	CMB-C2B-C1B	-5.98	119.41	128.62
7	M	312	BPH	CMD-C2D-C3D	5.98	134.39	124.97
6	L	283	BCL	C3D-CAD-CBD	5.95	116.01	107.60
7	M	312	BPH	CMB-C2B-C1B	-5.89	119.69	128.65
6	L	283	BCL	CMD-C2D-C3D	5.76	134.05	124.97
6	M	310	BCL	CMB-C2B-C1B	-5.69	119.87	128.62
6	M	311	BCL	CMB-C2B-C3B	5.58	133.76	124.97
6	L	282	BCL	CMB-C2B-C1B	-5.41	120.30	128.62
7	L	284	BPH	CMB-C2B-C1B	-5.37	120.47	128.65
6	L	282	BCL	OBD-CAD-C3D	-5.18	118.27	127.91
6	M	310	BCL	C4D-CHA-CBD	-5.18	97.17	109.37
8	L	285	U10	C27-C28-C29	-5.17	116.64	127.80
7	L	284	BPH	O1D-CGD-CBD	-5.14	113.89	124.42
7	L	284	BPH	CMD-C2D-C1D	-5.10	117.55	125.81
7	M	312	BPH	CMB-C2B-C3B	5.10	133.01	124.97
7	M	312	BPH	CMD-C2D-C1D	-5.09	117.58	125.81
7	M	312	BPH	O1D-CGD-CBD	-5.08	114.02	124.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	L	284	BPH	C3D-CAD-CBD	5.06	114.75	107.60
6	L	283	BCL	CMB-C2B-C3B	5.03	132.90	124.97
7	L	284	BPH	C1B-CHB-C4A	4.89	143.16	127.62
8	M	313	U10	C17-C18-C19	-4.82	117.40	127.80
6	M	311	BCL	C3D-CAD-CBD	4.76	114.33	107.60
6	M	310	BCL	CMB-C2B-C3B	4.73	132.41	124.97
7	M	312	BPH	C3D-CAD-CBD	4.72	114.26	107.60
6	M	311	BCL	CAA-C2A-C3A	-4.69	101.95	113.04
7	L	284	BPH	C4D-CHA-CBD	-4.66	98.62	110.15
7	M	312	BPH	C6-C7-C8	-4.66	101.73	115.14
8	M	313	U10	C7-C8-C9	-4.63	118.93	126.76
7	L	284	BPH	CMB-C2B-C3B	4.56	132.16	124.97
7	M	312	BPH	C4D-CHA-CBD	-4.57	98.85	110.15
6	M	310	BCL	C3D-CAD-CBD	4.54	114.02	107.60
6	M	310	BCL	O2D-CGD-CBD	4.49	120.47	111.33
8	M	313	U10	C22-C23-C24	-4.48	118.14	127.80
6	L	282	BCL	CMD-C2D-C1D	-4.43	117.40	126.16
7	M	312	BPH	OBD-CAD-C3D	-4.43	119.66	127.91
6	M	311	BCL	OBB-CAB-C3B	4.40	126.67	120.07
6	L	282	BCL	C1-C2-C3	-4.39	118.38	126.19
6	M	311	BCL	CMD-C2D-C1D	-4.36	117.54	126.16
8	M	313	U10	C30-C29-C31	4.34	121.99	115.39
6	M	310	BCL	CMD-C2D-C1D	-4.34	117.58	126.16
6	M	310	BCL	C4-C3-C5	4.33	121.98	115.39
6	L	282	BCL	CMB-C2B-C3B	4.30	131.74	124.97
7	L	284	BPH	O2D-CGD-O1D	4.28	132.49	123.79
6	M	311	BCL	CAA-CBA-CGA	4.24	126.94	113.27
8	M	313	U10	C32-C33-C34	-4.22	118.70	127.80
6	L	282	BCL	C4D-CHA-CBD	-4.21	99.47	109.37
6	L	283	BCL	C4D-CHA-CBD	-4.15	99.60	109.37
6	L	283	BCL	CMD-C2D-C1D	-4.07	118.11	126.16
6	M	310	BCL	OBD-CAD-C3D	-4.04	120.39	127.91
6	L	282	BCL	O2D-CGD-CBD	4.04	119.55	111.33
6	M	310	BCL	O1D-CGD-CBD	-3.92	116.40	124.42
6	M	311	BCL	OBD-CAD-C3D	-3.77	120.89	127.91
6	L	283	BCL	C1-C2-C3	-3.77	119.49	126.19
7	L	284	BPH	CAC-C3C-C2C	-3.73	105.32	113.89
7	M	312	BPH	O2D-CGD-CBD	3.67	118.81	111.33
8	M	313	U10	C16-C14-C13	-3.60	114.16	121.08
8	M	313	U10	C25-C24-C26	3.52	120.75	115.39
8	M	313	U10	C27-C28-C29	-3.51	120.23	127.80
6	M	311	BCL	C4D-ND-C1D	3.51	110.81	106.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	M	311	BCL	CAD-CBD-CHA	3.46	113.59	103.30
7	L	284	BPH	C16-C15-C13	-3.45	105.20	115.14
8	M	313	U10	C17-C16-C14	-3.43	101.38	112.74
6	L	283	BCL	C16-C15-C13	-3.42	105.28	115.14
8	L	285	U10	C10-C9-C11	3.41	120.58	115.39
6	M	311	BCL	CBB-CAB-C3B	-3.37	110.44	120.30
8	L	285	U10	C20-C19-C21	3.33	120.45	115.39
7	L	284	BPH	OBD-CAD-C3D	-3.30	121.77	127.91
7	L	284	BPH	C1-C2-C3	-3.26	120.39	126.19
8	L	285	U10	C30-C29-C31	3.26	120.34	115.39
6	M	310	BCL	CAC-C3C-C2C	-3.23	106.47	113.89
7	L	284	BPH	OBB-CAB-C3B	-3.22	115.24	120.07
6	L	283	BCL	C11-C12-C13	-3.21	105.89	115.14
6	L	283	BCL	OBD-CAD-CBD	-3.17	121.15	125.94
6	M	311	BCL	O2A-CGA-O1A	-3.16	114.80	123.43
7	M	312	BPH	CBD-CHA-C1A	3.13	131.77	123.62
8	M	313	U10	C12-C13-C14	-3.12	121.07	127.80
6	L	283	BCL	C5-C3-C2	-3.11	115.11	121.08
8	M	313	U10	C10-C9-C11	3.08	120.07	115.39
8	L	285	U10	C11-C12-C13	-3.02	102.98	111.62
6	M	310	BCL	C4D-CHA-C1A	3.02	129.07	120.32
4	M	308	BOG	O5-C1-C2	-3.01	104.14	110.31
8	M	313	U10	C1M-C1-C6	-3.01	118.22	124.20
4	M	308	BOG	O5-C5-C6	2.99	113.70	106.34
6	M	311	BCL	CGD-CBD-CHA	-2.99	100.79	110.96
6	L	282	BCL	C2B-C1B-NB	-2.98	107.16	109.41
8	L	285	U10	C17-C18-C19	-2.97	121.39	127.80
6	L	283	BCL	C4D-CHA-C1A	2.95	128.87	120.32
6	M	310	BCL	C2D-C3D-CAD	2.93	158.12	138.46
7	M	312	BPH	C2D-C3D-CAD	2.92	158.10	138.46
8	M	313	U10	C20-C19-C21	2.91	119.81	115.39
8	L	285	U10	C25-C24-C26	2.91	119.81	115.39
6	M	311	BCL	CGD-CBD-CAD	-2.91	101.08	110.96
7	L	284	BPH	CBD-CHA-C1A	2.90	131.17	123.62
6	M	311	BCL	CHB-C4A-NA	2.90	128.01	124.58
6	M	311	BCL	C2D-C3D-CAD	2.90	157.94	138.46
6	L	282	BCL	C4D-CHA-C1A	2.88	128.65	120.32
8	M	313	U10	C35-C34-C33	-2.87	117.83	123.52
6	M	310	BCL	CBD-CHA-C1A	2.84	132.48	128.77
7	L	284	BPH	OBB-CAB-CBB	2.83	127.18	120.13
6	L	283	BCL	OBD-CAD-C3D	-2.81	122.68	127.91
6	L	283	BCL	C1-O2A-CGA	-2.80	109.14	116.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L	283	BCL	C2D-C3D-CAD	2.77	157.06	138.46
6	M	310	BCL	OBD-CAD-CBD	-2.77	121.76	125.94
6	M	310	BCL	C3A-C2A-C1A	2.75	104.97	101.08
6	M	310	BCL	CMC-C2C-C1C	-2.72	103.86	111.76
7	M	312	BPH	CED-O2D-CGD	2.71	122.46	116.02
6	M	311	BCL	C2D-C1D-ND	-2.70	107.37	109.41
7	M	312	BPH	O2A-C1-C2	2.70	114.39	108.55
6	L	282	BCL	C2D-C3D-CAD	2.68	156.45	138.46
6	L	283	BCL	CMA-C3A-C2A	-2.67	102.66	114.14
6	L	283	BCL	C4-C3-C2	-2.66	118.24	123.52
7	M	312	BPH	CAA-C2A-C3A	-2.66	106.75	113.04
4	M	308	BOG	C1'-O1-C1	2.65	118.72	113.96
8	M	313	U10	C35-C34-C36	2.65	119.41	115.39
7	M	312	BPH	C1-O2A-CGA	-2.62	109.64	116.98
8	L	285	U10	C7-C8-C9	-2.62	122.34	126.76
6	M	310	BCL	C4D-ND-C1D	2.61	109.72	106.57
7	L	284	BPH	C2D-C3D-CAD	2.57	155.75	138.46
7	L	284	BPH	C1-O2A-CGA	2.56	124.16	116.98
8	L	285	U10	C20-C19-C18	-2.54	118.49	123.52
7	L	284	BPH	CED-O2D-CGD	2.54	122.06	116.02
6	L	282	BCL	C1D-CHD-C4C	2.53	129.91	125.55
6	L	282	BCL	CAC-C3C-C2C	-2.53	108.08	113.89
6	M	310	BCL	C4-C3-C2	-2.51	118.55	123.52
6	L	283	BCL	C11-C10-C8	-2.51	107.91	115.14
6	L	283	BCL	CAA-CBA-CGA	-2.50	105.22	113.27
6	L	283	BCL	C4D-ND-C1D	2.48	109.57	106.57
6	M	310	BCL	C1-C2-C3	-2.47	121.79	126.19
8	L	285	U10	C15-C14-C16	2.47	119.14	115.39
6	L	283	BCL	CAA-C2A-C1A	2.45	117.75	111.62
6	M	311	BCL	O2A-C1-C2	2.44	113.84	108.55
6	M	310	BCL	C11-C12-C13	-2.43	108.14	115.14
6	M	310	BCL	C2B-C1B-NB	-2.42	107.58	109.41
6	M	311	BCL	CMA-C3A-C4A	2.39	118.71	111.76
8	L	285	U10	C30-C29-C28	-2.39	118.79	123.52
8	M	313	U10	C37-C38-C39	-2.36	122.70	127.80
8	M	313	U10	C27-C26-C24	-2.36	104.93	112.74
8	M	313	U10	C31-C29-C28	-2.35	116.56	121.08
6	M	311	BCL	O2D-CGD-CBD	2.31	116.04	111.33
8	M	313	U10	C40-C39-C38	-2.30	118.96	123.52
6	L	282	BCL	O1D-CGD-CBD	-2.30	119.71	124.42
7	L	284	BPH	CBB-CAB-C3B	-2.30	113.59	120.30
6	L	283	BCL	C3A-C2A-C1A	2.29	104.32	101.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	M	310	BCL	C2D-C1D-ND	-2.29	107.68	109.41
8	M	313	U10	C40-C39-C41	2.29	118.87	115.39
6	L	283	BCL	C2C-C3C-C4C	2.29	104.22	101.05
7	M	312	BPH	OBB-CAB-CBB	2.28	125.80	120.13
6	L	282	BCL	CMA-C3A-C2A	-2.26	104.41	114.14
7	M	312	BPH	CBB-CAB-C3B	-2.26	113.68	120.30
6	L	282	BCL	C4D-ND-C1D	2.26	109.29	106.57
6	L	283	BCL	C2D-C1D-ND	-2.25	107.72	109.41
8	M	313	U10	C26-C24-C23	-2.22	116.81	121.08
6	M	311	BCL	C1-C2-C3	-2.22	122.24	126.19
8	L	285	U10	C17-C16-C14	-2.20	105.44	112.74
6	L	282	BCL	CAC-C3C-C4C	2.20	117.46	112.58
6	L	283	BCL	O2A-CGA-CBA	2.19	118.82	111.94
6	L	282	BCL	C2C-C3C-C4C	2.18	104.07	101.05
8	L	285	U10	C22-C23-C24	-2.16	123.14	127.80
8	L	285	U10	C1M-C1-C6	-2.12	119.98	124.20
6	M	311	BCL	O1D-CGD-CBD	-2.11	120.10	124.42
6	M	311	BCL	C2C-C3C-C4C	2.07	103.92	101.05
6	L	283	BCL	C1D-CHD-C4C	2.05	129.08	125.55
6	M	311	BCL	C3A-C4A-CHB	-2.04	120.09	124.33
6	L	282	BCL	C2D-C1D-ND	-2.04	107.87	109.41
6	M	311	BCL	C3C-C2C-C1C	2.03	104.52	101.40
6	L	283	BCL	C2B-C1B-NB	-2.03	107.88	109.41
6	L	283	BCL	C6-C5-C3	2.01	117.55	112.78
6	M	310	BCL	C4A-NA-C1A	2.00	109.28	106.52
6	L	283	BCL	C1B-CHB-C4A	-2.00	125.89	130.06

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	M	308	BOG	C1
7	L	284	BPH	C8
7	L	284	BPH	C13
7	M	312	BPH	C8
7	M	312	BPH	C13

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.