



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 05:31 am 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 X-ray Structure 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/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

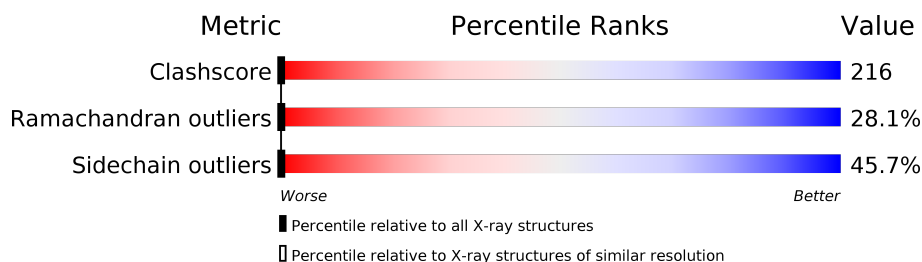
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

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	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (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. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

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

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	BOG	M	308	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	BCL	L	283	-	-	X	-
6	BCL	M	310	-	-	X	-
6	BCL	M	311	-	-	X	-
7	BPH	L	284	-	-	X	-
7	BPH	M	312	-	-	X	-
8	U10	L	285	-	-	X	-
8	U10	M	313	-	-	X	-

2 Entry composition [i](#)

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

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			

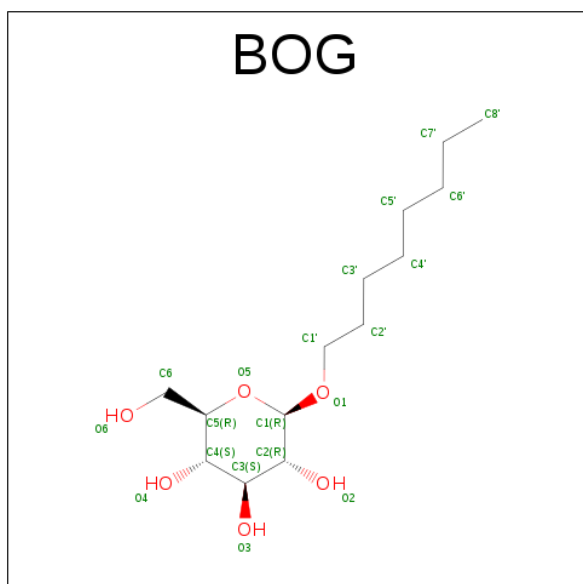
- Molecule 2 is a protein called PHOTOSYNTHETIC REACTION CENTER.

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: $C_{14}H_{28}O_6$).

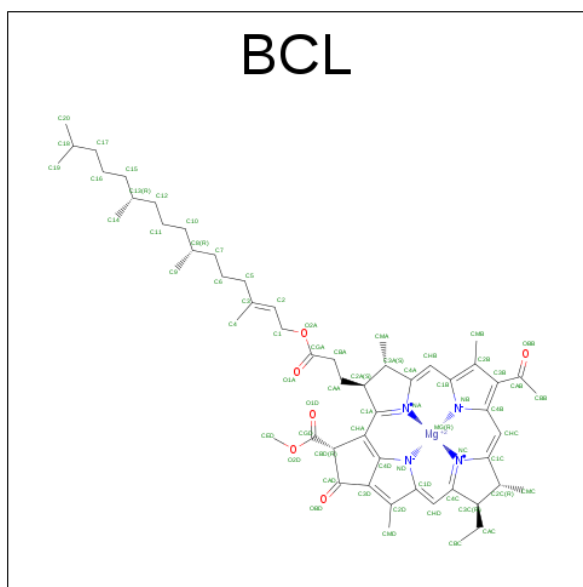


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	M	1	Total	C	O	0	0
			20	14	6		

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

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

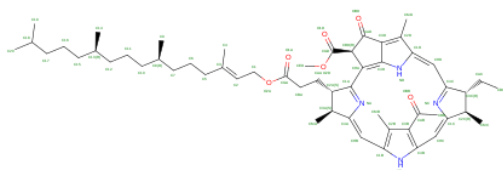
- Molecule 6 is BACTERIOCHLOROPHYLL A (three-letter code: BCL) (formula: $\text{C}_{55}\text{H}_{74}\text{MgN}_4\text{O}_6$).



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

- Molecule 7 is BACTERIOPHEOPHYTIN A (three-letter code: BPH) (formula: $\text{C}_{55}\text{H}_{76}\text{N}_4\text{O}_6$).

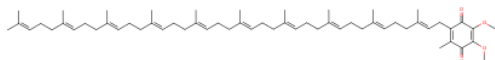
BPH



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: $C_{59}H_{90}O_4$).

U10



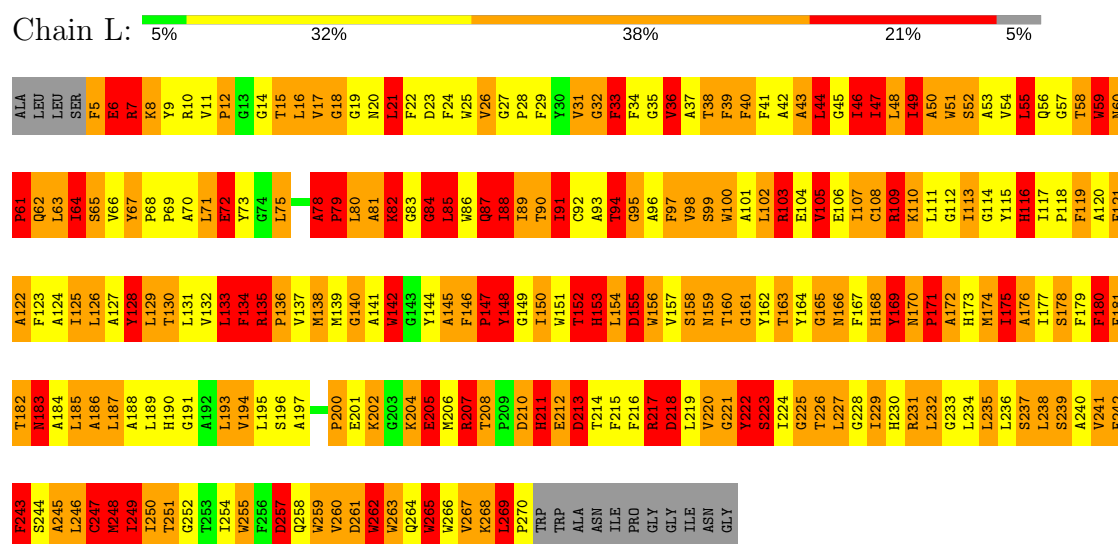
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	M	1	Total	C	O	0	0
			51	47	4		
8	L	1	Total	C	O	0	0
			41	37	4		

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 the various outlier classes 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





4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore 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

5.1 Standard geometry

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 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	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

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 216.

All (2900) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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	Interatomic distance (Å)	Clash overlap (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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:183:ASN:O	1:L:183:ASN:ND2	1.67	1.26
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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:204:LEU:HA	2:M:207:ALA:CB	1.77	1.15
1:L:205:GLU:HA	3:H:65:ILE:CG2	1.76	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:269:LEU:CB	1:L:270:PRO:HD2	1.76	1.15
2:M:21:THR:HB	2:M:139:ALA:HB1	1.20	1.15
1:L:53:ALA:HB2	1:L:64:ILE:CD1	1.76	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
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
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:C	3:H:56:PHE:HD1	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
2:M:17:ASP:C	2:M:18:LEU:HD12	1.68	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
1:L:227:LEU:HD23	1:L:231:ARG:HD2	1.21	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:94:LEU:HD11	2:M:114:LEU:HD23	1.21	1.10
2:M:114:LEU:O	2:M:117:ILE:HB	1.48	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
1:L:267:VAL:HG13	2:M:87:ARG:HD3	1.34	1.08
2:M:135:LEU:HD12	2:M:135:LEU:H	1.13	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:216:PHE:HD2	8:L:285:U10:H71	0.95	1.08
1:L:186:ALA:O	2:M:216:PHE:HE2	1.35	1.08
2:M:109:LEU:HD23	2:M:114:LEU:HD11	1.34	1.07
2:M:54:SER:O	2:M:57:VAL:HG13	1.51	1.07
2:M:90:PHE:HA	2:M:179:ILE:HD12	1.31	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:L:205:GLU:HA	3:H:65:ILE:HG21	1.29	1.07
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: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
2:M:299:GLN:HE21	2:M:299:GLN:HA	1.13	1.06
3:H:14:SER:O	3:H:18:TYR:HB3	1.51	1.06
3:H:37:ARG:NH2	3:H:41:PRO:O	1.87	1.06
1:L:242:PHE:HD1	1:L:243:PHE:N	1.51	1.06
1:L:232:LEU:HG	2:M:42:PHE:CZ	1.90	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
6:L:283:BCL:CMC	6:M:310:BCL:HBC1	1.87	1.04
2:M:185:TRP:CE3	2:M:185:TRP:O	2.09	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
6:L:283:BCL:HBD	6:M:311:BCL:HBC1	1.36	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:135:LEU:HB3	2:M:138:GLN:OE1	1.57	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
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:170:ASP:OD2	3:H:177:ARG:NH2	1.92	1.03
3:H:151:LEU:HD22	3:H:203:VAL:CG2	1.89	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
2:M:299:GLN:NE2	2:M:299:GLN:HA	1.64	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:283:BCL:HMC1	6:M:310:BCL:HBC1	1.42	1.01
2:M:205:SER:OG	2:M:279:THR:HG22	1.61	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
1:L:267:VAL:CG1	2:M:87:ARG:HD3	1.89	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
1:L:179:PHE:HB2	1:L:240:ALA:HB2	1.01	1.01
1:L:8:LYS:HA	3:H:87:LEU:HD22	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:96:PRO:CB	2:M:97:PRO:HD2	1.91	1.00
2:M:99:PRO:HB2	2:M:111:GLU:CG	1.92	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:HE21	2:M:299:GLN:CA	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:204:LYS:HB3	1:L:207:ARG:HH12	1.25	0.98
1:L:53:ALA:HB2	1:L:64:ILE:HD13	1.43	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
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:227:LEU:CD2	1:L:231:ARG:HD2	1.94	0.97
1:L:22:PHE:HE2	1:L:36:VAL:HG11	1.26	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:208:THR:CB	1:L:211:HIS:HD2	1.76	0.97
1:L:34:PHE:O	1:L:38:THR:N	1.97	0.97
2:M:238:ILE:CG2	2:M:238:ILE:O	2.13	0.97
2:M:164:ARG:NH2	2:M:168:MET:HE1	1.80	0.96
1:L:180:PHE:HE1	2:M:213:ALA:HB2	1.29	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
1:L:268:LYS:HG2	1:L:269:LEU:H	0.88	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:122:MET:HG2	2:M:122:MET:O	1.65	0.95
2:M:15:PRO:HD2	3:H:140:PHE:CE1	2.00	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:73:TRP:NE1	2:M:114:LEU:CG	2.23	0.94
2:M:249:ALA:HB2	8:M:313:U10:H4M1	0.98	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
1:L:24:PHE:CE2	1:L:31:VAL:HG21	2.02	0.94
8:L:285:U10:H261	8:L:285:U10:H303	1.48	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
2:M:227:SER:HB3	3:H:194:GLN:HG2	1.50	0.93
1:L:156:TRP:CE3	1:L:156:TRP:O	2.20	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:268:LYS:CG	1:L:269:LEU:H	1.81	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
1:L:113:ILE:HD11	2:M:226:VAL:HG22	1.49	0.91
3:H:183:LEU:N	3:H:183:LEU:HD23	1.84	0.91
3:H:161:ALA:HB2	3:H:210:SER:CB	1.99	0.91
3:H:20:PHE:O	3:H:22:ILE:N	2.03	0.91
3:H:111:PRO:HG2	3:H:242:MET:HB3	1.51	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
1:L:33:PHE:HD1	1:L:33:PHE:O	1.44	0.90
2:M:87:ARG:CG	2:M:88:ASP:H	1.84	0.90
1:L:187:LEU:HD22	2:M:216:PHE:CD2	2.07	0.90
1:L:232:LEU:O	1:L:235:LEU:HB2	1.70	0.90
6:M:311:BCL:CBB	6:M:311:BCL:HMB1	2.02	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
3:H:63:THR:HG23	3:H:74:THR:HG23	1.55	0.89
2:M:105:PHE:HD1	2:M:106:ALA:N	1.69	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
1:L:17:VAL:HG13	1:L:18:GLY:N	1.85	0.89
2:M:90:PHE:CE2	2:M:180:PHE:CE1	2.61	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
2:M:233:ARG:NH2	3:H:122:GLU:OE1	2.05	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:L:285:U10:H153	8:L:285:U10:C11	2.02	0.88
3:H:56:PHE:CD1	3:H:56:PHE:C	2.25	0.88
1:L:51:TRP:CD1	1:L:51:TRP:C	2.33	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:17:VAL:CG1	1:L:18:GLY:H	1.87	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
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
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
1:L:269:LEU:CB	1:L:270:PRO:CD	2.53	0.87
2:M:33:GLY:O	2:M:34:PRO:O	1.91	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:296:VAL:O	2:M:298:GLY:N	2.09	0.86
2:M:99:PRO:HB2	2:M:111:GLU:HG3	1.57	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
2:M:136:ARG:HA	2:M:136:ARG:HE	1.41	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
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
2:M:271:TRP:CZ3	3:H:31:LEU:HD23	2.10	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:131:GLY:O	2:M:134:TYR:CB	2.23	0.85
2:M:17:ASP:C	2:M:18:LEU:CD1	2.45	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
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
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:103:ASP:OD1	3:H:106:LYS:NZ	2.09	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:HBB2	6:L:282:BCL:HHC	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
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
1:L:205:GLU:CA	3:H:65:ILE:CG2	2.57	0.82
2:M:87:ARG:HD2	2:M:88:ASP:OD2	1.76	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: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
1:L:214:THR:HG22	2:M:140:LEU:CD2	2.08	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:24:PHE:O	1:L:31:VAL:HG23	1.78	0.82
1:L:234:LEU:HD12	2:M:221:ALA:CA	2.10	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
1:L:33:PHE:C	1:L:33:PHE:CD1	2.50	0.82
2:M:175:VAL:HG22	2:M:185:TRP:CZ2	2.14	0.82
3:H:134:MET:HE1	3:H:167:ILE:HD12	1.61	0.82
3:H:15:LEU:HA	3:H:18:TYR:HD2	1.45	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
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:14:SER:O	3:H:18:TYR:CB	2.27	0.81
3:H:17:ILE:HD13	3:H:17:ILE:O	1.81	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
1:L:54:VAL:O	1:L:56:GLN:N	2.13	0.81
7:M:312:BPH:C6	7:M:312:BPH:C8	2.58	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
2:M:102:GLY:C	2:M:104:SER:H	1.84	0.81
1:L:232:LEU:CA	2:M:42:PHE:HZ	1.94	0.81
3:H:56:PHE:O	3:H:58:LEU:N	2.14	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
1:L:135:ARG:CG	1:L:139:MET:CE	2.57	0.81
1:L:260:VAL:O	1:L:260:VAL:HG12	1.81	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:65:MET:CG	2:M:66:TRP:N	2.38	0.81
2:M:64:LEU:O	2:M:68:PHE:N	2.14	0.81
1:L:75:LEU:HG	1:L:140:GLY:O	1.81	0.81
1:L:219:LEU:CA	2:M:132:ARG:HH21	1.93	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:219:LEU:O	2:M:132:ARG:NH2	2.14	0.80
1:L:22:PHE:HB3	1:L:32:GLY:HA2	1.63	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
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
3:H:60:LYS:HG3	3:H:60:LYS:O	1.81	0.80
1:L:195:LEU:HD21	2:M:267:ARG:HD3	1.64	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:204:LYS:HD2	1:L:207:ARG:HH22	1.47	0.80
1:L:224:ILE:CD1	1:L:232:LEU:HD12	2.11	0.80
1:L:219:LEU:HD21	2:M:133:THR:CG2	2.11	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:226:THR:HG22	2:M:232:GLU:HB3	1.65	0.78
1:L:179:PHE:HB3	1:L:240:ALA:HB2	1.64	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:205:GLU:CA	3:H:65:ILE:HG21	2.13	0.78
1:L:101:ALA:O	1:L:104:GLU:HB2	1.83	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
1:L:116:HIS:HE1	2:M:225:ALA:HA	1.48	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:225:GLY:HA3	3:H:173:GLU:OE2	1.84	0.78
1:L:183:ASN:HD22	1:L:183:ASN:C	1.85	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:234:CYS:O	3:H:237:VAL:HG23	1.83	0.78
3:H:111:PRO:HG2	3:H:242:MET:CG	2.12	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:17:ASP:HA	2:M:18:LEU:HD12	1.65	0.78
2:M:241:ARG:NH1	2:M:241:ARG:CB	2.47	0.78
2:M:296:VAL:O	2:M:297:TRP:C	2.22	0.78
2:M:89:LEU:HA	2:M:92:PHE:HD2	1.46	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:177:ILE:HD13	6:L:283:BCL:HNB	1.65	0.78
1:L:25:TRP:CH2	1:L:110:LYS:NZ	2.51	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:103:ASP:HB3	3:H:106:LYS:HE3	1.66	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:C2C	6:M:310:BCL:HBC2	2.13	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
3:H:117:ARG:HB2	3:H:227:LEU:HB3	1.65	0.77
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
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:180:PHE:HE1	2:M:213:ALA:CB	1.97	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:269:LEU:CG	1:L:270:PRO:CD	2.62	0.77
1:L:269:LEU:HB3	1:L:270:PRO:CD	2.11	0.77
1:L:48:LEU:HD12	1:L:89:ILE:CD1	2.14	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:CBC	7:M:312:BPH:HHD	2.12	0.77
3:H:44:ASN:ND2	3:H:44:ASN:N	2.29	0.76
3:H:52:ASN:O	3:H:53:GLN:HB2	1.83	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
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
2:M:11:GLN:HB3	3:H:143:SER:O	1.85	0.76
1:L:21:LEU:CD1	1:L:22:PHE:HE1	1.95	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:236:GLU:CG	3:H:122:GLU:HG3	2.16	0.76
2:M:205:SER:O	6:M:310:BCL:HMA2	1.85	0.76
3:H:124:ASP:O	3:H:126:HIS:N	2.18	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:L:208:THR:H	1:L:211:HIS:CG	2.04	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: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: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
2:M:163:ILE:HG21	2:M:285:LEU:HD13	1.68	0.75
3:H:142:VAL:O	3:H:142:VAL:HG12	1.87	0.75
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:194:GLY:O	2:M:195:ASN:C	2.24	0.75
2:M:264:GLY:CA	2:M:267:ARG:HB2	2.17	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
1:L:15:THR:HG21	1:L:19:GLY:CA	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:206:MET:H	3:H:65:ILE:HG22	0.69	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
8:L:285:U10:O4	8:L:285:U10:C3M	2.33	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:226:THR:HG22	2:M:232:GLU:CB	2.17	0.74
1:L:39:PHE:C	1:L:41:PHE:H	1.91	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:6:GLU:HG2	1:L:10:ARG:HG2	1.68	0.74
8:L:285:U10:O4	8:L:285:U10:H3M3	1.87	0.74
1:L:95:GLY:O	1:L:99:SER:HB3	1.87	0.74
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
3:H:116:ALA:CA	3:H:228:LEU:CD1	2.65	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
3:H:198:VAL:O	3:H:198:VAL:HG12	1.86	0.73
3:H:82:ASP:O	3:H:84:PRO:CD	2.36	0.73
1:L:135:ARG:NH1	1:L:139:MET:HE1	2.01	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
1:L:197:ALA:HB1	2:M:235:LEU:CD2	2.16	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
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
1:L:269:LEU:HD22	1:L:270:PRO:HD3	0.78	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:268:TRP:NE1	8:M:313:U10:H111	2.05	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
1:L:266:TRP:HE1	2:M:87:ARG:HA	1.52	0.72
2:M:109:LEU:C	2:M:109:LEU:CD2	2.57	0.72
2:M:90:PHE:CG	2:M:179:ILE:HD12	2.24	0.72
2:M:28:ASN:C	2:M:29:ARG:O	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:97:PHE:CE1	6:L:283:BCL:C11	2.73	0.72
1:L:84:GLY:C	1:L:86:TRP:N	2.41	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
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:167:PHE:CZ	1:L:251:THR:HG21	2.25	0.72
1:L:114:GLY:H	2:M:225:ALA:HB1	1.55	0.72
1:L:113:ILE:CD1	2:M:226:VAL:CG2	2.68	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:L:6:GLU:HG2	1:L:10:ARG:CG	2.19	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: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:136:ARG:NE	2:M:136:ARG:CA	2.53	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
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:136:ARG:NE	2:M:136:ARG:HA	2.04	0.71
2:M:205:SER:N	2:M:279:THR:HG21	2.05	0.71
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:146:PHE:O	1:L:147:PRO:O	2.07	0.71
1:L:16:LEU:HB3	1:L:106:GLU:OE2	1.91	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:146:LYS:NZ	3:H:198:VAL:HG12	2.06	0.70
3:H:12:LEU:O	3:H:14:SER:N	2.24	0.70
3:H:82:ASP:O	3:H:84:PRO:HD2	1.92	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
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
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:73:TRP:CG	2:M:114:LEU:CG	2.71	0.70
2:M:73:TRP:CE2	2:M:114:LEU:HD11	2.25	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
3:H:134:MET:CE	3:H:141:HIS:HE1	2.05	0.70
6:L:283:BCL:HMC2	6:M:310:BCL:HBC1	1.66	0.70
1:L:97:PHE:CE1	6:L:283:BCL:C12	2.75	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:208:THR:H	1:L:211:HIS:CD2	2.10	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
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
3:H:48:THR:HG23	3:H:51:ALA:O	1.92	0.69
1:L:11:VAL:HG13	3:H:87:LEU:HD21	1.73	0.69
1:L:269:LEU:CD1	1:L:270:PRO:HD2	2.23	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: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
1:L:165:GLY:HA3	1:L:258:GLN:HG2	1.74	0.69
2:M:197:PHE:HE1	6:M:311:BCL:HMD3	1.57	0.69
1:L:25:TRP:HZ2	1:L:110:LYS:HE3	1.57	0.69
1:L:231:ARG:NH2	2:M:7:PHE:CA	2.50	0.69
2:M:206:ILE:CG1	6:M:310:BCL:CHB	2.71	0.69
1:L:177:ILE:HD12	6:L:283:BCL:C2B	2.23	0.69
1:L:195:LEU:CB	2:M:145:HIS:HD2	2.04	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
1:L:208:THR:OG1	1:L:211:HIS:CD2	2.46	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:197:PHE:CE1	6:M:311:BCL:HMD3	2.28	0.69
3:H:111:PRO:HB2	3:H:239:GLY:HA2	1.74	0.69
3:H:238:ALA:O	3:H:239:GLY:C	2.31	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
3:H:63:THR:HG23	3:H:74:THR:CG2	2.23	0.68
2:M:88:ASP:C	2:M:92:PHE:CD2	2.67	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: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
2:M:73:TRP:NE1	2:M:114:LEU:CD1	2.57	0.68
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:98:ALA:HB2	2:M:172:SER:HA	1.75	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
1:L:101:ALA:HB2	1:L:121:PHE:HE1	1.59	0.67
1:L:107:ILE:HG22	2:M:254:TRP:HE3	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:232:LEU:HA	2:M:42:PHE:CZ	2.23	0.67
1:L:269:LEU:HD13	1:L:270:PRO:HD2	1.76	0.67
1:L:167:PHE:CD2	6:L:283:BCL:CHD	2.73	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
1:L:208:THR:O	1:L:211:HIS:CB	2.31	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
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
1:L:17:VAL:O	1:L:19:GLY:N	2.28	0.67
2:M:187:ASN:C	2:M:190:SER:H	1.97	0.67
2:M:90:PHE:HA	2:M:179:ILE:CD1	2.18	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
3:H:103:ASP:C	3:H:106:LYS:HZ1	1.98	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
1:L:202:LYS:O	1:L:202:LYS:HG2	1.94	0.67
1:L:248:MET:CE	6:L:283:BCL:CMD	2.73	0.67
1:L:35:GLY:HA3	8:M:313:U10:H402	1.77	0.67
2:M:284:ILE:CG1	6:M:310:BCL:HED1	2.25	0.67
3:H:80:SER:O	3:H:81:GLU:HG3	1.95	0.67
1:L:174:MET:CE	2:M:180:PHE:CZ	2.78	0.67
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:146:LYS:NZ	3:H:198:VAL:O	2.28	0.66
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:157:TRP:HB2	6:M:310:BCL:H92	1.77	0.66
2:M:238:ILE:HD11	2:M:263:GLU:N	2.10	0.66
2:M:82:PRO:O	2:M:83:ALA:C	2.33	0.66
3:H:103:ASP:C	3:H:106:LYS:NZ	2.49	0.66
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
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
3:H:105:MET:N	3:H:106:LYS:NZ	2.44	0.66
1:L:232:LEU:C	1:L:235:LEU:HB2	2.15	0.66
1:L:33:PHE:CG	1:L:33:PHE:O	2.39	0.66
2:M:228:ARG:HH12	3:H:241:LEU:HD11	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
3:H:104:PRO:HG3	3:H:243:TYR:CE2	2.31	0.65
3:H:206:ASN:O	3:H:207:ALA:C	2.35	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:208:THR:CB	1:L:211:HIS:CD2	2.69	0.65
1:L:47:ILE:CG2	1:L:48:LEU:N	2.59	0.65
1:L:48:LEU:CD1	1:L:89:ILE:CG1	2.73	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
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:21:THR:HG22	2:M:140:LEU:HD11	1.79	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
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
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
2:M:236:GLU:OE2	3:H:122:GLU:HA	1.97	0.65
1:L:208:THR:HG23	1:L:211:HIS:NE2	2.08	0.65
1:L:20:ASN:O	1:L:23:ASP:N	2.30	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:105:MET:N	3:H:106:LYS:HZ1	1.95	0.64
3:H:182:GLU:CA	3:H:187:SER:O	2.45	0.64
1:L:25:TRP:CZ2	1:L:110:LYS:HE3	2.33	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
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
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
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:205:GLU:HA	3:H:65:ILE:HG23	1.75	0.64
1:L:241:VAL:HG21	7:L:284:BPH:HBC3	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:85:LEU:O	1:L:89:ILE:HB	1.98	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:206:MET:CB	3:H:65:ILE:O	2.46	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: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:109:ARG:CA	1:L:109:ARG:HE	2.10	0.63
1:L:108:CYS:O	1:L:110:LYS:N	2.32	0.63
1:L:135:ARG:HG2	1:L:139:MET:CE	2.29	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
1:L:226:THR:CG2	2:M:232:GLU:O	2.47	0.63
3:H:12:LEU:HD22	3:H:13:ALA:N	2.14	0.63
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:48:LEU:CD1	1:L:89:ILE:CD1	2.77	0.63
2:M:25:ASN:HD22	2:M:26:LEU:N	1.97	0.63
2:M:152:SER:HB3	2:M:277:THR:CG2	2.29	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
1:L:54:VAL:HG12	1:L:55:LEU:H	1.64	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
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
3:H:56:PHE:CE1	3:H:57:PRO:HD2	2.32	0.62
1:L:159:ASN:O	1:L:163:THR:N	2.33	0.62
1:L:54:VAL:HG12	1:L:55:LEU:N	2.13	0.62
2:M:215:LEU:HA	2:M:218:MET:HB2	1.81	0.62
1:L:113:ILE:HD12	2:M:225:ALA:O	2.00	0.62
2:M:242:GLY:O	2:M:243:THR:C	2.37	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:44:ASN:H	3:H:44:ASN:ND2	1.97	0.62
1:L:206:MET:HB3	3:H:65:ILE:O	1.98	0.62
1:L:111:LEU:HD21	2:M:251:PHE:HB2	1.81	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
3:H:115:VAL:HG12	3:H:116:ALA:H	1.62	0.62
1:L:15:THR:HG21	1:L:19:GLY:N	2.15	0.62
1:L:193:LEU:HD23	8:L:285:U10:C2	2.30	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:208:THR:OG1	1:L:211:HIS:HD2	1.82	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:219:LEU:HA	2:M:132:ARG:NH2	2.06	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
6:L:282:BCL:C1	7:M:312:BPH:OBB	2.48	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
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
6:L:283:BCL:C14	7:L:284:BPH:O2A	2.47	0.61
2:M:199:ASN:ND2	2:M:294:TRP:CZ2	2.68	0.61
2:M:290:VAL:CG1	2:M:290:VAL:O	2.47	0.61
2:M:284:ILE:CD1	6:M:310:BCL:CED	2.78	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:222:TYR:HE1	2:M:44:ASN:HB3	1.64	0.61
2:M:78:ALA:HB1	2:M:84:VAL:HG12	1.81	0.61
3:H:106:LYS:NZ	3:H:106:LYS:H	1.98	0.61
1:L:206:MET:N	3:H:65:ILE:CG2	2.34	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
3:H:199:GLN:HE21	3:H:200:SER:N	1.99	0.61
2:M:102:GLY:C	2:M:104:SER:N	2.48	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:261:THR:HB	3:H:36:MET:HA	1.82	0.61
1:L:204:LYS:CB	1:L:207:ARG:HH12	2.09	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
3:H:213:PHE:CD1	3:H:216:ILE:CD1	2.84	0.60
1:L:174:MET:HE3	2:M:180:PHE:CZ	2.36	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
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:H71	6:L:283:BCL:H41	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
2:M:13:ARG:CD	3:H:143:SER:OG	2.49	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
1:L:28:PRO:O	2:M:254:TRP:HA	2.01	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
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
2:M:17:ASP:C	2:M:18:LEU:CG	2.70	0.60
8:M:313:U10:H361	8:M:313:U10:H402	1.83	0.60
1:L:169:TYR:O	1:L:170:ASN:C	2.40	0.59
1:L:53:ALA:CB	1:L:64:ILE:CB	2.80	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:49:ILE:HG12	1:L:89:ILE:HD13	1.84	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
3:H:60:LYS:CG	3:H:60:LYS:O	2.48	0.59
2:M:238:ILE:HG23	3:H:64:PHE:CE2	2.37	0.59
2:M:291:VAL:HG21	2:M:294:TRP:CZ3	2.37	0.59
2:M:27:ALA:CB	2:M:51:TYR:HA	2.32	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
2:M:164:ARG:HH11	2:M:164:ARG:HG2	1.67	0.59
1:L:113:ILE:HD13	2:M:229:PHE:HE1	1.68	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:95:GLU:OE1	2:M:176:PRO:HB2	2.03	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:37:THR:HG22	2:M:38:LEU:CG	2.31	0.59
2:M:35:PHE:HE1	2:M:38:LEU:HD13	1.67	0.59
3:H:103:ASP:O	3:H:106:LYS:CE	2.50	0.59
3:H:204:HIS:HE1	3:H:213:PHE:CZ	2.20	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
1:L:8:LYS:O	1:L:11:VAL:CG1	2.50	0.59
2:M:24:VAL:C	2:M:26:LEU:H	2.05	0.59
2:M:205:SER:CA	2:M:279:THR:HG21	2.31	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
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:167:PHE:HZ	1:L:251:THR:HG21	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:227:LEU:HD12	2:M:232:GLU:CD	2.23	0.59
1:L:237:SER:O	1:L:238:LEU:C	2.41	0.59
1:L:10:ARG:NH2	1:L:25:TRP:CB	2.63	0.59
1:L:268:LYS:HD2	1:L:269:LEU:HB2	1.84	0.59
1:L:67:TYR:HB3	1:L:68:PRO:HD2	1.85	0.59
2:M:11:GLN:NE2	3:H:144:ALA:HB3	2.18	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:238:ALA:C	3:H:240:GLY:N	2.53	0.58
3:H:239:GLY:O	3:H:243:TYR:N	2.26	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:187:ASN:HD22	2:M:188:ASN:H	0.61	0.58
2:M:46:GLN:HG2	2:M:47:LEU:N	2.05	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:68:PHE:O	2:M:72:ILE:N	2.36	0.58
2:M:71:GLY:O	2:M:74:PHE:HB2	2.04	0.58
3:H:116:ALA:CB	3:H:228:LEU:CD1	2.82	0.58
3:H:57:PRO:O	3:H:58:LEU:HB2	2.02	0.58
1:L:226:THR:HG21	2:M:232:GLU:HB2	1.85	0.58
1:L:269:LEU:HD13	1:L:270:PRO:CD	2.34	0.58
2:M:114:LEU:O	2:M:117:ILE:N	2.35	0.58
2:M:201:PHE:CE1	2:M:282:ILE:HG21	2.38	0.58
2:M:25:ASN:HD22	2:M:25:ASN:C	2.06	0.58
1:L:151:TRP:O	1:L:154:LEU:HD13	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:213:PHE:HD1	3:H:216:ILE:HD13	1.69	0.58
3:H:212:LEU:C	3:H:214:ALA:H	2.07	0.58
3:H:39:GLY:N	3:H:42:LEU:HD11	2.18	0.58
3:H:56:PHE:CE1	3:H:57:PRO:CD	2.85	0.58
3:H:96:PHE:C	3:H:97:PRO:O	2.42	0.58
2:M:155:TRP:NE1	2:M:278:LEU:O	2.36	0.58
2:M:204:LEU:C	2:M:207:ALA:CB	2.73	0.58
3:H:116:ALA:CA	3:H:228:LEU:HD12	2.31	0.58
3:H:183:LEU:HD11	3:H:189:ARG:HD2	1.86	0.58
1:L:15:THR:HG22	1:L:15:THR:O	2.04	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
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: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
1:L:98:VAL:CG2	1:L:125:ILE:HD11	2.35	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:146:LYS:HZ3	3:H:198:VAL:HG12	1.67	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
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
2:M:182:HIS:CE1	2:M:183:LEU:HD12	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:48:THR:CG2	3:H:51:ALA:C	2.73	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: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
2:M:260:ALA:CB	3:H:36:MET:CG	2.83	0.57
1:L:75:LEU:CD2	1:L:141:ALA:C	2.73	0.57
1:L:69:PRO:CB	1:L:78:ALA:CB	2.81	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
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:135:ARG:HG2	1:L:139:MET:HE3	1.87	0.56
1:L:98:VAL:O	1:L:102:LEU:HD23	2.05	0.56
3:H:49:PRO:HD2	3:H:50:ALA:O	2.04	0.56
1:L:263:TRP:CE3	1:L:263:TRP:HA	2.38	0.56
1:L:121:PHE:HB2	7:L:284:BPH:C2D	2.35	0.56
2:M:135:LEU:O	2:M:138:GLN:N	2.39	0.56
2:M:17:ASP:O	2:M:18:LEU:CG	2.52	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
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	Interatomic distance (Å)	Clash overlap (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
2:M:13:ARG:HE	3:H:143:SER:CB	2.18	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: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:187:ASN:O	2:M:188:ASN:C	2.43	0.56
2:M:206:ILE:CD1	6:M:310:BCL:C2B	2.83	0.56
3:H:96:PHE:O	3:H:97:PRO:O	2.23	0.56
1:L:8:LYS:O	1:L:11:VAL:HG13	2.05	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
2:M:132:ARG:C	2:M:134:TYR:H	2.07	0.56
1:L:219:LEU:C	2:M:132:ARG:NH2	2.58	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:103:ASP:CG	3:H:106:LYS:HZ2	2.04	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:147:PRO:HG2	1:L:152:THR:CG2	2.31	0.56
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:18:LEU:N	2:M:18:LEU:CD1	2.64	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
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
1:L:173:HIS:CB	1:L:247:CYS:SG	2.92	0.55
2:M:238:ILE:HG23	3:H:64:PHE:CZ	2.40	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
1:L:208:THR:N	1:L:211:HIS:CD2	2.73	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
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
3:H:103:ASP:O	3:H:106:LYS:NZ	2.39	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:M:37:THR:CG2	2:M:38:LEU:CD1	2.76	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:260:VAL:O	1:L:260:VAL:CG1	2.53	0.55
1:L:53:ALA:HB2	1:L:64:ILE:CB	2.37	0.55
1:L:189:LEU:HD11	7:M:312:BPH:HED3	1.89	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
1:L:205:GLU:OE1	3:H:68:HIS:HA	2.06	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
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: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
2:M:13:ARG:CZ	2:M:34:PRO:HB3	2.37	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L:284:BPH:H162	6:M:311:BCL:HBB3	1.87	0.54
1:L:64:ILE:HD12	1:L:65:SER:H	1.72	0.54
1:L:48:LEU:CD1	1:L:85:LEU:HD12	2.38	0.54
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
2:M:260:ALA:HB1	3:H:36:MET:SD	2.47	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
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
1:L:54:VAL:CG1	1:L:55:LEU:N	2.71	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
3:H:105:MET:HB3	3:H:106:LYS:HZ3	1.73	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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
2:M:238:ILE:CG2	3:H:64:PHE:CZ	2.91	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:HG2	1:L:79:PRO:O	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: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
2:M:150:PHE:HD1	7:M:312:BPH:C2D	2.21	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
3:H:63:THR:HA	3:H:74:THR:HA	1.91	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:187:ASN:O	2:M:190:SER:HB3	2.08	0.53
2:M:6:ILE:HG22	2:M:7:PHE:HB3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:199:GLN:NE2	3:H:200:SER:OG	2.41	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
2:M:152:SER:C	2:M:154:ILE:N	2.61	0.53
2:M:289:THR:C	2:M:291:VAL:N	2.53	0.53
2:M:206:ILE:HG12	6:M:310:BCL:HHB	1.90	0.53
3:H:19:SER:HA	3:H:22:ILE:HD12	1.91	0.53
3:H:65:ILE:O	3:H:65:ILE:HG22	2.09	0.53
1:L:94:THR:HG21	1:L:129:LEU:HD11	1.79	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: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
1:L:114:GLY:CA	2:M:225:ALA:HB1	2.39	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
3:H:63:THR:HG23	3:H:74:THR:CB	2.38	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:106:LYS:H	3:H:106:LYS:CE	2.23	0.52
3:H:128:HIS:C	3:H:130:LYS:N	2.63	0.52
3:H:196:VAL:O	3:H:196:VAL:CG2	2.57	0.52
3:H:191:LEU:HD11	3:H:205:VAL:HG12	1.89	0.52
3:H:121:PRO:HB3	3:H:225:VAL:O	2.09	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:81:ASN:O	2:M:82:PRO:O	2.27	0.52
3:H:108:GLY:CA	3:H:114:TRP:CZ3	2.89	0.52
3:H:191:LEU:CD2	3:H:213:PHE:CZ	2.92	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
1:L:15:THR:HG21	1:L:19:GLY:O	2.10	0.52
1:L:33:PHE:CE1	1:L:33:PHE:O	2.50	0.52
2:M:162:PHE:O	2:M:163:ILE:O	2.28	0.52
3:H:142:VAL:CG1	3:H:142:VAL:O	2.57	0.52
1:L:15:THR:CG2	1:L:19:GLY:N	2.72	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
2:M:200:PRO:HG3	2:M:297:TRP:CZ3	2.45	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:232:LEU:CD1	2:M:42:PHE:HE2	2.22	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
3:H:151:LEU:HB3	3:H:203:VAL:HG23	1.89	0.52
3:H:31:LEU:O	3:H:34:GLU:N	2.43	0.52
3:H:31:LEU:O	3:H:34:GLU:HB2	2.10	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:261:THR:OG1	3:H:40:TYR:CD1	2.63	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
2:M:236:GLU:CB	3:H:122:GLU:HG3	2.40	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:117:ILE:HG21	2:M:252:TRP:CH2	2.45	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
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: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
1:L:181:PHE:HE1	6:M:310:BCL:CBA	2.24	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:208:THR:C	1:L:211:HIS:HB2	2.26	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:16:ALA:HB1	2:M:32:VAL:CG2	2.29	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:185:LEU:HB3	7:M:312:BPH:C3C	2.38	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
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
2:M:35:PHE:CG	2:M:39:LEU:HD23	2.44	0.51
2:M:236:GLU:HG2	3:H:122:GLU:HG3	1.91	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:234:LEU:HD12	2:M:221:ALA:CB	2.40	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
3:H:239:GLY:O	3:H:240:GLY:C	2.48	0.51
2:M:13:ARG:NE	3:H:143:SER:OG	2.44	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:23:ASP:OD1	2:M:24:VAL:HG23	2.11	0.50
2:M:241:ARG:NH1	2:M:241:ARG:HB3	2.09	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
6:L:282:BCL:HMD2	6:L:283:BCL:CAB	2.41	0.50
1:L:189:LEU:HD21	7:M:312:BPH:CAD	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:6:GLU:HA	1:L:9:TYR:HD1	1.75	0.50
1:L:94:THR:O	1:L:94:THR:HG22	2.11	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:205:GLU:O	1:L:207:ARG:HD3	2.12	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
2:M:236:GLU:CD	3:H:122:GLU:HG3	2.32	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
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:112:ALA:O	3:H:235:GLY:HA3	2.12	0.50
2:M:13:ARG:NE	3:H:143:SER:CB	2.75	0.50
3:H:193:MET:C	3:H:195:MET:H	2.15	0.50
3:H:199:GLN:NE2	3:H:200:SER:N	2.59	0.50
3:H:204:HIS:HD2	3:H:206:ASN:HA	1.76	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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:207:ALA:C	3:H:247:LYS:NZ	2.62	0.49
3:H:82:ASP:O	3:H:84:PRO:HD3	2.11	0.49
1:L:8:LYS:HB3	3:H:85:ILE:CG2	2.42	0.49
1:L:12:PRO:HG2	3:H:99:ALA:HA	1.93	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: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
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
1:L:54:VAL:C	1:L:56:GLN:N	2.64	0.49
1:L:108:CYS:SG	2:M:251:PHE:HE2	2.36	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
3:H:198:VAL:O	3:H:198:VAL:CG1	2.58	0.49
1:L:79:PRO:O	1:L:79:PRO:CG	2.61	0.49
1:L:49:ILE:HA	1:L:89:ILE:CD1	2.42	0.49
2:M:230:GLY:C	2:M:232:GLU:N	2.66	0.49
1:L:25:TRP:HZ2	2:M:254:TRP:CH2	2.31	0.49
2:M:208:PHE:CE2	2:M:275:LEU:HB3	2.47	0.49
2:M:50:ILE:HG23	2:M:52:LEU:HG	1.95	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:146:LYS:HZ2	3:H:198:VAL:HG12	1.75	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:113:ILE:CD1	2:M:229:PHE:HE1	2.26	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:225:GLY:HA2	8:L:285:U10:H4M1	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:241:VAL:HG21	7:L:284:BPH:H2C	1.95	0.49
1:L:36:VAL:O	1:L:39:PHE:HB3	2.13	0.49
2:M:191:LEU:H	2:M:191:LEU:HD13	1.76	0.49
2:M:206:ILE:HD11	6:M:310:BCL:NB	2.25	0.49
2:M:64:LEU:HD12	7:M:312:BPH:C7	2.24	0.49
3:H:124:ASP:C	3:H:126:HIS:N	2.64	0.49
3:H:48:THR:HG23	3:H:51:ALA:C	2.33	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
1:L:98:VAL:HG23	1:L:125:ILE:HD11	1.95	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
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
2:M:256:MET:O	2:M:257:GLY:O	2.30	0.49
1:L:181:PHE:HE1	6:M:310:BCL:CGA	2.25	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
1:L:66:VAL:O	1:L:147:PRO:HA	2.13	0.49
2:M:102:GLY:O	2:M:104:SER:CA	2.59	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
7:L:284:BPH:HMC3	2:M:213:ALA:HB1	1.95	0.49
2:M:228:ARG:HH12	3:H:241:LEU:CD1	2.24	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
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
1:L:187:LEU:HA	2:M:216:PHE:CE2	2.48	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:15:THR:HG21	1:L:19:GLY:HA2	1.93	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:296:VAL:C	2:M:298:GLY:N	2.67	0.48
2:M:89:LEU:HA	2:M:92:PHE:CE2	2.47	0.48
3:H:52:ASN:O	3:H:53:GLN:CB	2.59	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:56:PHE:CD1	3:H:57:PRO:CA	2.92	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
1:L:269:LEU:HD22	1:L:270:PRO:N	2.20	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
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:73:TYR:CE1	1:L:78:ALA:HA	2.48	0.48
1:L:34:PHE:HB3	1:L:99:SER:O	2.13	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
3:H:80:SER:O	3:H:81:GLU:CG	2.61	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:154:ILE:HD12	2:M:157:TRP:CE3	2.49	0.48
2:M:119:SER:HB2	2:M:177:TYR:CZ	2.48	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: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:265:TRP:CH2	1:L:266:TRP:HE3	2.31	0.48
1:L:167:PHE:HE2	6:L:283:BCL:C2D	2.26	0.48
2:M:97:PRO:HB3	2:M:112:GLY:HA2	1.94	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
3:H:30:TYR:O	3:H:31:LEU:O	2.30	0.48
3:H:82:ASP:CG	3:H:82:ASP:O	2.52	0.48
1:L:15:THR:O	1:L:15:THR:CG2	2.61	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
3:H:208:LEU:C	3:H:208:LEU:HD12	2.30	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:295:TYR:HB3	2:M:296:VAL:H	1.24	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
3:H:153:VAL:HG21	3:H:181:VAL:CG1	2.44	0.48
1:L:116:HIS:NE2	2:M:224:LEU:HB3	2.28	0.48
1:L:15:THR:CG2	1:L:19:GLY:H	2.26	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
2:M:201:PHE:CD2	2:M:282:ILE:CG2	2.97	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
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
1:L:224:ILE:HA	2:M:44:ASN:HB2	1.96	0.48
2:M:94:LEU:CD2	2:M:114:LEU:HB3	2.31	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
3:H:56:PHE:CG	3:H:57:PRO:HD2	2.37	0.47
1:L:169:TYR:O	1:L:171:PRO:N	2.47	0.47
1:L:208:THR:H	1:L:211:HIS:CB	2.26	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
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
3:H:199:GLN:HE21	3:H:200:SER:H	1.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:146:PHE:CE2	6:M:311:BCL:CMC	2.97	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:69:GLY:O	3:H:70:ARG:HB2	2.14	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
1:L:113:ILE:CD1	2:M:226:VAL:HG23	2.37	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
2:M:88:ASP:OD1	2:M:91:PHE:HD2	1.97	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:17:VAL:CG1	1:L:18:GLY:N	2.51	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
1:L:25:TRP:HB2	3:H:95:GLY:O	2.15	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:208:PHE:CD2	2:M:275:LEU:HB3	2.50	0.47
2:M:214:LEU:CG	2:M:215:LEU:N	2.74	0.47
2:M:39:LEU:N	2:M:39:LEU:HD22	2.27	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:177:ILE:HD12	6:L:283:BCL:CMB	2.44	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:78:ALA:CB	1:L:79:PRO:HD3	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:13:ARG:HD3	3:H:143:SER:OG	2.15	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
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
1:L:202:LYS:O	1:L:202:LYS:CG	2.63	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
2:M:95:GLU:OE1	2:M:176:PRO:CB	2.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:118:ARG:HH11	3:H:227:LEU:CD1	2.28	0.46
3:H:161:ALA:CB	3:H:210:SER:CB	2.80	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
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:295:TYR:O	2:M:296:VAL:C	2.53	0.46
2:M:35:PHE:HE1	2:M:38:LEU:HD22	1.80	0.46
3:H:219:ILE:HG22	3:H:229:GLU:CD	2.36	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
8:L:285:U10:C32	2:M:60:LEU:HD21	2.45	0.46
3:H:83:ARG:HA	3:H:83:ARG:HE	1.80	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:168:MET:HE1	2:M:288:GLY:HA3	1.96	0.46
2:M:165:PRO:CB	2:M:173:GLU:HB2	2.46	0.46
2:M:186:THR:HG22	6:M:310:BCL:HHD	1.97	0.46
2:M:278:LEU:C	2:M:278:LEU:HD12	2.36	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:150:PHE:CD1	7:M:312:BPH:C3D	2.99	0.46
2:M:164:ARG:NH1	2:M:164:ARG:HG2	2.28	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:17:ILE:HD11	3:H:21:TRP:HE1	1.80	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:204:LYS:CD	1:L:207:ARG:HH22	2.23	0.45
1:L:216:PHE:HD1	1:L:216:PHE:HA	1.54	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
2:M:218:MET:HE1	8:M:313:U10:C1M	2.47	0.45
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
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:193:LEU:HD23	8:L:285:U10:O3	2.14	0.45
1:L:170:ASN:ND2	1:L:247:CYS:O	2.49	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:252:TRP:CD1	8:M:313:U10:C6	2.99	0.45
2:M:152:SER:CA	2:M:277:THR:HG22	2.42	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:54:VAL:C	1:L:56:GLN:H	2.20	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
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
1:L:185:LEU:O	1:L:188:ALA:CA	2.61	0.44
1:L:241:VAL:HG21	7:L:284:BPH:CBC	2.46	0.44
1:L:268:LYS:HB3	1:L:268:LYS:HE2	1.43	0.44
2:M:133:THR:HG21	2:M:146:THR:HG21	2.00	0.44
2:M:191:LEU:N	2:M:191:LEU:CD1	2.80	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
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: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:16:LEU:HB2	1:L:106:GLU:OE2	2.17	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
1:L:244:SER:HB3	6:L:283:BCL:HBA2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:L:285:U10:C4M	8:L:285:U10:H3M3	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:11:GLN:NE2	3:H:144:ALA:CB	2.79	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
3:H:83:ARG:HA	3:H:84:PRO:HD2	1.78	0.44
1:L:102:LEU:C	1:L:104:GLU:N	2.68	0.44
1:L:17:VAL:C	1:L:19:GLY:H	2.20	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:77:GLN:HE21	2:M:77:GLN:HB2	1.54	0.44
2:M:93:SER:HB2	2:M:178:GLY:CA	2.44	0.44
1:L:150:ILE:HG22	1:L:151:TRP:CD1	2.53	0.44
1:L:200:PRO:HB2	1:L:201:GLU:H	1.63	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
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
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
3:H:57:PRO:C	3:H:58:LEU:HD12	2.37	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
8:L:285:U10:H321	2:M:60:LEU:HD21	1.99	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
2:M:81:ASN:O	2:M:82:PRO:C	2.56	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: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:131:LEU:HD13	1:L:146:PHE:HE2	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:161:GLY:O	1:L:163:THR:N	2.51	0.44
1:L:10:ARG:CZ	1:L:25:TRP:CG	3.01	0.44
1:L:98:VAL:HG23	1:L:125:ILE:CD1	2.47	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:105:MET:CB	3:H:106:LYS:HZ3	2.30	0.43
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: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:102:GLY:O	3:H:103:ASP:C	2.57	0.43
3:H:140:PHE:CE2	3:H:169:VAL:HG11	2.50	0.43
3:H:88:ALA:C	3:H:89:ARG:HG2	2.38	0.43
1:L:110:LYS:C	1:L:112:GLY:N	2.70	0.43
1:L:177:ILE:HD11	6:L:283:BCL:C1B	2.47	0.43
1:L:225:GLY:HA2	8:L:285:U10:H4M2	1.97	0.43
7:L:284:BPH:CMC	2:M:213:ALA:HB1	2.49	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
1:L:113:ILE:CD1	2:M:225:ALA:O	2.64	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:73:TRP:CH2	2:M:109:LEU:CD2	3.00	0.43
2:M:201:PHE:CZ	2:M:282:ILE:HG21	2.53	0.43
2:M:150:PHE:CD1	7:M:312:BPH:C2D	3.01	0.43
2:M:60:LEU:O	2:M:61:PHE:C	2.56	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
3:H:116:ALA:HB1	3:H:228:LEU:CD1	2.48	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:231:ARG:NH2	2:M:7:PHE:CB	2.82	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
3:H:210:SER:O	3:H:212:LEU:CA	2.63	0.43
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
1:L:54:VAL:O	1:L:55:LEU:C	2.56	0.43
2:M:12:VAL:HG22	3:H:141:HIS:O	2.18	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
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:31:VAL:HG13	8:M:313:U10:C40	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:9:TYR:O	1:L:11:VAL:HG22	2.19	0.43
2:M:96:PRO:O	2:M:98:ALA:N	2.50	0.43
3:H:106:LYS:HB2	3:H:106:LYS:HE2	1.43	0.43
3:H:58:LEU:N	3:H:58:LEU:HD12	2.34	0.43
3:H:65:ILE:O	3:H:65:ILE:CG2	2.66	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
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
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:166:ASN:OD1	1:L:166:ASN:C	2.57	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
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:160:LEU:HD21	6:M:310:BCL:OBD	2.20	0.42
2:M:242:GLY:HA3	3:H:117:ARG:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
3:H:105:MET:H	3:H:106:LYS:NZ	2.14	0.42
3:H:116:ALA:CA	3:H:228:LEU:HD11	2.43	0.42
1:L:75:LEU:HD23	1:L:141:ALA:HA	2.01	0.42
1:L:139:MET:C	1:L:141:ALA:N	2.72	0.42
1:L:246:LEU:O	1:L:247:CYS:C	2.57	0.42
6:L:282:BCL:CBB	6:L:282:BCL:HHC	2.41	0.42
1:L:91:ILE:O	1:L:91:ILE:HG22	2.19	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: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
2:M:290:VAL:HG21	3:H:12:LEU:HD13	2.01	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
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
3:H:60:LYS:HD2	3:H:62:LYS:HG2	2.00	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:111:PRO:CD	3:H:243:TYR:CZ	2.97	0.42
1:L:111:LEU:HD22	2:M:251:PHE:HA	2.01	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:6:GLU:HG2	1:L:10:ARG:CD	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:64:PHE:HB2	3:H:73:LEU:O	2.19	0.42
3:H:83:ARG:HA	3:H:83:ARG:NE	2.35	0.42
1:L:127:ALA:HB3	6:L:283:BCL:C2	2.46	0.42
1:L:174:MET:SD	6:L:282:BCL:O1D	2.78	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: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: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
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
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
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
3:H:121:PRO:HG3	3:H:224:GLU:HG2	2.02	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:16:ALA:HB2	2:M:32:VAL:HG21	1.96	0.41
2:M:35:PHE:HB3	2:M:39:LEU:HD22	2.02	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:94:LEU:HD11	2:M:114:LEU:CB	2.50	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
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:269:LEU:CD1	1:L:270:PRO:CD	2.90	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
3:H:155:GLY:HA3	3:H:210:SER:H	1.86	0.41
1:L:15:THR:HG21	1:L:19:GLY:C	2.40	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
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
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:206:MET:HB2	3:H:65:ILE:O	2.19	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
1:L:55:LEU:HA	1:L:55:LEU:HD23	1.56	0.40
2:M:168:MET:HG3	2:M:173:GLU:CD	2.42	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:M:233:ARG:HD3	2:M:233:ARG:HH11	1.65	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
3:H:117:ARG:H	3:H:117:ARG:HG2	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 [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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 [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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	40,59,74	1.91	5 (12%)	47,97,115	2.35	14 (29%)
6	BCL	L	283	1	55,74,74	1.62	6 (10%)	65,115,115	2.22	21 (32%)
7	BPH	L	284	-	65,70,70	2.20	9 (13%)	75,101,101	3.79	23 (30%)
8	U10	L	285	-	41,41,63	0.97	0	49,52,79	1.82	13 (26%)
4	BOG	M	308	-	20,20,20	0.67	0	25,25,25	1.43	3 (12%)
6	BCL	M	310	2	55,74,74	1.59	5 (9%)	65,115,115	2.04	15 (23%)
6	BCL	M	311	-	40,59,74	2.72	9 (22%)	47,97,115	2.44	17 (36%)
7	BPH	M	312	2	65,70,70	1.56	7 (10%)	75,101,101	3.68	21 (28%)
8	U10	M	313	-	51,51,63	0.92	1 (1%)	61,64,79	1.93	20 (32%)

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	-	0/19/119/137	0/0/9/9
6	BCL	L	283	1	-	0/37/137/137	0/0/9/9
7	BPH	L	284	-	-	0/54/105/105	0/1/6/6
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	-	0/37/137/137	0/0/9/9
6	BCL	M	311	-	-	0/19/119/137	0/0/9/9
7	BPH	M	312	2	-	2/54/105/105	0/1/6/6
8	U10	M	313	-	-	0/49/73/87	0/1/1/1

All (42) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	M	311	BCL	CHB-C4A	-11.51	1.19	1.33
7	L	284	BPH	O2D-CGD	-4.69	1.21	1.33
7	M	312	BPH	O2D-CGD	-4.63	1.21	1.33
6	M	310	BCL	O2D-CGD	-3.96	1.23	1.33
6	M	311	BCL	CMA-C3A	-3.63	1.45	1.53
6	L	282	BCL	CAC-C3C	-3.37	1.47	1.54
6	L	282	BCL	O2D-CGD	-3.27	1.24	1.33
7	M	312	BPH	CAC-C3C	-3.24	1.47	1.54
6	L	283	BCL	O2D-CGD	-3.21	1.25	1.33
6	M	311	BCL	CAC-C3C	-2.98	1.48	1.54
6	L	283	BCL	CAC-C3C	-2.96	1.48	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	M	311	BCL	O2D-CGD	-2.76	1.26	1.33
6	M	310	BCL	CAC-C3C	-2.38	1.49	1.54
7	L	284	BPH	CAC-C3C	-2.26	1.49	1.54
7	L	284	BPH	C3B-C2B	-2.11	1.32	1.38
7	L	284	BPH	CAA-C2A	2.18	1.58	1.54
8	M	313	U10	C16-C14	2.22	1.56	1.51
7	L	284	BPH	C3D-C4D	2.23	1.44	1.41
6	L	283	BCL	O2A-C1	2.26	1.52	1.46
7	M	312	BPH	CAA-C2A	2.28	1.58	1.54
6	M	311	BCL	O2D-CED	2.64	1.51	1.45
7	L	284	BPH	CHC-C1C	2.78	1.41	1.36
7	M	312	BPH	C3D-C4D	2.89	1.44	1.41
6	M	311	BCL	C1A-CHA	3.19	1.56	1.43
7	L	284	BPH	O1D-CGD	4.25	1.31	1.21
6	M	311	BCL	CAA-C2A	4.65	1.63	1.54
6	L	283	BCL	CHC-C1C	4.91	1.39	1.33
6	M	310	BCL	CHB-C4A	4.94	1.39	1.33
7	M	312	BPH	O1D-CGD	4.99	1.33	1.21
6	M	311	BCL	O1D-CGD	5.04	1.33	1.21
6	L	283	BCL	O1D-CGD	5.26	1.34	1.21
6	M	310	BCL	O1D-CGD	5.32	1.34	1.21
7	M	312	BPH	C11-C10	5.39	1.76	1.52
6	L	282	BCL	CHB-C4A	5.40	1.40	1.33
6	L	282	BCL	O1D-CGD	5.68	1.35	1.21
6	L	282	BCL	CHC-C1C	5.93	1.41	1.33
7	M	312	BPH	C6-C7	5.98	1.78	1.52
6	M	310	BCL	CHC-C1C	6.04	1.41	1.33
6	L	283	BCL	CHB-C4A	6.34	1.41	1.33
6	M	311	BCL	CHC-C1C	6.95	1.42	1.33
7	L	284	BPH	CHC-C4B	8.22	1.60	1.40
7	L	284	BPH	CHB-C1B	12.13	1.62	1.38

All (147) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	M	312	BPH	C4D-C3D-CAD	-25.19	93.37	107.78
7	L	284	BPH	C4D-C3D-CAD	-23.99	94.06	107.78
7	L	284	BPH	CHB-C1B-NB	-9.92	105.20	124.64
6	L	283	BCL	CMB-C2B-C1B	-6.31	118.76	128.46
7	L	284	BPH	O1D-CGD-CBD	-5.96	113.89	124.60
7	M	312	BPH	O1D-CGD-CBD	-5.89	114.02	124.60
6	M	311	BCL	CMB-C2B-C1B	-5.89	119.41	128.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	M	310	BCL	CMB-C2B-C1B	-5.59	119.87	128.46
6	L	282	BCL	CMB-C2B-C1B	-5.31	120.30	128.46
6	L	282	BCL	OBD-CAD-C3D	-5.29	118.27	128.03
6	L	282	BCL	C1-C2-C3	-5.25	118.38	126.68
8	L	285	U10	C12-C13-C14	-5.18	114.68	127.68
8	M	313	U10	C7-C8-C9	-4.65	118.93	126.71
6	M	310	BCL	O1D-CGD-CBD	-4.57	116.40	124.60
7	M	312	BPH	OBD-CAD-C3D	-4.54	119.66	128.03
8	L	285	U10	C27-C28-C29	-4.39	116.64	127.68
7	M	312	BPH	C6-C7-C8	-4.26	101.73	115.73
6	M	310	BCL	OBD-CAD-C3D	-4.15	120.39	128.03
8	M	313	U10	C17-C18-C19	-4.09	117.40	127.68
6	M	311	BCL	CAA-C2A-C3A	-3.96	101.95	112.81
6	M	311	BCL	OBD-CAD-C3D	-3.87	120.89	128.03
8	M	313	U10	C22-C23-C24	-3.80	118.14	127.68
8	M	313	U10	C32-C33-C34	-3.57	118.70	127.68
7	L	284	BPH	CAC-C3C-C2C	-3.55	105.32	114.24
6	M	311	BCL	O2A-CGA-O1A	-3.53	114.80	123.55
6	L	283	BCL	C1-C2-C3	-3.51	119.49	125.96
7	M	312	BPH	CMB-C2B-C1B	-3.44	119.69	125.04
6	M	311	BCL	CBB-CAB-C3B	-3.42	110.44	120.39
8	M	313	U10	C17-C16-C14	-3.42	101.38	112.93
7	L	284	BPH	OBD-CAD-C3D	-3.40	121.77	128.03
8	M	313	U10	C16-C14-C13	-3.39	114.16	121.10
7	L	284	BPH	C4B-C3B-CAB	-3.30	117.91	130.09
7	L	284	BPH	CBB-CAB-C3B	-3.24	113.59	120.52
7	L	284	BPH	C16-C15-C13	-3.21	105.20	115.73
4	M	308	BOG	O5-C1-C2	-3.19	104.14	110.30
7	M	312	BPH	CBB-CAB-C3B	-3.19	113.68	120.52
6	L	283	BCL	C16-C15-C13	-3.18	105.28	115.73
6	L	283	BCL	C1-O2A-CGA	-3.18	109.14	116.77
6	L	283	BCL	OBD-CAD-CBD	-3.17	121.15	125.94
7	L	284	BPH	C1C-NC-C4C	-3.14	107.71	110.54
6	M	310	BCL	CAC-C3C-C2C	-3.09	106.47	114.24
7	L	284	BPH	C1-C2-C3	-3.02	120.39	125.96
6	L	283	BCL	C11-C12-C13	-3.00	105.89	115.73
7	M	312	BPH	C1-O2A-CGA	-2.97	109.64	116.77
8	M	313	U10	C27-C28-C29	-2.97	120.23	127.68
8	M	313	U10	C1M-C1-C6	-2.95	118.22	124.20
6	M	310	BCL	CMC-C2C-C1C	-2.94	103.86	111.77
7	L	284	BPH	CMB-C2B-C1B	-2.93	120.47	125.04
6	L	283	BCL	C5-C3-C2	-2.93	115.11	121.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L	283	BCL	OBD-CAD-C3D	-2.90	122.68	128.03
6	M	311	BCL	CGD-CBD-CAD	-2.87	101.08	110.71
7	M	312	BPH	C1C-NC-C4C	-2.86	107.97	110.54
7	L	284	BPH	OBB-CAB-C3B	-2.83	115.24	120.37
6	M	311	BCL	C1-C2-C3	-2.81	122.24	126.68
6	M	310	BCL	OBD-CAD-CBD	-2.77	121.76	125.94
6	L	283	BCL	CMA-C3A-C2A	-2.74	102.66	113.77
6	L	282	BCL	O1D-CGD-CBD	-2.72	119.71	124.60
6	L	283	BCL	CAA-CBA-CGA	-2.70	105.22	113.35
8	M	313	U10	C12-C13-C14	-2.63	121.07	127.68
8	L	285	U10	C11-C12-C13	-2.62	102.98	111.97
8	L	285	U10	C7-C8-C9	-2.61	122.34	126.71
7	M	312	BPH	C4B-C3B-CAB	-2.61	120.46	130.09
8	L	285	U10	C17-C18-C19	-2.50	121.39	127.68
6	M	311	BCL	O1D-CGD-CBD	-2.50	120.10	124.60
7	L	284	BPH	C2B-C1B-NB	-2.50	106.12	109.82
6	L	282	BCL	CAC-C3C-C2C	-2.45	108.08	114.24
6	L	283	BCL	C11-C10-C8	-2.38	107.91	115.73
8	M	313	U10	C27-C26-C24	-2.36	104.93	112.93
6	M	310	BCL	C11-C12-C13	-2.31	108.14	115.73
6	L	282	BCL	CMA-C3A-C2A	-2.31	104.41	113.77
6	M	310	BCL	C1-C2-C3	-2.26	121.79	125.96
8	M	313	U10	C31-C29-C28	-2.22	116.56	121.10
8	L	285	U10	C17-C16-C14	-2.21	105.44	112.93
7	M	312	BPH	CAA-C2A-C3A	-2.21	106.75	112.81
8	M	313	U10	C35-C34-C33	-2.19	117.83	123.69
6	L	282	BCL	C1-O2A-CGA	-2.15	111.61	116.77
6	L	283	BCL	C1B-CHB-C4A	-2.13	125.89	130.12
8	M	313	U10	C26-C24-C23	-2.10	116.81	121.10
8	L	285	U10	C1M-C1-C6	-2.08	119.98	124.20
7	M	312	BPH	O2A-CGA-O1A	-2.06	118.44	123.55
8	L	285	U10	C7-C6-C1	-2.05	119.43	123.47
6	L	283	BCL	C4-C3-C2	-2.04	118.24	123.69
7	L	284	BPH	C14-C13-C15	-2.03	103.97	111.36
8	M	313	U10	C7-C6-C1	-2.00	119.53	123.47
6	L	283	BCL	O2D-CGD-CBD	2.03	114.93	111.30
7	L	284	BPH	CBD-CHA-C1A	2.04	131.17	126.36
8	M	313	U10	C40-C39-C41	2.06	118.87	115.29
6	M	311	BCL	C4A-NA-C1A	2.08	109.04	106.45
6	L	283	BCL	C1D-CHD-C4C	2.12	129.08	125.92
7	M	312	BPH	CMB-C2B-C3B	2.12	133.01	127.86
6	L	283	BCL	C6-C5-C3	2.16	117.55	112.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L	282	BCL	CAC-C3C-C4C	2.20	117.46	112.58
8	L	285	U10	C15-C14-C16	2.22	119.14	115.29
6	M	310	BCL	C4A-NA-C1A	2.28	109.28	106.45
7	M	312	BPH	CBD-CHA-C1A	2.30	131.77	126.36
6	L	282	BCL	C5-C3-C4	2.33	120.05	114.60
6	L	283	BCL	O2A-CGA-CBA	2.38	118.82	111.90
8	M	313	U10	C35-C34-C36	2.38	119.41	115.29
6	M	310	BCL	C3A-C2A-C1A	2.42	104.97	101.34
6	M	311	BCL	CHB-C4A-NA	2.53	128.01	124.51
6	M	311	BCL	CMA-C3A-C4A	2.58	118.71	111.77
7	L	284	BPH	CED-O2D-CGD	2.60	122.06	115.97
8	M	313	U10	C20-C19-C21	2.61	119.81	115.29
8	L	285	U10	C25-C24-C26	2.61	119.81	115.29
6	M	311	BCL	O2D-CGD-CBD	2.66	116.04	111.30
6	L	282	BCL	C1D-CHD-C4C	2.68	129.91	125.92
7	M	312	BPH	OB B-CAB-CBB	2.70	125.80	119.71
8	M	313	U10	C10-C9-C11	2.75	120.07	115.29
7	M	312	BPH	CED-O2D-CGD	2.77	122.46	115.97
4	M	308	BOG	C1'-O1-C1	2.83	118.72	113.87
8	L	285	U10	C30-C29-C31	2.91	120.34	115.29
8	L	285	U10	C20-C19-C21	2.97	120.45	115.29
4	M	308	BOG	O5-C5-C6	3.04	113.70	106.41
8	L	285	U10	C10-C9-C11	3.05	120.58	115.29
7	L	284	BPH	C1-O2A-CGA	3.08	124.16	116.77
8	M	313	U10	C25-C24-C26	3.15	120.75	115.29
7	L	284	BPH	OB B-CAB-CBB	3.31	127.18	119.71
6	M	311	BCL	OB B-CAB-C3B	3.52	126.67	119.95
6	L	282	BCL	CMB-C2B-C3B	3.69	131.74	124.89
7	M	312	BPH	C3C-C4C-NC	3.80	111.55	107.97
6	M	310	BCL	C4-C3-C5	3.86	121.98	115.29
8	M	313	U10	C30-C29-C31	3.86	121.99	115.29
6	M	310	BCL	CMB-C2B-C3B	4.05	132.41	124.89
7	M	312	BPH	O2D-CGD-CBD	4.20	118.81	111.30
7	L	284	BPH	O2D-CGD-O1D	4.31	132.49	123.82
6	L	283	BCL	CMB-C2B-C3B	4.31	132.90	124.89
6	M	311	BCL	CAA-CBA-CGA	4.51	126.94	113.35
6	M	310	BCL	C3D-CAD-CBD	4.54	114.02	107.60
6	L	282	BCL	O2D-CGD-CBD	4.62	119.55	111.30
7	L	284	BPH	C3C-C4C-NC	4.68	112.38	107.97
7	M	312	BPH	C3D-CAD-CBD	4.72	114.26	107.60
6	M	311	BCL	C3D-CAD-CBD	4.76	114.33	107.60
6	M	311	BCL	CMB-C2B-C3B	4.78	133.76	124.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L	283	BCL	CMD-C2D-C3D	4.94	134.05	124.89
7	L	284	BPH	C3D-CAD-CBD	5.06	114.75	107.60
7	M	312	BPH	CMD-C2D-C3D	5.12	134.39	124.89
6	M	310	BCL	O2D-CGD-CBD	5.13	120.47	111.30
6	L	282	BCL	CMD-C2D-C3D	5.13	134.41	124.89
6	M	310	BCL	CMD-C2D-C3D	5.16	134.47	124.89
6	M	311	BCL	CMD-C2D-C3D	5.25	134.64	124.89
7	L	284	BPH	CMD-C2D-C3D	5.30	134.72	124.89
6	L	283	BCL	C4-C3-C5	5.83	125.41	115.29
6	L	283	BCL	C3D-CAD-CBD	5.95	116.01	107.60
6	L	282	BCL	C3D-CAD-CBD	6.19	116.35	107.60
7	M	312	BPH	C11-C10-C8	6.71	137.75	115.73
7	M	312	BPH	C7-C6-C5	7.29	133.38	113.11
7	L	284	BPH	CHB-C1B-C2B	9.38	147.13	125.62

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	M	308	BOG	C1

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	M	312	BPH	OBB-CAB-C3B-C4B
7	M	312	BPH	C4B-C3B-CAB-CBB

There are no ring outliers.

9 monomers are involved in 327 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	L	282	BCL	19	0
6	L	283	BCL	100	0
7	L	284	BPH	44	0
8	L	285	U10	31	0
4	M	308	BOG	7	0
6	M	310	BCL	68	0
6	M	311	BCL	25	0
7	M	312	BPH	47	0
8	M	313	U10	43	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.