



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 11:31 PM UTC

PDB ID : 4KJZ / pdb_00004kzj
Title : Crystal Structure of Thermus Thermophilus IF2, Apo and GDP-bound Forms (2-474)
Authors : Eiler, D.R.; Lin, J.; Steitz, T.A.
Deposited on : 2013-05-04
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

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

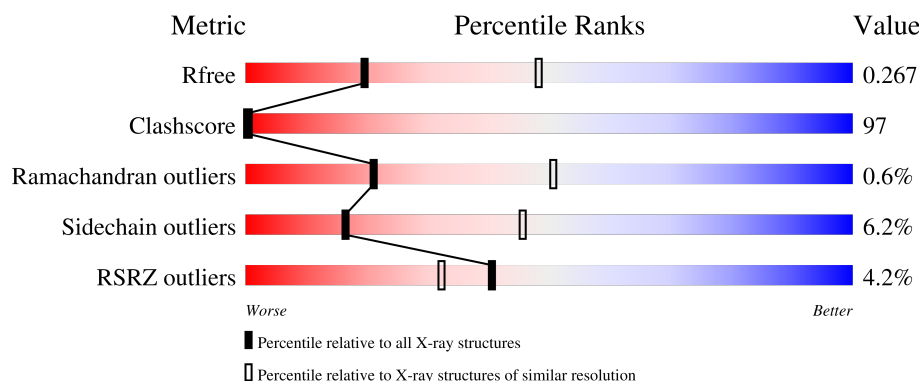
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

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))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	473	 4% 23% 53% 19% • 5%
1	B	473	 5% 22% 48% 24% • •
1	C	473	 4% 26% 51% 18% • •
1	D	473	 3% 25% 51% 17% • 5%

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
2	GDP	A	900	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13708 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.

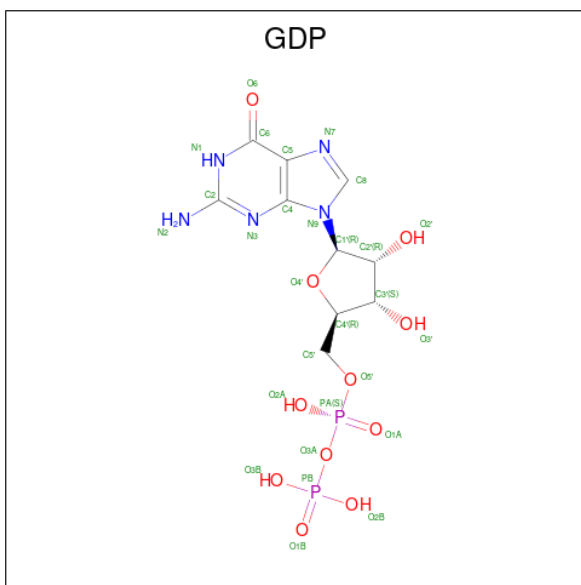
- Molecule 1 is a protein called Translation initiation factor IF-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	451	Total	C	N	O	S	0	0	0
			3375	2116	588	659	12			
1	D	447	Total	C	N	O	S	0	0	0
			3410	2131	609	657	13			
1	B	457	Total	C	N	O	S	0	0	0
			3435	2158	607	657	13			
1	C	458	Total	C	N	O	S	0	0	0
			3417	2137	605	663	12			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	CYS	THR	engineered mutation	UNP P48515
A	319	PRO	ALA	SEE REMARK 999	UNP P48515
D	17	CYS	THR	engineered mutation	UNP P48515
D	319	PRO	ALA	SEE REMARK 999	UNP P48515
B	17	CYS	THR	engineered mutation	UNP P48515
B	319	PRO	ALA	SEE REMARK 999	UNP P48515
C	17	CYS	THR	engineered mutation	UNP P48515
C	319	PRO	ALA	SEE REMARK 999	UNP P48515

- Molecule 2 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 28	C 10	N 5	O 11	P 2	0	0
2	C	1	Total 28	C 10	N 5	O 11	P 2	0	0

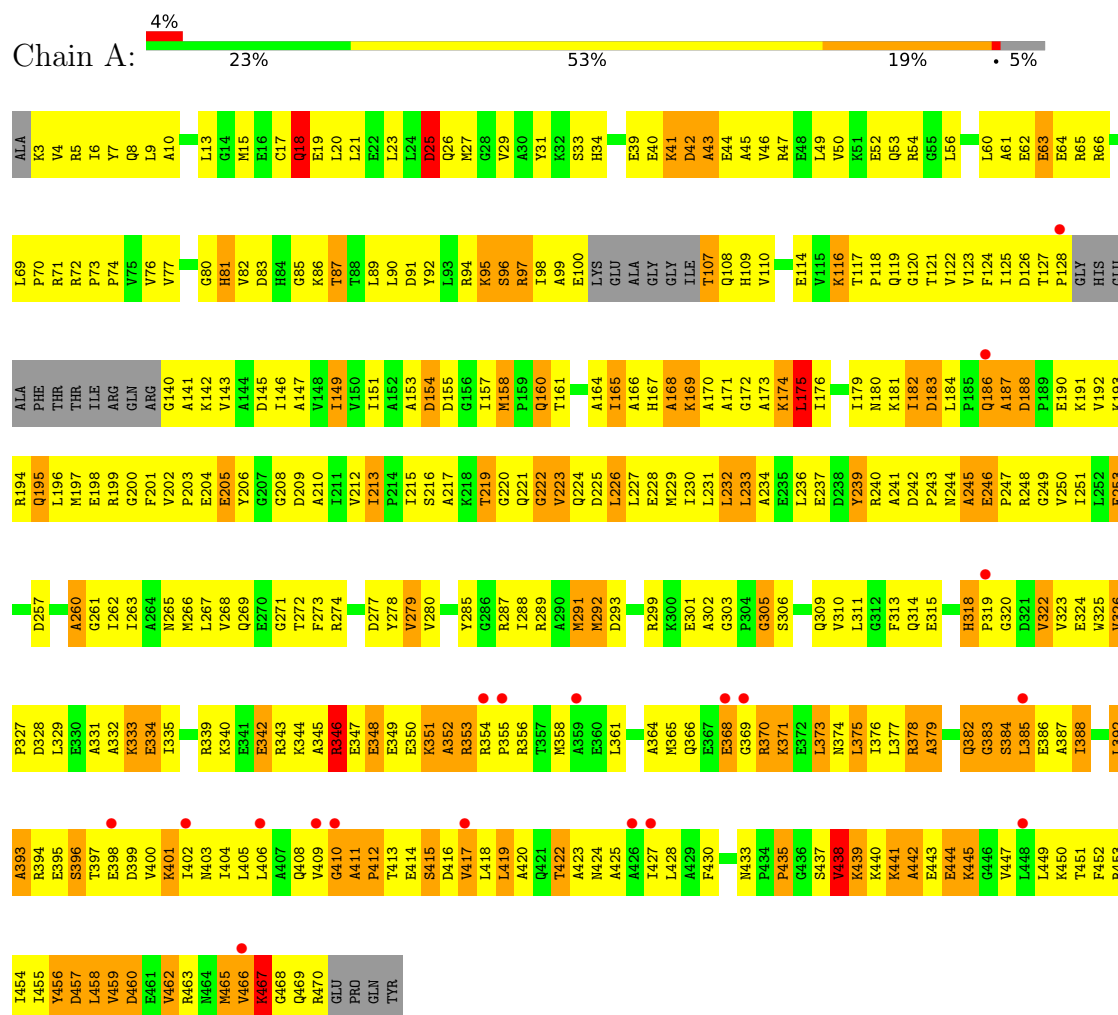
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O 1 1	0	0
3	D	2	Total O 2 2	0	0
3	B	8	Total O 8 8	0	0
3	C	4	Total O 4 4	0	0

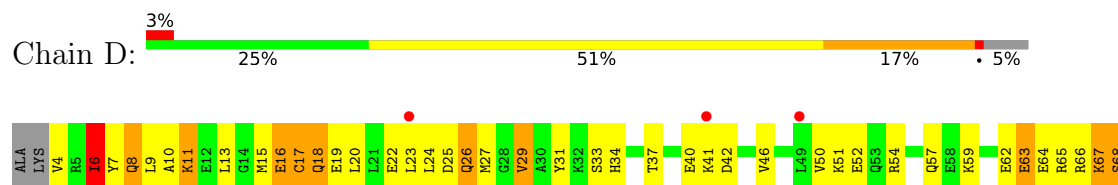
3 Residue-property plots

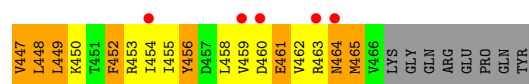
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

• Molecule 1: Translation initiation factor IF-2

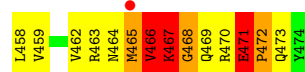
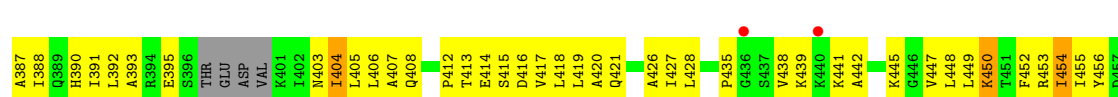
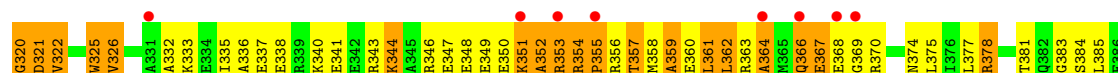
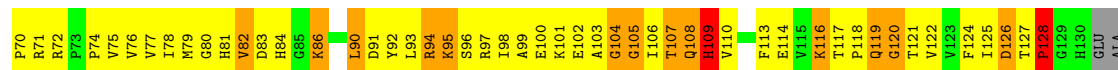
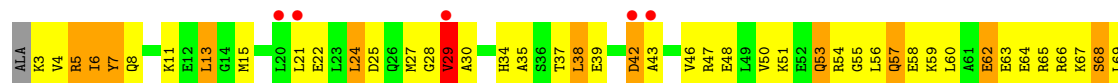


• Molecule 1: Translation initiation factor IF-2





● Molecule 1: Translation initiation factor IF-2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	119.83Å 177.82Å 61.79Å 90.00° 89.87° 90.00°	Depositor
Resolution (Å)	46.76 – 2.80 46.76 – 2.80	Depositor EDS
% Data completeness (in resolution range)	97.3 (46.76-2.80) 98.5 (46.76-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.240 , 0.276 0.232 , 0.267	Depositor DCC
R_{free} test set	3107 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	43.1	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 37.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	0.106 for -h,-k,l	Xtriage
Reported twinning fraction	0.506 for H, K, L 0.494 for h,-k,-l	Depositor
Outliers	0 of 62632 reflections	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	13708	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 23.50 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.6065e-03.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GDP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.53	44/3416 (1.3%)	1.65	76/4624 (1.6%)
1	B	1.66	69/3478 (2.0%)	1.80	111/4703 (2.4%)
1	C	1.63	66/3459 (1.9%)	1.73	95/4674 (2.0%)
1	D	1.53	53/3449 (1.5%)	1.70	92/4651 (2.0%)
All	All	1.59	232/13802 (1.7%)	1.72	374/18652 (2.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
1	B	0	9
1	C	0	11
1	D	0	2
All	All	0	27

All (232) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	205	GLU	C-O	-9.30	1.13	1.24
1	D	177	PHE	C-O	-8.93	1.13	1.24
1	C	202	VAL	CA-C	-8.89	1.43	1.52
1	B	78	ILE	C-O	-8.80	1.14	1.24
1	C	78	ILE	C-O	-8.56	1.14	1.24
1	C	202	VAL	N-CA	-8.43	1.36	1.46
1	C	202	VAL	C-O	-8.41	1.13	1.24
1	D	174	LYS	C-O	-8.29	1.14	1.23
1	D	167	HIS	CG-ND1	-8.11	1.29	1.38
1	D	167	HIS	CD2-NE2	-8.09	1.28	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	109	HIS	N-CA	-7.86	1.36	1.46
1	B	35	ALA	C-O	-7.72	1.12	1.24
1	B	202	VAL	CA-C	-7.65	1.46	1.52
1	D	408	GLN	CA-C	-7.63	1.43	1.52
1	D	318	HIS	CA-C	-7.55	1.43	1.53
1	D	168	ALA	C-O	-7.51	1.15	1.24
1	B	323	VAL	C-O	-7.51	1.14	1.24
1	A	176	ILE	C-O	-7.50	1.15	1.24
1	D	406	LEU	C-O	-7.45	1.15	1.24
1	C	253	GLU	C-O	-7.43	1.14	1.23
1	D	122	VAL	C-O	-7.37	1.16	1.24
1	D	324	GLU	C-O	-7.35	1.14	1.23
1	A	233	LEU	C-O	-7.30	1.15	1.24
1	B	320	GLY	C-O	-7.28	1.13	1.24
1	D	165	ILE	C-O	-7.28	1.15	1.24
1	B	239	TYR	C-O	-7.27	1.15	1.23
1	D	274	ARG	C-O	-7.23	1.15	1.23
1	B	176	ILE	N-CA	-7.22	1.37	1.46
1	C	295	ASP	C-O	-7.20	1.14	1.23
1	D	463	ARG	N-CA	-7.19	1.37	1.46
1	C	473	GLN	CA-C	-7.14	1.43	1.52
1	D	427	ILE	CA-C	-7.12	1.43	1.52
1	B	291	MET	C-O	-7.11	1.16	1.24
1	A	123	VAL	C-O	-7.10	1.15	1.24
1	C	326	VAL	C-O	-7.06	1.19	1.24
1	A	174	LYS	C-O	-7.03	1.15	1.24
1	B	80	GLY	C-O	-7.00	1.15	1.23
1	C	187	ALA	C-O	-6.99	1.16	1.24
1	A	165	ILE	C-O	-6.97	1.16	1.24
1	C	120	GLY	C-O	-6.94	1.17	1.23
1	A	246	GLU	CA-C	-6.92	1.46	1.53
1	D	407	ALA	CA-C	-6.88	1.44	1.52
1	B	346	ARG	N-CA	-6.87	1.38	1.46
1	B	252	LEU	C-O	-6.85	1.16	1.24
1	B	175	LEU	CA-C	-6.81	1.44	1.52
1	D	16	GLU	CA-C	-6.81	1.44	1.52
1	A	168	ALA	C-O	-6.79	1.16	1.24
1	B	143	VAL	C-O	-6.79	1.16	1.24
1	B	281	ALA	CA-C	-6.77	1.46	1.53
1	D	195	GLN	C-O	-6.76	1.16	1.24
1	D	212	VAL	C-O	-6.76	1.16	1.24
1	A	120	GLY	C-O	-6.68	1.17	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	469	GLN	CA-C	-6.67	1.46	1.53
1	B	216	SER	C-O	-6.67	1.16	1.24
1	B	237	GLU	C-O	-6.62	1.15	1.24
1	B	324	GLU	C-O	-6.62	1.16	1.23
1	A	318	HIS	CA-C	-6.61	1.43	1.53
1	D	79	MET	C-O	-6.61	1.15	1.23
1	C	362	LEU	CA-C	-6.60	1.44	1.52
1	C	232	LEU	C-O	-6.56	1.16	1.24
1	A	196	LEU	C-O	-6.54	1.16	1.24
1	A	239	TYR	C-O	-6.54	1.15	1.23
1	D	194	ARG	C-O	-6.53	1.16	1.24
1	A	166	ALA	C-O	-6.52	1.16	1.24
1	D	27	MET	CA-C	-6.51	1.45	1.52
1	B	134	THR	CA-C	-6.51	1.44	1.52
1	B	302	ALA	C-O	-6.51	1.16	1.24
1	B	174	LYS	C-O	-6.49	1.15	1.23
1	B	169	LYS	C-O	-6.45	1.16	1.24
1	D	277	ASP	C-O	-6.45	1.16	1.24
1	D	402	ILE	N-CA	6.43	1.54	1.46
1	A	160	GLN	C-O	-6.42	1.16	1.24
1	B	167	HIS	ND1-CE1	6.41	1.39	1.32
1	C	145	ASP	C-O	-6.39	1.15	1.24
1	C	321	ASP	CA-C	-6.37	1.44	1.53
1	B	98	ILE	C-O	-6.35	1.16	1.24
1	D	323	VAL	C-O	-6.34	1.17	1.24
1	C	264	ALA	C-O	-6.31	1.16	1.24
1	D	81	HIS	ND1-CE1	6.29	1.38	1.32
1	C	298	GLN	CA-C	-6.29	1.45	1.52
1	C	352	ALA	CA-C	-6.27	1.44	1.52
1	A	81	HIS	C-O	-6.26	1.16	1.23
1	B	360	GLU	N-CA	-6.26	1.39	1.46
1	A	387	ALA	C-O	-6.25	1.16	1.23
1	D	429	ALA	C-O	-6.25	1.16	1.24
1	C	378	ARG	C-O	-6.25	1.15	1.23
1	B	444	GLU	CA-C	-6.24	1.47	1.53
1	D	167	HIS	N-CA	-6.24	1.38	1.46
1	C	230	ILE	C-O	-6.21	1.17	1.24
1	A	233	LEU	N-CA	-6.19	1.38	1.46
1	D	164	ALA	C-O	-6.18	1.16	1.24
1	C	187	ALA	N-CA	-6.18	1.38	1.46
1	D	113	PHE	C-O	-6.18	1.16	1.23
1	B	325	TRP	NE1-CE2	-6.17	1.30	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	115	VAL	C-O	-6.14	1.17	1.24
1	A	318	HIS	CD2-NE2	-6.13	1.31	1.37
1	A	246	GLU	C-O	-6.12	1.17	1.24
1	B	252	LEU	CA-C	-6.10	1.45	1.52
1	C	297	ASN	CA-C	-6.10	1.44	1.52
1	C	262	ILE	C-O	-6.08	1.17	1.24
1	A	318	HIS	C-O	-6.07	1.16	1.24
1	C	187	ALA	CA-C	-6.07	1.45	1.52
1	C	363	ARG	N-CA	-6.06	1.39	1.46
1	B	134	THR	CB-CG2	-6.05	1.32	1.52
1	D	404	ILE	CA-CB	6.04	1.62	1.54
1	C	287	ARG	C-O	-6.01	1.17	1.23
1	B	250	VAL	C-O	-6.00	1.17	1.23
1	C	229	MET	C-O	-6.00	1.17	1.24
1	C	189	PRO	C-O	-5.97	1.16	1.24
1	A	25	ASP	N-CA	-5.97	1.39	1.46
1	C	322	VAL	C-O	-5.95	1.16	1.24
1	C	223	VAL	C-O	-5.93	1.17	1.24
1	B	35	ALA	N-CA	-5.92	1.37	1.46
1	C	156	GLY	CA-C	-5.91	1.46	1.52
1	D	327	PRO	C-O	-5.91	1.16	1.24
1	C	359	ALA	CA-C	-5.89	1.44	1.52
1	A	441	LYS	CA-C	-5.88	1.44	1.52
1	C	86	LYS	C-O	-5.88	1.17	1.24
1	C	167	HIS	CG-CD2	5.88	1.42	1.35
1	C	248	ARG	C-O	-5.87	1.16	1.23
1	A	384	SER	C-O	-5.85	1.15	1.23
1	C	466	VAL	N-CA	-5.85	1.39	1.46
1	C	320	GLY	C-O	-5.83	1.16	1.23
1	D	117	THR	CA-C	-5.82	1.46	1.52
1	D	425	ALA	CA-C	-5.82	1.45	1.52
1	D	324	GLU	CA-C	-5.81	1.45	1.52
1	B	120	GLY	C-O	-5.81	1.16	1.23
1	C	109	HIS	CG-ND1	-5.81	1.31	1.38
1	D	351	LYS	C-O	-5.80	1.17	1.24
1	C	179	ILE	C-O	-5.77	1.17	1.24
1	B	140	GLY	C-O	-5.77	1.17	1.23
1	C	211	ILE	C-O	-5.75	1.17	1.24
1	D	152	ALA	C-O	5.75	1.30	1.23
1	B	427	ILE	CA-C	-5.73	1.47	1.53
1	A	234	ALA	C-O	-5.72	1.17	1.24
1	D	256	LEU	C-O	-5.70	1.16	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	251	ILE	C-O	-5.70	1.15	1.23
1	B	202	VAL	N-CA	-5.69	1.40	1.46
1	B	4	VAL	CA-C	-5.68	1.45	1.52
1	B	388	ILE	C-O	-5.68	1.17	1.24
1	D	270	GLU	C-O	-5.67	1.16	1.23
1	B	145	ASP	C-O	-5.67	1.15	1.23
1	B	306	SER	C-O	-5.66	1.17	1.24
1	B	109	HIS	CA-C	-5.64	1.46	1.53
1	D	77	VAL	N-CA	-5.63	1.39	1.46
1	A	393	ALA	C-O	-5.63	1.16	1.24
1	B	141	ALA	C-O	-5.63	1.17	1.24
1	B	428	LEU	CA-C	-5.63	1.46	1.52
1	C	361	LEU	CA-C	-5.62	1.45	1.53
1	A	365	MET	CA-C	-5.62	1.47	1.52
1	B	308	VAL	C-O	-5.62	1.17	1.23
1	B	78	ILE	CA-C	-5.61	1.45	1.52
1	A	187	ALA	C-O	-5.60	1.17	1.24
1	C	206	TYR	C-O	-5.59	1.16	1.24
1	D	121	THR	C-O	-5.58	1.17	1.24
1	D	81	HIS	CG-CD2	5.58	1.42	1.35
1	B	177	PHE	CA-C	-5.58	1.46	1.52
1	D	324	GLU	N-CA	-5.57	1.38	1.45
1	C	167	HIS	ND1-CE1	5.56	1.38	1.32
1	C	109	HIS	CA-C	-5.54	1.46	1.52
1	A	114	GLU	C-O	-5.54	1.17	1.23
1	B	175	LEU	C-O	-5.53	1.16	1.23
1	C	119	GLN	C-O	-5.51	1.17	1.24
1	B	427	ILE	C-O	-5.50	1.16	1.23
1	A	116	LYS	C-O	-5.50	1.17	1.24
1	C	222	GLY	C-O	-5.49	1.16	1.23
1	A	222	GLY	C-O	-5.48	1.16	1.24
1	B	426	ALA	N-CA	-5.47	1.39	1.46
1	B	444	GLU	C-O	-5.47	1.19	1.24
1	D	408	GLN	C-O	-5.46	1.17	1.23
1	B	445	LYS	CA-C	-5.45	1.45	1.52
1	C	441	LYS	C-O	-5.45	1.17	1.24
1	A	174	LYS	CA-C	-5.44	1.45	1.52
1	C	325	TRP	CD2-CE2	5.44	1.50	1.41
1	C	297	ASN	N-CA	-5.42	1.39	1.46
1	A	318	HIS	CG-ND1	-5.41	1.32	1.38
1	C	157	ILE	C-O	-5.39	1.18	1.24
1	C	103	ALA	CA-C	-5.38	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	201	PHE	C-O	-5.38	1.17	1.24
1	C	109	HIS	CD2-NE2	-5.37	1.31	1.37
1	A	232	LEU	C-N	-5.37	1.26	1.33
1	C	156	GLY	C-O	-5.36	1.16	1.23
1	B	37	THR	CA-C	-5.36	1.46	1.52
1	A	442	ALA	N-CA	-5.36	1.40	1.46
1	D	166	ALA	C-O	-5.36	1.17	1.24
1	D	426	ALA	CA-C	-5.36	1.46	1.52
1	A	379	ALA	CA-C	-5.34	1.46	1.52
1	C	179	ILE	CA-CB	-5.33	1.47	1.53
1	A	239	TYR	N-CA	-5.33	1.40	1.46
1	A	396	SER	CA-C	-5.31	1.45	1.53
1	A	97	ARG	N-CA	-5.29	1.39	1.46
1	B	307	ALA	C-O	-5.29	1.18	1.24
1	C	94	ARG	C-O	-5.28	1.17	1.24
1	C	262	ILE	CA-C	-5.28	1.46	1.52
1	B	148	VAL	N-CA	-5.27	1.39	1.46
1	D	407	ALA	C-O	-5.26	1.17	1.24
1	D	286	GLY	C-O	-5.25	1.18	1.24
1	B	135	THR	C-O	-5.21	1.17	1.23
1	D	409	VAL	C-O	-5.21	1.18	1.24
1	C	95	LYS	CA-C	-5.21	1.45	1.52
1	B	167	HIS	N-CA	5.19	1.52	1.46
1	D	427	ILE	C-O	-5.19	1.18	1.24
1	B	325	TRP	CA-C	-5.19	1.46	1.53
1	C	209	ASP	N-CA	5.18	1.52	1.46
1	B	185	PRO	N-CD	5.18	1.54	1.47
1	B	359	ALA	CA-C	-5.17	1.46	1.52
1	B	176	ILE	C-O	-5.16	1.18	1.24
1	B	345	ALA	C-N	-5.16	1.27	1.33
1	C	292	MET	C-O	-5.16	1.17	1.23
1	C	321	ASP	N-CA	-5.15	1.39	1.45
1	A	195	GLN	C-O	-5.13	1.18	1.24
1	D	169	LYS	C-O	-5.12	1.17	1.24
1	B	72	ARG	C-O	-5.12	1.17	1.24
1	C	78	ILE	CA-C	-5.11	1.46	1.52
1	C	6	ILE	N-CA	-5.11	1.40	1.46
1	D	175	LEU	C-O	-5.10	1.17	1.24
1	A	167	HIS	CA-C	-5.09	1.46	1.52
1	B	5	ARG	C-O	-5.09	1.17	1.23
1	B	145	ASP	CG-OD1	-5.09	1.15	1.25
1	A	182	ILE	C-O	-5.08	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	359	ALA	C-O	-5.08	1.18	1.24
1	A	169	LYS	C-O	-5.06	1.17	1.24
1	A	253	GLU	C-O	-5.05	1.17	1.23
1	D	468	GLY	CA-C	-5.05	1.47	1.52
1	B	184	LEU	CA-C	-5.05	1.46	1.52
1	B	303	GLY	C-O	-5.04	1.17	1.24
1	B	175	LEU	N-CA	-5.03	1.39	1.45
1	B	456	TYR	CA-C	5.03	1.59	1.52
1	C	221	GLN	C-O	-5.03	1.18	1.24
1	B	184	LEU	N-CA	-5.02	1.37	1.46
1	A	378	ARG	C-O	-5.00	1.17	1.24
1	C	363	ARG	CA-C	-5.00	1.48	1.53

All (374) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	463	ARG	N-CA-C	-18.04	89.51	111.33
1	B	465	MET	N-CA-C	14.65	127.25	111.28
1	C	467	LYS	CA-C-N	13.23	134.67	119.98
1	C	467	LYS	C-N-CA	13.23	134.67	119.98
1	C	180	ASN	N-CA-C	12.93	125.46	111.36
1	A	41	LYS	N-CA-C	-12.67	96.00	111.33
1	A	269	GLN	N-CA-C	12.29	124.42	111.14
1	A	422	THR	N-CA-C	-12.08	98.15	111.07
1	B	140	GLY	N-CA-C	12.06	127.08	112.49
1	A	43	ALA	N-CA-C	-11.61	98.65	111.07
1	C	105	GLY	N-CA-C	11.61	125.97	112.50
1	B	394	ARG	N-CA-C	-11.51	93.25	110.28
1	D	97	ARG	N-CA-C	11.50	125.43	111.40
1	D	68	SER	N-CA-C	11.42	123.81	111.36
1	D	323	VAL	CB-CA-C	-11.40	94.32	110.96
1	C	221	GLN	N-CA-C	11.38	123.69	111.28
1	B	388	ILE	CB-CA-C	-11.16	97.42	112.04
1	D	402	ILE	N-CA-C	11.03	132.27	109.34
1	D	343	ARG	N-CA-C	-11.01	99.28	111.28
1	A	246	GLU	N-CA-C	-10.91	97.05	109.60
1	B	53	GLN	N-CA-C	-10.70	99.62	111.28
1	A	366	GLN	N-CA-C	-10.34	100.01	111.28
1	C	270	GLU	N-CA-C	-10.30	92.82	108.99
1	C	368	GLU	N-CA-C	10.19	122.47	111.36
1	A	97	ARG	N-CA-C	-10.16	89.17	110.80
1	D	403	ASN	N-CA-C	-10.15	94.13	107.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	123	VAL	CB-CA-C	-10.07	97.18	110.98
1	C	319	PRO	N-CA-CB	9.97	112.03	103.35
1	A	368	GLU	N-CA-C	9.76	121.51	111.07
1	A	442	ALA	N-CA-C	-9.76	100.34	110.97
1	B	118	PRO	N-CA-C	-9.69	99.75	113.81
1	B	142	LYS	N-CA-C	-9.58	97.78	110.24
1	B	168	ALA	N-CA-C	-9.58	98.25	112.04
1	C	128	PRO	CA-C-N	9.51	129.38	120.34
1	C	128	PRO	C-N-CA	9.51	129.38	120.34
1	D	270	GLU	N-CA-C	-9.50	93.75	108.76
1	C	363	ARG	N-CA-C	-9.49	95.99	110.70
1	C	104	GLY	CA-C-N	9.42	130.40	119.94
1	C	104	GLY	C-N-CA	9.42	130.40	119.94
1	D	271	GLY	N-CA-C	9.42	125.36	112.17
1	A	438	VAL	N-CA-C	-9.38	101.64	111.58
1	B	170	ALA	N-CA-C	9.34	122.63	111.33
1	C	354	ARG	N-CA-C	9.27	124.77	112.35
1	A	319	PRO	CA-C-N	9.20	139.44	121.41
1	A	319	PRO	C-N-CA	9.20	139.44	121.41
1	B	137	ARG	N-CA-C	9.16	121.34	111.36
1	A	379	ALA	N-CA-C	9.13	123.03	109.24
1	C	68	SER	N-CA-C	-9.13	101.24	112.38
1	C	370	ARG	N-CA-C	9.02	121.94	111.11
1	A	410	GLY	N-CA-C	9.00	126.41	112.45
1	A	18	GLN	N-CA-C	-8.97	100.35	111.11
1	D	319	PRO	N-CA-CB	8.88	111.62	103.19
1	C	179	ILE	CB-CA-C	-8.88	98.88	111.31
1	C	354	ARG	CA-C-N	-8.86	110.02	119.24
1	C	354	ARG	C-N-CA	-8.86	110.02	119.24
1	C	29	VAL	N-CA-C	8.81	122.10	108.44
1	C	6	ILE	CB-CA-C	-8.78	100.73	111.97
1	C	367	GLU	N-CA-C	-8.74	97.39	110.24
1	B	389	GLN	N-CA-C	-8.74	100.98	112.34
1	A	226	LEU	N-CA-C	-8.73	100.58	111.75
1	D	465	MET	CB-CA-C	-8.71	96.88	110.81
1	B	313	PHE	CA-C-N	-8.68	109.16	120.44
1	B	313	PHE	C-N-CA	-8.68	109.16	120.44
1	D	17	CYS	N-CA-C	8.66	120.72	111.28
1	C	355	PRO	N-CA-C	-8.61	99.83	113.78
1	D	346	ARG	N-CA-C	-8.59	100.80	111.11
1	C	57	GLN	N-CA-C	-8.57	101.94	111.28
1	A	348	GLU	N-CA-C	-8.52	101.92	111.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	459	VAL	N-CA-C	8.50	118.52	110.53
1	A	439	LYS	N-CA-C	-8.46	102.13	111.36
1	D	63	GLU	N-CA-C	-8.44	100.95	111.75
1	D	441	LYS	N-CA-C	-8.34	102.19	111.28
1	B	361	LEU	N-CA-C	8.31	119.97	111.07
1	D	427	ILE	CB-CA-C	-8.28	98.87	110.96
1	C	188	ASP	CA-C-N	-8.28	110.63	119.24
1	C	188	ASP	C-N-CA	-8.28	110.63	119.24
1	B	64	GLU	N-CA-C	-8.27	102.26	111.28
1	A	460	ASP	N-CA-C	-8.25	102.28	111.28
1	C	357	THR	N-CA-C	-8.23	101.33	112.94
1	C	361	LEU	N-CA-C	-8.20	91.20	107.69
1	B	52	GLU	CA-C-N	-8.19	109.30	120.28
1	B	52	GLU	C-N-CA	-8.19	109.30	120.28
1	B	312	GLY	CA-C-N	-8.05	109.28	120.71
1	B	312	GLY	C-N-CA	-8.05	109.28	120.71
1	B	396	SER	N-CA-C	-7.97	98.21	109.69
1	A	382	GLN	N-CA-C	-7.92	102.53	112.90
1	A	445	LYS	N-CA-C	7.91	122.75	113.18
1	B	452	PHE	N-CA-C	7.89	121.96	109.50
1	B	211	ILE	N-CA-C	7.83	119.18	108.84
1	B	144	ALA	N-CA-C	7.82	120.85	110.53
1	B	388	ILE	N-CA-C	7.78	118.37	110.82
1	A	444	GLU	N-CA-C	-7.75	102.79	111.71
1	A	383	GLY	N-CA-C	-7.75	102.96	113.27
1	A	385	LEU	N-CA-C	-7.74	104.36	113.88
1	A	370	ARG	N-CA-C	7.73	122.39	112.34
1	D	321	ASP	CA-C-N	-7.73	112.40	122.37
1	D	321	ASP	C-N-CA	-7.73	112.40	122.37
1	D	388	ILE	CB-CA-C	-7.72	102.08	111.97
1	D	406	LEU	CA-C-N	-7.72	111.73	122.93
1	D	406	LEU	C-N-CA	-7.72	111.73	122.93
1	B	34	HIS	N-CA-C	-7.70	102.86	111.71
1	A	394	ARG	N-CA-C	-7.67	103.81	113.01
1	D	69	LEU	N-CA-C	7.61	121.15	110.20
1	A	81	HIS	N-CA-C	7.51	121.40	110.28
1	A	417	VAL	N-CA-C	-7.50	102.97	110.62
1	B	259	GLN	N-CA-C	7.42	123.37	113.72
1	D	18	GLN	CA-C-N	7.42	131.59	120.31
1	D	18	GLN	C-N-CA	7.42	131.59	120.31
1	D	128	PRO	N-CA-CB	7.41	111.14	103.00
1	B	202	VAL	N-CA-C	-7.38	99.34	108.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	319	PRO	N-CA-CB	7.38	111.00	103.25
1	B	58	GLU	CA-C-N	-7.37	110.61	120.63
1	B	58	GLU	C-N-CA	-7.37	110.61	120.63
1	D	347	GLU	N-CA-C	-7.33	103.43	112.38
1	B	184	LEU	N-CA-C	-7.33	96.17	109.44
1	B	393	ALA	N-CA-C	-7.31	98.13	109.76
1	B	60	LEU	N-CA-C	-7.26	102.46	111.75
1	A	405	LEU	N-CA-C	7.25	118.83	111.07
1	C	38	LEU	N-CA-C	7.24	120.70	108.90
1	A	353	ARG	N-CA-C	-7.23	102.44	111.11
1	C	213	ILE	CA-C-N	7.23	128.88	119.84
1	C	213	ILE	C-N-CA	7.23	128.88	119.84
1	B	230	ILE	CA-C-N	-7.20	110.64	120.44
1	B	230	ILE	C-N-CA	-7.20	110.64	120.44
1	A	145	ASP	N-CA-C	-7.18	103.50	111.82
1	D	168	ALA	N-CA-C	7.18	119.10	111.28
1	C	11	LYS	N-CA-C	-7.14	103.49	111.28
1	D	298	GLN	N-CA-C	-7.11	97.66	109.24
1	D	310	VAL	N-CA-C	7.09	118.26	107.77
1	C	208	GLY	N-CA-C	7.08	124.96	112.64
1	A	66	ARG	N-CA-C	7.07	118.78	111.14
1	A	260	ALA	N-CA-C	7.06	119.05	111.36
1	D	361	LEU	N-CA-C	7.05	118.76	111.14
1	A	87	THR	N-CA-C	-7.05	103.68	111.36
1	A	441	LYS	N-CA-C	-7.05	104.49	113.23
1	B	72	ARG	N-CA-C	-7.00	98.17	109.58
1	D	285	TYR	N-CA-C	-6.96	98.44	109.23
1	C	108	GLN	N-CA-C	6.92	120.26	110.50
1	B	392	LEU	N-CA-C	-6.92	104.71	113.02
1	C	369	GLY	CA-C-N	6.90	129.85	120.54
1	C	369	GLY	C-N-CA	6.90	129.85	120.54
1	B	426	ALA	N-CA-C	-6.89	98.02	109.46
1	A	351	LYS	N-CA-C	-6.88	102.94	111.75
1	B	427	ILE	N-CA-C	-6.85	102.58	110.05
1	D	72	ARG	N-CA-C	-6.85	101.18	110.36
1	B	168	ALA	CA-C-N	6.79	129.38	120.28
1	B	168	ALA	C-N-CA	6.79	129.38	120.28
1	B	400	VAL	N-CA-C	6.77	118.51	109.37
1	C	465	MET	N-CA-C	-6.76	105.00	113.18
1	D	86	LYS	N-CA-C	-6.75	103.85	111.07
1	A	319	PRO	N-CA-CB	6.75	110.34	103.25
1	A	63	GLU	N-CA-C	-6.74	104.16	112.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	168	ALA	N-CA-C	6.73	118.69	111.36
1	C	5	ARG	N-CA-C	-6.73	101.62	110.43
1	D	153	ALA	CA-C-N	6.70	129.81	120.29
1	D	153	ALA	C-N-CA	6.70	129.81	120.29
1	D	154	ASP	N-CA-C	6.67	118.64	111.36
1	D	11	LYS	N-CA-C	-6.67	103.94	111.07
1	A	172	GLY	N-CA-C	-6.66	106.14	115.32
1	D	373	LEU	CA-CB-CG	-6.64	93.07	116.30
1	B	344	LYS	N-CA-C	-6.58	103.22	111.11
1	A	245	ALA	N-CA-C	-6.56	101.84	110.43
1	D	126	ASP	N-CA-C	6.55	118.50	111.36
1	D	26	GLN	N-CA-C	6.54	118.96	111.11
1	A	356	ARG	N-CA-C	6.53	121.45	112.04
1	C	452	PHE	CA-C-N	6.53	129.32	120.44
1	C	452	PHE	C-N-CA	6.53	129.32	120.44
1	C	209	ASP	N-CA-C	6.52	119.22	111.33
1	B	366	GLN	N-CA-C	-6.51	106.07	112.97
1	B	386	GLU	N-CA-C	6.46	119.28	111.40
1	D	429	ALA	CA-C-O	-6.45	113.23	120.32
1	D	374	ASN	CA-C-N	-6.43	111.89	122.11
1	D	374	ASN	C-N-CA	-6.43	111.89	122.11
1	D	194	ARG	CA-C-N	6.43	128.89	120.28
1	D	194	ARG	C-N-CA	6.43	128.89	120.28
1	D	386	GLU	N-CA-C	6.42	118.07	111.14
1	C	7	TYR	N-CA-C	-6.41	105.18	112.87
1	C	450	LYS	N-CA-C	6.41	118.92	109.24
1	A	352	ALA	N-CA-C	6.40	121.12	113.12
1	C	95	LYS	CA-C-N	6.36	128.81	120.28
1	C	95	LYS	C-N-CA	6.36	128.81	120.28
1	B	236	LEU	N-CA-C	6.35	118.00	111.14
1	D	110	VAL	N-CA-C	-6.34	106.14	112.17
1	A	42	ASP	N-CA-C	-6.30	104.85	112.54
1	A	412	PRO	N-CA-C	6.30	122.24	111.03
1	D	175	LEU	N-CA-C	6.29	119.19	109.07
1	A	186	GLN	N-CA-C	6.22	120.50	112.41
1	D	234	ALA	N-CA-C	-6.21	104.59	111.36
1	B	347	GLU	N-CA-C	6.21	118.57	111.11
1	C	472	PRO	CA-N-CD	-6.21	103.31	112.00
1	D	179	ILE	CB-CA-C	-6.21	103.08	111.15
1	D	95	LYS	N-CA-C	-6.18	105.67	112.72
1	B	148	VAL	CA-C-N	-6.17	115.05	123.14
1	B	148	VAL	C-N-CA	-6.17	115.05	123.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	122	VAL	N-CA-C	-6.17	99.23	108.12
1	C	110	VAL	N-CA-C	-6.17	107.12	113.10
1	C	179	ILE	N-CA-CB	-6.15	103.72	111.41
1	B	445	LYS	N-CA-C	-6.14	97.71	110.80
1	C	469	GLN	N-CA-C	-6.13	101.19	110.70
1	C	364	ALA	N-CA-C	6.12	119.49	109.76
1	B	238	ASP	N-CA-C	6.11	120.08	111.52
1	B	173	ALA	N-CA-C	6.08	119.48	110.48
1	B	338	GLU	N-CA-C	-6.08	104.57	111.07
1	B	205	GLU	CA-C-N	-6.07	112.96	122.73
1	B	205	GLU	C-N-CA	-6.07	112.96	122.73
1	C	259	GLN	N-CA-C	6.06	122.13	114.31
1	D	323	VAL	N-CA-C	6.05	116.57	107.80
1	B	461	GLU	N-CA-C	-6.04	105.81	113.43
1	B	271	GLY	CA-C-N	-6.04	114.17	122.93
1	B	271	GLY	C-N-CA	-6.04	114.17	122.93
1	C	321	ASP	N-CA-C	-6.04	102.52	110.43
1	A	415	SER	N-CA-C	-6.03	104.71	111.28
1	D	112	ALA	N-CA-C	6.02	118.08	107.61
1	B	246	GLU	CA-C-N	-6.00	113.77	119.89
1	B	246	GLU	C-N-CA	-6.00	113.77	119.89
1	A	219	THR	N-CA-C	-5.99	106.01	113.38
1	C	62	GLU	N-CA-C	-5.99	104.76	111.28
1	A	183	ASP	N-CA-C	-5.98	104.83	111.71
1	D	460	ASP	CA-C-N	-5.96	112.30	120.28
1	D	460	ASP	C-N-CA	-5.96	112.30	120.28
1	A	406	LEU	N-CA-C	-5.95	98.57	108.75
1	D	322	VAL	N-CA-CB	5.95	117.21	110.72
1	B	133	PHE	CA-C-N	5.94	129.34	120.31
1	B	133	PHE	C-N-CA	5.94	129.34	120.31
1	A	95	LYS	N-CA-C	5.93	119.34	111.75
1	B	183	ASP	N-CA-C	5.93	119.77	112.54
1	C	471	GLU	CA-C-N	-5.92	113.59	119.92
1	C	471	GLU	C-N-CA	-5.92	113.59	119.92
1	C	109	HIS	CB-CA-C	5.89	119.47	109.75
1	B	129	GLY	N-CA-C	-5.88	99.24	113.18
1	B	231	LEU	CA-C-N	-5.87	112.01	120.82
1	B	231	LEU	C-N-CA	-5.87	112.01	120.82
1	B	359	ALA	N-CA-C	-5.87	104.88	111.28
1	D	238	ASP	N-CA-C	5.85	119.47	111.39
1	B	270	GLU	N-CA-C	5.85	119.09	109.72
1	D	374	ASN	O-C-N	-5.85	116.55	123.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	467	LYS	N-CA-C	-5.84	105.26	113.20
1	B	148	VAL	CB-CA-C	-5.83	101.88	111.51
1	A	175	LEU	N-CA-C	5.81	118.43	109.07
1	C	297	ASN	O-C-N	5.80	129.96	122.89
1	A	279	VAL	N-CA-C	5.79	118.31	108.86
1	B	449	LEU	N-CA-C	5.79	117.65	108.79
1	C	167	HIS	N-CA-CB	5.79	118.41	110.01
1	D	172	GLY	N-CA-C	5.79	126.90	113.18
1	C	305	GLY	N-CA-C	-5.79	107.33	115.32
1	D	125	ILE	CB-CA-C	-5.78	103.58	111.33
1	B	73	PRO	CA-C-N	-5.78	114.01	120.14
1	B	73	PRO	C-N-CA	-5.78	114.01	120.14
1	D	224	GLN	N-CA-C	5.77	117.24	111.07
1	D	248	ARG	N-CA-C	5.75	118.82	108.48
1	D	401	LYS	CA-C-N	5.74	132.30	121.97
1	D	401	LYS	C-N-CA	5.74	132.30	121.97
1	C	271	GLY	N-CA-C	5.73	123.14	112.77
1	D	265	ASN	N-CA-C	5.71	117.98	109.59
1	B	244	ASN	N-CA-C	5.71	119.47	111.30
1	B	422	THR	CB-CA-C	-5.71	101.92	110.88
1	C	295	ASP	N-CA-C	-5.68	103.03	110.53
1	A	456	TYR	CB-CA-C	-5.68	101.96	110.88
1	B	249	GLY	N-CA-C	-5.68	99.98	110.83
1	B	236	LEU	CB-CA-C	-5.67	101.94	110.90
1	A	369	GLY	N-CA-C	5.64	121.48	114.37
1	C	183	ASP	N-CA-C	5.64	117.51	111.36
1	D	297	ASN	N-CA-C	5.63	118.01	110.35
1	B	52	GLU	O-C-N	-5.63	116.17	122.03
1	D	331	ALA	N-CA-C	5.62	117.48	111.36
1	C	261	GLY	N-CA-C	-5.62	99.87	113.18
1	D	146	ILE	N-CA-C	5.61	118.01	108.86
1	C	179	ILE	N-CA-C	5.61	115.87	107.51
1	B	419	LEU	N-CA-C	-5.61	104.38	111.11
1	D	195	GLN	CA-C-N	5.61	128.05	120.65
1	D	195	GLN	C-N-CA	5.61	128.05	120.65
1	D	201	PHE	CB-CA-C	-5.61	101.65	110.79
1	B	346	ARG	N-CA-C	-5.60	105.18	111.28
1	D	143	VAL	N-CA-C	5.59	115.79	110.42
1	C	326	VAL	CB-CA-C	5.59	114.81	109.33
1	A	223	VAL	N-CA-C	-5.59	104.92	110.62
1	A	305	GLY	N-CA-C	-5.59	106.47	115.08
1	A	25	ASP	CB-CA-C	5.58	120.14	110.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	401	LYS	N-CA-C	-5.57	99.34	108.76
1	D	406	LEU	O-C-N	-5.55	116.83	123.27
1	C	166	ALA	N-CA-C	5.55	117.41	111.36
1	B	239	TYR	N-CA-C	5.54	118.28	109.96
1	B	421	GLN	CA-C-N	5.54	127.64	120.44
1	B	421	GLN	C-N-CA	5.54	127.64	120.44
1	C	316	LEU	N-CA-C	5.53	117.71	110.08
1	B	187	ALA	N-CA-C	-5.52	103.20	110.43
1	D	230	ILE	N-CA-C	-5.51	104.96	110.30
1	B	169	LYS	CA-C-N	5.50	127.91	120.38
1	B	169	LYS	C-N-CA	5.50	127.91	120.38
1	C	237	GLU	N-CA-C	-5.47	106.65	113.38
1	C	24	LEU	CA-C-N	5.46	127.54	120.44
1	C	24	LEU	C-N-CA	5.46	127.54	120.44
1	D	201	PHE	N-CA-C	5.45	117.64	107.99
1	B	256	LEU	N-CA-C	5.45	117.63	108.96
1	C	227	LEU	CA-C-N	5.45	129.32	120.60
1	C	227	LEU	C-N-CA	5.45	129.32	120.60
1	B	169	LYS	N-CA-C	5.45	117.22	111.28
1	B	365	MET	N-CA-C	-5.44	107.29	114.31
1	B	450	LYS	N-CA-C	-5.44	100.45	108.99
1	C	291	MET	O-C-N	-5.44	116.72	123.36
1	B	50	VAL	N-CA-C	-5.43	105.08	110.62
1	C	466	VAL	N-CA-C	-5.41	105.11	110.62
1	D	27	MET	N-CA-C	-5.40	105.81	112.72
1	B	322	VAL	N-CA-C	-5.40	99.46	107.51
1	C	178	ALA	CA-C-N	5.39	130.00	122.93
1	C	178	ALA	C-N-CA	5.39	130.00	122.93
1	C	210	ALA	N-CA-C	5.39	118.71	110.20
1	C	126	ASP	N-CA-C	-5.38	105.40	113.89
1	C	53	GLN	CA-C-N	-5.37	113.47	120.44
1	C	53	GLN	C-N-CA	-5.37	113.47	120.44
1	B	427	ILE	CB-CA-C	-5.34	105.72	111.59
1	B	464	ASN	N-CA-C	-5.33	99.45	110.80
1	B	435	PRO	N-CA-C	-5.32	105.87	113.47
1	C	167	HIS	CB-CA-C	-5.31	102.54	110.88
1	C	260	ALA	N-CA-C	5.30	120.40	113.30
1	D	6	ILE	CB-CA-C	-5.29	103.96	112.16
1	A	411	ALA	CA-C-N	5.28	126.56	120.85
1	A	411	ALA	C-N-CA	5.28	126.56	120.85
1	D	445	LYS	CB-CA-C	-5.28	101.78	110.08
1	B	372	GLU	CA-C-N	-5.28	115.15	123.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	372	GLU	C-N-CA	-5.28	115.15	123.13
1	B	448	LEU	N-CA-C	5.28	117.36	108.96
1	A	212	VAL	CB-CA-C	5.27	117.54	110.42
1	B	23	LEU	N-CA-C	5.26	116.82	111.14
1	B	201	PHE	CA-C-N	-5.24	118.22	123.04
1	B	201	PHE	C-N-CA	-5.24	118.22	123.04
1	A	342	GLU	N-CA-C	-5.24	104.50	112.04
1	A	346	ARG	N-CA-C	-5.24	104.63	111.02
1	B	416	ASP	N-CA-C	-5.24	104.99	111.33
1	D	117	THR	N-CA-C	-5.24	99.98	109.09
1	A	96	SER	CA-C-N	-5.23	111.55	121.54
1	A	96	SER	C-N-CA	-5.23	111.55	121.54
1	A	457	ASP	N-CA-C	-5.21	106.99	113.19
1	C	453	ARG	N-CA-C	5.20	116.76	111.14
1	A	462	VAL	N-CA-C	-5.20	105.32	110.62
1	C	110	VAL	N-CA-CB	-5.19	105.61	112.36
1	D	351	LYS	CA-C-N	5.18	128.19	120.31
1	D	351	LYS	C-N-CA	5.18	128.19	120.31
1	B	209	ASP	CB-CA-C	-5.17	103.95	111.14
1	B	377	LEU	CA-CB-CG	5.17	134.38	116.30
1	D	319	PRO	O-C-N	5.16	129.57	123.06
1	C	205	GLU	N-CA-C	-5.16	105.66	111.28
1	A	458	LEU	N-CA-C	-5.15	105.29	112.45
1	D	319	PRO	N-CA-C	-5.15	102.51	111.32
1	C	202	VAL	N-CA-C	-5.15	97.75	108.88
1	A	371	LYS	N-CA-C	5.15	117.81	110.24
1	C	227	LEU	O-C-N	5.15	127.58	122.12
1	C	468	GLY	N-CA-C	5.12	118.87	112.73
1	B	38	LEU	N-CA-C	5.11	116.84	109.07
1	D	8	GLN	N-CA-C	-5.11	105.88	112.68
1	A	291	MET	CB-CG-SD	-5.11	97.37	112.70
1	B	117	THR	N-CA-C	-5.10	101.26	109.58
1	D	166	ALA	N-CA-C	5.10	116.84	111.28
1	B	322	VAL	CA-C-N	5.09	129.35	121.71
1	B	322	VAL	C-N-CA	5.09	129.35	121.71
1	D	292	MET	N-CA-C	5.09	117.70	109.40
1	A	213	ILE	CA-C-N	5.09	126.20	119.84
1	A	213	ILE	C-N-CA	5.09	126.20	119.84
1	D	264	ALA	N-CA-C	5.09	116.70	108.26
1	A	169	LYS	N-CA-C	5.07	117.70	111.82
1	C	463	ARG	N-CA-C	-5.05	106.38	112.54
1	B	403	ASN	N-CA-C	5.05	117.56	107.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	13	LEU	N-CA-C	-5.05	106.90	113.16
1	D	443	GLU	N-CA-C	-5.04	105.92	111.71
1	C	363	ARG	CA-C-N	-5.04	114.30	121.50
1	C	363	ARG	C-N-CA	-5.04	114.30	121.50
1	A	154	ASP	N-CA-C	5.03	119.44	112.45
1	D	356	ARG	CB-CA-C	-5.03	105.13	111.86
1	D	409	VAL	CB-CA-C	-5.02	103.64	110.77
1	D	433	ASN	CA-C-N	5.02	123.32	119.66
1	D	433	ASN	C-N-CA	5.02	123.32	119.66
1	C	42	ASP	N-CA-C	-5.02	107.71	113.88
1	B	16	GLU	CA-C-N	-5.02	113.56	120.28
1	B	16	GLU	C-N-CA	-5.02	113.56	120.28

There are no chirality outliers.

All (27) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	107	THR	Peptide
1	A	158	MET	Peptide
1	A	25	ASP	Peptide
1	A	346	ARG	Peptide
1	A	467	LYS	Peptide
1	B	311	LEU	Mainchain
1	B	365	MET	Peptide
1	B	366	GLN	Peptide
1	B	394	ARG	Peptide
1	B	446	GLY	Peptide
1	B	460	ASP	Peptide
1	B	53	GLN	Peptide
1	B	55	GLY	Peptide
1	B	59	LYS	Peptide
1	C	102	GLU	Peptide
1	C	104	GLY	Peptide
1	C	128	PRO	Peptide
1	C	351	LYS	Mainchain
1	C	353	ARG	Peptide
1	C	358	MET	Mainchain
1	C	360	GLU	Peptide
1	C	404	ILE	Mainchain
1	C	466	VAL	Peptide
1	C	467	LYS	Mainchain,Peptide
1	D	271	GLY	Peptide

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Mol	Chain	Res	Type	Group
1	D	447	VAL	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3375	0	3330	666	10
1	B	3435	0	3417	741	14
1	C	3417	0	3363	660	4
1	D	3410	0	3413	644	3
2	A	28	0	11	36	0
2	C	28	0	12	8	0
3	A	1	0	0	1	0
3	B	8	0	0	3	0
3	C	4	0	0	0	0
3	D	2	0	0	0	0
All	All	13708	0	13546	2646	16

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 97.

All (2646) 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)
1:C:95:LYS:CG	1:C:98:ILE:HG21	1.18	1.66
1:C:95:LYS:HG3	1:C:98:ILE:CG2	1.25	1.63
1:D:452:PHE:CE2	1:D:458:LEU:HD13	1.27	1.60
1:C:421:GLN:CA	1:C:445:LYS:HZ2	1.16	1.59
1:D:452:PHE:CD2	1:D:458:LEU:HD13	1.32	1.58
1:C:255:LYS:CE	1:C:263:ILE:HD11	1.28	1.55
1:B:79:MET:CE	1:B:164:ALA:HA	1.36	1.55
1:A:157:ILE:CD1	1:A:199:ARG:HH12	0.92	1.54
1:C:81:HIS:HB3	1:C:84:HIS:CD2	1.42	1.53
1:B:262:ILE:HG21	1:B:316:LEU:CD2	1.34	1.52
1:D:421:GLN:CG	1:D:445:LYS:HB2	1.30	1.51
1:A:413:THR:CG2	1:A:416:ASP:CG	1.78	1.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:38:LEU:CD2	1:B:39:GLU:N	1.75	1.48
1:B:79:MET:HE2	1:B:164:ALA:CA	1.44	1.47
1:D:452:PHE:CE2	1:D:458:LEU:CD1	1.96	1.46
1:A:40:GLU:CA	1:A:43:ALA:HB2	1.45	1.44
1:A:413:THR:HG22	1:A:416:ASP:CG	1.01	1.42
1:C:385:LEU:HD11	1:C:407:ALA:CB	1.48	1.42
1:A:184:LEU:HD21	2:A:900:GDP:N2	1.35	1.42
1:C:255:LYS:CE	1:C:263:ILE:CD1	1.98	1.41
1:C:81:HIS:HB3	1:C:84:HIS:NE2	1.13	1.41
1:B:286:GLY:HA2	1:B:314:GLN:CD	1.48	1.39
1:C:255:LYS:HE3	1:C:263:ILE:CD1	1.47	1.39
1:C:385:LEU:CD1	1:C:407:ALA:HB1	1.48	1.39
1:B:286:GLY:HA2	1:B:314:GLN:NE2	1.37	1.39
1:C:71:ARG:HG2	1:C:240:ARG:CG	1.51	1.38
1:B:419:LEU:O	1:B:422:THR:CG2	1.67	1.38
1:A:285:TYR:CE1	1:A:314:GLN:OE1	1.77	1.38
1:C:421:GLN:CA	1:C:445:LYS:NZ	1.74	1.38
1:D:182:ILE:CD1	1:D:214:PRO:HB2	1.54	1.37
1:D:421:GLN:HG2	1:D:445:LYS:CB	1.53	1.36
1:D:293:ASP:CG	1:D:299:ARG:HH12	1.29	1.36
1:D:374:ASN:CA	1:D:404:ILE:HG22	1.56	1.36
1:C:421:GLN:HA	1:C:445:LYS:NZ	1.08	1.36
1:B:411:ALA:N	1:B:434:PRO:HG2	1.36	1.36
1:D:122:VAL:HB	1:D:124:PHE:CE1	1.60	1.35
1:B:411:ALA:H	1:B:434:PRO:CG	1.37	1.35
1:C:95:LYS:HG3	1:C:98:ILE:CB	1.55	1.35
1:D:69:LEU:CD1	1:D:242:ASP:HB2	1.54	1.34
1:B:286:GLY:CA	1:B:314:GLN:OE1	1.75	1.34
1:B:12:GLU:CG	1:B:13:LEU:HD12	1.56	1.34
1:C:95:LYS:CA	1:C:98:ILE:HG23	1.58	1.34
1:C:203:PRO:HB2	1:C:205:GLU:OE1	1.24	1.33
1:C:69:LEU:O	1:C:240:ARG:HD3	1.15	1.32
1:C:4:VAL:CG1	1:C:8:GLN:HG3	1.59	1.32
1:D:182:ILE:HD11	1:D:214:PRO:CB	1.59	1.31
1:C:95:LYS:CG	1:C:98:ILE:CG2	1.89	1.31
1:B:38:LEU:HD23	1:B:39:GLU:CA	1.60	1.31
1:B:12:GLU:HG3	1:B:13:LEU:CD1	1.59	1.30
1:C:427:ILE:HD12	1:C:449:LEU:CD1	1.61	1.30
1:A:285:TYR:HE1	1:A:314:GLN:OE1	1.02	1.29
1:B:12:GLU:CG	1:B:13:LEU:CD1	2.07	1.29
1:A:352:ALA:O	1:A:355:PRO:HD2	1.32	1.29

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:66:ARG:O	1:C:69:LEU:HB2	1.17	1.29
1:D:421:GLN:CG	1:D:445:LYS:CB	2.06	1.28
1:A:76:VAL:HG11	1:A:124:PHE:CE1	1.67	1.27
1:C:125:ILE:CG2	1:C:127:THR:HG22	1.64	1.27
1:A:40:GLU:HA	1:A:43:ALA:CB	1.63	1.27
1:A:413:THR:HG22	1:A:416:ASP:OD2	1.33	1.27
1:D:178:ALA:HA	1:D:213:ILE:O	1.15	1.27
1:A:420:ALA:O	1:A:424:ASN:N	1.66	1.27
1:B:29:VAL:HG12	3:B:901:HOH:O	1.35	1.27
1:C:95:LYS:CG	1:C:98:ILE:HG12	1.65	1.27
1:B:262:ILE:CG2	1:B:316:LEU:HD21	1.62	1.26
1:B:6:ILE:HB	1:B:34:HIS:O	1.26	1.26
1:B:405:LEU:HD11	1:B:406:LEU:CD1	1.64	1.26
1:A:198:GLU:OE2	1:B:256:LEU:HD23	1.20	1.25
1:A:378:ARG:NH2	1:A:416:ASP:OD2	1.69	1.25
1:B:462:VAL:O	1:B:465:MET:HB3	1.23	1.25
1:C:59:LYS:HA	1:C:62:GLU:CB	1.64	1.25
1:C:203:PRO:CB	1:C:205:GLU:OE1	1.83	1.25
1:C:4:VAL:HG12	1:C:8:GLN:CG	1.65	1.25
1:B:272:THR:HG23	1:B:302:ALA:O	1.34	1.24
1:D:345:ALA:HA	1:D:348:GLU:CB	1.65	1.24
1:A:197:MET:SD	1:A:206:TYR:CE2	2.30	1.24
1:A:97:ARG:HG2	1:A:100:GLU:CB	1.67	1.23
1:A:82:VAL:O	2:A:900:GDP:O1B	1.56	1.23
1:B:255:LYS:O	1:B:262:ILE:HG23	1.38	1.23
1:C:116:LYS:HE2	1:C:121:THR:CG2	1.69	1.23
1:C:378:ARG:NH1	1:C:408:GLN:HB2	1.54	1.22
1:C:95:LYS:CD	1:C:98:ILE:HG21	1.69	1.22
1:C:95:LYS:HG3	1:C:98:ILE:CG1	1.67	1.22
1:D:345:ALA:O	1:D:348:GLU:N	1.73	1.22
1:C:55:GLY:O	1:C:58:GLU:HB3	1.37	1.22
1:A:352:ALA:C	1:A:355:PRO:HD2	1.64	1.21
1:C:81:HIS:CB	1:C:84:HIS:CD2	2.21	1.21
1:A:415:SER:O	1:A:419:LEU:N	1.71	1.21
1:A:39:GLU:O	1:A:42:ASP:CB	1.87	1.21
1:C:466:VAL:O	1:C:468:GLY:N	1.74	1.21
1:D:178:ALA:CA	1:D:213:ILE:O	1.89	1.21
1:A:184:LEU:CD2	2:A:900:GDP:N2	2.03	1.21
1:A:39:GLU:O	1:A:42:ASP:HB2	1.03	1.20
1:D:205:GLU:HG3	1:D:206:TYR:CE1	1.77	1.20
1:A:61:ALA:O	1:A:64:GLU:CB	1.90	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:71:ARG:HA	1:C:240:ARG:HA	1.22	1.20
1:C:95:LYS:CB	1:C:98:ILE:HG21	1.72	1.20
1:B:405:LEU:HD12	1:B:406:LEU:CG	1.71	1.19
1:A:378:ARG:CZ	1:A:416:ASP:OD2	1.88	1.19
1:D:108:GLN:NE2	1:D:292:MET:HE1	1.57	1.18
1:A:460:ASP:OD1	1:A:463:ARG:NH2	1.75	1.18
1:A:157:ILE:HD13	1:A:199:ARG:NH1	0.86	1.18
1:B:38:LEU:HD23	1:B:39:GLU:N	0.85	1.18
1:B:264:ALA:HB3	1:B:313:PHE:CE2	1.79	1.18
1:B:137:ARG:HD3	1:B:319:PRO:O	1.41	1.17
1:C:81:HIS:CB	1:C:84:HIS:NE2	2.08	1.17
1:D:293:ASP:OD2	1:D:299:ARG:NH1	1.75	1.17
1:B:62:GLU:O	1:B:65:ARG:HB3	1.43	1.17
1:B:38:LEU:HD23	1:B:38:LEU:C	1.64	1.17
1:B:117:THR:CG2	1:B:119:GLN:HG3	1.73	1.17
1:D:374:ASN:HA	1:D:404:ILE:HG22	1.17	1.16
1:D:452:PHE:CD2	1:D:458:LEU:CD1	2.23	1.16
1:C:274:ARG:NH1	1:C:301:GLU:OE2	1.77	1.16
1:D:99:ALA:CB	1:B:99:ALA:HA	1.75	1.15
1:D:340:LYS:O	1:D:344:LYS:HG3	1.46	1.15
1:B:427:ILE:HD11	1:B:449:LEU:HD22	1.26	1.15
1:C:285:TYR:CZ	1:C:333:LYS:HD3	1.81	1.15
1:C:95:LYS:CB	1:C:98:ILE:CG2	2.25	1.15
1:C:466:VAL:C	1:C:468:GLY:H	1.45	1.15
1:B:117:THR:HG23	1:B:119:GLN:HG3	1.24	1.15
1:B:405:LEU:HD12	1:B:406:LEU:HG	1.23	1.15
1:A:46:VAL:CG1	1:A:50:VAL:CG2	2.23	1.14
1:A:46:VAL:HG12	1:A:50:VAL:CG2	1.76	1.14
1:D:345:ALA:C	1:D:348:GLU:H	1.54	1.14
1:B:262:ILE:CG2	1:B:316:LEU:CD2	2.22	1.14
1:C:271:GLY:O	1:C:304:PRO:HD3	1.46	1.14
1:C:421:GLN:CB	1:C:445:LYS:HZ2	1.59	1.14
1:A:376:ILE:HD11	1:A:427:ILE:HG12	1.16	1.14
1:D:24:LEU:HB3	1:D:29:VAL:HG11	1.20	1.14
1:D:374:ASN:HA	1:D:404:ILE:CG2	1.77	1.14
1:B:405:LEU:CD1	1:B:406:LEU:CD1	2.24	1.14
1:B:411:ALA:CB	1:B:434:PRO:HB2	1.76	1.14
1:C:285:TYR:OH	1:C:333:LYS:HD3	1.48	1.14
1:B:4:VAL:HG21	1:B:8:GLN:OE1	1.45	1.14
1:B:393:ALA:HB2	1:B:398:GLU:N	1.60	1.13
1:D:99:ALA:HB3	1:B:99:ALA:HA	1.14	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:GLU:CA	1:A:43:ALA:CB	2.24	1.13
1:B:427:ILE:HD11	1:B:449:LEU:CD2	1.79	1.12
1:C:427:ILE:HB	1:C:449:LEU:CD1	1.78	1.12
1:A:96:SER:O	1:A:98:ILE:N	1.83	1.12
1:A:141:ALA:HB3	1:A:250:VAL:CG2	1.78	1.12
1:D:318:HIS:N	1:D:321:ASP:OD2	1.81	1.12
1:C:95:LYS:HE2	1:C:98:ILE:HB	1.28	1.12
1:C:105:GLY:O	1:C:295:ASP:HA	1.44	1.12
1:C:427:ILE:CD1	1:C:449:LEU:CD1	2.26	1.12
1:A:293:ASP:OD2	1:A:299:ARG:HD2	1.49	1.12
1:D:94:ARG:NH2	1:D:126:ASP:OD2	1.83	1.12
1:B:38:LEU:HD22	1:B:39:GLU:O	1.49	1.12
1:A:199:ARG:O	1:A:386:GLU:OE1	1.66	1.12
1:A:413:THR:HG23	1:A:416:ASP:N	1.63	1.12
1:B:278:TYR:CE1	1:B:329:LEU:HB3	1.85	1.12
1:D:278:TYR:O	1:D:326:VAL:HG22	1.50	1.11
1:D:388:ILE:O	1:D:391:ILE:HG22	1.50	1.11
1:A:118:PRO:HG3	1:B:366:GLN:HA	1.13	1.11
1:B:6:ILE:CG2	1:B:34:HIS:HB2	1.79	1.11
1:A:413:THR:HG22	1:A:416:ASP:CB	1.80	1.11
1:A:437:SER:HA	1:A:440:LYS:CB	1.79	1.11
1:C:418:LEU:HD12	1:C:421:GLN:OE1	1.47	1.11
1:D:159:PRO:HA	1:D:162:GLU:HG3	1.33	1.10
1:C:125:ILE:HG23	1:C:127:THR:HG22	1.29	1.10
1:D:442:ALA:O	1:D:447:VAL:HG13	1.48	1.10
1:D:465:MET:HG3	1:D:466:VAL:N	1.52	1.10
1:B:38:LEU:CD2	1:B:39:GLU:O	1.99	1.10
1:C:74:PRO:HG3	1:C:234:ALA:HB2	1.26	1.10
1:D:16:GLU:OE1	1:D:18:GLN:N	1.85	1.10
1:B:184:LEU:HB3	1:B:186:GLN:HE22	1.13	1.10
1:A:76:VAL:CG1	1:A:124:PHE:HE1	1.64	1.10
1:D:278:TYR:C	1:D:326:VAL:CG2	2.25	1.10
1:D:293:ASP:HB2	1:D:299:ARG:NH1	1.65	1.10
1:B:62:GLU:CG	1:B:65:ARG:HH21	1.64	1.09
1:C:378:ARG:HH11	1:C:408:GLN:HB2	0.94	1.09
1:A:40:GLU:CB	1:A:43:ALA:HB2	1.81	1.09
1:A:118:PRO:CG	1:B:366:GLN:HA	1.82	1.09
1:A:184:LEU:CD2	2:A:900:GDP:HN22	1.62	1.09
1:B:4:VAL:CG2	1:B:5:ARG:H	1.62	1.09
1:B:379:ALA:CB	1:B:384:SER:OG	2.01	1.09
1:B:405:LEU:CD1	1:B:406:LEU:HG	1.82	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:TYR:HE2	1:A:223:VAL:HG21	1.12	1.09
1:B:379:ALA:HB1	1:B:384:SER:OG	1.51	1.09
1:C:71:ARG:HG2	1:C:240:ARG:HG2	1.15	1.09
1:C:90:LEU:CD2	1:C:113:PHE:CE1	2.35	1.09
1:C:427:ILE:HB	1:C:449:LEU:CG	1.81	1.09
1:D:99:ALA:HB3	1:B:99:ALA:CA	1.82	1.09
1:D:468:GLY:O	1:D:469:GLN:C	1.93	1.09
1:C:470:ARG:O	1:C:472:PRO:HD3	1.52	1.08
1:A:80:GLY:O	1:A:86:LYS:NZ	1.86	1.08
1:A:141:ALA:HB3	1:A:250:VAL:HG21	1.13	1.08
1:B:262:ILE:HG21	1:B:316:LEU:HD23	1.17	1.08
1:C:66:ARG:O	1:C:69:LEU:CB	1.99	1.08
1:C:353:ARG:HB3	1:C:357:THR:CG2	1.81	1.08
1:A:76:VAL:CG1	1:A:124:PHE:CE1	2.34	1.08
1:B:380:ASP:CA	1:B:409:VAL:HG12	1.83	1.08
1:C:126:ASP:O	1:C:128:PRO:HD3	1.52	1.08
1:A:378:ARG:HH22	1:A:416:ASP:CG	1.60	1.08
1:D:99:ALA:CB	1:B:99:ALA:C	2.27	1.08
1:D:452:PHE:CZ	1:D:458:LEU:HD13	1.88	1.08
1:B:405:LEU:CD1	1:B:406:LEU:HD11	1.80	1.08
1:A:72:ARG:HD3	1:A:241:ALA:HB2	1.10	1.08
1:A:198:GLU:OE2	1:B:256:LEU:CD2	1.99	1.08
1:D:247:PRO:HG2	1:D:325:TRP:CD1	1.86	1.08
1:D:278:TYR:O	1:D:326:VAL:CG2	2.00	1.08
1:D:345:ALA:HA	1:D:348:GLU:HB2	1.25	1.08
1:C:255:LYS:HE2	1:C:263:ILE:CD1	1.74	1.07
1:C:287:ARG:O	1:C:312:GLY:HA3	1.51	1.07
1:D:341:GLU:OE1	1:D:344:LYS:NZ	1.88	1.07
1:B:380:ASP:HA	1:B:409:VAL:HG12	1.14	1.07
1:B:405:LEU:HD11	1:B:406:LEU:HD11	1.12	1.07
1:B:411:ALA:HB3	1:B:434:PRO:HB2	1.34	1.07
1:A:72:ARG:HD3	1:A:241:ALA:CB	1.85	1.07
1:A:92:TYR:HE1	1:B:356:ARG:O	1.34	1.07
1:A:413:THR:HG23	1:A:416:ASP:H	0.90	1.07
1:A:376:ILE:HD11	1:A:427:ILE:CG1	1.85	1.06
1:D:434:PRO:HB3	1:D:449:LEU:HD21	1.34	1.06
1:C:353:ARG:HB3	1:C:357:THR:HG21	1.10	1.06
1:A:326:VAL:HG13	1:A:327:PRO:HD2	1.35	1.06
1:D:10:ALA:HB2	1:D:20:LEU:HD22	1.12	1.06
1:D:452:PHE:CZ	1:D:458:LEU:CD1	2.38	1.06
1:B:4:VAL:HG22	1:B:5:ARG:N	1.63	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:413:THR:HG21	1:D:415:SER:OG	1.53	1.06
1:C:59:LYS:CA	1:C:62:GLU:HB2	1.85	1.06
1:B:442:ALA:O	1:B:447:VAL:CG2	2.03	1.06
1:B:258:LYS:HG3	1:B:259:GLN:HG2	1.33	1.06
1:C:66:ARG:HA	1:C:69:LEU:HG	1.30	1.06
1:C:90:LEU:CD2	1:C:113:PHE:CZ	2.38	1.06
1:A:61:ALA:O	1:A:64:GLU:N	1.89	1.05
1:D:293:ASP:CG	1:D:299:ARG:NH1	2.11	1.05
1:D:293:ASP:CB	1:D:299:ARG:HH12	1.69	1.05
1:A:86:LYS:HG2	2:A:900:GDP:PB	1.95	1.05
1:A:188:ASP:OD1	1:A:191:LYS:N	1.88	1.05
1:A:72:ARG:HH11	1:A:240:ARG:C	1.64	1.05
1:D:413:THR:CG2	1:D:415:SER:OG	2.05	1.05
1:D:69:LEU:HD13	1:D:242:ASP:HB2	1.31	1.05
1:B:405:LEU:CD1	1:B:406:LEU:CG	2.34	1.05
1:C:90:LEU:HD23	1:C:113:PHE:CZ	1.90	1.05
1:A:92:TYR:CE1	1:B:356:ARG:O	2.09	1.04
1:D:385:LEU:HD13	1:D:407:ALA:HB1	1.37	1.04
1:D:385:LEU:O	1:D:388:ILE:HG22	1.54	1.04
1:B:262:ILE:HG21	1:B:316:LEU:HD21	1.05	1.04
1:C:95:LYS:HA	1:C:98:ILE:CG2	1.85	1.04
1:C:155:ASP:O	1:C:158:MET:HE2	1.55	1.04
1:C:170:ALA:HA	1:C:455:ILE:HB	1.29	1.04
1:B:59:LYS:O	1:B:62:GLU:N	1.87	1.04
1:C:71:ARG:HG2	1:C:240:ARG:HG3	1.29	1.04
1:A:87:THR:HB	2:A:900:GDP:O2A	1.55	1.04
1:D:388:ILE:HG23	1:D:389:GLN:N	1.72	1.04
1:C:179:ILE:O	1:C:179:ILE:HG22	1.54	1.04
1:B:4:VAL:HG22	1:B:5:ARG:H	0.89	1.04
1:A:416:ASP:HA	1:A:419:LEU:HB2	1.34	1.04
1:D:110:VAL:HG11	1:D:307:ALA:O	1.58	1.04
1:D:276:GLY:HA2	1:D:287:ARG:HE	1.21	1.04
1:B:12:GLU:OE2	1:B:13:LEU:HD11	1.57	1.04
1:B:38:LEU:HD13	1:B:42:ASP:HB2	1.39	1.04
1:B:44:GLU:OE2	1:B:47:ARG:NH2	1.91	1.04
1:C:50:VAL:HG13	1:C:54:ARG:HE	1.20	1.04
1:A:45:ALA:O	1:A:49:LEU:HD13	1.57	1.03
1:B:290:ALA:CB	1:B:311:LEU:HD12	1.87	1.03
1:C:53:GLN:O	1:C:56:LEU:HG	1.57	1.03
1:D:293:ASP:CB	1:D:299:ARG:NH1	2.21	1.03
1:D:454:ILE:O	1:D:457:ASP:OD1	1.77	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:345:ALA:HA	1:D:348:GLU:HB3	1.41	1.03
1:D:461:GLU:OE1	1:D:464:ASN:CB	2.07	1.03
1:C:95:LYS:HG2	1:C:98:ILE:HG12	1.35	1.03
1:A:92:TYR:OH	1:B:361:LEU:HD23	1.59	1.02
1:A:413:THR:CG2	1:A:416:ASP:OD1	2.06	1.02
1:B:263:ILE:HG22	1:B:311:LEU:HD21	1.38	1.02
1:B:357:THR:CB	1:B:360:GLU:HG3	1.89	1.02
1:B:462:VAL:O	1:B:465:MET:CB	2.06	1.02
1:D:409:VAL:O	1:D:409:VAL:HG12	1.59	1.02
1:D:69:LEU:HD13	1:D:242:ASP:CB	1.88	1.02
1:D:99:ALA:CB	1:B:99:ALA:CA	2.36	1.02
1:B:380:ASP:OD1	1:B:381:THR:HG23	1.59	1.02
1:C:4:VAL:CG1	1:C:8:GLN:CG	2.29	1.02
1:A:46:VAL:CG1	1:A:50:VAL:HG23	1.88	1.02
1:B:463:ARG:C	1:B:465:MET:H	1.59	1.02
1:A:376:ILE:CD1	1:A:427:ILE:HG12	1.89	1.02
1:C:95:LYS:HE2	1:C:98:ILE:CB	1.90	1.02
1:C:116:LYS:CE	1:C:121:THR:HG23	1.87	1.02
1:A:350:GLU:OE2	1:A:354:ARG:CB	2.08	1.01
1:B:256:LEU:HD12	1:B:262:ILE:HG12	1.42	1.01
1:A:72:ARG:NH1	1:A:240:ARG:O	1.93	1.01
1:A:153:ALA:HB1	1:A:187:ALA:HB1	1.43	1.01
1:D:69:LEU:HD11	1:D:242:ASP:HB2	1.42	1.01
1:B:353:ARG:HG2	1:B:355:PRO:HD3	1.37	1.01
1:C:427:ILE:HD12	1:C:449:LEU:HD12	1.03	1.01
1:D:94:ARG:HG2	1:D:113:PHE:CZ	1.95	1.01
1:D:98:ILE:CG2	1:D:99:ALA:H	1.72	1.01
1:D:427:ILE:C	1:D:449:LEU:HD12	1.85	1.01
1:B:247:PRO:HG3	1:B:272:THR:O	1.58	1.01
1:B:286:GLY:CA	1:B:314:GLN:CD	2.24	1.01
1:C:95:LYS:CA	1:C:98:ILE:CG2	2.38	1.01
1:B:455:ILE:HD11	1:B:456:TYR:CD1	1.94	1.01
1:A:72:ARG:CD	1:A:241:ALA:HB2	1.90	1.00
1:A:278:TYR:CD2	1:A:328:ASP:HA	1.96	1.00
1:D:108:GLN:CD	1:D:292:MET:CE	2.34	1.00
1:D:205:GLU:HG3	1:D:206:TYR:CD1	1.95	1.00
1:D:421:GLN:HG3	1:D:445:LYS:CB	1.91	1.00
1:A:437:SER:O	1:A:441:LYS:N	1.93	1.00
1:D:247:PRO:CG	1:D:325:TRP:CD1	2.43	1.00
1:B:4:VAL:CG2	1:B:8:GLN:OE1	2.09	1.00
1:C:90:LEU:HD23	1:C:113:PHE:HZ	1.16	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:434:PRO:HB3	1:D:449:LEU:CD2	1.90	1.00
1:B:263:ILE:HG22	1:B:311:LEU:CD2	1.92	1.00
1:C:421:GLN:N	1:C:445:LYS:NZ	2.08	1.00
1:B:328:ASP:OD1	1:B:331:ALA:N	1.94	1.00
1:A:227:LEU:HD11	1:B:358:MET:HE1	1.02	1.00
1:D:465:MET:CG	1:D:466:VAL:H	1.73	1.00
1:B:79:MET:HE1	1:B:164:ALA:HA	1.44	1.00
1:B:393:ALA:CB	1:B:398:GLU:N	2.24	1.00
1:C:69:LEU:O	1:C:240:ARG:CD	2.09	1.00
1:A:76:VAL:HB	1:A:124:PHE:CD1	1.97	0.99
1:B:6:ILE:CB	1:B:34:HIS:O	2.10	0.99
1:B:427:ILE:CG1	1:B:449:LEU:CD2	2.40	0.99
1:C:277:ASP:HB2	1:C:288:ILE:HD12	1.39	0.99
1:A:61:ALA:O	1:A:64:GLU:CA	2.09	0.99
1:B:6:ILE:HB	1:B:34:HIS:C	1.87	0.99
1:C:415:SER:O	1:C:419:LEU:HG	1.63	0.99
1:B:380:ASP:CA	1:B:409:VAL:CG1	2.40	0.99
1:B:442:ALA:O	1:B:447:VAL:HG22	1.58	0.99
1:C:59:LYS:HA	1:C:62:GLU:HB2	1.03	0.99
1:A:442:ALA:HB1	1:A:449:LEU:HD22	1.41	0.99
1:B:417:VAL:O	1:B:420:ALA:N	1.95	0.99
1:C:116:LYS:HE2	1:C:121:THR:HG23	1.02	0.99
1:A:118:PRO:HG3	1:B:366:GLN:CA	1.93	0.98
1:D:69:LEU:HD13	1:D:242:ASP:CA	1.93	0.98
1:A:378:ARG:NH1	1:A:416:ASP:OD2	1.96	0.98
1:D:452:PHE:CG	1:D:458:LEU:HD13	1.97	0.98
1:B:38:LEU:HD23	1:B:39:GLU:H	1.24	0.98
1:D:205:GLU:C	1:D:206:TYR:HD1	1.71	0.98
1:D:179:ILE:HD11	1:D:212:VAL:HG13	1.41	0.98
1:C:155:ASP:HB3	1:C:158:MET:HE3	1.44	0.98
1:C:427:ILE:HB	1:C:449:LEU:HG	1.44	0.98
1:A:416:ASP:OD1	1:A:419:LEU:HD12	1.64	0.98
1:A:350:GLU:OE2	1:A:354:ARG:N	1.96	0.98
1:D:122:VAL:HB	1:D:124:PHE:HE1	1.21	0.98
1:D:94:ARG:NH1	1:D:126:ASP:OD1	1.98	0.97
1:B:81:HIS:ND1	1:B:160:GLN:OE1	1.98	0.97
1:B:184:LEU:HB3	1:B:186:GLN:NE2	1.79	0.97
1:C:427:ILE:CD1	1:C:449:LEU:HD12	1.89	0.97
1:A:46:VAL:HG12	1:A:50:VAL:HG21	1.44	0.97
1:A:92:TYR:CE2	1:A:223:VAL:HG21	1.97	0.97
1:B:427:ILE:HG12	1:B:449:LEU:HD21	1.46	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:71:ARG:CG	1:C:240:ARG:HG2	1.93	0.97
1:D:372:GLU:HG2	1:D:404:ILE:HD13	1.44	0.97
1:B:403:ASN:C	1:B:404:ILE:HG12	1.86	0.97
1:A:227:LEU:CD1	1:B:358:MET:HE1	1.94	0.97
1:C:427:ILE:CD1	1:C:449:LEU:HD11	1.92	0.97
1:D:374:ASN:HA	1:D:404:ILE:CB	1.95	0.96
1:B:443:GLU:CA	1:B:447:VAL:CG2	2.30	0.96
1:B:33:SER:O	1:B:36:SER:N	1.97	0.96
1:D:465:MET:HG3	1:D:466:VAL:H	0.81	0.96
1:C:348:GLU:O	1:C:352:ALA:HB2	1.64	0.96
1:B:357:THR:CB	1:B:360:GLU:CG	2.42	0.96
1:C:291:MET:HA	1:C:309:GLN:O	1.65	0.96
1:B:380:ASP:HA	1:B:409:VAL:CG1	1.95	0.96
1:B:427:ILE:CD1	1:B:449:LEU:CD2	2.43	0.96
1:A:46:VAL:HG12	1:A:50:VAL:HG23	1.45	0.96
1:B:133:PHE:O	1:B:139:ARG:HD3	1.66	0.96
1:A:352:ALA:O	1:A:355:PRO:CD	2.13	0.96
1:B:191:LYS:O	1:B:195:GLN:HG3	1.64	0.96
1:A:76:VAL:HG11	1:A:124:PHE:HE1	0.80	0.95
1:A:206:TYR:HE2	1:B:316:LEU:HD13	1.30	0.95
1:D:69:LEU:CD1	1:D:242:ASP:CB	2.42	0.95
1:C:255:LYS:HE2	1:C:263:ILE:HD12	1.48	0.95
1:A:413:THR:CG2	1:A:416:ASP:CB	2.41	0.95
1:B:5:ARG:HG2	1:B:35:ALA:O	1.65	0.95
1:B:443:GLU:CA	1:B:447:VAL:HG21	1.64	0.95
1:C:359:ALA:HA	1:C:362:LEU:HA	1.48	0.95
1:D:122:VAL:CB	1:D:124:PHE:CE1	2.49	0.95
1:B:303:GLY:O	1:B:306:SER:HB2	1.66	0.95
1:B:376:ILE:O	1:B:427:ILE:HA	1.66	0.95
1:C:5:ARG:CB	1:C:35:ALA:O	2.14	0.95
1:A:86:LYS:CG	2:A:900:GDP:O2B	2.15	0.95
1:A:314:GLN:O	1:A:315:GLU:HG3	1.66	0.95
1:B:79:MET:HE2	1:B:164:ALA:CB	1.97	0.95
1:B:264:ALA:CB	1:B:313:PHE:CE2	2.49	0.95
1:C:359:ALA:O	1:C:362:LEU:N	2.00	0.95
1:C:378:ARG:NH2	1:C:416:ASP:OD2	1.98	0.95
1:A:96:SER:O	1:A:97:ARG:C	2.05	0.94
1:C:95:LYS:HA	1:C:98:ILE:HG23	0.96	0.94
1:A:97:ARG:CG	1:A:100:GLU:CB	2.43	0.94
1:D:374:ASN:CG	1:D:404:ILE:HG22	1.91	0.94
1:A:233:LEU:O	1:A:237:GLU:OE1	1.84	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:ALA:O	1:A:15:MET:O	1.85	0.94
1:A:157:ILE:CD1	1:A:199:ARG:NH1	1.72	0.94
1:D:442:ALA:C	1:D:447:VAL:CG1	2.39	0.94
1:B:62:GLU:CG	1:B:65:ARG:NH2	2.30	0.94
1:B:419:LEU:O	1:B:422:THR:HG22	0.76	0.94
1:A:69:LEU:O	1:A:240:ARG:HD3	1.68	0.94
1:B:81:HIS:HD1	1:B:160:GLN:CD	1.76	0.94
1:A:418:LEU:HD21	1:C:408:GLN:NE2	1.81	0.94
1:A:420:ALA:HA	1:A:423:ALA:HB3	1.49	0.94
1:D:42:ASP:O	1:D:46:VAL:HG23	1.67	0.94
1:A:399:ASP:OD1	1:A:400:VAL:HG23	1.66	0.93
1:A:50:VAL:O	1:A:54:ARG:HG2	1.69	0.93
1:C:223:VAL:O	1:C:227:LEU:HD23	1.67	0.93
1:B:12:GLU:CD	1:B:13:LEU:CD1	2.42	0.93
1:B:357:THR:CB	1:B:360:GLU:CD	2.41	0.93
1:C:427:ILE:HB	1:C:449:LEU:HD11	1.47	0.93
1:D:427:ILE:O	1:D:449:LEU:HA	1.69	0.93
1:C:255:LYS:CE	1:C:263:ILE:HD12	1.99	0.93
1:C:359:ALA:HA	1:C:362:LEU:CA	1.98	0.93
1:A:340:LYS:O	1:A:343:ARG:HG2	1.69	0.93
1:C:71:ARG:CG	1:C:240:ARG:CG	2.46	0.93
1:D:10:ALA:HB2	1:D:20:LEU:CD2	1.99	0.92
1:D:442:ALA:HB1	1:D:447:VAL:HG12	1.49	0.92
1:B:7:TYR:HB3	1:B:34:HIS:CE1	2.03	0.92
1:B:286:GLY:CA	1:B:314:GLN:NE2	2.30	0.92
1:C:421:GLN:CG	1:C:445:LYS:HZ2	1.82	0.92
1:B:411:ALA:HB3	1:B:434:PRO:CB	2.00	0.92
1:B:62:GLU:HG3	1:B:65:ARG:NH2	1.84	0.92
1:B:411:ALA:CA	1:B:434:PRO:HG2	2.00	0.92
1:C:116:LYS:CE	1:C:121:THR:CG2	2.45	0.92
1:A:191:LYS:O	1:A:195:GLN:HG3	1.70	0.92
1:A:182:ILE:O	1:A:182:ILE:HG22	1.68	0.92
1:A:413:THR:HG21	1:A:416:ASP:OD1	1.68	0.92
1:A:350:GLU:OE2	1:A:354:ARG:CA	2.18	0.92
1:B:117:THR:HG23	1:B:119:GLN:CG	2.00	0.92
1:B:137:ARG:CD	1:B:319:PRO:O	2.16	0.92
1:B:272:THR:HG21	1:B:301:GLU:HB3	1.49	0.92
1:A:206:TYR:CE2	1:B:316:LEU:HD13	2.04	0.92
1:C:22:GLU:O	1:C:25:ASP:HB3	1.70	0.92
1:D:86:LYS:HG3	1:D:87:THR:N	1.83	0.92
1:B:69:LEU:HD22	1:B:70:PRO:HD2	1.49	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:372:GLU:CG	1:D:404:ILE:HD13	2.00	0.92
1:B:419:LEU:C	1:B:422:THR:HG22	1.95	0.92
1:C:5:ARG:HA	1:C:37:THR:HA	1.52	0.92
1:A:368:GLU:HA	3:A:1001:HOH:O	1.70	0.91
1:D:375:LEU:C	1:D:375:LEU:HD12	1.95	0.91
1:D:388:ILE:CG2	1:D:389:GLN:N	2.33	0.91
1:A:46:VAL:HG13	1:A:50:VAL:CG2	1.98	0.91
1:D:421:GLN:CD	1:D:445:LYS:HB2	1.94	0.91
1:B:463:ARG:HA	1:B:465:MET:HG2	1.51	0.91
1:C:90:LEU:CD2	1:C:113:PHE:HE1	1.84	0.91
1:C:418:LEU:CD1	1:C:421:GLN:OE1	2.19	0.91
1:D:16:GLU:CD	1:D:17:CYS:N	2.28	0.91
1:D:441:LYS:O	1:D:444:GLU:HB3	1.70	0.91
1:C:15:MET:HG3	1:C:54:ARG:NH2	1.86	0.91
1:D:122:VAL:HB	1:D:124:PHE:CZ	2.05	0.91
1:B:59:LYS:O	1:B:61:ALA:N	2.02	0.91
1:A:94:ARG:NH1	1:A:109:HIS:CE1	2.38	0.91
1:B:362:LEU:O	1:B:366:GLN:OE1	1.89	0.91
1:B:393:ALA:CB	1:B:396:SER:O	2.19	0.91
1:B:444:GLU:HB2	1:B:447:VAL:HB	1.51	0.91
1:A:350:GLU:OE1	1:A:354:ARG:CB	2.19	0.91
1:A:346:ARG:O	1:A:349:GLU:HB2	1.71	0.91
1:A:157:ILE:HD13	1:A:199:ARG:HH11	1.34	0.90
1:B:186:GLN:OE1	1:B:186:GLN:N	2.03	0.90
1:C:59:LYS:O	1:C:62:GLU:HB3	1.71	0.90
1:C:421:GLN:HA	1:C:445:LYS:HZ1	1.10	0.90
1:A:378:ARG:NH2	1:A:416:ASP:CG	2.22	0.90
1:D:278:TYR:C	1:D:326:VAL:HG23	1.94	0.90
1:A:94:ARG:NH1	1:A:126:ASP:OD2	2.04	0.90
1:A:350:GLU:CD	1:A:354:ARG:CB	2.44	0.90
1:D:247:PRO:HD2	1:D:325:TRP:CD1	2.06	0.90
1:B:411:ALA:CB	1:B:434:PRO:CB	2.48	0.90
1:C:79:MET:HG3	1:C:164:ALA:HB1	1.50	0.90
1:C:427:ILE:CB	1:C:449:LEU:HD11	2.02	0.90
1:A:25:ASP:OD1	1:A:31:TYR:CE2	2.20	0.90
1:C:94:ARG:C	1:C:96:SER:H	1.73	0.90
1:B:183:ASP:OD1	1:B:184:LEU:HD12	1.69	0.90
1:A:40:GLU:HA	1:A:43:ALA:HB2	0.91	0.90
1:A:373:LEU:O	1:A:403:ASN:N	2.05	0.90
1:C:155:ASP:HB3	1:C:158:MET:CE	2.01	0.90
1:C:203:PRO:HB3	1:C:205:GLU:OE1	1.71	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:327:PRO:HG2	1:A:328:ASP:H	1.36	0.90
1:D:338:GLU:HG3	1:D:339:ARG:N	1.84	0.90
1:D:374:ASN:ND2	1:D:404:ILE:CG2	2.35	0.90
1:C:119:GLN:HB3	1:C:231:LEU:HD23	1.52	0.90
1:B:274:ARG:O	1:B:288:ILE:HD12	1.72	0.89
1:B:190:GLU:O	1:B:194:ARG:HG3	1.70	0.89
1:C:5:ARG:O	1:C:8:GLN:HB2	1.72	0.89
1:B:6:ILE:HG22	1:B:34:HIS:HB2	1.54	0.89
1:D:293:ASP:OD1	1:D:294:ALA:N	2.05	0.89
1:C:4:VAL:HG12	1:C:8:GLN:HG3	0.90	0.89
1:A:310:VAL:HG12	1:A:313:PHE:CE2	2.08	0.89
1:A:371:LYS:CB	1:A:400:VAL:HG22	2.02	0.89
1:B:422:THR:HG23	1:B:423:ALA:N	1.87	0.89
1:C:353:ARG:O	1:C:357:THR:HG23	1.71	0.89
1:C:421:GLN:HA	1:C:445:LYS:CE	2.00	0.89
1:D:374:ASN:CA	1:D:404:ILE:CG2	2.43	0.89
1:A:99:ALA:O	1:A:100:GLU:C	2.14	0.89
1:B:12:GLU:CG	1:B:13:LEU:HD13	2.02	0.89
1:B:411:ALA:H	1:B:434:PRO:HG2	0.72	0.89
1:C:6:ILE:HG12	1:C:38:LEU:HD11	1.55	0.89
1:C:84:HIS:HD1	1:C:151:ILE:HA	1.38	0.89
1:A:460:ASP:HA	1:A:463:ARG:HE	1.38	0.89
1:D:111:GLY:HA2	1:D:127:THR:HG23	1.55	0.89
1:D:98:ILE:HG22	1:D:99:ALA:N	1.86	0.88
1:B:264:ALA:HB3	1:B:313:PHE:HE2	1.36	0.88
1:D:108:GLN:CD	1:D:292:MET:HE1	1.97	0.88
1:C:66:ARG:CA	1:C:69:LEU:HG	2.03	0.88
1:D:179:ILE:N	1:D:213:ILE:O	2.06	0.88
1:D:374:ASN:CB	1:D:404:ILE:HG22	2.03	0.88
1:D:442:ALA:C	1:D:447:VAL:HG13	1.96	0.88
1:B:38:LEU:CD2	1:B:39:GLU:CA	2.41	0.88
1:C:155:ASP:O	1:C:158:MET:CE	2.20	0.88
1:D:376:ILE:HG23	1:D:406:LEU:HB3	1.53	0.88
1:A:86:LYS:HG3	2:A:900:GDP:O2B	1.74	0.88
1:B:44:GLU:CD	1:B:47:ARG:NH2	2.31	0.88
1:D:278:TYR:CE1	1:D:329:LEU:HD23	2.08	0.88
1:C:236:LEU:O	1:C:236:LEU:HD23	1.74	0.88
1:A:27:MET:SD	1:A:29:VAL:HG23	2.14	0.88
1:C:84:HIS:ND1	1:C:151:ILE:HA	1.89	0.88
1:A:198:GLU:OE2	1:B:256:LEU:HB3	1.72	0.87
1:B:46:VAL:O	1:B:50:VAL:HG23	1.73	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:393:ALA:HB1	1:B:397:THR:C	1.98	0.87
1:C:203:PRO:HB3	1:C:205:GLU:CD	1.99	0.87
1:D:345:ALA:O	1:D:348:GLU:CA	2.22	0.87
1:B:79:MET:HE2	1:B:164:ALA:HA	0.89	0.87
1:C:91:ASP:OD1	1:C:94:ARG:NH2	2.07	0.87
1:A:352:ALA:HA	1:A:355:PRO:HG2	1.56	0.87
1:B:362:LEU:O	1:B:366:GLN:HB3	1.74	0.87
1:D:385:LEU:O	1:D:388:ILE:CG2	2.23	0.87
1:B:411:ALA:HB2	1:B:434:PRO:HB2	1.57	0.87
1:D:442:ALA:O	1:D:447:VAL:CG1	2.23	0.87
1:C:90:LEU:HD21	1:C:113:PHE:CE1	2.07	0.87
1:D:352:ALA:O	1:D:355:PRO:HG3	1.74	0.87
1:D:374:ASN:CG	1:D:404:ILE:CG2	2.48	0.87
1:D:163:GLU:OE1	1:C:236:LEU:HD12	1.74	0.86
1:B:237:GLU:O	1:B:238:ASP:OD1	1.93	0.86
1:B:411:ALA:CB	1:B:434:PRO:HG2	2.04	0.86
1:A:197:MET:SD	1:A:206:TYR:CZ	2.67	0.86
1:D:452:PHE:CE2	1:D:458:LEU:HD11	2.06	0.86
1:D:462:VAL:O	1:D:463:ARG:C	2.18	0.86
1:D:16:GLU:CD	1:D:17:CYS:H	1.84	0.86
1:B:5:ARG:HG3	1:B:37:THR:HG22	1.57	0.86
1:B:231:LEU:O	1:B:232:LEU:C	2.15	0.86
1:B:286:GLY:HA2	1:B:314:GLN:HE22	1.12	0.86
1:B:448:LEU:O	1:B:449:LEU:HG	1.76	0.86
1:C:95:LYS:NZ	1:C:98:ILE:HD13	1.89	0.86
1:A:413:THR:HG21	1:A:416:ASP:CG	2.01	0.86
1:A:437:SER:CA	1:A:440:LYS:CB	2.53	0.86
1:A:127:THR:HG23	1:A:128:PRO:CD	2.06	0.86
1:A:206:TYR:HE2	1:B:316:LEU:CD1	1.88	0.86
1:A:227:LEU:HD11	1:B:358:MET:CE	1.98	0.86
1:D:421:GLN:HG3	1:D:445:LYS:HB3	1.57	0.86
1:B:38:LEU:CD2	1:B:39:GLU:C	2.48	0.86
1:B:69:LEU:HD22	1:B:70:PRO:CD	2.04	0.86
1:A:361:LEU:CB	1:A:364:ALA:HA	2.06	0.86
1:D:288:ILE:HD13	1:D:291:MET:HE3	1.58	0.86
1:B:157:ILE:H	1:B:195:GLN:HE22	1.23	0.86
1:A:73:PRO:HG2	1:A:305:GLY:HA3	1.58	0.85
1:B:38:LEU:CD2	1:B:38:LEU:C	2.28	0.85
1:A:253:GLU:OE2	1:A:265:ASN:ND2	2.08	0.85
1:A:262:ILE:HG21	1:A:315:GLU:O	1.76	0.85
1:A:348:GLU:HA	1:A:351:LYS:CB	2.07	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:427:ILE:HG13	1:B:449:LEU:HD23	1.58	0.85
1:C:151:ILE:HG12	1:C:161:THR:HG21	1.59	0.85
1:A:70:PRO:O	1:A:240:ARG:HB3	1.76	0.85
1:C:116:LYS:CD	1:C:121:THR:HG22	2.06	0.85
1:D:205:GLU:HG3	1:D:206:TYR:HE1	1.35	0.85
1:B:79:MET:CE	1:B:164:ALA:CA	2.23	0.85
1:B:53:GLN:O	1:B:54:ARG:C	2.18	0.85
1:B:376:ILE:O	1:B:427:ILE:CA	2.24	0.85
1:B:442:ALA:C	1:B:447:VAL:CG2	2.50	0.85
1:D:233:LEU:O	1:D:237:GLU:HB2	1.75	0.85
1:A:141:ALA:CB	1:A:250:VAL:CG2	2.55	0.85
1:C:67:LYS:O	1:C:240:ARG:NH1	2.10	0.85
1:A:247:PRO:O	1:A:248:ARG:HG3	1.77	0.85
1:A:285:TYR:CD1	1:A:314:GLN:OE1	2.30	0.85
1:B:376:ILE:O	1:B:428:LEU:N	2.10	0.85
1:C:359:ALA:HA	1:C:362:LEU:CB	2.07	0.85
1:D:94:ARG:CZ	1:D:126:ASP:CG	2.50	0.84
1:C:391:ILE:O	1:C:395:GLU:HG2	1.77	0.84
1:D:285:TYR:HE2	1:D:333:LYS:HE2	1.42	0.84
1:D:98:ILE:CG2	1:D:99:ALA:N	2.35	0.84
1:D:455:ILE:O	1:D:459:VAL:HG12	1.76	0.84
1:B:6:ILE:HG21	1:B:34:HIS:HB2	1.57	0.84
1:C:95:LYS:HE2	1:C:98:ILE:CG2	2.06	0.84
1:C:188:ASP:CG	1:C:191:LYS:HB2	2.01	0.84
1:D:179:ILE:HD11	1:D:212:VAL:CG1	2.06	0.84
1:B:376:ILE:CG2	1:B:427:ILE:HG22	2.07	0.84
1:C:63:GLU:O	1:C:67:LYS:HG3	1.77	0.84
1:A:455:ILE:O	1:A:458:LEU:HB3	1.76	0.84
1:D:278:TYR:C	1:D:326:VAL:HG22	1.96	0.84
1:A:201:PHE:CZ	1:A:383:GLY:O	2.31	0.84
1:B:155:ASP:O	1:B:158:MET:HE3	1.77	0.84
1:C:59:LYS:CA	1:C:62:GLU:CB	2.48	0.84
1:A:422:THR:HB	1:C:406:LEU:HD22	1.60	0.84
1:A:76:VAL:CB	1:A:124:PHE:CE1	2.61	0.84
1:C:79:MET:CG	1:C:164:ALA:HB1	2.06	0.84
1:D:108:GLN:NE2	1:D:292:MET:CE	2.38	0.84
1:B:262:ILE:HG23	1:B:316:LEU:HD21	1.60	0.84
1:C:186:GLN:HG2	1:C:186:GLN:O	1.78	0.84
1:A:157:ILE:HD13	1:A:199:ARG:CZ	2.04	0.84
1:D:421:GLN:HG2	1:D:445:LYS:HB2	0.85	0.84
1:B:12:GLU:HG2	1:B:13:LEU:HD13	1.60	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:251:ILE:HG22	1:C:319:PRO:HA	1.60	0.84
1:A:143:VAL:HG22	1:A:250:VAL:HG11	1.59	0.83
1:A:442:ALA:O	1:A:447:VAL:HG22	1.76	0.83
1:D:94:ARG:HG2	1:D:113:PHE:CE2	2.11	0.83
1:B:463:ARG:C	1:B:465:MET:N	2.27	0.83
1:A:127:THR:CG2	1:A:128:PRO:CD	2.56	0.83
1:D:375:LEU:HD12	1:D:376:ILE:N	1.93	0.83
1:B:345:ALA:O	1:B:349:GLU:HG3	1.78	0.83
1:D:421:GLN:HG2	1:D:445:LYS:CG	2.07	0.83
1:B:278:TYR:CE1	1:B:329:LEU:HD23	2.13	0.83
1:B:343:ARG:NH1	1:B:347:GLU:OE2	2.10	0.83
1:B:427:ILE:CG1	1:B:449:LEU:HD23	2.08	0.83
1:C:427:ILE:CB	1:C:449:LEU:CD1	2.56	0.83
1:A:354:ARG:O	1:A:358:MET:HB2	1.78	0.83
1:B:62:GLU:HG2	1:B:65:ARG:HH21	1.43	0.83
1:B:393:ALA:HB1	1:B:396:SER:O	1.76	0.83
1:C:116:LYS:CG	1:C:121:THR:HG22	2.08	0.83
1:D:94:ARG:CZ	1:D:126:ASP:OD2	2.26	0.83
1:B:380:ASP:C	1:B:409:VAL:CG1	2.51	0.83
1:C:203:PRO:CB	1:C:205:GLU:CD	2.52	0.83
1:D:78:ILE:HD12	1:D:90:LEU:HG	1.61	0.83
1:B:38:LEU:CD1	1:B:42:ASP:HB2	2.09	0.83
1:C:188:ASP:OD2	1:C:191:LYS:HB2	1.77	0.83
1:A:72:ARG:NH1	1:A:240:ARG:C	2.32	0.83
1:D:345:ALA:CA	1:D:348:GLU:CB	2.53	0.83
1:A:92:TYR:HE2	1:A:223:VAL:CG2	1.92	0.83
1:D:374:ASN:N	1:D:404:ILE:HG22	1.93	0.83
1:A:190:GLU:HG3	1:A:194:ARG:HE	1.43	0.82
1:D:247:PRO:CD	1:D:325:TRP:CD1	2.62	0.82
1:D:345:ALA:CA	1:D:348:GLU:HB3	2.09	0.82
1:C:170:ALA:O	1:C:454:ILE:HG22	1.76	0.82
1:A:82:VAL:O	1:A:83:ASP:OD1	1.97	0.82
1:A:278:TYR:CE2	1:A:328:ASP:HA	2.13	0.82
1:D:461:GLU:OE1	1:D:464:ASN:HB2	1.76	0.82
1:D:366:GLN:C	1:D:368:GLU:H	1.84	0.82
1:B:354:ARG:N	1:B:355:PRO:HD3	1.94	0.82
1:C:4:VAL:HG12	1:C:8:GLN:CB	2.08	0.82
1:C:47:ARG:O	1:C:47:ARG:HD2	1.78	0.82
1:C:95:LYS:CE	1:C:98:ILE:HB	2.10	0.82
1:A:40:GLU:HA	1:A:43:ALA:CA	2.05	0.82
1:A:127:THR:HG23	1:A:128:PRO:HD2	1.62	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:ARG:O	1:A:349:GLU:N	2.12	0.82
1:D:411:ALA:HA	1:D:432:VAL:HG11	1.60	0.82
1:C:80:GLY:N	1:C:86:LYS:HD3	1.94	0.82
1:D:318:HIS:O	1:D:321:ASP:CG	2.22	0.82
1:C:79:MET:SD	1:C:164:ALA:HB1	2.18	0.82
1:A:173:ALA:O	1:A:175:LEU:CD1	2.27	0.82
1:D:23:LEU:O	1:D:26:GLN:HG2	1.79	0.82
1:D:385:LEU:HB3	1:D:389:GLN:NE2	1.95	0.82
1:B:38:LEU:CG	1:B:39:GLU:N	2.43	0.82
1:C:353:ARG:CB	1:C:357:THR:HG21	2.04	0.82
1:B:264:ALA:HB3	1:B:313:PHE:CZ	2.15	0.82
1:A:5:ARG:HG3	1:A:5:ARG:O	1.79	0.82
1:A:375:LEU:HD11	1:A:404:ILE:HD13	1.62	0.82
1:D:108:GLN:HE22	1:D:292:MET:HE1	1.43	0.82
1:D:452:PHE:CG	1:D:458:LEU:HB2	2.14	0.82
1:A:354:ARG:O	1:A:358:MET:CB	2.27	0.81
1:D:375:LEU:N	1:D:404:ILE:O	2.10	0.81
1:B:38:LEU:HD13	1:B:42:ASP:CB	2.09	0.81
1:D:69:LEU:HD13	1:D:242:ASP:HA	1.61	0.81
1:D:461:GLU:O	1:D:464:ASN:CB	2.28	0.81
1:B:411:ALA:H	1:B:434:PRO:CD	1.94	0.81
1:C:109:HIS:CD2	1:C:109:HIS:N	2.43	0.81
1:C:353:ARG:O	1:C:357:THR:N	2.13	0.81
1:A:413:THR:O	1:A:416:ASP:HB2	1.79	0.81
1:B:369:GLY:O	1:B:371:LYS:N	2.12	0.81
1:A:169:LYS:O	1:A:455:ILE:HD12	1.80	0.81
1:A:346:ARG:O	1:A:349:GLU:CB	2.28	0.81
1:A:149:ILE:HG21	1:A:165:ILE:HD11	1.61	0.81
1:A:181:LYS:CD	2:A:900:GDP:C4	2.64	0.81
1:D:157:ILE:HG21	1:D:199:ARG:CZ	2.11	0.81
1:B:158:MET:HB3	1:B:159:PRO:HD2	1.62	0.81
1:C:74:PRO:CG	1:C:234:ALA:HB2	2.09	0.81
1:A:416:ASP:OD1	1:A:419:LEU:CD1	2.28	0.81
1:A:278:TYR:HD2	1:A:328:ASP:HA	1.45	0.81
1:B:286:GLY:HA2	1:B:314:GLN:OE1	1.49	0.81
1:A:184:LEU:CD2	2:A:900:GDP:HN21	1.92	0.81
1:B:122:VAL:CG2	1:B:231:LEU:HD21	2.11	0.81
1:A:81:HIS:ND1	1:A:160:GLN:HB2	1.97	0.80
1:D:75:VAL:N	1:D:145:ASP:OD2	2.13	0.80
1:B:38:LEU:HD23	1:B:39:GLU:C	2.06	0.80
1:B:354:ARG:O	1:B:356:ARG:N	2.14	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:353:ARG:O	1:C:356:ARG:HB2	1.82	0.80
1:C:421:GLN:CG	1:C:445:LYS:NZ	2.42	0.80
1:D:99:ALA:HB1	1:B:99:ALA:C	2.04	0.80
1:D:288:ILE:HG21	1:D:291:MET:HE3	1.63	0.80
1:B:272:THR:CG2	1:B:302:ALA:O	2.26	0.80
1:C:404:ILE:HG22	1:C:405:LEU:O	1.81	0.80
1:C:378:ARG:HH11	1:C:408:GLN:CB	1.86	0.80
1:A:27:MET:SD	1:A:29:VAL:CG2	2.70	0.80
1:A:157:ILE:HD12	1:A:195:GLN:HB3	1.63	0.80
1:D:97:ARG:NH1	1:D:295:ASP:OD1	2.10	0.80
1:D:146:ILE:HG12	1:D:174:LYS:HB3	1.63	0.80
1:D:262:ILE:HG23	1:D:316:LEU:CD2	2.12	0.80
1:B:278:TYR:CD1	1:B:329:LEU:HB3	2.16	0.80
1:B:12:GLU:OE2	1:B:13:LEU:CD1	2.29	0.80
1:D:262:ILE:HG23	1:D:316:LEU:HD23	1.63	0.79
1:C:116:LYS:HG2	1:C:121:THR:HG22	1.64	0.79
1:A:140:GLY:HA2	1:A:320:GLY:HA3	1.64	0.79
1:B:122:VAL:HG23	1:B:231:LEU:HD21	1.64	0.79
1:C:155:ASP:C	1:C:158:MET:HE2	2.07	0.79
1:A:127:THR:CG2	1:A:128:PRO:HD2	2.12	0.79
1:B:20:LEU:HD12	1:B:20:LEU:O	1.83	0.79
1:B:443:GLU:N	1:B:447:VAL:HG21	1.96	0.79
1:C:470:ARG:O	1:C:472:PRO:CD	2.29	0.79
1:D:388:ILE:CG2	1:D:389:GLN:H	1.94	0.79
1:B:411:ALA:CB	1:B:434:PRO:CG	2.61	0.79
1:A:374:ASN:O	1:A:425:ALA:HA	1.81	0.79
1:C:116:LYS:CD	1:C:121:THR:CG2	2.61	0.79
1:A:92:TYR:CE2	1:A:223:VAL:HG11	2.17	0.79
1:A:182:ILE:O	1:A:182:ILE:CG2	2.30	0.79
1:D:24:LEU:CB	1:D:29:VAL:HG11	2.10	0.79
1:D:99:ALA:HB1	1:B:99:ALA:CA	2.13	0.79
1:D:10:ALA:CB	1:D:20:LEU:HD22	2.06	0.79
1:D:98:ILE:HG23	1:D:99:ALA:H	1.47	0.79
1:C:15:MET:HG3	1:C:54:ARG:HH22	1.45	0.79
1:B:52:GLU:O	1:B:53:GLN:C	2.18	0.79
1:A:329:LEU:O	1:A:329:LEU:HD23	1.81	0.79
1:D:98:ILE:HG22	1:D:99:ALA:H	1.42	0.79
1:D:427:ILE:HB	1:D:449:LEU:HB2	1.64	0.79
1:D:461:GLU:OE1	1:D:464:ASN:HB3	1.81	0.79
1:B:393:ALA:HB2	1:B:398:GLU:CA	2.12	0.79
1:A:154:ASP:OD1	1:A:155:ASP:OD2	2.01	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:397:THR:HG22	1:A:397:THR:O	1.83	0.78
1:B:303:GLY:O	1:B:306:SER:CB	2.30	0.78
1:C:250:VAL:HG12	1:C:267:LEU:HB3	1.62	0.78
1:D:457:ASP:OD1	1:D:458:LEU:N	2.16	0.78
1:B:38:LEU:CD2	1:B:39:GLU:H	1.80	0.78
1:B:117:THR:HG21	1:B:119:GLN:HG3	1.61	0.78
1:B:380:ASP:H	1:B:409:VAL:HG13	1.46	0.78
1:A:61:ALA:C	1:A:64:GLU:H	1.92	0.78
1:D:81:HIS:HA	1:D:160:GLN:CB	2.13	0.78
1:B:5:ARG:HG3	1:B:5:ARG:HH11	1.48	0.78
1:B:7:TYR:CE2	1:B:8:GLN:HG3	2.18	0.78
1:C:188:ASP:HB3	1:C:191:LYS:HB3	1.64	0.78
1:A:86:LYS:HG2	2:A:900:GDP:O2B	1.77	0.78
1:C:188:ASP:HB3	1:C:191:LYS:CB	2.13	0.78
1:D:205:GLU:C	1:D:206:TYR:CD1	2.60	0.78
1:C:62:GLU:HB3	1:C:63:GLU:OE1	1.84	0.78
1:A:190:GLU:HG3	1:A:194:ARG:NE	1.98	0.78
1:B:176:ILE:HG21	1:B:226:LEU:HD11	1.65	0.78
1:B:403:ASN:O	1:B:404:ILE:HG12	1.82	0.78
1:C:374:ASN:OD1	1:C:403:ASN:HB3	1.84	0.78
1:A:343:ARG:HG3	1:A:344:LYS:N	1.99	0.78
1:C:82:VAL:O	1:C:83:ASP:HB2	1.83	0.78
1:C:182:ILE:HG22	1:C:216:SER:HB2	1.65	0.78
1:D:25:ASP:HA	1:D:29:VAL:HB	1.65	0.78
1:B:379:ALA:HB1	1:B:384:SER:HG	1.46	0.78
1:B:443:GLU:HA	1:B:447:VAL:CG2	2.14	0.78
1:C:95:LYS:CG	1:C:98:ILE:CG1	2.37	0.78
1:A:278:TYR:CD2	1:A:328:ASP:CA	2.67	0.77
1:A:83:ASP:HB3	2:A:900:GDP:C5'	2.14	0.77
1:A:153:ALA:CB	1:A:187:ALA:HB1	2.14	0.77
1:D:433:ASN:OD1	1:D:434:PRO:HD2	1.83	0.77
1:A:76:VAL:HB	1:A:124:PHE:CE1	2.20	0.77
1:D:122:VAL:CG1	1:D:124:PHE:CZ	2.67	0.77
1:D:373:LEU:HG	1:D:374:ASN:N	1.98	0.77
1:B:431:GLY:O	1:B:432:VAL:HG13	1.83	0.77
1:D:178:ALA:C	1:D:213:ILE:O	2.28	0.77
1:D:285:TYR:CE2	1:D:333:LYS:HE2	2.19	0.77
1:D:432:VAL:HG12	1:D:433:ASN:N	1.99	0.77
1:C:90:LEU:HD22	1:C:113:PHE:CE1	2.19	0.77
1:D:78:ILE:CD1	1:D:90:LEU:HG	2.13	0.77
1:B:69:LEU:CD2	1:B:70:PRO:HD3	2.15	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:255:LYS:HE2	1:B:263:ILE:HD11	1.67	0.77
1:A:385:LEU:O	1:A:385:LEU:HD13	1.85	0.77
1:C:185:PRO:HD2	1:C:186:GLN:OE1	1.85	0.77
1:C:287:ARG:O	1:C:312:GLY:CA	2.31	0.77
1:B:247:PRO:CG	1:B:272:THR:O	2.32	0.77
1:C:81:HIS:CA	1:C:84:HIS:CD2	2.68	0.77
1:C:94:ARG:C	1:C:96:SER:N	2.40	0.77
1:A:82:VAL:O	2:A:900:GDP:PB	2.42	0.77
1:A:460:ASP:CG	1:A:463:ARG:HH21	1.92	0.77
1:C:71:ARG:HA	1:C:240:ARG:CA	2.10	0.77
1:A:40:GLU:CB	1:A:43:ALA:CB	2.59	0.77
1:A:416:ASP:CA	1:A:419:LEU:HB2	2.13	0.77
1:D:23:LEU:HD12	1:D:24:LEU:N	2.00	0.77
1:B:363:ARG:CA	1:B:366:GLN:NE2	2.26	0.77
1:C:223:VAL:HG12	1:C:227:LEU:HD21	1.65	0.77
1:A:157:ILE:HD12	1:A:199:ARG:HH12	1.38	0.76
1:A:224:GLN:O	1:A:227:LEU:HB2	1.84	0.76
1:D:119:GLN:OE1	1:D:228:GLU:HG2	1.85	0.76
1:C:218:LYS:HG3	2:C:900:GDP:N1	2.00	0.76
1:D:108:GLN:CD	1:D:292:MET:HE3	2.08	0.76
1:B:6:ILE:HD12	1:B:36:SER:O	1.85	0.76
1:B:158:MET:HB3	1:B:159:PRO:CD	2.16	0.76
1:B:290:ALA:HB2	1:B:311:LEU:HD12	1.66	0.76
1:B:405:LEU:HD12	1:B:406:LEU:CD2	2.15	0.76
1:C:203:PRO:HB3	1:C:205:GLU:OE2	1.85	0.76
1:D:122:VAL:HG11	1:D:124:PHE:CZ	2.21	0.76
1:D:180:ASN:OD1	1:D:181:LYS:N	2.17	0.76
1:B:255:LYS:O	1:B:262:ILE:CG2	2.28	0.76
1:C:74:PRO:HB3	1:C:239:TYR:CE2	2.20	0.76
1:D:179:ILE:CD1	1:D:212:VAL:HG13	2.16	0.76
1:C:15:MET:CG	1:C:54:ARG:NH2	2.49	0.76
1:A:198:GLU:CD	1:B:256:LEU:HD23	2.09	0.76
1:A:201:PHE:CE1	1:A:383:GLY:O	2.39	0.76
1:D:276:GLY:CA	1:D:287:ARG:HE	1.97	0.76
1:B:286:GLY:CA	1:B:314:GLN:HE22	1.92	0.76
1:C:95:LYS:HZ3	1:C:98:ILE:HD13	1.50	0.76
1:D:310:VAL:CG1	1:D:313:PHE:HE1	1.99	0.76
1:D:413:THR:HG23	1:D:415:SER:OG	1.86	0.76
1:B:33:SER:O	1:B:36:SER:OG	2.03	0.76
1:B:433:ASN:O	1:B:435:PRO:CD	2.34	0.76
1:B:62:GLU:HG3	1:B:65:ARG:CZ	2.15	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:378:ARG:HB3	1:A:410:GLY:O	1.85	0.76
1:A:198:GLU:OE2	1:B:256:LEU:CB	2.34	0.75
1:D:412:PRO:HD2	1:D:435:PRO:HD3	1.68	0.75
1:B:405:LEU:CG	1:B:406:LEU:HG	2.15	0.75
1:B:448:LEU:C	1:B:449:LEU:HG	2.12	0.75
1:C:90:LEU:HD21	1:C:113:PHE:HE1	1.46	0.75
1:A:326:VAL:HG13	1:A:327:PRO:CD	2.15	0.75
1:D:452:PHE:CZ	1:D:458:LEU:HD12	2.21	0.75
1:C:81:HIS:O	1:C:84:HIS:CD2	2.39	0.75
1:C:466:VAL:C	1:C:468:GLY:N	2.21	0.75
1:A:184:LEU:HD21	2:A:900:GDP:HN22	0.69	0.75
1:A:247:PRO:HA	1:A:271:GLY:HA3	1.66	0.75
1:D:293:ASP:OD1	1:D:295:ASP:N	2.19	0.75
1:D:392:LEU:CD2	1:D:459:VAL:HG23	2.16	0.75
1:C:28:GLY:O	1:C:29:VAL:HG23	1.86	0.75
1:C:47:ARG:HD2	1:C:51:LYS:NZ	2.02	0.75
1:A:181:LYS:HD2	2:A:900:GDP:C4	2.22	0.75
1:D:439:LYS:O	1:D:442:ALA:HB3	1.86	0.75
1:B:278:TYR:HE1	1:B:329:LEU:HD23	1.47	0.75
1:C:125:ILE:HG23	1:C:127:THR:CG2	2.14	0.75
1:C:188:ASP:O	1:C:189:PRO:C	2.21	0.75
1:A:76:VAL:CG1	1:A:124:PHE:CD1	2.70	0.75
1:B:53:GLN:HE21	1:B:57:GLN:CB	2.00	0.75
1:D:122:VAL:CB	1:D:124:PHE:CZ	2.68	0.75
1:B:427:ILE:CG1	1:B:449:LEU:HD21	2.06	0.75
1:C:29:VAL:HG13	1:C:30:ALA:N	2.00	0.75
1:A:388:ILE:HD13	1:A:455:ILE:HG23	1.69	0.75
1:C:151:ILE:HG21	1:C:157:ILE:HG13	1.69	0.75
1:D:174:LYS:HE2	1:D:233:LEU:HD22	1.69	0.74
1:D:206:TYR:HD1	1:D:206:TYR:N	1.84	0.74
1:B:380:ASP:N	1:B:409:VAL:HG13	2.00	0.74
1:A:46:VAL:CG1	1:A:50:VAL:HG21	2.04	0.74
1:A:86:LYS:CG	2:A:900:GDP:PB	2.75	0.74
1:A:170:ALA:HA	1:A:455:ILE:HB	1.69	0.74
1:A:180:ASN:HD21	1:A:217:ALA:CB	2.00	0.74
1:D:361:LEU:HD22	1:C:224:GLN:HB2	1.67	0.74
1:B:13:LEU:HD21	1:B:47:ARG:HG2	1.66	0.74
1:B:379:ALA:CB	1:B:384:SER:HG	1.94	0.74
1:C:218:LYS:HG3	2:C:900:GDP:C2	2.22	0.74
1:A:442:ALA:CB	1:A:449:LEU:HD22	2.18	0.74
1:D:456:TYR:O	1:D:460:ASP:HB2	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:433:ASN:H	1:B:434:PRO:HD2	1.52	0.74
1:A:6:ILE:HB	1:A:34:HIS:O	1.86	0.74
1:A:40:GLU:HB2	1:A:43:ALA:CB	2.17	0.74
1:C:84:HIS:CE1	1:C:151:ILE:HA	2.22	0.74
1:C:377:LEU:HA	1:C:428:LEU:O	1.88	0.74
1:B:110:VAL:HG21	1:B:293:ASP:O	1.87	0.74
1:C:15:MET:CG	1:C:54:ARG:HH22	2.00	0.74
1:D:278:TYR:CD1	1:D:287:ARG:HB2	2.23	0.74
1:B:69:LEU:CD2	1:B:70:PRO:CD	2.66	0.74
1:C:70:PRO:O	1:C:240:ARG:HB3	1.87	0.74
1:D:86:LYS:HG3	1:D:87:THR:H	1.53	0.74
1:B:78:ILE:HG21	1:B:89:LEU:HD23	1.70	0.74
1:C:72:ARG:HG2	1:C:241:ALA:HB2	1.67	0.74
1:C:116:LYS:HG2	1:C:121:THR:CG2	2.17	0.74
1:C:378:ARG:HH21	1:C:416:ASP:CG	1.95	0.74
1:A:10:ALA:O	1:A:15:MET:HG3	1.86	0.74
1:A:77:VAL:HG23	1:A:125:ILE:HB	1.69	0.74
1:A:310:VAL:CG1	1:A:313:PHE:CE2	2.71	0.74
1:B:5:ARG:CG	1:B:35:ALA:O	2.36	0.74
1:B:393:ALA:HB3	1:B:396:SER:O	1.86	0.74
1:C:4:VAL:CG1	1:C:8:GLN:CB	2.66	0.74
1:A:441:LYS:O	1:A:445:LYS:CB	2.35	0.74
1:D:81:HIS:HA	1:D:160:GLN:HB3	1.70	0.74
1:B:247:PRO:HA	1:B:270:GLU:O	1.87	0.74
1:B:350:GLU:O	1:B:350:GLU:HG2	1.88	0.74
1:D:335:ILE:O	1:D:338:GLU:HG2	1.88	0.73
1:B:12:GLU:CD	1:B:13:LEU:HD11	2.09	0.73
1:B:204:GLU:HG2	1:B:208:GLY:O	1.88	0.73
1:B:346:ARG:O	1:B:349:GLU:HB2	1.88	0.73
1:B:411:ALA:HB2	1:B:434:PRO:CB	2.17	0.73
1:C:293:ASP:O	1:C:295:ASP:N	2.18	0.73
1:A:184:LEU:CG	2:A:900:GDP:N2	2.50	0.73
1:D:89:LEU:HD22	1:D:215:ILE:HD11	1.69	0.73
1:B:271:GLY:O	1:B:304:PRO:HD3	1.88	0.73
1:B:326:VAL:CG1	1:B:331:ALA:CB	2.66	0.73
1:C:293:ASP:OD2	1:C:295:ASP:HB2	1.89	0.73
1:D:178:ALA:HA	1:D:213:ILE:C	2.10	0.73
1:B:442:ALA:C	1:B:447:VAL:HG21	2.12	0.73
1:A:17:CYS:O	1:A:18:GLN:C	2.29	0.73
1:A:94:ARG:HH12	1:A:109:HIS:CE1	2.06	0.73
1:D:22:GLU:OE2	1:D:26:GLN:NE2	2.22	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:197:MET:HG2	1:B:203:PRO:HD2	1.70	0.73
1:B:211:ILE:HD13	1:B:229:MET:HE2	1.69	0.73
1:C:205:GLU:CD	1:C:205:GLU:H	1.96	0.73
1:A:180:ASN:HD21	1:A:217:ALA:HB2	1.53	0.73
1:A:179:ILE:O	1:A:215:ILE:O	2.06	0.73
1:B:286:GLY:HA3	1:B:314:GLN:OE1	1.87	0.73
1:C:378:ARG:CZ	1:C:416:ASP:OD2	2.36	0.73
1:A:76:VAL:CB	1:A:124:PHE:CD1	2.72	0.73
1:A:420:ALA:CA	1:A:423:ALA:HB3	2.17	0.73
1:D:127:THR:OG1	1:D:253:GLU:OE1	2.07	0.73
1:D:255:LYS:HA	1:C:197:MET:HE1	1.69	0.73
1:B:69:LEU:HD23	1:B:70:PRO:HD3	1.71	0.73
1:C:161:THR:O	1:C:165:ILE:HG13	1.88	0.73
1:D:278:TYR:O	1:D:326:VAL:HG23	1.80	0.73
1:D:278:TYR:CB	1:D:326:VAL:HG23	2.18	0.73
1:C:3:LYS:HA	1:C:38:LEU:O	1.88	0.73
1:B:422:THR:CG2	1:B:423:ALA:N	2.50	0.73
1:A:245:ALA:O	1:A:246:GLU:C	2.29	0.72
1:C:79:MET:HG3	1:C:164:ALA:CB	2.19	0.72
1:C:236:LEU:HD23	1:C:236:LEU:C	2.13	0.72
1:A:157:ILE:HG21	1:A:199:ARG:CZ	2.19	0.72
1:D:373:LEU:C	1:D:404:ILE:HG21	2.12	0.72
1:D:454:ILE:O	1:D:457:ASP:CG	2.32	0.72
1:B:131:GLU:CB	1:B:138:GLN:OE1	2.36	0.72
1:D:247:PRO:HG2	1:D:325:TRP:NE1	2.04	0.72
1:D:375:LEU:O	1:D:405:LEU:HA	1.89	0.72
1:A:373:LEU:CD2	1:A:465:MET:O	2.38	0.72
1:A:439:LYS:C	1:A:442:ALA:HB3	2.14	0.72
1:B:433:ASN:CB	1:B:434:PRO:HD3	2.18	0.72
1:C:108:GLN:C	1:C:109:HIS:CD2	2.67	0.72
1:A:39:GLU:C	1:A:42:ASP:HB2	2.07	0.72
1:B:5:ARG:HD3	1:B:35:ALA:O	1.89	0.72
1:B:272:THR:HG23	1:B:302:ALA:C	2.12	0.72
1:B:203:PRO:O	1:B:208:GLY:HA3	1.89	0.72
1:B:268:VAL:O	1:B:305:GLY:N	2.17	0.72
1:C:218:LYS:CG	2:C:900:GDP:C6	2.72	0.72
1:A:97:ARG:CB	1:A:100:GLU:CB	2.68	0.72
1:A:117:THR:HG22	1:B:362:LEU:HD23	1.71	0.72
1:D:4:VAL:O	1:D:37:THR:HA	1.90	0.72
1:D:374:ASN:ND2	1:D:404:ILE:HG22	2.03	0.72
1:D:465:MET:CG	1:D:466:VAL:N	2.33	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:455:ILE:HD11	1:B:456:TYR:CE1	2.24	0.72
1:C:466:VAL:O	1:C:468:GLY:CA	2.37	0.72
1:A:257:ASP:HB2	1:A:263:ILE:HG12	1.70	0.72
1:C:59:LYS:O	1:C:63:GLU:OE1	2.06	0.72
1:A:92:TYR:CD2	1:A:223:VAL:HG11	2.25	0.72
1:D:374:ASN:ND2	1:D:404:ILE:HG23	2.05	0.72
1:B:204:GLU:HA	1:B:208:GLY:O	1.90	0.72
1:D:341:GLU:CD	1:D:344:LYS:NZ	2.48	0.71
1:B:353:ARG:HG2	1:B:355:PRO:CD	2.19	0.71
1:B:393:ALA:CB	1:B:397:THR:C	2.60	0.71
1:B:433:ASN:CB	1:B:434:PRO:CD	2.68	0.71
1:C:119:GLN:HB3	1:C:231:LEU:CD2	2.20	0.71
1:C:151:ILE:CG1	1:C:161:THR:HG21	2.19	0.71
1:C:421:GLN:HG3	1:C:445:LYS:NZ	2.04	0.71
1:A:188:ASP:OD1	1:A:191:LYS:HB2	1.90	0.71
1:D:75:VAL:HB	1:D:144:ALA:HA	1.73	0.71
1:D:159:PRO:CA	1:D:162:GLU:HG3	2.18	0.71
1:D:373:LEU:C	1:D:404:ILE:CG2	2.63	0.71
1:C:412:PRO:HD2	1:C:435:PRO:HD3	1.70	0.71
1:D:154:ASP:C	1:D:154:ASP:OD1	2.30	0.71
1:C:95:LYS:CE	1:C:98:ILE:HG21	2.19	0.71
1:B:127:THR:HG23	1:B:127:THR:O	1.91	0.71
1:B:290:ALA:HB3	1:B:311:LEU:HD12	1.71	0.71
1:B:376:ILE:HB	1:B:427:ILE:HG22	1.71	0.71
1:C:65:ARG:O	1:C:68:SER:OG	2.07	0.71
1:B:263:ILE:HD12	1:B:309:GLN:NE2	2.06	0.71
1:B:348:GLU:O	1:B:349:GLU:C	2.33	0.71
1:B:445:LYS:O	1:B:447:VAL:HG12	1.91	0.71
1:A:97:ARG:HA	1:A:100:GLU:CB	2.20	0.71
1:D:86:LYS:CG	1:D:87:THR:N	2.52	0.71
1:D:283:GLU:CD	1:D:343:ARG:NE	2.49	0.71
1:B:312:GLY:O	1:B:313:PHE:C	2.32	0.71
1:B:379:ALA:HB2	1:B:384:SER:OG	1.89	0.71
1:B:6:ILE:CD1	1:B:36:SER:O	2.38	0.71
1:B:293:ASP:OD1	1:B:296:GLY:N	2.24	0.71
1:B:388:ILE:C	1:B:390:HIS:H	1.96	0.71
1:A:181:LYS:HD2	2:A:900:GDP:N3	2.06	0.71
1:D:427:ILE:O	1:D:449:LEU:HD12	1.91	0.71
1:C:47:ARG:HG3	1:C:51:LYS:NZ	2.04	0.71
1:C:125:ILE:CG2	1:C:127:THR:CG2	2.58	0.71
1:A:69:LEU:HD13	1:A:242:ASP:HB2	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:373:LEU:HB3	1:A:402:ILE:HG22	1.71	0.71
1:D:247:PRO:HD2	1:D:325:TRP:CG	2.26	0.71
1:B:12:GLU:HG3	1:B:13:LEU:HD12	0.75	0.71
1:C:3:LYS:CB	1:C:38:LEU:C	2.64	0.71
1:C:50:VAL:CG1	1:C:54:ARG:HE	2.00	0.71
1:C:119:GLN:CB	1:C:231:LEU:CD2	2.69	0.71
1:A:46:VAL:HG13	1:A:50:VAL:HG23	1.66	0.70
1:A:230:ILE:HA	1:A:233:LEU:HD12	1.72	0.70
1:D:31:TYR:CG	1:D:31:TYR:O	2.44	0.70
1:B:110:VAL:O	1:B:265:ASN:HB3	1.91	0.70
1:C:55:GLY:O	1:C:58:GLU:CB	2.29	0.70
1:D:81:HIS:ND1	1:D:160:GLN:HG3	2.05	0.70
1:D:378:ARG:NH2	1:D:406:LEU:HD21	2.06	0.70
1:C:95:LYS:CE	1:C:98:ILE:CB	2.68	0.70
1:A:371:LYS:CG	1:A:400:VAL:HG22	2.22	0.70
1:A:198:GLU:OE2	1:B:256:LEU:CG	2.39	0.70
1:A:232:LEU:O	1:A:236:LEU:HG	1.91	0.70
1:D:127:THR:CB	1:D:253:GLU:OE1	2.39	0.70
1:B:257:ASP:HB3	1:B:261:GLY:O	1.91	0.70
1:A:40:GLU:HB2	1:A:43:ALA:HB2	1.72	0.70
1:A:65:ARG:O	1:A:69:LEU:HG	1.90	0.70
1:A:340:LYS:O	1:A:343:ARG:CG	2.39	0.70
1:D:343:ARG:HA	1:D:346:ARG:NH1	2.07	0.70
1:B:390:HIS:HA	3:B:902:HOH:O	1.90	0.70
1:A:327:PRO:HG2	1:A:328:ASP:N	2.05	0.70
1:A:442:ALA:O	1:A:447:VAL:CG2	2.39	0.70
1:D:94:ARG:CZ	1:D:126:ASP:OD1	2.40	0.70
1:B:277:ASP:HB2	1:B:288:ILE:CD1	2.22	0.70
1:C:6:ILE:C	1:C:8:GLN:H	2.00	0.70
1:D:122:VAL:O	1:D:124:PHE:CE1	2.44	0.70
1:D:163:GLU:OE1	1:C:236:LEU:CD1	2.39	0.70
1:D:373:LEU:O	1:D:404:ILE:HG21	1.91	0.70
1:A:174:LYS:C	1:A:175:LEU:HD12	2.16	0.70
1:A:215:ILE:HG22	1:A:222:GLY:HA3	1.74	0.70
1:D:110:VAL:O	1:D:110:VAL:HG12	1.90	0.70
1:D:310:VAL:HG12	1:D:313:PHE:CE1	2.26	0.70
1:C:96:SER:OG	1:C:97:ARG:N	2.21	0.70
1:A:110:VAL:HG12	1:A:309:GLN:HB2	1.74	0.69
1:A:193:LYS:O	1:A:197:MET:HG3	1.92	0.69
1:D:99:ALA:HB1	1:B:99:ALA:O	1.92	0.69
1:D:159:PRO:HA	1:D:162:GLU:CG	2.20	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:269:GLN:O	1:B:304:PRO:HB3	1.92	0.69
1:C:50:VAL:HG13	1:C:54:ARG:NE	2.01	0.69
1:A:179:ILE:O	1:A:215:ILE:HG13	1.93	0.69
1:A:278:TYR:HD2	1:A:328:ASP:CA	2.02	0.69
1:B:176:ILE:CG2	1:B:226:LEU:HD11	2.22	0.69
1:A:371:LYS:HB2	1:A:400:VAL:HA	1.74	0.69
1:B:53:GLN:O	1:B:55:GLY:N	2.24	0.69
1:B:387:ALA:O	1:B:391:ILE:HG12	1.93	0.69
1:A:5:ARG:HG3	1:A:8:GLN:H	1.58	0.69
1:A:39:GLU:O	1:A:42:ASP:CA	2.40	0.69
1:A:141:ALA:CB	1:A:250:VAL:HG23	2.22	0.69
1:B:280:VAL:HG23	1:B:284:ALA:O	1.92	0.69
1:A:42:ASP:O	1:A:43:ALA:C	2.30	0.69
1:A:379:ALA:HB2	1:A:385:LEU:HD23	1.74	0.69
1:B:333:LYS:O	1:B:337:GLU:HB2	1.92	0.69
1:B:346:ARG:HA	1:B:349:GLU:CD	2.17	0.69
1:C:182:ILE:HB	1:C:215:ILE:O	1.91	0.69
1:D:440:LYS:HA	1:D:443:GLU:HG2	1.75	0.69
1:B:353:ARG:C	1:B:355:PRO:HD3	2.17	0.69
1:B:361:LEU:HD12	1:B:362:LEU:N	2.07	0.69
1:B:384:SER:O	1:B:388:ILE:HG13	1.92	0.69
1:B:393:ALA:HA	1:B:398:GLU:HA	1.75	0.69
1:C:74:PRO:HB3	1:C:239:TYR:CD2	2.27	0.69
1:A:314:GLN:O	1:A:315:GLU:CG	2.38	0.69
1:D:251:ILE:HG12	1:D:323:VAL:HG23	1.75	0.69
1:C:59:LYS:O	1:C:62:GLU:CB	2.41	0.69
1:D:323:VAL:O	1:D:323:VAL:HG12	1.84	0.69
1:B:5:ARG:CG	1:B:37:THR:HG22	2.21	0.69
1:B:126:ASP:OD1	1:B:126:ASP:O	2.10	0.69
1:B:133:PHE:O	1:B:139:ARG:CD	2.39	0.69
1:B:433:ASN:O	1:B:435:PRO:N	2.25	0.69
1:C:195:GLN:HA	1:C:198:GLU:HG3	1.73	0.69
1:A:213:ILE:HG22	1:A:215:ILE:HG23	1.73	0.69
1:C:353:ARG:C	1:C:357:THR:OG1	2.36	0.69
1:A:439:LYS:CA	1:A:442:ALA:HB3	2.23	0.69
1:D:120:GLY:HA3	1:D:231:LEU:HD22	1.74	0.68
1:D:248:ARG:HB3	1:D:270:GLU:HB3	1.73	0.68
1:D:392:LEU:HD23	1:D:459:VAL:HG23	1.74	0.68
1:B:53:GLN:HA	1:B:56:LEU:HB2	1.75	0.68
1:B:190:GLU:OE1	1:B:206:TYR:OH	2.11	0.68
1:A:161:THR:O	1:A:165:ILE:HD12	1.92	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:272:THR:CG2	1:B:301:GLU:HB3	2.20	0.68
1:B:273:PHE:HZ	1:B:323:VAL:CG1	2.05	0.68
1:B:274:ARG:HG2	1:B:301:GLU:HG2	1.74	0.68
1:B:393:ALA:HB2	1:B:398:GLU:H	1.54	0.68
1:C:378:ARG:NH1	1:C:408:GLN:CB	2.45	0.68
1:A:60:LEU:O	1:A:63:GLU:HB2	1.94	0.68
1:D:288:ILE:HD13	1:D:291:MET:CE	2.23	0.68
1:C:47:ARG:HD2	1:C:51:LYS:HZ3	1.56	0.68
1:C:218:LYS:HG2	2:C:900:GDP:C6	2.28	0.68
1:D:247:PRO:HG2	1:D:325:TRP:HD1	1.56	0.68
1:C:47:ARG:CD	1:C:51:LYS:NZ	2.56	0.68
1:D:310:VAL:CG1	1:D:313:PHE:CE1	2.76	0.68
1:B:69:LEU:O	1:B:240:ARG:HD3	1.93	0.68
1:B:277:ASP:HB2	1:B:288:ILE:HD12	1.76	0.68
1:B:461:GLU:O	1:B:462:VAL:C	2.36	0.68
1:C:285:TYR:OH	1:C:333:LYS:CD	2.33	0.68
1:B:117:THR:C	1:B:119:GLN:N	2.46	0.68
1:C:94:ARG:O	1:C:96:SER:N	2.27	0.68
1:A:310:VAL:CG1	1:A:313:PHE:CZ	2.76	0.68
1:D:62:GLU:OE1	1:D:65:ARG:CZ	2.42	0.68
1:B:273:PHE:CZ	1:B:323:VAL:CG1	2.77	0.68
1:C:251:ILE:CG2	1:C:319:PRO:HA	2.23	0.68
1:D:293:ASP:N	1:D:297:ASN:O	2.24	0.67
1:B:128:PRO:CD	1:B:253:GLU:OE2	2.42	0.67
1:A:243:PRO:O	1:A:271:GLY:HA2	1.94	0.67
1:D:108:GLN:OE1	1:D:292:MET:CE	2.42	0.67
1:D:111:GLY:HA2	1:D:127:THR:CG2	2.23	0.67
1:B:388:ILE:HA	1:B:391:ILE:HG12	1.76	0.67
1:C:47:ARG:CD	1:C:51:LYS:HZ2	2.07	0.67
1:C:59:LYS:HA	1:C:62:GLU:HB3	1.70	0.67
1:C:95:LYS:CE	1:C:98:ILE:CG2	2.71	0.67
1:A:343:ARG:HG3	1:A:344:LYS:H	1.57	0.67
1:B:5:ARG:HH11	1:B:37:THR:CG2	2.07	0.67
1:B:326:VAL:CG1	1:B:331:ALA:HB1	2.24	0.67
1:C:63:GLU:O	1:C:67:LYS:CG	2.42	0.67
1:A:69:LEU:O	1:A:240:ARG:CD	2.41	0.67
1:B:188:ASP:HB3	1:B:191:LYS:HB2	1.76	0.67
1:C:29:VAL:HG13	1:C:30:ALA:H	1.59	0.67
1:D:179:ILE:CD1	1:D:212:VAL:CG1	2.72	0.67
1:B:6:ILE:HB	1:B:34:HIS:CA	2.25	0.67
1:C:5:ARG:O	1:C:8:GLN:CB	2.42	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:310:VAL:HG11	1:A:313:PHE:CZ	2.30	0.67
1:D:110:VAL:O	1:D:110:VAL:CG1	2.42	0.67
1:B:79:MET:HE2	1:B:164:ALA:C	2.19	0.67
1:B:147:ALA:CB	1:B:168:ALA:HB1	2.25	0.67
1:B:157:ILE:H	1:B:195:GLN:NE2	1.93	0.67
1:C:81:HIS:C	1:C:84:HIS:CD2	2.73	0.67
1:C:378:ARG:NH2	1:C:416:ASP:CG	2.51	0.67
1:D:143:VAL:HG22	1:D:250:VAL:HG11	1.76	0.67
1:B:110:VAL:HG21	1:B:293:ASP:C	2.19	0.67
1:B:137:ARG:CG	1:B:319:PRO:O	2.43	0.67
1:B:376:ILE:HG21	1:B:427:ILE:HG22	1.77	0.67
1:B:411:ALA:N	1:B:434:PRO:CG	2.20	0.67
1:D:345:ALA:O	1:D:348:GLU:HB3	1.95	0.67
1:D:462:VAL:C	1:D:464:ASN:N	2.40	0.67
1:B:75:VAL:CG1	1:B:144:ALA:HA	2.25	0.67
1:B:376:ILE:CB	1:B:427:ILE:HG22	2.24	0.67
1:B:393:ALA:CB	1:B:398:GLU:CA	2.71	0.67
1:B:429:ALA:O	1:B:452:PHE:N	2.25	0.67
1:B:436:GLY:O	1:B:437:SER:C	2.38	0.67
1:C:70:PRO:O	1:C:240:ARG:CB	2.42	0.67
1:C:71:ARG:CG	1:C:240:ARG:HG3	2.18	0.67
1:C:71:ARG:NH1	1:C:71:ARG:HB3	2.10	0.67
1:A:314:GLN:C	1:A:315:GLU:HG3	2.20	0.67
1:A:352:ALA:HA	1:A:355:PRO:CG	2.25	0.66
1:D:344:LYS:O	1:D:348:GLU:N	2.28	0.66
1:B:117:THR:CG2	1:B:119:GLN:CG	2.62	0.66
1:C:53:GLN:HA	1:C:56:LEU:HD21	1.77	0.66
1:C:223:VAL:O	1:C:224:GLN:C	2.37	0.66
1:C:467:LYS:H	1:C:467:LYS:CD	2.09	0.66
1:A:183:ASP:HA	1:B:351:LYS:HE2	1.77	0.66
1:A:326:VAL:CG1	1:A:328:ASP:O	2.44	0.66
1:B:405:LEU:HD11	1:B:406:LEU:HD12	1.71	0.66
1:C:69:LEU:HD22	1:C:70:PRO:HD2	1.77	0.66
1:A:379:ALA:CB	1:A:385:LEU:HD23	2.24	0.66
1:D:78:ILE:HD12	1:D:90:LEU:CG	2.26	0.66
1:B:53:GLN:NE2	1:B:57:GLN:CB	2.58	0.66
1:B:123:VAL:O	1:B:123:VAL:HG12	1.95	0.66
1:A:452:PHE:CD1	1:A:457:ASP:O	2.48	0.66
1:B:117:THR:O	1:B:118:PRO:C	2.36	0.66
1:B:128:PRO:HD2	1:B:253:GLU:OE2	1.94	0.66
1:B:354:ARG:N	1:B:355:PRO:CD	2.59	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:327:PRO:CG	1:A:328:ASP:H	2.08	0.66
1:D:65:ARG:O	1:D:66:ARG:C	2.36	0.66
1:D:413:THR:HG21	1:D:415:SER:HG	1.61	0.66
1:B:183:ASP:OD1	1:B:184:LEU:CD1	2.41	0.66
1:C:116:LYS:HD3	1:C:121:THR:HG22	1.77	0.66
1:C:467:LYS:H	1:C:467:LYS:HD2	1.60	0.66
1:D:293:ASP:CB	1:D:297:ASN:O	2.44	0.66
1:B:376:ILE:HG22	1:B:427:ILE:HB	1.76	0.66
1:C:178:ALA:HA	1:C:213:ILE:O	1.96	0.66
1:A:83:ASP:OD1	2:A:900:GDP:O3A	2.14	0.66
1:A:441:LYS:O	1:A:445:LYS:HB2	1.93	0.66
1:D:135:THR:HG22	1:D:137:ARG:H	1.60	0.66
1:B:12:GLU:HG2	1:B:13:LEU:CD1	2.09	0.66
1:B:369:GLY:C	1:B:371:LYS:H	2.00	0.66
1:C:6:ILE:O	1:C:8:GLN:N	2.27	0.66
1:D:345:ALA:O	1:D:348:GLU:CB	2.43	0.66
1:D:461:GLU:O	1:D:464:ASN:HB3	1.94	0.66
1:C:108:GLN:C	1:C:109:HIS:HD2	2.03	0.66
1:A:175:LEU:HD12	1:A:175:LEU:N	2.11	0.66
1:A:181:LYS:HD3	2:A:900:GDP:C4	2.29	0.66
1:A:329:LEU:O	1:A:329:LEU:CD2	2.43	0.66
1:A:352:ALA:O	1:A:353:ARG:C	2.39	0.66
1:D:372:GLU:HG3	1:D:404:ILE:CD1	2.26	0.66
1:B:388:ILE:C	1:B:390:HIS:N	2.40	0.66
1:A:40:GLU:C	1:A:43:ALA:CB	2.64	0.66
1:A:61:ALA:C	1:A:64:GLU:CB	2.69	0.66
1:A:157:ILE:HG21	1:A:199:ARG:NH2	2.11	0.66
1:D:388:ILE:O	1:D:391:ILE:CG2	2.37	0.66
1:D:442:ALA:CB	1:D:447:VAL:HG12	2.25	0.66
1:C:6:ILE:HB	1:C:34:HIS:O	1.96	0.66
1:C:293:ASP:O	1:C:294:ALA:C	2.38	0.66
1:D:205:GLU:CG	1:D:206:TYR:CE1	2.68	0.65
1:B:273:PHE:CZ	1:B:323:VAL:HG11	2.31	0.65
1:B:351:LYS:CG	1:B:351:LYS:O	2.43	0.65
1:A:441:LYS:O	1:A:445:LYS:HB3	1.96	0.65
1:D:345:ALA:CA	1:D:348:GLU:HB2	2.15	0.65
1:C:224:GLN:O	1:C:228:GLU:CG	2.44	0.65
1:D:205:GLU:CG	1:D:206:TYR:HE1	2.07	0.65
1:D:338:GLU:HG3	1:D:339:ARG:H	1.62	0.65
1:D:376:ILE:CG2	1:D:406:LEU:HB3	2.26	0.65
1:A:86:LYS:O	1:A:90:LEU:HG	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:6:ILE:O	1:D:6:ILE:CG2	2.43	0.65
1:B:326:VAL:CG1	1:B:331:ALA:HB3	2.27	0.65
1:C:151:ILE:CG2	1:C:156:GLY:O	2.44	0.65
1:A:40:GLU:O	1:A:41:LYS:C	2.40	0.65
1:D:78:ILE:HD12	1:D:90:LEU:CD2	2.27	0.65
1:D:110:VAL:HG11	1:D:307:ALA:C	2.21	0.65
1:D:247:PRO:CG	1:D:325:TRP:HD1	2.05	0.65
1:D:350:GLU:HA	1:D:353:ARG:HG3	1.79	0.65
1:D:385:LEU:HB3	1:D:389:GLN:HE21	1.61	0.65
1:A:221:GLN:NE2	1:B:350:GLU:OE1	2.30	0.65
1:D:290:ALA:HB3	1:D:311:LEU:HD22	1.78	0.65
1:D:417:VAL:HG21	1:D:438:VAL:HG13	1.78	0.65
1:B:326:VAL:HG12	1:B:331:ALA:HB3	1.79	0.65
1:B:417:VAL:O	1:B:418:LEU:C	2.38	0.65
1:A:188:ASP:OD1	1:A:191:LYS:CB	2.44	0.65
1:C:6:ILE:C	1:C:8:GLN:N	2.47	0.65
1:C:109:HIS:N	1:C:109:HIS:HD2	1.95	0.65
1:C:183:ASP:OD1	1:C:184:LEU:N	2.30	0.65
1:A:186:GLN:N	1:A:186:GLN:OE1	2.30	0.65
1:A:439:LYS:O	1:A:442:ALA:HB3	1.97	0.65
1:C:90:LEU:CD2	1:C:113:PHE:HZ	1.90	0.65
1:C:375:LEU:CD2	1:C:426:ALA:HB3	2.26	0.65
1:B:59:LYS:O	1:B:60:LEU:C	2.40	0.65
1:B:62:GLU:OE2	1:B:65:ARG:NH2	2.29	0.65
1:C:418:LEU:O	1:C:421:GLN:HB2	1.97	0.65
1:C:427:ILE:HD13	1:C:449:LEU:HD11	1.77	0.65
1:A:83:ASP:HB3	2:A:900:GDP:H5''	1.79	0.64
1:D:463:ARG:O	1:D:465:MET:HG2	1.96	0.64
1:C:247:PRO:HA	1:C:271:GLY:HA3	1.79	0.64
1:B:203:PRO:C	1:B:208:GLY:HA3	2.22	0.64
1:C:95:LYS:HG3	1:C:98:ILE:HG23	1.61	0.64
1:A:293:ASP:HB3	1:A:299:ARG:HD3	1.79	0.64
1:D:432:VAL:CG1	1:D:433:ASN:N	2.60	0.64
1:B:117:THR:C	1:B:119:GLN:H	2.04	0.64
1:B:264:ALA:CB	1:B:313:PHE:HE2	2.01	0.64
1:C:24:LEU:HD23	1:C:27:MET:SD	2.37	0.64
1:A:149:ILE:HG13	1:A:165:ILE:HG13	1.77	0.64
1:A:183:ASP:OD1	1:A:183:ASP:N	2.30	0.64
1:B:5:ARG:HG3	1:B:5:ARG:NH1	2.06	0.64
1:A:119:GLN:HB3	1:A:231:LEU:HD13	1.79	0.64
1:B:6:ILE:N	1:B:34:HIS:O	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:31:TYR:O	1:D:31:TYR:CD1	2.51	0.64
1:D:99:ALA:HB3	1:B:99:ALA:C	2.10	0.64
1:D:417:VAL:CG2	1:D:438:VAL:HG13	2.28	0.64
1:B:379:ALA:O	1:B:380:ASP:CG	2.41	0.64
1:C:255:LYS:HE3	1:C:263:ILE:HD11	0.65	0.64
1:C:349:GLU:O	1:C:353:ARG:HG3	1.96	0.64
1:A:81:HIS:HD1	1:A:160:GLN:HB2	1.61	0.64
1:A:417:VAL:HG11	1:A:441:LYS:O	1.98	0.64
1:B:5:ARG:CD	1:B:35:ALA:O	2.45	0.64
1:B:133:PHE:HB3	1:B:167:HIS:HB3	1.80	0.64
1:A:94:ARG:NH1	1:A:109:HIS:NE2	2.45	0.64
1:D:276:GLY:HA2	1:D:287:ARG:NE	2.04	0.64
1:B:7:TYR:HB3	1:B:34:HIS:ND1	2.12	0.64
1:C:268:VAL:HB	1:C:304:PRO:HA	1.78	0.64
1:A:397:THR:O	1:A:397:THR:CG2	2.45	0.64
1:D:373:LEU:O	1:D:404:ILE:CG2	2.46	0.64
1:B:443:GLU:HA	1:B:447:VAL:HG22	1.79	0.64
1:A:204:GLU:HA	1:A:208:GLY:O	1.98	0.63
1:D:283:GLU:OE1	1:D:343:ARG:NH2	2.30	0.63
1:B:262:ILE:CG2	1:B:316:LEU:HD23	2.07	0.63
1:A:61:ALA:HA	1:A:64:GLU:CB	2.28	0.63
1:D:318:HIS:O	1:D:321:ASP:OD2	2.17	0.63
1:D:452:PHE:CB	1:D:458:LEU:HB2	2.28	0.63
1:B:199:ARG:HB3	1:B:201:PHE:HE2	1.63	0.63
1:A:413:THR:CG2	1:A:416:ASP:N	2.52	0.63
1:B:62:GLU:O	1:B:65:ARG:CB	2.33	0.63
1:B:124:PHE:HZ	1:B:227:LEU:HD21	1.63	0.63
1:C:143:VAL:HG11	1:C:252:LEU:HD21	1.80	0.63
1:A:354:ARG:O	1:A:358:MET:HB3	1.98	0.63
1:B:405:LEU:C	1:B:406:LEU:HG	2.21	0.63
1:C:420:ALA:C	1:C:445:LYS:HZ1	2.07	0.63
1:C:421:GLN:N	1:C:445:LYS:HZ1	1.81	0.63
1:A:82:VAL:C	2:A:900:GDP:O1B	2.42	0.63
1:D:182:ILE:HD11	1:D:214:PRO:HB2	0.72	0.63
1:D:461:GLU:O	1:D:464:ASN:N	2.31	0.63
1:B:124:PHE:HZ	1:B:227:LEU:CD2	2.10	0.63
1:A:352:ALA:CA	1:A:355:PRO:HD2	2.29	0.63
1:D:385:LEU:C	1:D:389:GLN:HE21	2.06	0.63
1:C:70:PRO:O	1:C:240:ARG:CA	2.47	0.63
1:C:182:ILE:CG2	1:C:216:SER:HB2	2.27	0.63
1:C:285:TYR:CZ	1:C:333:LYS:CD	2.73	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:ILE:HD13	1:B:229:MET:CE	2.29	0.62
1:D:24:LEU:HB3	1:D:29:VAL:CG1	2.13	0.62
1:B:354:ARG:O	1:B:354:ARG:HG2	1.97	0.62
1:B:448:LEU:O	1:B:449:LEU:CG	2.47	0.62
1:C:340:LYS:O	1:C:341:GLU:C	2.38	0.62
1:A:23:LEU:HD23	1:A:23:LEU:C	2.23	0.62
1:D:338:GLU:CG	1:D:339:ARG:N	2.60	0.62
1:B:117:THR:O	1:B:119:GLN:N	2.32	0.62
1:C:54:ARG:O	1:C:57:GLN:HB2	1.99	0.62
1:A:69:LEU:HD22	1:A:242:ASP:OD1	1.99	0.62
1:A:329:LEU:O	1:A:329:LEU:CG	2.47	0.62
1:D:94:ARG:CG	1:D:113:PHE:CZ	2.78	0.62
1:B:256:LEU:HD13	1:B:316:LEU:HD11	1.81	0.62
1:C:125:ILE:HG22	1:C:127:THR:HG22	1.73	0.62
1:C:263:ILE:HG22	1:C:311:LEU:CD2	2.29	0.62
1:C:421:GLN:CA	1:C:445:LYS:HZ1	1.70	0.62
1:A:253:GLU:HB2	1:A:265:ASN:HB2	1.80	0.62
1:A:456:TYR:O	1:A:459:VAL:N	2.32	0.62
1:B:137:ARG:HG2	1:B:319:PRO:O	2.00	0.62
1:B:184:LEU:HD12	1:B:184:LEU:N	2.15	0.62
1:C:81:HIS:CD2	1:C:158:MET:HG3	2.34	0.62
1:C:141:ALA:CB	1:C:250:VAL:HG23	2.29	0.62
1:A:416:ASP:HA	1:A:419:LEU:HD12	1.82	0.62
1:C:255:LYS:CD	1:C:263:ILE:HD11	2.24	0.62
1:C:362:LEU:O	1:C:364:ALA:N	2.31	0.62
1:D:127:THR:HB	1:D:253:GLU:OE1	1.99	0.62
1:B:141:ALA:O	1:B:143:VAL:HG23	2.00	0.62
1:B:310:VAL:HB	1:B:313:PHE:CZ	2.35	0.62
1:C:80:GLY:H	1:C:86:LYS:HZ3	1.46	0.62
1:D:6:ILE:HD11	1:D:24:LEU:HD11	1.81	0.62
1:D:247:PRO:HB2	1:D:325:TRP:HD1	1.64	0.62
1:B:274:ARG:O	1:B:288:ILE:CD1	2.46	0.62
1:C:59:LYS:C	1:C:62:GLU:HB3	2.25	0.62
1:D:191:LYS:O	1:D:194:ARG:N	2.32	0.62
1:B:127:THR:OG1	1:B:129:GLY:O	2.16	0.62
1:C:287:ARG:O	1:C:287:ARG:HG3	1.98	0.62
1:A:230:ILE:O	1:A:233:LEU:HB2	2.00	0.61
1:D:206:TYR:CD1	1:D:206:TYR:N	2.55	0.61
1:D:374:ASN:CG	1:D:404:ILE:HG23	2.24	0.61
1:B:122:VAL:CG2	1:B:231:LEU:CD2	2.78	0.61
1:C:29:VAL:CG1	1:C:30:ALA:N	2.61	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:81:HIS:ND1	1:C:160:GLN:OE1	2.33	0.61
1:D:434:PRO:CB	1:D:449:LEU:CD2	2.73	0.61
1:B:62:GLU:HG3	1:B:65:ARG:NE	2.16	0.61
1:B:191:LYS:HE3	3:B:903:HOH:O	1.99	0.61
1:B:255:LYS:C	1:B:262:ILE:HG23	2.21	0.61
1:B:405:LEU:HG	1:B:406:LEU:HG	1.82	0.61
1:C:67:LYS:C	1:C:69:LEU:H	2.07	0.61
1:A:184:LEU:HG	2:A:900:GDP:N2	2.15	0.61
1:D:283:GLU:CD	1:D:343:ARG:HE	2.08	0.61
1:D:354:ARG:HB3	1:D:357:THR:HG22	1.81	0.61
1:B:447:VAL:O	1:B:447:VAL:HG13	2.00	0.61
1:C:466:VAL:HG23	1:C:467:LYS:HA	1.81	0.61
1:D:76:VAL:HG22	1:D:146:ILE:HB	1.82	0.61
1:D:213:ILE:HG22	1:D:215:ILE:HG23	1.82	0.61
1:B:59:LYS:C	1:B:61:ALA:N	2.49	0.61
1:B:343:ARG:O	1:B:344:LYS:C	2.42	0.61
1:C:70:PRO:O	1:C:241:ALA:N	2.31	0.61
1:C:95:LYS:O	1:C:98:ILE:HG12	2.00	0.61
1:A:460:ASP:OD1	1:A:463:ARG:CZ	2.44	0.61
1:D:233:LEU:O	1:D:237:GLU:CB	2.48	0.61
1:C:381:THR:HG22	1:C:383:GLY:H	1.65	0.61
1:C:427:ILE:CG1	1:C:449:LEU:CD1	2.78	0.61
1:A:293:ASP:OD2	1:A:299:ARG:CD	2.37	0.61
1:D:23:LEU:HD12	1:D:23:LEU:C	2.25	0.61
1:D:420:ALA:HA	1:D:425:ALA:HB3	1.81	0.61
1:B:3:LYS:N	1:B:40:GLU:OE2	2.34	0.61
1:A:39:GLU:O	1:A:42:ASP:N	2.33	0.61
1:D:69:LEU:O	1:D:240:ARG:HD2	1.99	0.61
1:D:385:LEU:C	1:D:388:ILE:HG22	2.26	0.61
1:B:62:GLU:CD	1:B:65:ARG:NH2	2.58	0.61
1:B:251:ILE:HG22	1:B:319:PRO:HA	1.81	0.61
1:C:343:ARG:NH1	1:C:347:GLU:OE2	2.34	0.61
1:A:345:ALA:O	1:A:346:ARG:C	2.41	0.61
1:B:199:ARG:HB3	1:B:201:PHE:CE2	2.36	0.61
1:B:411:ALA:HB3	1:B:434:PRO:CG	2.28	0.61
1:C:81:HIS:HD1	1:C:160:GLN:CD	2.09	0.61
1:A:385:LEU:HD13	1:A:385:LEU:C	2.25	0.61
1:B:81:HIS:ND1	1:B:160:GLN:CD	2.49	0.61
1:B:124:PHE:CZ	1:B:227:LEU:HD21	2.35	0.61
1:B:438:VAL:HG13	1:B:439:LYS:N	2.16	0.61
1:C:162:GLU:HB3	1:C:390:HIS:HE1	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:371:LYS:HB2	1:A:400:VAL:HG22	1.82	0.61
1:D:146:ILE:CG1	1:D:174:LYS:HB3	2.31	0.61
1:B:202:VAL:O	1:B:208:GLY:HA3	2.00	0.61
1:C:66:ARG:O	1:C:69:LEU:CG	2.48	0.61
1:C:84:HIS:ND1	1:C:150:VAL:O	2.34	0.61
1:C:216:SER:HB3	1:C:219:THR:OG1	2.01	0.61
1:D:76:VAL:HG21	1:D:230:ILE:HD13	1.82	0.60
1:D:97:ARG:HE	1:D:114:GLU:CB	2.14	0.60
1:B:44:GLU:O	1:B:48:GLU:HG2	2.00	0.60
1:D:86:LYS:CG	1:D:87:THR:H	2.12	0.60
1:D:372:GLU:CG	1:D:404:ILE:CD1	2.74	0.60
1:B:380:ASP:C	1:B:409:VAL:HG11	2.26	0.60
1:C:81:HIS:HA	1:C:160:GLN:HB3	1.83	0.60
1:C:119:GLN:HB2	1:C:231:LEU:CD2	2.31	0.60
1:C:188:ASP:CB	1:C:191:LYS:HB2	2.30	0.60
1:C:350:GLU:HA	1:C:353:ARG:HG3	1.83	0.60
1:A:107:THR:O	1:A:108:GLN:C	2.44	0.60
1:B:12:GLU:HG3	1:B:13:LEU:N	2.17	0.60
1:C:273:PHE:O	1:C:302:ALA:N	2.30	0.60
1:A:413:THR:CG2	1:A:416:ASP:OD2	2.21	0.60
1:D:75:VAL:H	1:D:145:ASP:CG	2.09	0.60
1:D:247:PRO:CB	1:D:325:TRP:HD1	2.15	0.60
1:B:113:PHE:CZ	1:B:124:PHE:HB2	2.37	0.60
1:A:108:GLN:OE1	1:A:108:GLN:N	2.29	0.60
1:A:413:THR:CG2	1:A:415:SER:OG	2.50	0.60
1:A:439:LYS:HA	1:A:442:ALA:HB3	1.81	0.60
1:B:203:PRO:O	1:B:208:GLY:CA	2.49	0.60
1:B:422:THR:CG2	1:B:423:ALA:H	2.14	0.60
1:A:151:ILE:O	1:A:179:ILE:HA	2.01	0.60
1:A:203:PRO:HB2	1:A:205:GLU:HG2	1.82	0.60
1:A:310:VAL:HG12	1:A:313:PHE:HE2	1.66	0.60
1:D:122:VAL:O	1:D:124:PHE:CD1	2.55	0.60
1:B:203:PRO:O	1:B:208:GLY:N	2.34	0.60
1:C:93:LEU:HD13	1:C:124:PHE:CE2	2.36	0.60
1:C:447:VAL:HG12	1:C:448:LEU:N	2.17	0.60
1:A:416:ASP:HA	1:A:419:LEU:CB	2.23	0.60
1:D:16:GLU:OE1	1:D:17:CYS:C	2.45	0.60
1:B:376:ILE:O	1:B:427:ILE:C	2.45	0.60
1:A:433:ASN:OD1	1:A:451:THR:HG21	2.02	0.60
1:D:392:LEU:HD21	1:D:459:VAL:HG23	1.84	0.60
1:B:55:GLY:HA2	1:B:58:GLU:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:386:GLU:O	1:B:390:HIS:HB2	2.01	0.60
1:C:227:LEU:N	1:C:227:LEU:CD2	2.63	0.60
1:A:466:VAL:C	1:A:468:GLY:H	2.10	0.60
1:D:385:LEU:HD13	1:D:407:ALA:CB	2.24	0.60
1:D:445:LYS:O	1:D:445:LYS:HE3	2.01	0.60
1:C:350:GLU:HG3	1:C:351:LYS:N	2.16	0.60
1:C:354:ARG:O	1:C:355:PRO:C	2.36	0.60
1:D:428:LEU:N	1:D:449:LEU:HD12	2.17	0.60
1:B:362:LEU:O	1:B:366:GLN:N	2.35	0.60
1:B:404:ILE:HG22	1:B:406:LEU:H	1.67	0.60
1:C:344:LYS:O	1:C:347:GLU:HB2	2.02	0.60
1:A:209:ASP:HB3	1:B:130:HIS:H	1.67	0.59
1:D:461:GLU:O	1:D:464:ASN:HB2	2.01	0.59
1:B:153:ALA:N	1:B:180:ASN:O	2.35	0.59
1:B:447:VAL:HG22	1:B:447:VAL:O	2.01	0.59
1:C:116:LYS:CG	1:C:121:THR:CG2	2.78	0.59
1:C:353:ARG:O	1:C:357:THR:CG2	2.46	0.59
1:C:427:ILE:CG1	1:C:449:LEU:HD11	2.31	0.59
1:A:439:LYS:CA	1:A:442:ALA:CB	2.80	0.59
1:D:81:HIS:HA	1:D:160:GLN:HB2	1.81	0.59
1:C:84:HIS:HD1	1:C:151:ILE:CA	2.12	0.59
1:C:293:ASP:C	1:C:295:ASP:N	2.59	0.59
1:C:378:ARG:NE	1:C:416:ASP:OD2	2.35	0.59
1:B:63:GLU:HA	1:B:66:ARG:HG3	1.82	0.59
1:B:455:ILE:HD11	1:B:456:TYR:CG	2.36	0.59
1:D:31:TYR:HE1	1:D:33:SER:HA	1.68	0.59
1:B:38:LEU:CG	1:B:39:GLU:H	2.09	0.59
1:B:348:GLU:O	1:B:351:LYS:N	2.30	0.59
1:D:174:LYS:CE	1:D:233:LEU:HD22	2.33	0.59
1:D:201:PHE:N	1:D:201:PHE:CD1	2.70	0.59
1:D:293:ASP:HB3	1:D:297:ASN:O	2.03	0.59
1:A:278:TYR:CD2	1:A:328:ASP:C	2.81	0.59
1:D:64:GLU:O	1:D:64:GLU:CD	2.45	0.59
1:B:21:LEU:HD22	1:B:31:TYR:CE2	2.37	0.59
1:B:163:GLU:O	1:B:164:ALA:C	2.46	0.59
1:B:376:ILE:CG2	1:B:427:ILE:CG2	2.79	0.59
1:C:71:ARG:HD2	1:C:239:TYR:N	2.17	0.59
1:C:79:MET:C	1:C:86:LYS:HD3	2.27	0.59
1:C:391:ILE:HG21	1:C:459:VAL:HG21	1.83	0.59
1:A:197:MET:CE	1:A:206:TYR:CD2	2.85	0.59
1:B:250:VAL:HG22	1:B:251:ILE:N	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:346:ARG:HA	1:B:349:GLU:OE1	2.03	0.59
1:C:71:ARG:HB3	1:C:239:TYR:O	2.02	0.59
1:C:119:GLN:CB	1:C:231:LEU:HD23	2.28	0.59
1:A:413:THR:HG23	1:A:416:ASP:CA	2.31	0.59
1:D:16:GLU:OE1	1:D:17:CYS:CA	2.51	0.59
1:D:179:ILE:N	1:D:214:PRO:HA	2.18	0.59
1:B:128:PRO:HD2	1:B:129:GLY:N	2.17	0.59
1:B:275:VAL:HG12	1:B:276:GLY:H	1.67	0.59
1:A:44:GLU:HA	1:A:47:ARG:HB2	1.84	0.59
1:A:74:PRO:HD2	1:A:121:THR:O	2.02	0.59
1:A:91:ASP:O	1:A:95:LYS:HG2	2.03	0.59
1:A:223:VAL:CG2	1:B:361:LEU:HD22	2.33	0.59
1:D:99:ALA:HB1	1:B:99:ALA:HA	1.76	0.59
1:D:237:GLU:HB3	1:D:239:TYR:CE1	2.38	0.59
1:D:251:ILE:HB	1:D:321:ASP:HB2	1.84	0.59
1:C:56:LEU:HD12	1:C:57:GLN:N	2.18	0.59
1:C:95:LYS:HZ1	1:C:98:ILE:HD13	1.64	0.59
1:A:418:LEU:HD21	1:C:408:GLN:HE22	1.63	0.59
1:D:374:ASN:N	1:D:404:ILE:CG2	2.63	0.59
1:D:441:LYS:O	1:D:444:GLU:CB	2.48	0.59
1:C:224:GLN:O	1:C:228:GLU:HG3	2.02	0.59
1:C:225:ASP:HA	1:C:228:GLU:CD	2.27	0.59
1:A:442:ALA:HB1	1:A:449:LEU:CD2	2.26	0.58
1:B:290:ALA:CB	1:B:311:LEU:CD1	2.75	0.58
1:C:337:GLU:O	1:C:341:GLU:HG2	2.03	0.58
1:A:226:LEU:O	1:A:230:ILE:CD1	2.51	0.58
1:B:31:TYR:HB2	1:B:36:SER:CB	2.33	0.58
1:B:278:TYR:CE1	1:B:329:LEU:CB	2.76	0.58
1:A:223:VAL:HG21	1:B:361:LEU:CD2	2.33	0.58
1:A:417:VAL:HG12	1:A:445:LYS:HG2	1.86	0.58
1:B:344:LYS:O	1:B:347:GLU:N	2.37	0.58
1:C:59:LYS:O	1:C:60:LEU:C	2.45	0.58
1:C:277:ASP:HB2	1:C:288:ILE:CD1	2.25	0.58
1:C:348:GLU:O	1:C:352:ALA:CB	2.45	0.58
1:A:71:ARG:HA	1:A:240:ARG:HG2	1.85	0.58
1:A:376:ILE:HD11	1:A:427:ILE:CD1	2.34	0.58
1:B:54:ARG:O	1:B:57:GLN:N	2.36	0.58
1:A:263:ILE:HG22	1:A:311:LEU:HG	1.85	0.58
1:D:16:GLU:OE1	1:D:17:CYS:N	2.35	0.58
1:B:362:LEU:O	1:B:366:GLN:CB	2.51	0.58
1:B:380:ASP:C	1:B:409:VAL:HG12	2.22	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:95:LYS:CG	1:C:98:ILE:CB	2.49	0.58
1:C:227:LEU:N	1:C:227:LEU:HD22	2.17	0.58
1:C:274:ARG:HB2	1:C:277:ASP:OD1	2.02	0.58
1:A:439:LYS:HA	1:A:442:ALA:CB	2.33	0.58
1:D:75:VAL:O	1:D:145:ASP:HB2	2.03	0.58
1:D:146:ILE:HG21	1:D:176:ILE:HD12	1.86	0.58
1:D:317:PRO:C	1:D:321:ASP:OD2	2.46	0.58
1:D:366:GLN:C	1:D:368:GLU:N	2.53	0.58
1:D:421:GLN:HA	1:D:445:LYS:HG2	1.85	0.58
1:D:285:TYR:CE2	1:D:333:LYS:HG2	2.38	0.58
1:D:377:LEU:CD2	1:D:388:ILE:HD13	2.34	0.58
1:C:59:LYS:C	1:C:62:GLU:CB	2.77	0.58
1:C:466:VAL:HG23	1:C:467:LYS:CA	2.34	0.58
1:D:234:ALA:O	1:D:238:ASP:N	2.37	0.58
1:B:380:ASP:OD1	1:B:380:ASP:C	2.46	0.58
1:C:47:ARG:CG	1:C:51:LYS:NZ	2.67	0.58
1:C:392:LEU:HD22	1:C:462:VAL:HG11	1.85	0.58
1:D:65:ARG:O	1:D:68:SER:OG	2.18	0.58
1:D:278:TYR:HE1	1:D:329:LEU:HD23	1.66	0.58
1:D:345:ALA:C	1:D:348:GLU:HB3	2.28	0.58
1:B:403:ASN:O	1:B:404:ILE:CG1	2.51	0.58
1:D:178:ALA:HB1	1:D:215:ILE:HG12	1.85	0.58
1:A:345:ALA:O	1:A:349:GLU:HG2	2.04	0.57
1:B:146:ILE:HD13	1:B:230:ILE:HG23	1.84	0.57
1:C:388:ILE:HG12	1:C:455:ILE:HG23	1.85	0.57
1:D:143:VAL:HG11	1:D:252:LEU:HD21	1.86	0.57
1:D:375:LEU:O	1:D:404:ILE:O	2.21	0.57
1:B:5:ARG:NH1	1:B:37:THR:CG2	2.67	0.57
1:B:246:GLU:O	1:B:247:PRO:C	2.43	0.57
1:C:66:ARG:C	1:C:69:LEU:HG	2.29	0.57
1:C:170:ALA:HA	1:C:455:ILE:CB	2.20	0.57
1:A:460:ASP:HA	1:A:463:ARG:NE	2.15	0.57
1:C:141:ALA:CB	1:C:250:VAL:CG2	2.82	0.57
1:C:466:VAL:HG23	1:C:467:LYS:N	2.18	0.57
1:A:157:ILE:HD12	1:A:199:ARG:NH1	2.01	0.57
1:A:204:GLU:HG3	1:A:210:ALA:O	2.04	0.57
1:A:223:VAL:CG2	1:B:361:LEU:CD2	2.81	0.57
1:D:345:ALA:O	1:D:346:ARG:C	2.45	0.57
1:B:190:GLU:O	1:B:194:ARG:CG	2.48	0.57
1:B:290:ALA:HB3	1:B:311:LEU:CG	2.33	0.57
1:A:409:VAL:HG12	1:A:410:GLY:N	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:373:LEU:CG	1:D:374:ASN:N	2.68	0.57
1:A:205:GLU:HG3	1:A:206:TYR:HD1	1.70	0.57
1:A:413:THR:HG23	1:A:416:ASP:CB	2.25	0.57
1:D:99:ALA:CB	1:B:99:ALA:O	2.49	0.57
1:D:262:ILE:CG2	1:D:316:LEU:HD23	2.32	0.57
1:C:193:LYS:HG2	1:C:203:PRO:HG2	1.86	0.57
1:A:244:ASN:O	1:A:245:ALA:O	2.23	0.57
1:A:329:LEU:O	1:A:329:LEU:HG	2.04	0.57
1:D:182:ILE:HD11	1:D:214:PRO:CA	2.33	0.57
1:C:274:ARG:CZ	1:C:301:GLU:OE2	2.51	0.57
1:D:179:ILE:H	1:D:214:PRO:HA	1.69	0.57
1:B:55:GLY:O	1:B:56:LEU:HD22	2.04	0.57
1:B:137:ARG:HG3	1:B:320:GLY:HA3	1.85	0.57
1:B:193:LYS:HA	1:B:196:LEU:HD12	1.87	0.57
1:C:268:VAL:HG13	1:C:273:PHE:CD2	2.39	0.57
1:A:3:LYS:O	1:A:4:VAL:CG2	2.53	0.57
1:A:46:VAL:O	1:A:50:VAL:N	2.35	0.57
1:A:188:ASP:CG	1:A:191:LYS:HB2	2.29	0.57
1:D:181:LYS:HB3	1:D:184:LEU:HD13	1.87	0.57
1:D:374:ASN:HA	1:D:404:ILE:HB	1.84	0.57
1:B:290:ALA:HB3	1:B:311:LEU:CD1	2.34	0.57
1:B:290:ALA:HB3	1:B:311:LEU:HB2	1.87	0.57
1:C:59:LYS:CA	1:C:62:GLU:HB3	2.29	0.57
1:A:415:SER:HA	1:A:418:LEU:HB3	1.86	0.57
1:D:15:MET:HE1	1:D:19:GLU:C	2.30	0.57
1:D:74:PRO:HD2	1:D:121:THR:O	2.05	0.57
1:D:247:PRO:CB	1:D:325:TRP:CD1	2.88	0.57
1:D:452:PHE:CE1	1:D:458:LEU:HD13	2.38	0.57
1:C:268:VAL:O	1:C:305:GLY:N	2.25	0.57
1:A:274:ARG:O	1:A:277:ASP:CG	2.47	0.56
1:D:466:VAL:HG22	1:D:468:GLY:O	2.05	0.56
1:B:158:MET:CB	1:B:159:PRO:CD	2.82	0.56
1:C:213:ILE:HD13	1:C:226:LEU:HA	1.87	0.56
1:A:97:ARG:CA	1:A:100:GLU:CB	2.83	0.56
1:B:264:ALA:HB2	1:B:313:PHE:CE2	2.40	0.56
1:C:255:LYS:HG2	1:C:263:ILE:HG13	1.88	0.56
1:A:117:THR:HG22	1:B:362:LEU:CD2	2.34	0.56
1:A:188:ASP:OD1	1:A:191:LYS:CA	2.53	0.56
1:A:197:MET:HE1	1:A:206:TYR:CD2	2.40	0.56
1:D:31:TYR:CE1	1:D:33:SER:HA	2.40	0.56
1:D:179:ILE:HB	1:D:214:PRO:HB3	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:363:ARG:CB	1:B:366:GLN:NE2	2.68	0.56
1:C:67:LYS:C	1:C:69:LEU:N	2.59	0.56
1:C:81:HIS:CG	1:C:84:HIS:CD2	2.92	0.56
1:C:105:GLY:O	1:C:295:ASP:CA	2.37	0.56
1:A:72:ARG:NH1	1:A:240:ARG:N	2.53	0.56
1:A:127:THR:HG22	1:A:128:PRO:CD	2.35	0.56
1:D:157:ILE:HG21	1:D:199:ARG:NE	2.20	0.56
1:B:358:MET:SD	1:B:361:LEU:HD21	2.46	0.56
1:C:107:THR:O	1:C:109:HIS:NE2	2.38	0.56
1:C:366:GLN:O	1:C:367:GLU:C	2.44	0.56
1:D:465:MET:SD	1:D:466:VAL:HG12	2.44	0.56
1:C:143:VAL:HG11	1:C:252:LEU:CD2	2.35	0.56
1:A:9:LEU:O	1:A:13:LEU:HG	2.05	0.56
1:A:46:VAL:O	1:A:49:LEU:N	2.39	0.56
1:A:151:ILE:HG12	1:A:161:THR:HG21	1.88	0.56
1:D:318:HIS:HB2	1:D:321:ASP:OD1	2.06	0.56
1:C:63:GLU:O	1:C:67:LYS:CD	2.54	0.56
1:A:3:LYS:C	1:A:4:VAL:HG23	2.31	0.56
1:A:154:ASP:OD1	1:A:155:ASP:CG	2.49	0.56
1:A:180:ASN:ND2	1:A:217:ALA:HB2	2.20	0.56
1:B:353:ARG:C	1:B:355:PRO:CD	2.79	0.56
1:B:455:ILE:CD1	1:B:456:TYR:CD1	2.82	0.56
1:C:6:ILE:CG1	1:C:38:LEU:HD11	2.32	0.56
1:C:81:HIS:HD2	1:C:158:MET:HG3	1.70	0.56
1:A:278:TYR:HB2	1:A:326:VAL:O	2.06	0.56
1:A:435:PRO:HB2	1:A:438:VAL:HG21	1.87	0.56
1:D:91:ASP:HA	1:D:94:ARG:HD3	1.86	0.56
1:D:138:GLN:HE21	1:D:319:PRO:CB	2.19	0.56
1:D:354:ARG:O	1:D:355:PRO:C	2.48	0.56
1:B:110:VAL:O	1:B:265:ASN:CB	2.53	0.56
1:C:101:LYS:CB	1:C:106:ILE:CB	2.83	0.56
1:A:92:TYR:OH	1:B:361:LEU:CD2	2.45	0.56
1:B:31:TYR:HB2	1:B:36:SER:HB2	1.87	0.56
1:C:71:ARG:HB3	1:C:71:ARG:HH11	1.68	0.56
1:A:343:ARG:O	1:A:344:LYS:C	2.44	0.56
1:A:437:SER:C	1:A:440:LYS:H	2.14	0.56
1:D:452:PHE:CD1	1:D:458:LEU:HD13	2.41	0.56
1:C:79:MET:SD	1:C:164:ALA:CB	2.93	0.56
1:C:359:ALA:CA	1:C:362:LEU:CB	2.83	0.56
1:A:5:ARG:HG3	1:A:8:GLN:N	2.21	0.55
1:A:83:ASP:CB	2:A:900:GDP:C5'	2.84	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:455:ILE:O	1:A:458:LEU:CB	2.51	0.55
1:A:459:VAL:HA	1:A:462:VAL:HG23	1.88	0.55
1:D:434:PRO:HB3	1:D:449:LEU:HD23	1.86	0.55
1:B:326:VAL:HG12	1:B:331:ALA:CB	2.34	0.55
1:A:40:GLU:C	1:A:42:ASP:N	2.52	0.55
1:A:169:LYS:C	1:A:455:ILE:HD12	2.31	0.55
1:A:326:VAL:HG11	1:A:328:ASP:O	2.06	0.55
1:D:203:PRO:HA	1:D:210:ALA:O	2.05	0.55
1:D:213:ILE:CD1	1:D:226:LEU:HD13	2.37	0.55
1:B:204:GLU:O	1:B:207:GLY:N	2.34	0.55
1:B:233:LEU:O	1:B:237:GLU:HB2	2.06	0.55
1:B:255:LYS:CE	1:B:263:ILE:HD11	2.34	0.55
1:C:218:LYS:HG3	2:C:900:GDP:C6	2.41	0.55
1:C:245:ALA:O	1:C:246:GLU:C	2.48	0.55
1:B:388:ILE:O	1:B:389:GLN:C	2.49	0.55
1:B:455:ILE:HD12	1:B:456:TYR:N	2.21	0.55
1:A:175:LEU:CD1	1:A:175:LEU:N	2.70	0.55
1:A:205:GLU:HG3	1:A:206:TYR:CD1	2.41	0.55
1:D:86:LYS:O	1:D:87:THR:C	2.49	0.55
1:D:442:ALA:HB1	1:D:447:VAL:CG1	2.31	0.55
1:B:33:SER:O	1:B:35:ALA:N	2.40	0.55
1:B:38:LEU:HG	1:B:39:GLU:H	1.71	0.55
1:B:110:VAL:O	1:B:265:ASN:ND2	2.40	0.55
1:B:188:ASP:HB3	1:B:191:LYS:CB	2.35	0.55
1:A:5:ARG:O	1:A:6:ILE:C	2.49	0.55
1:A:83:ASP:CB	2:A:900:GDP:H5"	2.37	0.55
1:A:417:VAL:HG12	1:A:445:LYS:CG	2.36	0.55
1:D:62:GLU:C	1:D:64:GLU:N	2.59	0.55
1:D:114:GLU:HG2	1:D:123:VAL:HG22	1.89	0.55
1:D:345:ALA:O	1:D:349:GLU:N	2.38	0.55
1:B:388:ILE:O	1:B:390:HIS:N	2.40	0.55
1:C:289:ARG:N	1:C:311:LEU:O	2.33	0.55
1:A:188:ASP:OD1	1:A:188:ASP:O	2.24	0.55
1:A:288:ILE:HG23	1:A:310:VAL:HG13	1.88	0.55
1:A:435:PRO:HB2	1:A:438:VAL:CG2	2.37	0.55
1:D:6:ILE:O	1:D:6:ILE:HG23	2.05	0.55
1:D:137:ARG:HH22	1:C:205:GLU:HB3	1.71	0.55
1:B:209:ASP:C	1:B:209:ASP:OD1	2.45	0.55
1:B:380:ASP:N	1:B:409:VAL:CG1	2.65	0.55
1:C:71:ARG:CB	1:C:239:TYR:O	2.54	0.55
1:A:46:VAL:HG13	1:A:50:VAL:HG22	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118:PRO:HG2	1:B:366:GLN:HA	1.84	0.55
1:D:350:GLU:O	1:D:351:LYS:C	2.50	0.55
1:B:433:ASN:O	1:B:435:PRO:HD3	2.06	0.55
1:C:353:ARG:HB3	1:C:357:THR:CB	2.36	0.55
1:A:107:THR:O	1:A:108:GLN:O	2.25	0.55
1:A:373:LEU:HD22	1:A:465:MET:O	2.06	0.55
1:A:460:ASP:CA	1:A:463:ARG:HE	2.15	0.55
1:D:354:ARG:N	1:D:355:PRO:HD3	2.22	0.55
1:B:20:LEU:O	1:B:21:LEU:C	2.46	0.55
1:D:6:ILE:CD1	1:D:24:LEU:HD11	2.37	0.55
1:D:40:GLU:CG	1:D:41:LYS:N	2.70	0.55
1:B:404:ILE:HG22	1:B:405:LEU:N	2.21	0.55
1:C:53:GLN:HA	1:C:56:LEU:CD2	2.37	0.55
1:C:201:PHE:CD1	1:C:201:PHE:N	2.75	0.55
1:D:262:ILE:HG23	1:D:316:LEU:HD21	1.89	0.54
1:D:433:ASN:OD1	1:D:434:PRO:CD	2.54	0.54
1:B:393:ALA:HB2	1:B:398:GLU:CB	2.36	0.54
1:C:108:GLN:HA	1:C:109:HIS:HD2	1.72	0.54
1:A:83:ASP:HB3	2:A:900:GDP:H5'	1.90	0.54
1:A:127:THR:HG22	1:A:128:PRO:HD2	1.89	0.54
1:A:184:LEU:HG	2:A:900:GDP:HN21	1.69	0.54
1:A:245:ALA:C	1:A:246:GLU:O	2.38	0.54
1:D:50:VAL:O	1:D:54:ARG:HB2	2.07	0.54
1:D:250:VAL:HG13	1:D:250:VAL:O	2.07	0.54
1:C:153:ALA:HB3	1:C:181:LYS:HB2	1.89	0.54
1:C:263:ILE:HG22	1:C:311:LEU:HD21	1.88	0.54
1:C:353:ARG:CB	1:C:357:THR:CG2	2.72	0.54
1:A:143:VAL:HG13	1:A:267:LEU:HD22	1.88	0.54
1:A:226:LEU:O	1:A:230:ILE:HD12	2.06	0.54
1:A:371:LYS:HB3	1:A:400:VAL:HG22	1.87	0.54
1:A:415:SER:O	1:A:418:LEU:C	2.46	0.54
1:C:143:VAL:O	1:C:143:VAL:HG12	2.06	0.54
1:A:197:MET:CE	1:A:206:TYR:CE2	2.90	0.54
1:A:206:TYR:HD2	1:B:254:SER:O	1.90	0.54
1:A:415:SER:O	1:A:418:LEU:N	2.41	0.54
1:B:62:GLU:CD	1:B:65:ARG:HH21	2.14	0.54
1:C:47:ARG:HG3	1:C:51:LYS:HZ2	1.71	0.54
1:D:413:THR:HG23	1:D:416:ASP:H	1.72	0.54
1:B:128:PRO:CD	1:B:129:GLY:N	2.70	0.54
1:C:53:GLN:O	1:C:56:LEU:CG	2.45	0.54
1:C:71:ARG:HD3	1:C:238:ASP:OD1	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:95:LYS:O	1:C:98:ILE:CG1	2.54	0.54
1:B:69:LEU:HD11	1:B:242:ASP:HB2	1.89	0.54
1:B:362:LEU:C	1:B:366:GLN:HB3	2.32	0.54
1:B:405:LEU:HD12	1:B:406:LEU:HD21	1.88	0.54
1:B:418:LEU:O	1:B:419:LEU:C	2.50	0.54
1:A:216:SER:HB3	1:A:221:GLN:HB3	1.88	0.54
1:A:217:ALA:HB3	2:A:900:GDP:N7	2.23	0.54
1:C:471:GLU:O	1:C:472:PRO:C	2.46	0.54
1:A:266:MET:HE3	1:A:323:VAL:HG21	1.90	0.54
1:A:375:LEU:HA	1:A:425:ALA:HB1	1.89	0.54
1:D:97:ARG:NE	1:D:114:GLU:HB2	2.22	0.54
1:B:455:ILE:CG1	1:B:456:TYR:N	2.71	0.54
1:A:146:ILE:HG23	1:A:174:LYS:O	2.07	0.54
1:D:388:ILE:HG22	1:D:389:GLN:H	1.72	0.54
1:B:273:PHE:HZ	1:B:323:VAL:HG12	1.73	0.54
1:B:341:GLU:O	1:B:342:GLU:C	2.46	0.54
1:B:362:LEU:C	1:B:366:GLN:OE1	2.45	0.54
1:D:388:ILE:C	1:D:391:ILE:HG22	2.30	0.54
1:A:127:THR:HG23	1:A:128:PRO:HD3	1.86	0.53
1:A:303:GLY:O	1:A:306:SER:HB2	2.07	0.53
1:D:378:ARG:NH2	1:D:406:LEU:CD2	2.69	0.53
1:C:13:LEU:HD13	1:C:50:VAL:HG11	1.89	0.53
1:C:47:ARG:HD2	1:C:47:ARG:C	2.33	0.53
1:C:188:ASP:HB3	1:C:191:LYS:HB2	1.86	0.53
1:C:286:GLY:HA3	1:C:312:GLY:O	2.07	0.53
1:A:45:ALA:O	1:A:49:LEU:CD1	2.46	0.53
1:A:94:ARG:CZ	1:A:126:ASP:OD2	2.56	0.53
1:A:157:ILE:HG21	1:A:199:ARG:NH1	2.22	0.53
1:A:352:ALA:HA	1:A:355:PRO:CD	2.39	0.53
1:D:76:VAL:O	1:D:125:ILE:HG12	2.08	0.53
1:D:421:GLN:NE2	1:D:445:LYS:HB2	2.23	0.53
1:B:110:VAL:O	1:B:265:ASN:CG	2.51	0.53
1:B:128:PRO:HD2	1:B:129:GLY:H	1.74	0.53
1:C:4:VAL:HG11	1:C:8:GLN:HB3	1.90	0.53
1:C:141:ALA:HB1	1:C:250:VAL:CG2	2.38	0.53
1:A:373:LEU:CB	1:A:402:ILE:HG22	2.36	0.53
1:D:22:GLU:CD	1:D:26:GLN:NE2	2.66	0.53
1:D:59:LYS:O	1:D:63:GLU:HB2	2.08	0.53
1:D:253:GLU:O	1:D:265:ASN:N	2.41	0.53
1:C:6:ILE:O	1:C:7:TYR:C	2.50	0.53
1:A:409:VAL:CG1	1:A:410:GLY:N	2.71	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:70:PRO:O	1:B:240:ARG:HB3	2.08	0.53
1:C:71:ARG:CD	1:C:238:ASP:HA	2.39	0.53
1:C:95:LYS:HB2	1:C:98:ILE:HG21	1.76	0.53
1:A:142:LYS:HE2	1:A:171:ALA:O	2.08	0.53
1:A:149:ILE:HD13	1:A:149:ILE:N	2.24	0.53
1:A:184:LEU:CG	2:A:900:GDP:HN21	2.20	0.53
1:D:356:ARG:O	1:D:357:THR:C	2.48	0.53
1:B:234:ALA:HA	1:B:239:TYR:CE2	2.43	0.53
1:B:427:ILE:HG12	1:B:449:LEU:CD2	2.14	0.53
1:D:16:GLU:CG	1:D:17:CYS:N	2.71	0.53
1:B:256:LEU:HD13	1:B:316:LEU:CD1	2.38	0.53
1:C:3:LYS:CB	1:C:37:THR:OG1	2.55	0.53
1:B:4:VAL:HG23	1:B:8:GLN:OE1	2.01	0.53
1:B:141:ALA:O	1:B:142:LYS:C	2.49	0.53
1:D:16:GLU:OE2	1:D:17:CYS:HB2	2.08	0.53
1:D:143:VAL:HG11	1:D:252:LEU:CD2	2.39	0.53
1:D:352:ALA:O	1:D:355:PRO:CG	2.51	0.53
1:B:455:ILE:HG13	1:B:456:TYR:H	1.73	0.53
1:C:81:HIS:O	1:C:84:HIS:HB2	2.08	0.53
1:C:223:VAL:HG12	1:C:227:LEU:CD2	2.35	0.53
1:C:449:LEU:HD23	1:C:450:LYS:N	2.24	0.53
1:A:435:PRO:HD2	1:A:438:VAL:HB	1.91	0.53
1:D:23:LEU:HA	1:D:26:GLN:HG2	1.91	0.53
1:B:34:HIS:C	1:B:36:SER:H	2.16	0.53
1:B:38:LEU:CD1	1:B:42:ASP:CB	2.79	0.53
1:B:133:PHE:CB	1:B:167:HIS:HB3	2.39	0.53
1:D:62:GLU:O	1:D:65:ARG:N	2.41	0.53
1:D:89:LEU:HD12	1:D:89:LEU:O	2.09	0.53
1:D:452:PHE:CD2	1:D:458:LEU:HD22	2.45	0.53
1:B:433:ASN:O	1:B:435:PRO:CG	2.57	0.53
1:C:71:ARG:HD2	1:C:238:ASP:C	2.34	0.53
1:C:127:THR:O	1:C:127:THR:HG23	2.08	0.53
1:C:392:LEU:HA	1:C:395:GLU:HB2	1.91	0.53
1:A:420:ALA:C	1:A:423:ALA:HB3	2.34	0.52
1:D:345:ALA:C	1:D:348:GLU:N	2.35	0.52
1:B:93:LEU:HD21	1:B:227:LEU:HD11	1.91	0.52
1:C:4:VAL:O	1:C:5:ARG:C	2.47	0.52
1:C:54:ARG:O	1:C:57:GLN:N	2.41	0.52
1:A:73:PRO:CG	1:A:305:GLY:HA3	2.36	0.52
1:A:373:LEU:HB3	1:A:402:ILE:HA	1.91	0.52
1:D:113:PHE:HD2	1:D:126:ASP:HB2	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:81:HIS:O	1:C:84:HIS:HD2	1.91	0.52
1:C:227:LEU:CD2	1:C:227:LEU:H	2.20	0.52
1:C:346:ARG:O	1:C:350:GLU:N	2.42	0.52
1:D:31:TYR:CD1	1:D:31:TYR:C	2.87	0.52
1:D:142:LYS:O	1:D:142:LYS:HG2	2.09	0.52
1:B:84:HIS:NE2	1:B:155:ASP:HB2	2.24	0.52
1:B:363:ARG:HB3	1:B:366:GLN:NE2	2.24	0.52
1:A:371:LYS:HG3	1:A:400:VAL:HG22	1.90	0.52
1:D:374:ASN:HA	1:D:404:ILE:CA	2.39	0.52
1:B:34:HIS:C	1:B:36:SER:N	2.65	0.52
1:B:79:MET:HE2	1:B:164:ALA:HB1	1.87	0.52
1:B:157:ILE:C	1:B:158:MET:HG2	2.34	0.52
1:B:157:ILE:O	1:B:158:MET:HE2	2.09	0.52
1:C:117:THR:HB	1:C:118:PRO:HD2	1.91	0.52
1:A:9:LEU:HD23	1:A:20:LEU:HD21	1.91	0.52
1:A:443:GLU:O	1:A:444:GLU:C	2.52	0.52
1:A:453:ARG:HD3	1:A:453:ARG:N	2.25	0.52
1:D:372:GLU:N	1:D:372:GLU:OE1	2.43	0.52
1:B:285:TYR:O	1:B:314:GLN:N	2.36	0.52
1:C:466:VAL:O	1:C:468:GLY:HA3	2.08	0.52
1:A:87:THR:CB	2:A:900:GDP:O2A	2.45	0.52
1:B:351:LYS:O	1:B:351:LYS:HG2	2.08	0.52
1:C:120:GLY:N	1:C:231:LEU:HD21	2.24	0.52
1:C:170:ALA:CA	1:C:455:ILE:HB	2.20	0.52
1:A:412:PRO:HD2	1:A:435:PRO:HD3	1.92	0.52
1:B:463:ARG:O	1:B:465:MET:N	2.42	0.52
1:C:227:LEU:HD23	1:C:227:LEU:H	1.75	0.52
1:C:346:ARG:HA	1:C:349:GLU:HB2	1.92	0.52
1:D:338:GLU:CG	1:D:339:ARG:H	2.22	0.52
1:B:411:ALA:N	1:B:434:PRO:CD	2.66	0.52
1:C:151:ILE:HG22	1:C:156:GLY:O	2.10	0.52
1:A:86:LYS:HG2	2:A:900:GDP:O3B	2.09	0.52
1:A:293:ASP:CG	1:A:299:ARG:HD2	2.29	0.52
1:A:342:GLU:O	1:A:345:ALA:HB3	2.10	0.52
1:A:456:TYR:C	1:A:458:LEU:H	2.17	0.52
1:D:97:ARG:HE	1:D:114:GLU:HB2	1.74	0.52
1:D:343:ARG:O	1:D:347:GLU:HB2	2.10	0.52
1:B:53:GLN:CA	1:B:56:LEU:HB2	2.39	0.52
1:C:95:LYS:CG	1:C:95:LYS:O	2.57	0.52
1:A:422:THR:CB	1:C:406:LEU:HD22	2.36	0.52
1:A:468:GLY:O	1:A:469:GLN:C	2.53	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:247:PRO:O	1:D:325:TRP:HB2	2.10	0.52
1:B:6:ILE:HG21	1:B:34:HIS:CB	2.34	0.52
1:B:93:LEU:CD2	1:B:227:LEU:HD11	2.39	0.52
1:C:47:ARG:CG	1:C:51:LYS:HZ2	2.23	0.52
1:C:148:VAL:O	1:C:148:VAL:HG12	2.10	0.52
1:C:467:LYS:CD	1:C:467:LYS:N	2.72	0.52
1:A:143:VAL:O	1:A:143:VAL:HG12	2.09	0.51
1:D:157:ILE:CG2	1:D:199:ARG:NH2	2.73	0.51
1:B:21:LEU:O	1:B:22:GLU:C	2.53	0.51
1:B:256:LEU:CD1	1:B:316:LEU:HD11	2.40	0.51
1:B:346:ARG:O	1:B:349:GLU:N	2.43	0.51
1:A:272:THR:HA	1:A:302:ALA:O	2.09	0.51
1:A:310:VAL:HG11	1:A:313:PHE:HZ	1.75	0.51
1:A:396:SER:HB2	1:A:401:LYS:HA	1.92	0.51
1:B:433:ASN:O	1:B:435:PRO:HG3	2.10	0.51
1:B:462:VAL:O	1:B:465:MET:CG	2.59	0.51
1:C:81:HIS:C	1:C:84:HIS:HD2	2.15	0.51
1:D:412:PRO:HG2	1:D:435:PRO:HD2	1.91	0.51
1:D:435:PRO:HB2	1:D:438:VAL:HG23	1.93	0.51
1:B:5:ARG:CD	1:B:35:ALA:HB1	2.40	0.51
1:C:182:ILE:HG22	1:C:216:SER:CB	2.37	0.51
1:C:464:ASN:C	1:C:466:VAL:H	2.09	0.51
1:D:7:TYR:HD2	1:D:34:HIS:O	1.94	0.51
1:D:146:ILE:CG2	1:D:176:ILE:HD12	2.40	0.51
1:D:192:VAL:HA	1:D:195:GLN:OE1	2.10	0.51
1:B:422:THR:HG23	1:B:423:ALA:H	1.68	0.51
1:C:3:LYS:CA	1:C:38:LEU:O	2.56	0.51
1:C:15:MET:SD	1:C:54:ARG:NH2	2.84	0.51
1:C:249:GLY:O	1:C:322:VAL:HG13	2.11	0.51
1:A:40:GLU:O	1:A:44:GLU:N	2.43	0.51
1:D:143:VAL:CG1	1:D:252:LEU:HD21	2.41	0.51
1:B:128:PRO:HD3	1:B:253:GLU:OE2	2.10	0.51
1:B:277:ASP:HB2	1:B:288:ILE:HD11	1.93	0.51
1:B:377:LEU:HD23	1:B:428:LEU:CB	2.41	0.51
1:C:170:ALA:HB3	1:C:456:TYR:CE2	2.46	0.51
1:C:350:GLU:O	1:C:353:ARG:N	2.41	0.51
1:A:398:GLU:O	1:A:400:VAL:O	2.28	0.51
1:D:8:GLN:O	1:D:9:LEU:C	2.53	0.51
1:B:117:THR:O	1:B:120:GLY:N	2.34	0.51
1:B:251:ILE:HB	1:B:321:ASP:HB2	1.92	0.51
1:B:376:ILE:HG22	1:B:427:ILE:CB	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:414:GLU:O	1:A:418:LEU:N	2.40	0.51
1:B:342:GLU:O	1:B:345:ALA:N	2.43	0.51
1:B:345:ALA:O	1:B:346:ARG:C	2.50	0.51
1:C:218:LYS:HG2	2:C:900:GDP:C5	2.46	0.51
1:C:253:GLU:HB2	1:C:265:ASN:HB2	1.92	0.51
1:C:414:GLU:O	1:C:417:VAL:N	2.44	0.51
1:A:208:GLY:HA2	1:B:129:GLY:HA3	1.93	0.51
1:D:139:ARG:HD3	1:D:167:HIS:ND1	2.25	0.51
1:D:407:ALA:O	1:D:408:GLN:OE1	2.29	0.51
1:D:442:ALA:C	1:D:447:VAL:HG12	2.33	0.51
1:B:272:THR:HG22	1:B:273:PHE:N	2.26	0.51
1:C:125:ILE:HG21	1:C:127:THR:HG22	1.80	0.51
1:C:427:ILE:CB	1:C:449:LEU:HG	2.28	0.51
1:A:83:ASP:CG	2:A:900:GDP:H5"	2.36	0.51
1:A:278:TYR:CD2	1:A:329:LEU:N	2.78	0.51
1:A:452:PHE:CD1	1:A:458:LEU:HA	2.45	0.51
1:D:89:LEU:HA	1:D:217:ALA:HB1	1.92	0.51
1:D:310:VAL:HG12	1:D:313:PHE:HE1	1.64	0.51
1:C:59:LYS:O	1:C:62:GLU:N	2.44	0.51
1:C:162:GLU:HB3	1:C:390:HIS:CE1	2.46	0.51
1:A:190:GLU:CG	1:A:194:ARG:HH21	2.24	0.51
1:D:62:GLU:C	1:D:64:GLU:H	2.18	0.51
1:D:122:VAL:CG1	1:D:124:PHE:CE1	2.90	0.51
1:D:361:LEU:CD1	1:C:92:TYR:OH	2.59	0.51
1:D:374:ASN:HA	1:D:404:ILE:HA	1.93	0.51
1:D:412:PRO:CG	1:D:434:PRO:HA	2.41	0.51
1:B:33:SER:O	1:B:34:HIS:C	2.54	0.51
1:B:38:LEU:HD11	1:B:42:ASP:CG	2.35	0.51
1:B:118:PRO:HD2	1:B:119:GLN:HG2	1.92	0.51
1:B:455:ILE:HG13	1:B:456:TYR:N	2.26	0.51
1:C:71:ARG:CA	1:C:239:TYR:O	2.59	0.51
1:C:107:THR:O	1:C:109:HIS:CD2	2.63	0.51
1:C:169:LYS:HD2	1:C:201:PHE:CZ	2.46	0.51
1:C:283:GLU:O	1:C:336:ALA:HB1	2.12	0.51
1:C:362:LEU:C	1:C:364:ALA:N	2.66	0.51
1:C:466:VAL:CG2	1:C:467:LYS:N	2.73	0.51
1:A:61:ALA:CA	1:A:64:GLU:CB	2.89	0.50
1:A:164:ALA:O	1:A:168:ALA:CB	2.59	0.50
1:A:203:PRO:CB	1:A:205:GLU:HG2	2.41	0.50
1:A:340:LYS:C	1:A:343:ARG:HG2	2.36	0.50
1:D:94:ARG:HH22	1:D:109:HIS:CE1	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:75:VAL:HG12	1:B:144:ALA:HA	1.92	0.50
1:A:430:PHE:CZ	1:A:455:ILE:HG13	2.46	0.50
1:D:438:VAL:O	1:D:442:ALA:N	2.38	0.50
1:B:369:GLY:C	1:B:371:LYS:N	2.64	0.50
1:B:434:PRO:O	1:B:435:PRO:C	2.51	0.50
1:C:5:ARG:O	1:C:8:GLN:CG	2.59	0.50
1:C:83:ASP:HA	2:C:900:GDP:O3B	2.12	0.50
1:C:108:GLN:CA	1:C:109:HIS:HD2	2.23	0.50
1:A:244:ASN:O	1:A:245:ALA:C	2.52	0.50
1:D:89:LEU:HD23	1:D:150:VAL:HG21	1.93	0.50
1:D:345:ALA:C	1:D:348:GLU:CB	2.84	0.50
1:D:461:GLU:OE1	1:D:461:GLU:O	2.29	0.50
1:B:184:LEU:CD1	1:B:184:LEU:N	2.72	0.50
1:B:442:ALA:O	1:B:447:VAL:HG23	2.06	0.50
1:C:72:ARG:NH1	1:C:145:ASP:OD2	2.44	0.50
1:C:180:ASN:OD1	1:C:180:ASN:O	2.30	0.50
1:C:387:ALA:O	1:C:390:HIS:N	2.44	0.50
1:C:391:ILE:CG2	1:C:459:VAL:HG21	2.40	0.50
1:D:247:PRO:HB2	1:D:325:TRP:CD1	2.44	0.50
1:D:361:LEU:HD12	1:C:92:TYR:OH	2.10	0.50
1:B:188:ASP:O	1:B:191:LYS:HB3	2.11	0.50
1:B:411:ALA:HB3	1:B:434:PRO:HG2	1.83	0.50
1:C:320:GLY:O	1:C:321:ASP:O	2.28	0.50
1:A:232:LEU:HG	1:A:236:LEU:HD11	1.94	0.50
1:A:415:SER:OG	1:A:416:ASP:N	2.45	0.50
1:D:154:ASP:OD1	1:D:154:ASP:O	2.29	0.50
1:D:158:MET:O	1:D:162:GLU:HG3	2.12	0.50
1:D:180:ASN:CG	1:D:181:LYS:H	2.15	0.50
1:C:236:LEU:O	1:C:236:LEU:CD2	2.53	0.50
1:C:421:GLN:HG3	1:C:445:LYS:HZ3	1.74	0.50
1:A:23:LEU:C	1:A:23:LEU:CD2	2.85	0.50
1:A:326:VAL:CG1	1:A:327:PRO:HD2	2.25	0.50
1:A:340:LYS:HA	1:A:343:ARG:HG2	1.93	0.50
1:D:278:TYR:HB2	1:D:326:VAL:HG23	1.92	0.50
1:D:293:ASP:HB3	1:D:297:ASN:N	2.26	0.50
1:B:12:GLU:CG	1:B:13:LEU:N	2.74	0.50
1:B:13:LEU:HD12	1:B:13:LEU:N	2.25	0.50
1:B:147:ALA:N	1:B:174:LYS:O	2.38	0.50
1:B:303:GLY:O	1:B:306:SER:OG	2.29	0.50
1:A:220:GLY:O	1:A:223:VAL:HG22	2.11	0.50
1:D:74:PRO:HG2	1:D:122:VAL:HG13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:278:TYR:CE1	1:D:287:ARG:HB2	2.45	0.50
1:D:445:LYS:HG3	1:D:446:GLY:N	2.23	0.50
1:B:4:VAL:CG2	1:B:5:ARG:N	2.34	0.50
1:C:70:PRO:O	1:C:240:ARG:HA	2.11	0.50
1:C:193:LYS:O	1:C:197:MET:HG3	2.11	0.50
1:A:346:ARG:O	1:A:349:GLU:CA	2.60	0.50
1:A:413:THR:CG2	1:A:416:ASP:CA	2.90	0.50
1:D:434:PRO:CB	1:D:449:LEU:HD23	2.41	0.50
1:B:436:GLY:O	1:B:438:VAL:N	2.45	0.50
1:A:164:ALA:O	1:A:168:ALA:HB2	2.12	0.50
1:B:341:GLU:O	1:B:345:ALA:N	2.41	0.50
1:C:101:LYS:C	1:C:105:GLY:HA3	2.37	0.50
1:C:268:VAL:HG13	1:C:273:PHE:HD2	1.77	0.50
1:A:98:ILE:HG23	1:A:99:ALA:N	2.26	0.49
1:A:375:LEU:CA	1:A:425:ALA:HB1	2.41	0.49
1:D:25:ASP:CA	1:D:29:VAL:HB	2.39	0.49
1:D:278:TYR:CZ	1:D:329:LEU:HD23	2.47	0.49
1:B:346:ARG:O	1:B:349:GLU:CB	2.60	0.49
1:C:7:TYR:HB3	1:C:34:HIS:HD2	1.77	0.49
1:C:100:GLU:O	1:C:101:LYS:C	2.54	0.49
1:C:154:ASP:OD1	1:C:155:ASP:OD1	2.30	0.49
1:A:415:SER:O	1:A:418:LEU:CA	2.60	0.49
1:D:137:ARG:HH12	1:D:318:HIS:HB3	1.77	0.49
1:C:59:LYS:C	1:C:62:GLU:H	2.20	0.49
1:C:170:ALA:CB	1:C:456:TYR:CD2	2.95	0.49
1:C:353:ARG:CB	1:C:357:THR:OG1	2.60	0.49
1:A:343:ARG:CG	1:A:344:LYS:N	2.74	0.49
1:D:328:ASP:C	1:D:328:ASP:OD1	2.55	0.49
1:D:381:THR:C	1:D:383:GLY:N	2.70	0.49
1:D:417:VAL:HG11	1:D:441:LYS:HB3	1.94	0.49
1:B:263:ILE:HD12	1:B:309:GLN:HE22	1.77	0.49
1:D:62:GLU:O	1:D:64:GLU:N	2.46	0.49
1:B:156:GLY:HA2	1:B:192:VAL:HG22	1.94	0.49
1:B:411:ALA:N	1:B:434:PRO:HD2	2.26	0.49
1:A:245:ALA:O	1:A:246:GLU:O	2.29	0.49
1:A:413:THR:CG2	1:A:416:ASP:HB2	2.39	0.49
1:A:468:GLY:C	1:A:470:ARG:N	2.69	0.49
1:D:4:VAL:O	1:D:37:THR:CA	2.60	0.49
1:D:94:ARG:NH1	1:D:126:ASP:CG	2.62	0.49
1:D:377:LEU:HD22	1:D:388:ILE:HD13	1.93	0.49
1:D:417:VAL:HG11	1:D:441:LYS:CB	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:5:ARG:HG2	1:B:35:ALA:C	2.34	0.49
1:B:146:ILE:HD13	1:B:230:ILE:CG2	2.42	0.49
1:B:358:MET:O	1:B:361:LEU:HG	2.13	0.49
1:C:116:LYS:HD3	1:C:121:THR:CG2	2.40	0.49
1:C:375:LEU:HD21	1:C:426:ALA:HB3	1.94	0.49
1:C:388:ILE:HG21	1:C:458:LEU:HD22	1.94	0.49
1:C:447:VAL:CG1	1:C:448:LEU:N	2.75	0.49
1:A:23:LEU:HD23	1:A:23:LEU:O	2.11	0.49
1:A:81:HIS:HA	1:A:160:GLN:OE1	2.12	0.49
1:A:351:LYS:O	1:A:355:PRO:CG	2.61	0.49
1:A:450:LYS:HB3	1:A:452:PHE:CZ	2.48	0.49
1:D:113:PHE:CD2	1:D:126:ASP:HB2	2.46	0.49
1:C:69:LEU:C	1:C:240:ARG:HD3	2.20	0.49
1:A:273:PHE:HE1	1:A:279:VAL:HG12	1.78	0.49
1:A:287:ARG:O	1:A:288:ILE:C	2.52	0.49
1:A:459:VAL:O	1:A:462:VAL:HB	2.13	0.49
1:D:366:GLN:O	1:D:368:GLU:N	2.46	0.49
1:D:412:PRO:HG2	1:D:435:PRO:CD	2.42	0.49
1:B:226:LEU:O	1:B:230:ILE:HG13	2.13	0.49
1:C:4:VAL:HG11	1:C:8:GLN:CG	2.37	0.49
1:C:375:LEU:O	1:C:405:LEU:N	2.36	0.49
1:A:61:ALA:O	1:A:65:ARG:N	2.46	0.49
1:A:180:ASN:HD21	1:A:217:ALA:HB3	1.78	0.49
1:A:203:PRO:HG2	1:A:206:TYR:CE1	2.47	0.49
1:A:352:ALA:HA	1:A:355:PRO:HD2	1.95	0.49
1:D:51:LYS:O	1:D:52:GLU:C	2.55	0.49
1:D:92:TYR:O	1:D:96:SER:HB3	2.13	0.49
1:B:92:TYR:CE2	1:B:220:GLY:HA3	2.48	0.49
1:B:387:ALA:O	1:B:390:HIS:HB3	2.13	0.49
1:C:3:LYS:CB	1:C:38:LEU:O	2.60	0.49
1:C:81:HIS:O	1:C:84:HIS:CG	2.66	0.49
1:C:316:LEU:HB2	1:C:317:PRO:CD	2.43	0.49
1:A:382:GLN:C	1:A:384:SER:N	2.64	0.49
1:B:9:LEU:HD12	1:B:12:GLU:OE1	2.12	0.49
1:C:71:ARG:HA	1:C:239:TYR:O	2.13	0.49
1:C:285:TYR:O	1:C:314:GLN:HB3	2.12	0.49
1:A:418:LEU:CD2	1:C:408:GLN:NE2	2.67	0.49
1:D:85:GLY:O	1:D:89:LEU:N	2.44	0.49
1:B:17:CYS:O	1:B:18:GLN:C	2.51	0.49
1:B:326:VAL:HG11	1:B:331:ALA:CB	2.41	0.49
1:C:97:ARG:HH12	1:C:114:GLU:H	1.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81:HIS:O	1:A:82:VAL:C	2.56	0.48
1:A:420:ALA:O	1:A:423:ALA:HB3	2.13	0.48
1:D:344:LYS:O	1:D:348:GLU:HB2	2.13	0.48
1:B:153:ALA:CB	1:B:187:ALA:HB1	2.43	0.48
1:B:254:SER:HB2	1:B:317:PRO:HD2	1.95	0.48
1:C:197:MET:N	1:C:201:PHE:O	2.46	0.48
1:A:186:GLN:H	1:A:186:GLN:CD	2.20	0.48
1:D:69:LEU:HB3	1:D:70:PRO:HD2	1.95	0.48
1:D:90:LEU:O	1:D:93:LEU:N	2.40	0.48
1:D:310:VAL:HG11	1:D:313:PHE:HE1	1.78	0.48
1:D:411:ALA:HB1	1:D:412:PRO:HD2	1.94	0.48
1:B:5:ARG:HH11	1:B:5:ARG:CG	2.18	0.48
1:B:147:ALA:HB1	1:B:168:ALA:HB1	1.94	0.48
1:B:363:ARG:HA	1:B:366:GLN:CG	2.09	0.48
1:A:350:GLU:C	1:A:352:ALA:N	2.68	0.48
1:A:399:ASP:OD1	1:A:400:VAL:N	2.46	0.48
1:C:74:PRO:HB3	1:C:239:TYR:HE2	1.74	0.48
1:C:143:VAL:HG22	1:C:250:VAL:HG11	1.95	0.48
1:C:225:ASP:O	1:C:228:GLU:HB2	2.13	0.48
1:D:94:ARG:HG2	1:D:113:PHE:CE1	2.44	0.48
1:D:373:LEU:HG	1:D:374:ASN:H	1.73	0.48
1:D:445:LYS:O	1:D:445:LYS:CD	2.61	0.48
1:C:3:LYS:CB	1:C:38:LEU:N	2.76	0.48
1:A:398:GLU:O	1:A:400:VAL:N	2.47	0.48
1:A:445:LYS:HG3	1:A:445:LYS:O	2.13	0.48
1:D:215:ILE:HG22	1:D:222:GLY:HA3	1.95	0.48
1:B:162:GLU:O	1:B:162:GLU:CG	2.62	0.48
1:B:258:LYS:HG3	1:B:259:GLN:CG	2.24	0.48
1:A:85:GLY:HA3	1:A:180:ASN:HD22	1.77	0.48
1:D:78:ILE:HG22	1:D:86:LYS:HB2	1.94	0.48
1:D:94:ARG:CG	1:D:113:PHE:CE2	2.91	0.48
1:D:278:TYR:CE1	1:D:287:ARG:HD2	2.49	0.48
1:D:310:VAL:HG11	1:D:313:PHE:CE1	2.47	0.48
1:B:16:GLU:O	1:B:17:CYS:C	2.53	0.48
1:C:81:HIS:O	1:C:84:HIS:CB	2.62	0.48
1:C:347:GLU:O	1:C:350:GLU:HG2	2.13	0.48
1:A:62:GLU:C	1:A:64:GLU:N	2.70	0.48
1:D:278:TYR:CA	1:D:326:VAL:HG23	2.44	0.48
1:D:338:GLU:O	1:D:342:GLU:HG3	2.13	0.48
1:D:377:LEU:HD21	1:D:388:ILE:HD13	1.96	0.48
1:D:412:PRO:CD	1:D:435:PRO:HD3	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:38:LEU:HD21	1:B:39:GLU:HB2	1.95	0.48
1:B:122:VAL:HG12	1:B:124:PHE:CE1	2.49	0.48
1:B:443:GLU:N	1:B:447:VAL:CG2	2.69	0.48
1:C:90:LEU:HD22	1:C:113:PHE:HE1	1.63	0.48
1:C:154:ASP:OD1	1:C:155:ASP:N	2.47	0.48
1:C:155:ASP:C	1:C:158:MET:CE	2.78	0.48
1:C:190:GLU:O	1:C:193:LYS:HB2	2.13	0.48
1:C:287:ARG:N	1:C:312:GLY:O	2.42	0.48
1:C:392:LEU:O	1:C:393:ALA:C	2.57	0.48
1:A:27:MET:SD	1:A:29:VAL:HG21	2.54	0.48
1:A:173:ALA:O	1:A:175:LEU:HD12	2.11	0.48
1:D:385:LEU:CD1	1:D:407:ALA:HB1	2.26	0.48
1:B:38:LEU:CD1	1:B:42:ASP:CG	2.86	0.48
1:B:135:THR:OG1	1:B:138:GLN:HG3	2.14	0.48
1:B:280:VAL:HG22	1:B:281:ALA:N	2.28	0.48
1:C:190:GLU:C	1:C:190:GLU:CD	2.82	0.48
1:A:60:LEU:O	1:A:64:GLU:N	2.47	0.48
1:A:225:ASP:C	1:A:227:LEU:N	2.66	0.48
1:D:186:GLN:OE1	1:D:186:GLN:CA	2.62	0.48
1:D:373:LEU:HA	1:D:373:LEU:HD12	1.20	0.48
1:B:46:VAL:O	1:B:50:VAL:CG2	2.55	0.48
1:B:81:HIS:HD2	1:B:84:HIS:CD2	2.32	0.48
1:C:229:MET:HG3	1:C:233:LEU:HD11	1.95	0.48
1:C:352:ALA:C	1:C:354:ARG:H	2.21	0.48
1:A:23:LEU:HD13	1:A:46:VAL:HG13	1.96	0.48
1:B:124:PHE:CZ	1:B:227:LEU:CD2	2.94	0.48
1:C:56:LEU:O	1:C:57:GLN:C	2.55	0.48
1:C:74:PRO:HD3	1:C:234:ALA:HB1	1.96	0.48
1:C:284:ALA:HB1	1:C:315:GLU:O	2.14	0.48
1:A:197:MET:SD	1:A:206:TYR:CD2	3.00	0.47
1:A:467:LYS:O	1:A:469:GLN:N	2.47	0.47
1:D:81:HIS:CA	1:D:160:GLN:HB2	2.44	0.47
1:D:179:ILE:N	1:D:179:ILE:HD12	2.29	0.47
1:D:205:GLU:O	1:D:206:TYR:CD1	2.67	0.47
1:B:251:ILE:HD13	1:B:266:MET:HB3	1.96	0.47
1:B:324:GLU:O	1:B:326:VAL:HG23	2.13	0.47
1:C:359:ALA:CA	1:C:362:LEU:CA	2.84	0.47
1:A:3:LYS:C	1:A:4:VAL:CG2	2.87	0.47
1:A:247:PRO:HD2	1:A:325:TRP:HB3	1.94	0.47
1:A:293:ASP:HB3	1:A:299:ARG:CD	2.43	0.47
1:D:180:ASN:OD1	1:D:215:ILE:O	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:440:LYS:HA	1:D:443:GLU:CG	2.42	0.47
1:B:180:ASN:HD21	1:B:217:ALA:HB2	1.79	0.47
1:B:184:LEU:CD1	1:B:184:LEU:H	2.27	0.47
1:B:343:ARG:NH1	1:B:347:GLU:CD	2.72	0.47
1:B:433:ASN:H	1:B:434:PRO:CD	2.24	0.47
1:B:438:VAL:HG13	1:B:439:LYS:HG2	1.97	0.47
1:C:4:VAL:HG13	1:C:8:GLN:HG3	1.79	0.47
1:C:66:ARG:C	1:C:69:LEU:H	2.22	0.47
1:C:79:MET:HA	1:C:86:LYS:CD	2.44	0.47
1:C:197:MET:HE2	1:C:197:MET:HB3	1.81	0.47
1:C:268:VAL:CB	1:C:304:PRO:HA	2.43	0.47
1:C:375:LEU:O	1:C:405:LEU:HB2	2.14	0.47
1:D:16:GLU:CG	1:D:17:CYS:H	2.26	0.47
1:D:385:LEU:O	1:D:389:GLN:HG3	2.14	0.47
1:D:452:PHE:CD2	1:D:458:LEU:CG	2.93	0.47
1:C:95:LYS:HB2	1:C:98:ILE:CG2	2.34	0.47
1:C:143:VAL:CG1	1:C:267:LEU:HD22	2.44	0.47
1:C:392:LEU:O	1:C:395:GLU:N	2.46	0.47
1:A:398:GLU:C	1:A:400:VAL:N	2.70	0.47
1:D:241:ALA:O	1:D:243:PRO:HD3	2.15	0.47
1:D:452:PHE:CG	1:D:458:LEU:CD1	2.81	0.47
1:B:5:ARG:NH1	1:B:37:THR:HG21	2.29	0.47
1:B:77:VAL:HG12	1:B:146:ILE:O	2.13	0.47
1:B:84:HIS:HE2	1:B:155:ASP:HB2	1.79	0.47
1:C:254:SER:CB	1:C:317:PRO:HD2	2.44	0.47
1:A:157:ILE:CG2	1:A:199:ARG:NH2	2.78	0.47
1:A:466:VAL:C	1:A:468:GLY:N	2.73	0.47
1:D:136:ILE:H	1:D:136:ILE:HD12	1.80	0.47
1:B:5:ARG:HH11	1:B:37:THR:HG22	1.80	0.47
1:B:137:ARG:CG	1:B:320:GLY:HA3	2.44	0.47
1:C:7:TYR:HB3	1:C:34:HIS:CD2	2.50	0.47
1:C:72:ARG:HH12	1:C:145:ASP:CG	2.22	0.47
1:C:76:VAL:HG21	1:C:230:ILE:HD13	1.95	0.47
1:A:268:VAL:HG23	1:A:306:SER:O	2.14	0.47
1:B:323:VAL:C	1:B:324:GLU:HG3	2.38	0.47
1:C:79:MET:HA	1:C:86:LYS:NZ	2.30	0.47
1:A:168:ALA:O	1:A:171:ALA:HB3	2.13	0.47
1:A:186:GLN:N	1:A:186:GLN:CD	2.72	0.47
1:A:370:ARG:O	1:A:371:LYS:C	2.55	0.47
1:A:413:THR:HG23	1:A:415:SER:OG	2.15	0.47
1:A:456:TYR:C	1:A:458:LEU:N	2.67	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:337:GLU:O	1:D:341:GLU:HG2	2.14	0.47
1:B:29:VAL:HG12	1:B:30:ALA:H	1.80	0.47
1:C:117:THR:HG1	1:C:120:GLY:H	1.63	0.47
1:C:151:ILE:HG23	1:C:156:GLY:O	2.14	0.47
1:C:353:ARG:O	1:C:356:ARG:CB	2.59	0.47
1:C:421:GLN:HG2	1:C:445:LYS:HD2	1.96	0.47
1:A:247:PRO:C	1:A:248:ARG:HG3	2.37	0.47
1:B:32:LYS:N	1:B:36:SER:OG	2.47	0.47
1:C:146:ILE:HG22	1:C:147:ALA:N	2.29	0.47
1:C:177:PHE:HB2	1:C:212:VAL:HG22	1.96	0.47
1:A:72:ARG:HG2	1:A:239:TYR:O	2.15	0.47
1:D:110:VAL:CG1	1:D:307:ALA:C	2.88	0.47
1:D:158:MET:O	1:D:162:GLU:CG	2.62	0.47
1:D:428:LEU:CA	1:D:449:LEU:HD12	2.45	0.47
1:B:80:GLY:H	1:B:86:LYS:NZ	2.13	0.47
1:B:455:ILE:CD1	1:B:456:TYR:CG	2.98	0.47
1:A:205:GLU:HG3	1:A:206:TYR:N	2.29	0.47
1:B:365:MET:C	1:B:367:GLU:H	2.22	0.47
1:A:153:ALA:HB2	1:A:179:ILE:CG2	2.45	0.46
1:A:197:MET:SD	1:A:206:TYR:HE2	2.23	0.46
1:A:413:THR:HG22	1:A:416:ASP:HB2	1.86	0.46
1:A:452:PHE:HD1	1:A:457:ASP:O	1.95	0.46
1:D:251:ILE:HG12	1:D:323:VAL:CG2	2.42	0.46
1:D:373:LEU:CD1	1:D:374:ASN:H	2.28	0.46
1:D:452:PHE:CE1	1:D:458:LEU:CD1	2.94	0.46
1:B:357:THR:O	1:B:358:MET:C	2.51	0.46
1:C:218:LYS:CG	2:C:900:GDP:N1	2.72	0.46
1:A:173:ALA:O	1:A:175:LEU:HD11	2.14	0.46
1:A:197:MET:HG2	1:A:203:PRO:HD2	1.97	0.46
1:A:223:VAL:HG23	1:A:224:GLN:N	2.29	0.46
1:B:328:ASP:OD1	1:B:328:ASP:C	2.58	0.46
1:C:263:ILE:HG13	1:C:263:ILE:O	2.15	0.46
1:D:432:VAL:CG1	1:D:433:ASN:H	2.28	0.46
1:A:348:GLU:CA	1:A:351:LYS:CB	2.87	0.46
1:A:437:SER:CB	1:A:440:LYS:CB	2.94	0.46
1:D:78:ILE:HD13	1:D:90:LEU:HG	1.97	0.46
1:D:94:ARG:HH22	1:D:109:HIS:HE1	1.62	0.46
1:D:179:ILE:O	1:D:214:PRO:HA	2.16	0.46
1:D:452:PHE:CG	1:D:458:LEU:CB	2.93	0.46
1:B:59:LYS:O	1:B:61:ALA:C	2.56	0.46
1:B:359:ALA:O	1:B:360:GLU:C	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:386:GLU:O	1:B:390:HIS:CB	2.63	0.46
1:C:39:GLU:O	1:C:42:ASP:N	2.40	0.46
1:C:141:ALA:HB1	1:C:250:VAL:HG21	1.96	0.46
1:A:25:ASP:OD1	1:A:31:TYR:HE2	1.39	0.46
1:A:83:ASP:CB	2:A:900:GDP:H5'	2.46	0.46
1:D:20:LEU:O	1:D:23:LEU:HG	2.15	0.46
1:D:285:TYR:CE2	1:D:333:LYS:CG	2.99	0.46
1:B:33:SER:C	1:B:35:ALA:N	2.67	0.46
1:B:250:VAL:CG2	1:B:251:ILE:N	2.78	0.46
1:C:188:ASP:O	1:C:189:PRO:O	2.32	0.46
1:A:146:ILE:HG22	1:A:147:ALA:N	2.31	0.46
1:A:243:PRO:O	1:A:271:GLY:CA	2.61	0.46
1:D:174:LYS:HG2	1:D:233:LEU:HD13	1.98	0.46
1:B:278:TYR:CE1	1:B:329:LEU:CD2	2.93	0.46
1:C:47:ARG:HG3	1:C:51:LYS:HZ1	1.75	0.46
1:A:40:GLU:HB2	1:A:43:ALA:HB3	1.97	0.46
1:A:226:LEU:O	1:A:230:ILE:HG13	2.15	0.46
1:A:289:ARG:HB2	1:A:311:LEU:O	2.16	0.46
1:D:462:VAL:O	1:D:465:MET:HG2	2.15	0.46
1:B:13:LEU:HD21	1:B:47:ARG:CG	2.42	0.46
1:B:42:ASP:O	1:B:45:ALA:N	2.49	0.46
1:C:279:VAL:HG11	1:C:288:ILE:HD11	1.96	0.46
1:A:116:LYS:HA	1:A:121:THR:HG23	1.97	0.46
1:A:385:LEU:C	1:A:385:LEU:CD1	2.89	0.46
1:D:81:HIS:ND1	1:D:160:GLN:CG	2.78	0.46
1:D:99:ALA:HB2	1:B:99:ALA:C	2.33	0.46
1:D:191:LYS:O	1:D:192:VAL:C	2.58	0.46
1:D:245:ALA:HB3	1:D:270:GLU:HG2	1.96	0.46
1:D:318:HIS:CA	1:D:321:ASP:OD2	2.59	0.46
1:C:249:GLY:CA	1:C:267:LEU:O	2.64	0.46
1:C:320:GLY:O	1:C:321:ASP:C	2.59	0.46
1:C:468:GLY:C	1:C:470:ARG:N	2.71	0.46
1:A:108:GLN:H	1:A:108:GLN:CD	2.19	0.46
1:A:127:THR:HG22	1:A:128:PRO:N	2.30	0.46
1:D:254:SER:OG	1:D:316:LEU:HD22	2.16	0.46
1:D:310:VAL:HG12	1:D:313:PHE:CD1	2.51	0.46
1:D:434:PRO:HD2	1:D:451:THR:CG2	2.46	0.46
1:B:278:TYR:CZ	1:B:329:LEU:HD23	2.50	0.46
1:B:431:GLY:O	1:B:432:VAL:CG1	2.59	0.46
1:C:43:ALA:O	1:C:46:VAL:HG12	2.16	0.46
1:C:95:LYS:HG2	1:C:95:LYS:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:359:ALA:C	1:C:362:LEU:N	2.70	0.46
1:A:89:LEU:HD11	1:A:223:VAL:HG12	1.98	0.46
1:A:335:ILE:O	1:A:339:ARG:HG3	2.16	0.46
1:A:373:LEU:HD23	1:A:402:ILE:HG22	1.97	0.46
1:D:23:LEU:C	1:D:26:GLN:HG2	2.40	0.46
1:D:23:LEU:CD1	1:D:24:LEU:N	2.77	0.46
1:B:59:LYS:C	1:B:61:ALA:H	2.23	0.46
1:B:69:LEU:HD23	1:B:69:LEU:HA	1.35	0.46
1:C:24:LEU:CD2	1:C:27:MET:SD	3.02	0.46
1:A:98:ILE:CG2	1:A:99:ALA:N	2.80	0.45
1:A:165:ILE:CG2	1:A:201:PHE:CZ	2.99	0.45
1:A:377:LEU:HD23	1:A:428:LEU:O	2.16	0.45
1:A:427:ILE:C	1:A:428:LEU:HD12	2.41	0.45
1:D:440:LYS:O	1:D:444:GLU:N	2.49	0.45
1:B:6:ILE:CA	1:B:34:HIS:O	2.64	0.45
1:B:119:GLN:HE22	1:B:228:GLU:HG2	1.81	0.45
1:B:384:SER:OG	1:B:385:LEU:N	2.48	0.45
1:A:411:ALA:HA	1:A:412:PRO:HD3	1.62	0.45
1:A:416:ASP:HA	1:A:419:LEU:CD1	2.45	0.45
1:D:122:VAL:O	1:D:124:PHE:HE1	1.97	0.45
1:B:64:GLU:O	1:B:67:LYS:HB2	2.16	0.45
1:B:110:VAL:CG2	1:B:293:ASP:O	2.62	0.45
1:B:127:THR:O	1:B:127:THR:CG2	2.62	0.45
1:B:380:ASP:OD1	1:B:381:THR:CG2	2.49	0.45
1:C:54:ARG:HA	1:C:57:GLN:CD	2.42	0.45
1:C:97:ARG:NH1	1:C:114:GLU:H	2.14	0.45
1:D:256:LEU:HG	1:D:262:ILE:HA	1.96	0.45
1:D:293:ASP:OD1	1:D:293:ASP:C	2.56	0.45
1:D:341:GLU:CD	1:D:344:LYS:HZ2	2.23	0.45
1:B:313:PHE:O	1:B:314:GLN:C	2.53	0.45
1:B:433:ASN:N	1:B:434:PRO:CD	2.80	0.45
1:C:281:ALA:CB	1:C:317:PRO:HB3	2.46	0.45
1:C:449:LEU:C	1:C:450:LYS:HG3	2.42	0.45
1:A:87:THR:N	2:A:900:GDP:O2B	2.44	0.45
1:D:188:ASP:O	1:D:189:PRO:C	2.60	0.45
1:B:176:ILE:HG21	1:B:226:LEU:CD1	2.42	0.45
1:C:24:LEU:HA	1:C:27:MET:HB3	1.97	0.45
1:C:69:LEU:HD23	1:C:69:LEU:HA	1.77	0.45
1:A:220:GLY:C	1:A:223:VAL:HG13	2.42	0.45
1:A:347:GLU:O	1:A:351:LYS:N	2.44	0.45
1:D:242:ASP:C	1:D:242:ASP:OD1	2.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:268:VAL:HB	1:B:303:GLY:O	2.17	0.45
1:B:278:TYR:HE1	1:B:329:LEU:CD2	2.24	0.45
1:C:7:TYR:N	1:C:34:HIS:O	2.48	0.45
1:C:95:LYS:C	1:C:98:ILE:HG23	2.34	0.45
1:C:175:LEU:HD23	1:C:175:LEU:HA	1.57	0.45
1:D:62:GLU:OE1	1:D:65:ARG:NE	2.49	0.45
1:D:89:LEU:HD22	1:D:215:ILE:CD1	2.44	0.45
1:D:182:ILE:HD13	1:D:214:PRO:HB2	1.79	0.45
1:D:316:LEU:HA	1:D:317:PRO:HD3	1.66	0.45
1:B:5:ARG:HD2	1:B:35:ALA:HB1	1.98	0.45
1:B:21:LEU:HD22	1:B:31:TYR:CZ	2.52	0.45
1:C:48:GLU:HA	1:C:51:LYS:NZ	2.32	0.45
1:C:188:ASP:CB	1:C:191:LYS:CB	2.86	0.45
1:A:83:ASP:CA	2:A:900:GDP:H5'	2.46	0.45
1:A:223:VAL:HG23	1:B:361:LEU:HD22	1.98	0.45
1:A:292:MET:CE	1:A:311:LEU:HD13	2.46	0.45
1:A:331:ALA:O	1:A:332:ALA:C	2.59	0.45
1:A:437:SER:C	1:A:440:LYS:N	2.74	0.45
1:D:24:LEU:C	1:D:29:VAL:HG11	2.42	0.45
1:D:155:ASP:OD1	1:D:158:MET:SD	2.75	0.45
1:D:213:ILE:HD12	1:D:226:LEU:CD1	2.47	0.45
1:D:278:TYR:HB3	1:D:326:VAL:HG23	1.96	0.45
1:B:268:VAL:HG21	1:B:302:ALA:CB	2.47	0.45
1:B:461:GLU:O	1:B:464:ASN:N	2.50	0.45
1:C:79:MET:HA	1:C:86:LYS:HD2	1.98	0.45
1:A:3:LYS:O	1:A:4:VAL:HG22	2.17	0.45
1:A:6:ILE:HG21	1:A:21:LEU:HD23	1.98	0.45
1:A:65:ARG:O	1:A:69:LEU:CG	2.61	0.45
1:A:413:THR:HG21	1:A:415:SER:OG	2.16	0.45
1:D:291:MET:SD	1:D:308:VAL:HG21	2.57	0.45
1:D:445:LYS:O	1:D:445:LYS:CE	2.63	0.45
1:B:5:ARG:HD3	1:B:35:ALA:HB1	1.99	0.45
1:B:6:ILE:CB	1:B:34:HIS:HB2	2.44	0.45
1:B:6:ILE:HD13	1:B:36:SER:O	2.17	0.45
1:B:211:ILE:HG21	1:B:229:MET:HE2	1.99	0.45
1:C:274:ARG:O	1:C:277:ASP:OD1	2.35	0.45
1:A:181:LYS:HD3	2:A:900:GDP:C5	2.52	0.45
1:A:190:GLU:HG3	1:A:194:ARG:CZ	2.46	0.45
1:A:192:VAL:O	1:A:195:GLN:HB2	2.16	0.45
1:A:257:ASP:N	1:A:261:GLY:O	2.42	0.45
1:A:288:ILE:HD13	1:A:291:MET:HE3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:350:GLU:O	1:A:351:LYS:C	2.60	0.45
1:D:213:ILE:HD12	1:D:226:LEU:HD13	1.98	0.45
1:B:268:VAL:HG21	1:B:302:ALA:HB1	1.99	0.45
1:B:290:ALA:HB3	1:B:311:LEU:CB	2.46	0.45
1:C:77:VAL:O	1:C:147:ALA:HA	2.17	0.45
1:A:71:ARG:HA	1:A:240:ARG:CG	2.47	0.45
1:D:62:GLU:O	1:D:63:GLU:C	2.59	0.45
1:D:145:ASP:O	1:D:146:ILE:HG13	2.17	0.45
1:D:452:PHE:HB3	1:D:458:LEU:HB2	1.99	0.45
1:B:427:ILE:CD1	1:B:449:LEU:HD23	2.37	0.45
1:A:225:ASP:O	1:A:228:GLU:N	2.50	0.44
1:D:253:GLU:HB2	1:D:265:ASN:HB2	1.99	0.44
1:D:372:GLU:HG3	1:D:404:ILE:HD11	1.98	0.44
1:D:463:ARG:O	1:D:464:ASN:C	2.60	0.44
1:B:13:LEU:HD21	1:B:47:ARG:HA	1.99	0.44
1:B:381:THR:N	1:B:409:VAL:CG1	2.80	0.44
1:C:384:SER:OG	1:C:455:ILE:HD11	2.17	0.44
1:C:427:ILE:CG2	1:C:449:LEU:HD11	2.45	0.44
1:A:190:GLU:HG2	1:A:194:ARG:HH21	1.81	0.44
1:A:197:MET:HE1	1:B:255:LYS:HA	2.00	0.44
1:A:223:VAL:CG2	1:A:224:GLN:N	2.79	0.44
1:D:81:HIS:CB	1:D:160:GLN:HB2	2.47	0.44
1:D:464:ASN:O	1:D:465:MET:C	2.60	0.44
1:C:56:LEU:HD12	1:C:56:LEU:C	2.43	0.44
1:C:170:ALA:HB1	1:C:456:TYR:CD2	2.51	0.44
1:C:250:VAL:N	1:C:267:LEU:O	2.46	0.44
1:A:393:ALA:C	1:A:395:GLU:H	2.24	0.44
1:D:16:GLU:CD	1:D:17:CYS:CA	2.90	0.44
1:D:346:ARG:O	1:D:350:GLU:HG3	2.16	0.44
1:B:417:VAL:O	1:B:420:ALA:CA	2.65	0.44
1:A:257:ASP:OD2	1:A:260:ALA:HB3	2.17	0.44
1:A:278:TYR:CE2	1:A:329:LEU:N	2.86	0.44
1:D:157:ILE:HG22	1:D:199:ARG:NH2	2.33	0.44
1:D:354:ARG:O	1:D:357:THR:CG2	2.65	0.44
1:B:411:ALA:HB2	1:B:434:PRO:CG	2.42	0.44
1:C:367:GLU:H	1:C:367:GLU:HG2	1.61	0.44
1:C:462:VAL:O	1:C:466:VAL:CG1	2.65	0.44
1:A:190:GLU:CG	1:A:194:ARG:HE	2.22	0.44
1:A:219:THR:O	1:B:356:ARG:HA	2.18	0.44
1:A:253:GLU:CB	1:A:265:ASN:HB2	2.46	0.44
1:A:326:VAL:CG1	1:A:327:PRO:CD	2.93	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:114:GLU:HG2	1:D:123:VAL:CG2	2.47	0.44
1:B:21:LEU:HA	1:B:21:LEU:HD23	1.67	0.44
1:B:231:LEU:O	1:B:233:LEU:N	2.50	0.44
1:A:52:GLU:O	1:A:56:LEU:HG	2.17	0.44
1:A:377:LEU:CD2	1:A:428:LEU:HB2	2.47	0.44
1:D:22:GLU:O	1:D:25:ASP:HB2	2.17	0.44
1:D:176:ILE:HD11	1:D:233:LEU:CD1	2.48	0.44
1:D:378:ARG:HB3	1:D:410:GLY:O	2.17	0.44
1:B:326:VAL:HG13	1:B:327:PRO:HD2	1.99	0.44
1:C:274:ARG:O	1:C:275:VAL:C	2.58	0.44
1:A:44:GLU:CA	1:A:47:ARG:HB2	2.48	0.44
1:A:82:VAL:N	1:A:160:GLN:OE1	2.50	0.44
1:D:346:ARG:C	1:D:348:GLU:N	2.74	0.44
1:D:440:LYS:O	1:D:441:LYS:C	2.60	0.44
1:B:263:ILE:CG2	1:B:311:LEU:HD21	2.27	0.44
1:B:268:VAL:N	1:B:306:SER:O	2.40	0.44
1:B:381:THR:N	1:B:409:VAL:HG11	2.33	0.44
1:B:394:ARG:O	1:B:396:SER:N	2.28	0.44
1:C:47:ARG:CD	1:C:47:ARG:C	2.90	0.44
1:C:155:ASP:CB	1:C:158:MET:CE	2.86	0.44
1:C:184:LEU:HB3	1:C:185:PRO:HD2	2.00	0.44
1:C:229:MET:O	1:C:230:ILE:C	2.60	0.44
1:C:263:ILE:HG22	1:C:311:LEU:HD23	1.97	0.44
1:C:418:LEU:HA	1:C:421:GLN:OE1	2.18	0.44
1:A:72:ARG:HB2	1:A:73:PRO:HD2	2.00	0.44
1:A:291:MET:HG2	1:A:310:VAL:HG22	1.99	0.44
1:D:23:LEU:O	1:D:24:LEU:C	2.60	0.44
1:D:452:PHE:CD2	1:D:458:LEU:CD2	3.01	0.44
1:B:236:LEU:HD23	1:B:236:LEU:C	2.43	0.44
1:B:256:LEU:CD1	1:B:316:LEU:CD1	2.95	0.44
1:B:379:ALA:O	1:B:380:ASP:OD1	2.36	0.44
1:B:401:LYS:O	1:B:401:LYS:HG2	2.18	0.44
1:C:255:LYS:HG2	1:C:263:ILE:CG1	2.48	0.44
1:C:421:GLN:CG	1:C:445:LYS:CE	2.96	0.44
1:A:141:ALA:HB2	1:A:250:VAL:HG23	1.98	0.44
1:D:73:PRO:HD2	1:D:73:PRO:O	2.18	0.44
1:B:151:ILE:O	1:B:180:ASN:N	2.50	0.44
1:B:335:ILE:O	1:B:336:ALA:C	2.60	0.44
1:C:64:GLU:O	1:C:68:SER:N	2.51	0.44
1:C:71:ARG:CA	1:C:240:ARG:HG2	2.48	0.44
1:C:259:GLN:O	1:C:259:GLN:HG3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:353:ARG:O	1:C:357:THR:OG1	2.36	0.44
1:A:92:TYR:CE2	1:A:223:VAL:CG1	2.97	0.43
1:A:293:ASP:OD1	1:A:293:ASP:C	2.61	0.43
1:D:157:ILE:HG21	1:D:199:ARG:NH2	2.30	0.43
1:D:213:ILE:HD13	1:D:226:LEU:HD13	2.00	0.43
1:D:279:VAL:N	1:D:326:VAL:CG2	2.77	0.43
1:D:376:ILE:HG22	1:D:377:LEU:N	2.33	0.43
1:B:310:VAL:HB	1:B:313:PHE:HZ	1.83	0.43
1:B:342:GLU:O	1:B:343:ARG:C	2.57	0.43
1:A:4:VAL:HG12	1:A:5:ARG:N	2.33	0.43
1:A:81:HIS:O	1:A:83:ASP:N	2.50	0.43
1:D:13:LEU:N	1:D:13:LEU:HD23	2.23	0.43
1:D:376:ILE:HG23	1:D:406:LEU:O	2.18	0.43
1:B:147:ALA:HB3	1:B:168:ALA:HB1	1.97	0.43
1:C:84:HIS:CE1	1:C:161:THR:OG1	2.71	0.43
1:C:116:LYS:HG2	1:C:121:THR:HG21	1.99	0.43
1:C:414:GLU:O	1:C:415:SER:C	2.61	0.43
1:C:465:MET:HE2	1:C:465:MET:HB3	1.87	0.43
1:A:249:GLY:O	1:A:322:VAL:HG13	2.19	0.43
1:A:373:LEU:HD12	1:A:374:ASN:N	2.32	0.43
1:A:375:LEU:CD1	1:A:404:ILE:HD13	2.42	0.43
1:A:440:LYS:O	1:A:444:GLU:HG2	2.18	0.43
1:D:8:GLN:O	1:D:11:LYS:N	2.50	0.43
1:A:157:ILE:HB	1:A:199:ARG:HH22	1.83	0.43
1:A:303:GLY:O	1:A:306:SER:CB	2.66	0.43
1:A:376:ILE:HG13	1:A:427:ILE:HG23	2.00	0.43
1:D:193:LYS:O	1:D:197:MET:HG3	2.19	0.43
1:B:413:THR:O	1:B:416:ASP:HB2	2.17	0.43
1:B:434:PRO:HB3	1:B:437:SER:OG	2.18	0.43
1:C:66:ARG:O	1:C:69:LEU:HG	2.16	0.43
1:C:117:THR:OG1	1:C:119:GLN:N	2.51	0.43
1:C:170:ALA:O	1:C:454:ILE:CG2	2.59	0.43
1:C:202:VAL:O	1:C:210:ALA:HB3	2.18	0.43
1:A:206:TYR:CE2	1:B:316:LEU:CD1	2.77	0.43
1:A:423:ALA:HB1	1:A:425:ALA:H	1.83	0.43
1:A:424:ASN:CG	1:A:424:ASN:O	2.61	0.43
1:B:77:VAL:O	1:B:77:VAL:HG13	2.18	0.43
1:B:379:ALA:HB2	1:B:384:SER:HG	1.73	0.43
1:B:393:ALA:O	1:B:394:ARG:C	2.54	0.43
1:B:455:ILE:CD1	1:B:456:TYR:N	2.81	0.43
1:C:75:VAL:HB	1:C:144:ALA:HA	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:96:SER:OG	1:C:97:ARG:HG2	2.19	0.43
1:A:46:VAL:C	1:A:50:VAL:HG23	2.43	0.43
1:A:95:LYS:O	1:A:96:SER:C	2.58	0.43
1:D:54:ARG:O	1:D:57:GLN:HB2	2.19	0.43
1:D:188:ASP:CG	1:D:191:LYS:HB2	2.44	0.43
1:D:226:LEU:O	1:D:230:ILE:HG13	2.19	0.43
1:D:452:PHE:CD1	1:D:458:LEU:HB2	2.52	0.43
1:C:80:GLY:N	1:C:86:LYS:HZ3	2.15	0.43
1:A:414:GLU:O	1:A:417:VAL:HB	2.18	0.43
1:D:186:GLN:OE1	1:D:186:GLN:HA	2.18	0.43
1:D:271:GLY:O	1:D:304:PRO:HD3	2.18	0.43
1:B:6:ILE:CG2	1:B:34:HIS:CB	2.72	0.43
1:B:153:ALA:HB3	1:B:187:ALA:HB1	2.01	0.43
1:C:27:MET:HG2	1:C:27:MET:O	2.17	0.43
1:A:257:ASP:HB3	1:A:260:ALA:HB3	2.01	0.43
1:A:430:PHE:HB2	1:A:458:LEU:HD12	1.99	0.43
1:D:137:ARG:NH2	1:C:205:GLU:HB3	2.32	0.43
1:D:195:GLN:O	1:D:199:ARG:HD2	2.19	0.43
1:D:254:SER:HA	1:D:264:ALA:HA	1.99	0.43
1:D:375:LEU:CD1	1:D:376:ILE:N	2.73	0.43
1:C:347:GLU:HA	1:C:350:GLU:HG2	2.00	0.43
1:C:412:PRO:HD2	1:C:435:PRO:CD	2.45	0.43
1:D:88:THR:HG21	1:D:218:LYS:HD2	2.00	0.43
1:B:71:ARG:HA	1:B:240:ARG:HA	1.99	0.43
1:B:296:GLY:O	1:B:297:ASN:C	2.62	0.43
1:C:169:LYS:HD2	1:C:201:PHE:HZ	1.82	0.43
1:A:244:ASN:C	1:A:245:ALA:O	2.54	0.43
1:B:147:ALA:O	1:B:148:VAL:C	2.62	0.43
1:A:46:VAL:O	1:A:47:ARG:C	2.62	0.42
1:A:86:LYS:HG3	1:A:87:THR:N	2.34	0.42
1:A:157:ILE:HD12	1:A:195:GLN:CB	2.43	0.42
1:A:417:VAL:HG13	1:A:447:VAL:HG21	2.01	0.42
1:D:179:ILE:H	1:D:179:ILE:HD12	1.84	0.42
1:D:213:ILE:CD1	1:D:226:LEU:CD1	2.97	0.42
1:B:5:ARG:O	1:B:6:ILE:C	2.61	0.42
1:B:147:ALA:HB2	1:B:173:ALA:HB3	1.99	0.42
1:B:379:ALA:O	1:B:380:ASP:CB	2.67	0.42
1:B:419:LEU:O	1:B:422:THR:CB	2.58	0.42
1:C:151:ILE:CG2	1:C:156:GLY:C	2.92	0.42
1:A:419:LEU:O	1:A:423:ALA:CB	2.67	0.42
1:D:279:VAL:N	1:D:326:VAL:HG22	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:419:LEU:HA	1:D:422:THR:OG1	2.19	0.42
1:C:4:VAL:CG1	1:C:8:GLN:CD	2.90	0.42
1:C:335:ILE:O	1:C:338:GLU:CB	2.67	0.42
1:C:335:ILE:O	1:C:338:GLU:HB3	2.18	0.42
1:C:421:GLN:HG2	1:C:445:LYS:CE	2.49	0.42
1:A:379:ALA:HB3	1:A:385:LEU:HD23	1.99	0.42
1:A:450:LYS:HB3	1:A:452:PHE:CE2	2.54	0.42
1:B:392:LEU:HD21	1:B:459:VAL:HG22	2.01	0.42
1:C:74:PRO:HA	1:C:145:ASP:OD2	2.19	0.42
1:C:182:ILE:CG2	1:C:183:ASP:N	2.82	0.42
1:C:293:ASP:OD2	1:C:297:ASN:HB2	2.19	0.42
1:C:375:LEU:HD22	1:C:426:ALA:HB3	2.02	0.42
1:A:70:PRO:O	1:A:240:ARG:CB	2.59	0.42
1:A:280:VAL:HG13	1:A:324:GLU:HB2	2.02	0.42
1:D:380:ASP:OD2	1:D:431:GLY:HA3	2.19	0.42
1:B:414:GLU:O	1:B:417:VAL:N	2.46	0.42
1:C:195:GLN:HA	1:C:198:GLU:CG	2.45	0.42
1:C:250:VAL:HG22	1:C:320:GLY:O	2.19	0.42
1:C:285:TYR:HB2	1:C:332:ALA:HB1	2.01	0.42
1:C:361:LEU:O	1:C:364:ALA:HB2	2.20	0.42
1:C:387:ALA:O	1:C:388:ILE:C	2.62	0.42
1:D:64:GLU:CD	1:D:64:GLU:C	2.87	0.42
1:D:165:ILE:HD13	1:D:165:ILE:HG21	1.78	0.42
1:D:373:LEU:O	1:D:404:ILE:CB	2.66	0.42
1:D:461:GLU:OE1	1:D:464:ASN:CG	2.61	0.42
1:A:293:ASP:OD1	1:A:293:ASP:O	2.38	0.42
1:A:423:ALA:C	1:A:425:ALA:H	2.28	0.42
1:D:279:VAL:CA	1:D:326:VAL:HG22	2.49	0.42
1:D:439:LYS:C	1:D:442:ALA:HB3	2.45	0.42
1:C:21:LEU:O	1:C:25:ASP:HB2	2.19	0.42
1:C:51:LYS:HE2	1:C:51:LYS:HB2	1.82	0.42
1:A:377:LEU:HD21	1:A:428:LEU:HB2	2.01	0.42
1:D:153:ALA:CB	1:D:187:ALA:HB1	2.50	0.42
1:B:275:VAL:HG12	1:B:276:GLY:N	2.34	0.42
1:B:389:GLN:O	1:B:398:GLU:CB	2.67	0.42
1:B:427:ILE:CD1	1:B:449:LEU:HD21	2.36	0.42
1:C:74:PRO:HD3	1:C:234:ALA:CB	2.50	0.42
1:A:343:ARG:NH2	1:A:347:GLU:OE2	2.53	0.42
1:D:23:LEU:O	1:D:26:GLN:CG	2.60	0.42
1:D:89:LEU:HD23	1:D:150:VAL:CG2	2.50	0.42
1:D:223:VAL:O	1:D:227:LEU:HD12	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:278:TYR:CD1	1:D:329:LEU:HB3	2.54	0.42
1:D:283:GLU:OE1	1:D:343:ARG:NE	2.53	0.42
1:D:463:ARG:O	1:D:465:MET:N	2.52	0.42
1:B:20:LEU:HD12	1:B:20:LEU:C	2.36	0.42
1:B:193:LYS:HD3	1:B:205:GLU:OE1	2.20	0.42
1:B:251:ILE:HD13	1:B:251:ILE:HA	1.85	0.42
1:B:326:VAL:CG1	1:B:327:PRO:HD2	2.49	0.42
1:B:328:ASP:OD1	1:B:331:ALA:CB	2.68	0.42
1:B:393:ALA:CA	1:B:398:GLU:HA	2.48	0.42
1:C:94:ARG:O	1:C:96:SER:OG	2.30	0.42
1:C:248:ARG:HB2	1:C:270:GLU:HB2	2.02	0.42
1:A:229:MET:O	1:A:232:LEU:HB3	2.20	0.42
1:A:373:LEU:HD21	1:A:465:MET:O	2.16	0.42
1:D:378:ARG:HH22	1:D:406:LEU:HD21	1.81	0.42
1:B:79:MET:HA	1:B:86:LYS:HD3	2.01	0.42
1:B:277:ASP:HB3	1:B:325:TRP:CD1	2.55	0.42
1:B:280:VAL:HG11	1:B:335:ILE:CG2	2.50	0.42
1:B:285:TYR:O	1:B:314:GLN:HB2	2.19	0.42
1:B:348:GLU:O	1:B:350:GLU:N	2.53	0.42
1:C:236:LEU:C	1:C:236:LEU:CD2	2.82	0.42
1:C:428:LEU:HB3	1:C:458:LEU:HD11	2.02	0.42
1:A:5:ARG:NH2	1:A:8:GLN:HA	2.34	0.42
1:A:373:LEU:HD21	1:A:465:MET:HB3	2.02	0.42
1:A:376:ILE:CG1	1:A:427:ILE:HG12	2.47	0.42
1:A:422:THR:HB	1:C:406:LEU:CD2	2.41	0.42
1:D:272:THR:HG22	1:D:274:ARG:HG3	2.01	0.42
1:B:42:ASP:O	1:B:43:ALA:C	2.60	0.42
1:B:116:LYS:HD2	1:B:121:THR:HA	2.02	0.42
1:B:273:PHE:O	1:B:301:GLU:HA	2.20	0.42
1:B:419:LEU:C	1:B:422:THR:CG2	2.73	0.42
1:C:81:HIS:CB	1:C:84:HIS:HD2	2.16	0.42
1:C:101:LYS:CB	1:C:105:GLY:C	2.93	0.42
1:C:427:ILE:CG1	1:C:449:LEU:HD12	2.46	0.42
1:C:462:VAL:O	1:C:466:VAL:HG12	2.19	0.42
1:A:53:GLN:HA	1:A:56:LEU:HD12	2.00	0.41
1:A:143:VAL:HG13	1:A:267:LEU:CD2	2.50	0.41
1:A:430:PHE:HE1	1:A:454:ILE:HA	1.85	0.41
1:D:215:ILE:HG22	1:D:222:GLY:C	2.44	0.41
1:D:285:TYR:CD2	1:D:333:LYS:HG3	2.55	0.41
1:D:373:LEU:CG	1:D:374:ASN:H	2.28	0.41
1:C:64:GLU:O	1:C:68:SER:HB3	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:216:SER:CB	1:C:219:THR:OG1	2.67	0.41
1:C:359:ALA:CA	1:C:362:LEU:HA	2.34	0.41
1:C:384:SER:O	1:C:388:ILE:HG13	2.20	0.41
1:A:188:ASP:OD1	1:A:188:ASP:C	2.62	0.41
1:D:293:ASP:HB2	1:D:299:ARG:CZ	2.43	0.41
1:B:181:LYS:HB3	1:B:184:LEU:HD13	2.02	0.41
1:C:170:ALA:HB3	1:C:456:TYR:CD2	2.55	0.41
1:C:281:ALA:HB3	1:C:317:PRO:HB3	2.02	0.41
1:A:23:LEU:CD1	1:A:50:VAL:HG22	2.50	0.41
1:A:92:TYR:CZ	1:B:356:ARG:O	2.67	0.41
1:A:149:ILE:HG13	1:A:165:ILE:CG1	2.49	0.41
1:A:329:LEU:HD23	1:A:329:LEU:C	2.41	0.41
1:D:179:ILE:HB	1:D:214:PRO:CB	2.50	0.41
1:D:292:MET:HG3	1:D:293:ASP:N	2.35	0.41
1:B:59:LYS:HE2	1:B:59:LYS:HB2	1.69	0.41
1:C:353:ARG:O	1:C:357:THR:CB	2.68	0.41
1:A:3:LYS:O	1:A:4:VAL:HG23	2.20	0.41
1:A:15:MET:HE3	1:A:20:LEU:HD22	1.14	0.41
1:D:285:TYR:CD2	1:D:333:LYS:CG	3.04	0.41
1:B:186:GLN:N	1:B:186:GLN:CD	2.76	0.41
1:C:47:ARG:NH1	1:C:51:LYS:HG3	2.35	0.41
1:C:346:ARG:O	1:C:349:GLU:N	2.54	0.41
1:D:195:GLN:HB3	1:D:199:ARG:NH1	2.35	0.41
1:D:373:LEU:O	1:D:404:ILE:CD1	2.69	0.41
1:B:237:GLU:C	1:B:238:ASP:OD1	2.58	0.41
1:B:247:PRO:HG3	1:B:272:THR:C	2.37	0.41
1:B:444:GLU:CB	1:B:447:VAL:HB	2.36	0.41
1:B:462:VAL:HG12	1:B:465:MET:SD	2.61	0.41
1:C:47:ARG:C	1:C:51:LYS:HZ3	2.27	0.41
1:C:90:LEU:HD21	1:C:113:PHE:CZ	2.35	0.41
1:C:255:LYS:CG	1:C:263:ILE:HD11	2.50	0.41
1:C:359:ALA:CB	1:C:362:LEU:CB	2.98	0.41
1:A:108:GLN:N	1:A:108:GLN:CD	2.77	0.41
1:A:382:GLN:O	1:A:383:GLY:C	2.64	0.41
1:D:379:ALA:O	1:D:409:VAL:HG22	2.20	0.41
1:D:381:THR:O	1:D:384:SER:N	2.53	0.41
1:B:148:VAL:HG12	1:B:149:ILE:N	2.32	0.41
1:C:98:ILE:HD12	1:C:98:ILE:O	2.21	0.41
1:C:155:ASP:O	1:C:158:MET:HE1	2.11	0.41
1:A:92:TYR:CE1	1:B:358:MET:N	2.89	0.41
1:A:146:ILE:HG12	1:A:174:LYS:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:205:GLU:CG	1:A:206:TYR:HD1	2.33	0.41
1:A:373:LEU:HD12	1:A:374:ASN:H	1.86	0.41
1:A:388:ILE:O	1:A:392:LEU:HG	2.20	0.41
1:B:257:ASP:O	1:B:261:GLY:CA	2.69	0.41
1:C:340:LYS:HE2	1:C:344:LYS:HE2	2.02	0.41
1:D:64:GLU:HA	1:D:67:LYS:HG3	2.02	0.41
1:D:303:GLY:O	1:D:304:PRO:C	2.63	0.41
1:B:16:GLU:HG2	1:B:18:GLN:N	2.36	0.41
1:B:341:GLU:H	1:B:341:GLU:HG2	1.55	0.41
1:B:433:ASN:N	1:B:434:PRO:HD2	2.24	0.41
1:C:141:ALA:HB1	1:C:250:VAL:HG23	2.01	0.41
1:C:237:GLU:O	1:C:238:ASP:C	2.61	0.41
1:C:438:VAL:O	1:C:442:ALA:N	2.48	0.41
1:A:223:VAL:HG21	1:B:361:LEU:HD21	2.03	0.41
1:A:351:LYS:O	1:A:355:PRO:HG2	2.21	0.41
1:A:378:ARG:HA	1:A:408:GLN:O	2.21	0.41
1:D:6:ILE:HG23	1:D:20:LEU:HD21	2.03	0.41
1:D:23:LEU:CA	1:D:26:GLN:HG2	2.50	0.41
1:D:81:HIS:CE1	1:D:160:GLN:HG3	2.56	0.41
1:D:278:TYR:CE1	1:D:329:LEU:HB3	2.56	0.41
1:D:344:LYS:HB2	1:D:344:LYS:HE2	1.75	0.41
1:D:354:ARG:N	1:D:355:PRO:CD	2.82	0.41
1:D:428:LEU:HA	1:D:449:LEU:HD12	2.03	0.41
1:D:441:LYS:HA	1:D:444:GLU:HB2	2.03	0.41
1:B:31:TYR:HB2	1:B:36:SER:OG	2.21	0.41
1:B:62:GLU:HG3	1:B:65:ARG:HE	1.84	0.41
1:B:128:PRO:CD	1:B:129:GLY:H	2.30	0.41
1:B:143:VAL:HG22	1:B:250:VAL:HG11	2.03	0.41
1:B:242:ASP:C	1:B:244:ASN:H	2.29	0.41
1:B:280:VAL:HG11	1:B:335:ILE:HG21	2.02	0.41
1:B:333:LYS:O	1:B:333:LYS:HG2	2.21	0.41
1:B:385:LEU:CD2	1:B:409:VAL:HG22	2.51	0.41
1:B:458:LEU:HD23	1:B:458:LEU:C	2.46	0.41
1:C:92:TYR:CD1	1:C:92:TYR:C	2.99	0.41
1:C:168:ALA:HB1	1:C:173:ALA:HB3	2.02	0.41
1:C:354:ARG:HA	1:C:357:THR:OG1	2.21	0.41
1:C:413:THR:O	1:C:417:VAL:HG23	2.20	0.41
1:C:435:PRO:O	1:C:439:LYS:N	2.47	0.41
1:C:447:VAL:CG1	1:C:448:LEU:H	2.33	0.41
1:A:5:ARG:O	1:A:5:ARG:CG	2.55	0.41
1:A:76:VAL:CG2	1:A:230:ILE:HG21	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:6:ILE:HG23	1:D:20:LEU:CD2	2.50	0.41
1:D:205:GLU:CD	1:D:206:TYR:HE1	2.28	0.41
1:B:280:VAL:CG2	1:B:281:ALA:N	2.83	0.41
1:C:242:ASP:HA	1:C:243:PRO:HD2	1.90	0.41
1:A:74:PRO:HG2	1:A:122:VAL:HG13	2.03	0.40
1:A:82:VAL:HG13	1:A:83:ASP:N	2.35	0.40
1:A:157:ILE:CD1	1:A:199:ARG:CZ	2.77	0.40
1:A:354:ARG:N	1:A:355:PRO:CD	2.84	0.40
1:A:418:LEU:HD21	1:C:408:GLN:HE21	1.78	0.40
1:B:59:LYS:O	1:B:61:ALA:CA	2.67	0.40
1:C:277:ASP:OD2	1:C:325:TRP:HD1	2.03	0.40
1:C:346:ARG:O	1:C:347:GLU:C	2.63	0.40
1:A:376:ILE:CD1	1:A:427:ILE:HG23	2.51	0.40
1:A:378:ARG:HH12	1:A:416:ASP:CG	2.29	0.40
1:D:213:ILE:HD13	1:D:226:LEU:HA	2.03	0.40
1:B:376:ILE:C	1:B:427:ILE:HA	2.41	0.40
1:C:359:ALA:O	1:C:361:LEU:C	2.63	0.40
1:A:197:MET:O	1:A:200:GLY:N	2.53	0.40
1:A:439:LYS:C	1:A:442:ALA:CB	2.91	0.40
1:D:279:VAL:HA	1:D:326:VAL:HG22	2.03	0.40
1:D:351:LYS:NZ	1:C:182:ILE:O	2.52	0.40
1:B:33:SER:N	1:B:36:SER:OG	2.55	0.40
1:B:242:ASP:OD1	1:B:244:ASN:N	2.40	0.40
1:C:72:ARG:H	1:C:72:ARG:HG3	1.59	0.40
1:C:455:ILE:O	1:C:458:LEU:N	2.55	0.40
1:C:464:ASN:C	1:C:466:VAL:N	2.72	0.40
1:A:141:ALA:O	1:A:143:VAL:HG23	2.20	0.40
1:A:374:ASN:O	1:A:425:ALA:CA	2.62	0.40
1:D:82:VAL:HG12	1:D:160:GLN:NE2	2.36	0.40
1:D:283:GLU:OE1	1:D:343:ARG:CZ	2.70	0.40
1:B:67:LYS:C	1:B:69:LEU:H	2.30	0.40
1:B:147:ALA:HB3	1:B:175:LEU:HD23	2.03	0.40
1:B:252:LEU:O	1:B:253:GLU:HG3	2.22	0.40
1:B:278:TYR:OH	1:B:329:LEU:HD23	2.22	0.40
1:B:376:ILE:HG21	1:B:427:ILE:CG2	2.45	0.40
1:C:320:GLY:C	1:C:321:ASP:O	2.60	0.40
1:C:325:TRP:C	1:C:326:VAL:HG23	2.46	0.40
1:A:5:ARG:O	1:A:7:TYR:N	2.55	0.40
1:A:251:ILE:HD13	1:A:251:ILE:HA	1.96	0.40
1:A:274:ARG:NH1	1:A:301:GLU:OE2	2.54	0.40
1:D:22:GLU:OE1	1:D:26:GLN:NE2	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:293:ASP:HB3	1:D:297:ASN:CA	2.52	0.40
1:D:434:PRO:HA	1:D:435:PRO:HD3	1.85	0.40
1:B:76:VAL:CG2	1:B:230:ILE:HG21	2.52	0.40
1:B:257:ASP:O	1:B:261:GLY:N	2.54	0.40
1:B:336:ALA:O	1:B:339:ARG:N	2.55	0.40
1:B:351:LYS:O	1:B:351:LYS:HG3	2.19	0.40
1:B:453:ARG:O	1:B:454:ILE:HD13	2.21	0.40
1:C:108:GLN:CB	1:C:292:MET:HE1	2.51	0.40
1:C:205:GLU:CD	1:C:205:GLU:N	2.73	0.40
1:C:359:ALA:C	1:C:362:LEU:CA	2.95	0.40

All (16) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:354:ARG:NH2	1:C:99:ALA:O[1_455]	1.18	1.02
1:A:33:SER:OG	1:B:334:GLU:OE1[2_556]	1.49	0.71
1:A:18:GLN:NE2	1:A:333:LYS:NZ[1_556]	1.50	0.70
1:A:318:HIS:CE1	1:B:206:TYR:CE1[1_554]	1.77	0.43
1:B:354:ARG:CZ	1:C:99:ALA:O[1_455]	1.78	0.42
1:A:158:MET:CE	1:B:67:LYS:NZ[1_554]	1.84	0.36
1:A:33:SER:OG	1:B:334:GLU:CD[2_556]	1.88	0.32
1:A:334:GLU:OE2	1:B:33:SER:OG[2_556]	1.93	0.27
1:D:391:ILE:CD1	1:B:346:ARG:NH1[1_655]	1.97	0.23
1:D:170:ALA:O	1:B:383:GLY:N[1_655]	1.99	0.21
1:A:33:SER:OG	1:B:334:GLU:OE2[2_556]	2.00	0.20
1:A:33:SER:CB	1:B:334:GLU:OE1[2_556]	2.11	0.09
1:D:328:ASP:OD2	1:C:34:HIS:CE1[2_656]	2.13	0.07
1:A:397:THR:CG2	1:B:228:GLU:OE2[1_554]	2.17	0.03
1:B:354:ARG:NH1	1:C:99:ALA:O[1_455]	2.18	0.02
1:A:334:GLU:OE1	1:B:33:SER:CB[2_556]	2.19	0.01

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	445/473 (94%)	417 (94%)	27 (6%)	1 (0%)	43	72
1	B	453/473 (96%)	407 (90%)	42 (9%)	4 (1%)	14	41
1	C	452/473 (96%)	420 (93%)	28 (6%)	4 (1%)	14	41
1	D	439/473 (93%)	409 (93%)	28 (6%)	2 (0%)	24	55
All	All	1789/1892 (95%)	1653 (92%)	125 (7%)	11 (1%)	21	51

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	404	ILE
1	C	471	GLU
1	B	447	VAL
1	C	294	ALA
1	C	467	LYS
1	B	433	ASN
1	C	188	ASP
1	D	214	PRO
1	B	354	ARG
1	B	128	PRO
1	A	435	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	A	338/382 (88%)	318 (94%)	20 (6%)	18	48
1	B	341/382 (89%)	315 (92%)	26 (8%)	12	36
1	C	336/382 (88%)	319 (95%)	17 (5%)	21	54
1	D	345/382 (90%)	324 (94%)	21 (6%)	17	46
All	All	1360/1528 (89%)	1276 (94%)	84 (6%)	16	45

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

Mol	Chain	Res	Type
1	A	18	GLN
1	A	19	GLU
1	A	26	GLN
1	A	149	ILE
1	A	175	LEU
1	A	188	ASP
1	A	202	VAL
1	A	292	MET
1	A	322	VAL
1	A	326	VAL
1	A	333	LYS
1	A	334	GLU
1	A	373	LEU
1	A	375	LEU
1	A	388	ILE
1	A	392	LEU
1	A	419	LEU
1	A	438	VAL
1	A	465	MET
1	A	466	VAL
1	D	6	ILE
1	D	29	VAL
1	D	67	LYS
1	D	89	LEU
1	D	90	LEU
1	D	122	VAL
1	D	158	MET
1	D	161	THR
1	D	186	GLN
1	D	198	GLU
1	D	206	TYR
1	D	240	ARG
1	D	292	MET
1	D	298	GLN
1	D	301	GLU
1	D	322	VAL
1	D	344	LYS
1	D	351	LYS
1	D	405	LEU
1	D	409	VAL
1	D	444	GLU
1	B	5	ARG

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Mol	Chain	Res	Type
1	B	29	VAL
1	B	36	SER
1	B	38	LEU
1	B	46	VAL
1	B	82	VAL
1	B	86	LYS
1	B	115	VAL
1	B	150	VAL
1	B	158	MET
1	B	182	ILE
1	B	190	GLU
1	B	197	MET
1	B	199	ARG
1	B	224	GLN
1	B	231	LEU
1	B	232	LEU
1	B	323	VAL
1	B	334	GLU
1	B	335	ILE
1	B	341	GLU
1	B	347	GLU
1	B	376	ILE
1	B	404	ILE
1	B	405	LEU
1	B	439	LYS
1	C	29	VAL
1	C	82	VAL
1	C	90	LEU
1	C	107	THR
1	C	109	HIS
1	C	116	LYS
1	C	169	LYS
1	C	193	LYS
1	C	196	LEU
1	C	205	GLU
1	C	218	LYS
1	C	233	LEU
1	C	275	VAL
1	C	344	LYS
1	C	366	GLN
1	C	454	ILE
1	C	467	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	81	HIS
1	A	109	HIS
1	A	269	GLN
1	A	314	GLN
1	A	389	GLN
1	D	26	GLN
1	D	138	GLN
1	D	221	GLN
1	D	389	GLN
1	B	34	HIS
1	B	53	GLN
1	B	195	GLN
1	B	309	GLN
1	C	8	GLN
1	C	34	HIS
1	C	84	HIS
1	C	109	HIS
1	C	309	GLN
1	C	408	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GDP	A	900	-	29,30,30	0.89	1 (3%)	45,47,47	1.55	5 (11%)
2	GDP	C	900	-	29,30,30	0.86	1 (3%)	45,47,47	1.33	5 (11%)

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
2	GDP	A	900	-	-	4/16/32/32	0/3/3/3
2	GDP	C	900	-	-	3/16/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	900	GDP	C5-C4	2.34	1.45	1.38
2	A	900	GDP	C5-C4	2.19	1.44	1.38

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	900	GDP	C5-C4-N3	-5.06	120.33	128.39
2	A	900	GDP	C2-N3-C4	4.16	119.46	112.30
2	C	900	GDP	C5-C4-N3	-4.10	121.86	128.39
2	A	900	GDP	N9-C4-N3	3.73	133.42	125.95
2	C	900	GDP	C2-N3-C4	3.34	118.05	112.30
2	C	900	GDP	N9-C4-N3	3.31	132.57	125.95
2	A	900	GDP	C6-C5-N7	2.48	134.80	130.29
2	C	900	GDP	O2A-PA-O3A	2.21	113.25	107.27
2	A	900	GDP	O6-C6-C5	-2.08	121.05	126.53
2	C	900	GDP	O3A-PB-O1B	-2.04	100.32	111.04

There are no chirality outliers.

All (7) torsion outliers are listed below:

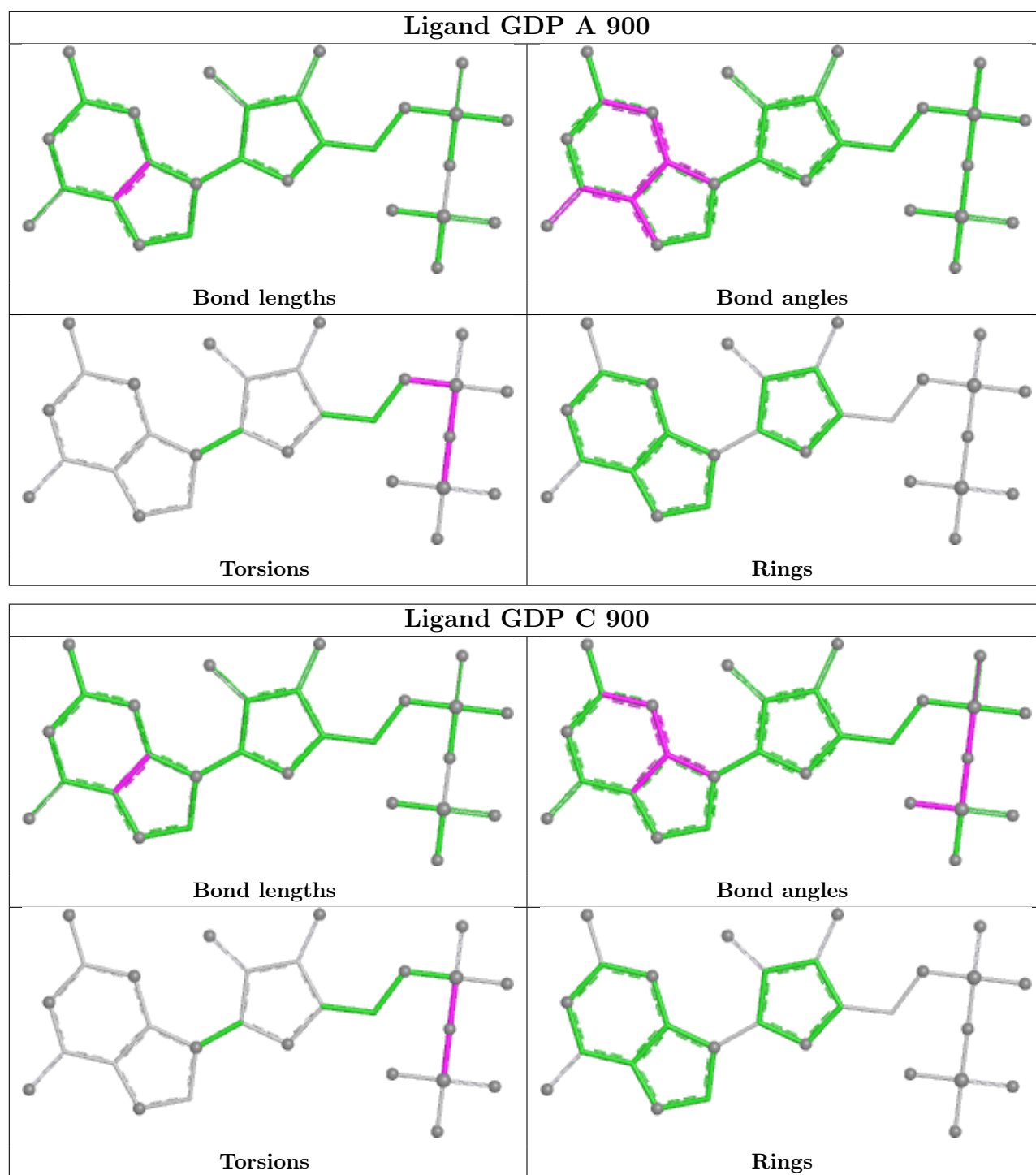
Mol	Chain	Res	Type	Atoms
2	A	900	GDP	PB-O3A-PA-O1A
2	A	900	GDP	C5'-O5'-PA-O1A
2	A	900	GDP	PB-O3A-PA-O2A
2	C	900	GDP	PB-O3A-PA-O1A
2	C	900	GDP	PB-O3A-PA-O2A
2	A	900	GDP	PA-O3A-PB-O1B
2	C	900	GDP	PA-O3A-PB-O1B

There are no ring outliers.

2 monomers are involved in 44 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	900	GDP	36	0
2	C	900	GDP	8	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	451/473 (95%)	0.25	19 (4%) 40 32	7, 36, 75, 93	0
1	B	457/473 (96%)	0.21	24 (5%) 32 24	2, 33, 79, 93	0
1	C	458/473 (96%)	0.21	17 (3%) 45 36	5, 33, 77, 111	0
1	D	447/473 (94%)	0.19	16 (3%) 46 37	2, 33, 70, 112	0
All	All	1813/1892 (95%)	0.21	76 (4%) 40 32	2, 34, 77, 112	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	359	ALA	6.0
1	B	442	ALA	5.5
1	D	184	LEU	4.9
1	A	186	GLN	4.6
1	B	410	GLY	4.5
1	B	30	ALA	4.1
1	D	410	GLY	4.0
1	D	448	LEU	3.9
1	A	466	VAL	3.7
1	A	128	PRO	3.3
1	A	319	PRO	3.3
1	C	355	PRO	3.2
1	B	444	GLU	3.2
1	B	49	LEU	3.2
1	D	357	THR	3.1
1	A	402	ILE	3.1
1	B	454	ILE	3.0
1	C	21	LEU	3.0
1	D	23	LEU	2.9
1	B	404	ILE	2.9
1	C	29	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	27	MET	2.9
1	B	29	VAL	2.9
1	C	43	ALA	2.9
1	B	463	ARG	2.8
1	B	26	GLN	2.8
1	A	409	VAL	2.8
1	B	432	VAL	2.8
1	D	49	LEU	2.7
1	B	459	VAL	2.7
1	C	368	GLU	2.7
1	B	460	ASP	2.7
1	A	354	ARG	2.6
1	C	20	LEU	2.6
1	C	294	ALA	2.6
1	C	440	LYS	2.6
1	D	393	ALA	2.5
1	B	23	LEU	2.5
1	A	417	VAL	2.5
1	A	427	ILE	2.5
1	C	351	LYS	2.5
1	B	416	ASP	2.4
1	A	410	GLY	2.4
1	B	367	GLU	2.4
1	C	331	ALA	2.4
1	D	417	VAL	2.3
1	B	97	ARG	2.3
1	B	443	GLU	2.3
1	D	355	PRO	2.3
1	C	366	GLN	2.3
1	B	31	TYR	2.3
1	A	448	LEU	2.3
1	A	355	PRO	2.3
1	A	368	GLU	2.3
1	C	369	GLY	2.2
1	C	436	GLY	2.2
1	B	399	ASP	2.2
1	A	369	GLY	2.2
1	B	24	LEU	2.2
1	D	41	LYS	2.1
1	A	406	LEU	2.1
1	C	353	ARG	2.1
1	D	459	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	464	ASN	2.1
1	A	385	LEU	2.1
1	C	42	ASP	2.1
1	D	429	ALA	2.1
1	D	434	PRO	2.1
1	C	364	ALA	2.1
1	B	50	VAL	2.0
1	A	426	ALA	2.0
1	D	425	ALA	2.0
1	A	398	GLU	2.0
1	D	446	GLY	2.0
1	C	465	MET	2.0
1	D	447	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

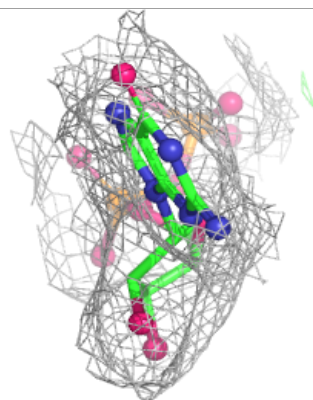
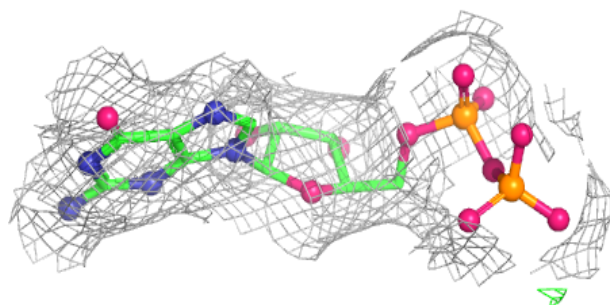
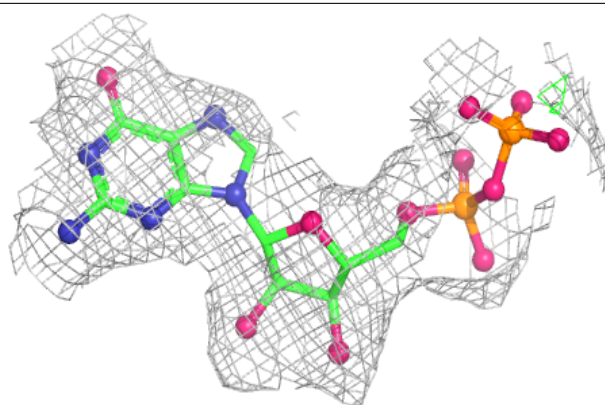
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GDP	A	900	28/28	0.91	0.09	42,49,58,59	0
2	GDP	C	900	28/28	0.91	0.11	46,51,53,54	0

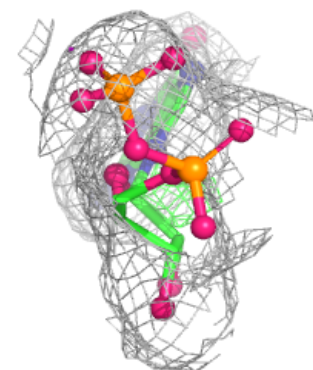
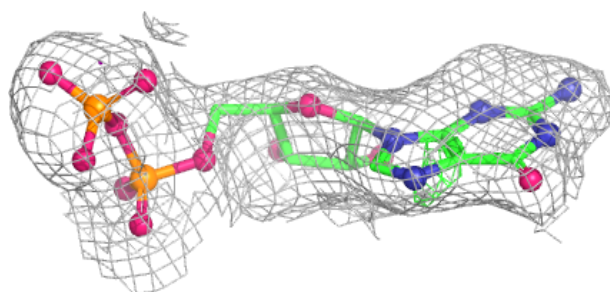
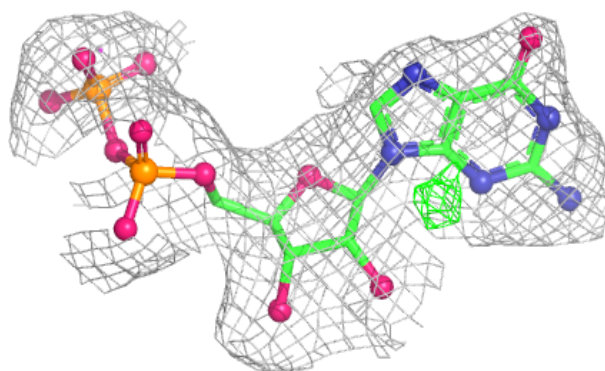
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around GDP A 900:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around GDP C 900:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.