



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 09:02 PM UTC

PDB ID : 2QE7 / pdb_00002qe7
Title : Crystal structure of the f1-atpase from the thermoalkaliphilic bacterium bacillus sp. ta2.a1
Authors : Stocker, A.; Keis, S.; Vonck, J.; Cook, G.M.; Dimroth, P.
Deposited on : 2007-06-25
Resolution : 3.06 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
Xtriage (Phenix)	:	2.0
EDS	:	3.0
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

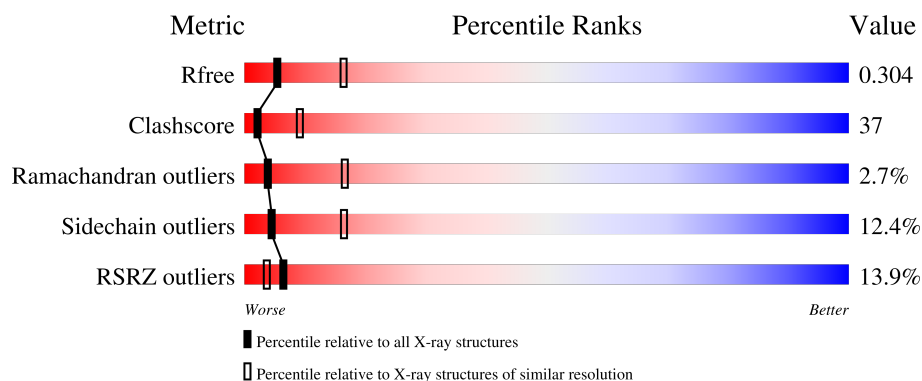
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.06 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	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)

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	502	5% 53% 33% 8% 6%
1	B	502	7% 52% 32% 10% 6%
1	C	502	5% 53% 33% 8% 6%
2	D	462	5% 52% 37% 9% .
2	E	462	3% 54% 35% 9% .

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Mol	Chain	Length	Quality of chain
2	F	462	4% 51% 38% 9%
3	G	286	68% 8% 55% 16% 21%
4	H	135	74% 13% 76% 11%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 30018 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 ATP synthase subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	474	Total	C	N	O	S	0	0	0
			3640	2295	628	703	14			
1	B	474	Total	C	N	O	S	0	0	0
			3640	2295	628	703	14			
1	C	474	Total	C	N	O	S	0	0	0
			3640	2295	628	703	14			

- Molecule 2 is a protein called ATP synthase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	461	Total	C	N	O	S	0	0	0
			3522	2218	608	683	13			
2	E	461	Total	C	N	O	S	0	0	0
			3522	2218	608	683	13			
2	F	461	Total	C	N	O	S	0	0	0
			3522	2218	608	683	13			

- Molecule 3 is a protein called ATP synthase subunit gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	227	Total	C	N	O	S	0	227	0
			5382	3396	954	1005	27			

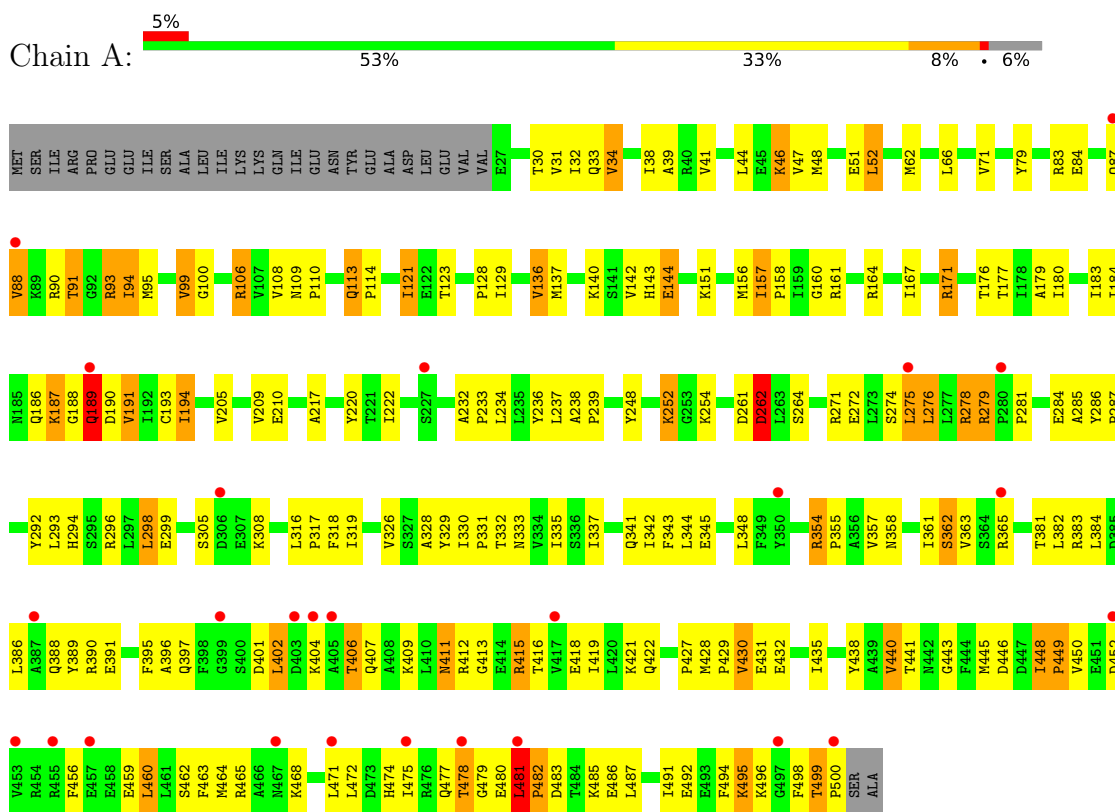
- Molecule 4 is a protein called ATP synthase subunit epsilon.

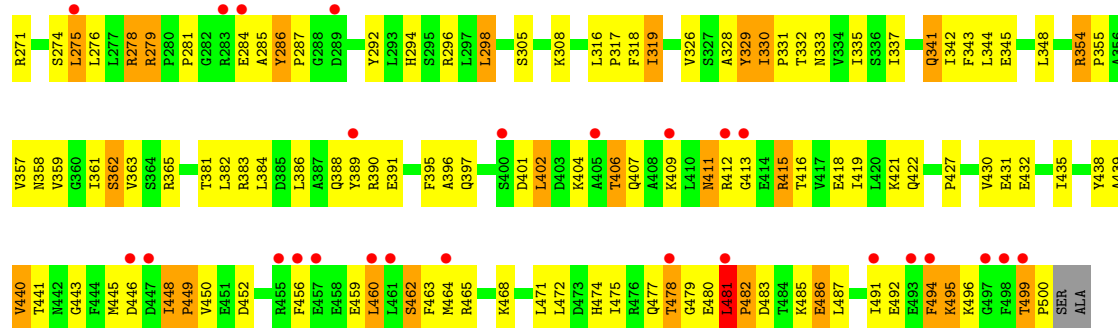
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	135	Total	C	N	O	S	0	135	0
			3150	1974	579	591	6			

3 Residue-property plots [i](#)

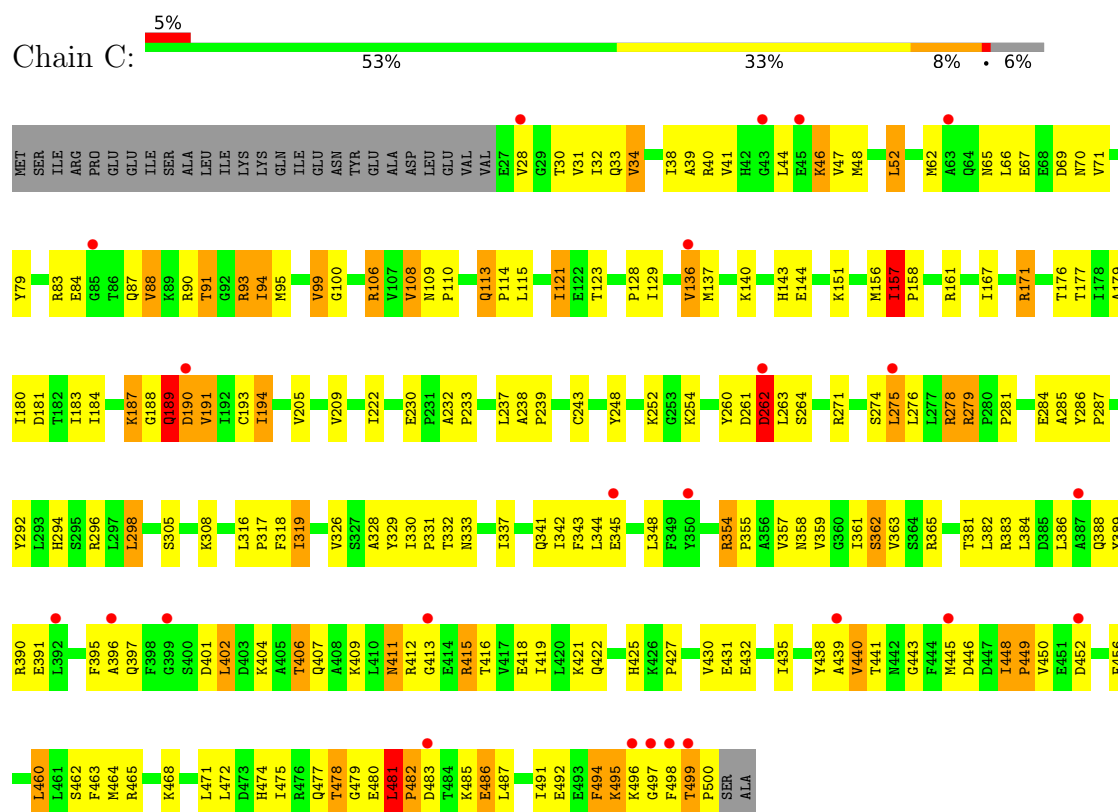
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

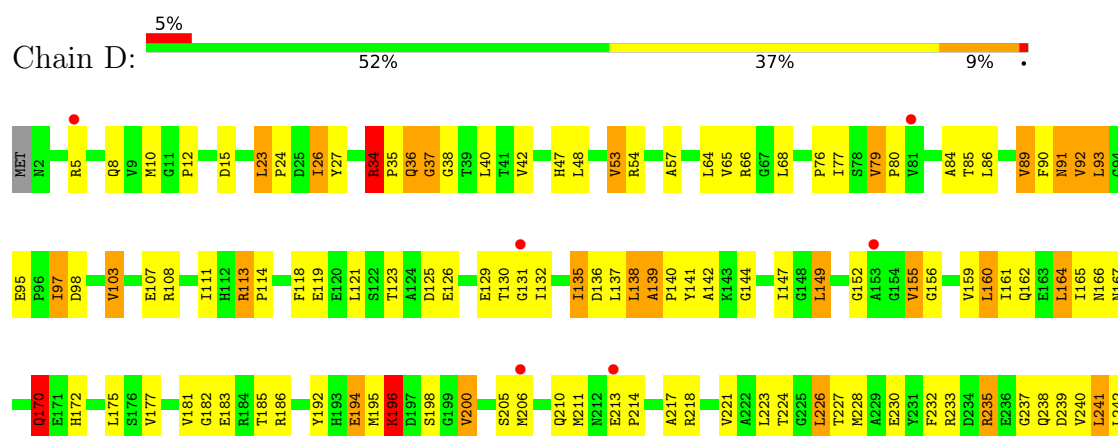


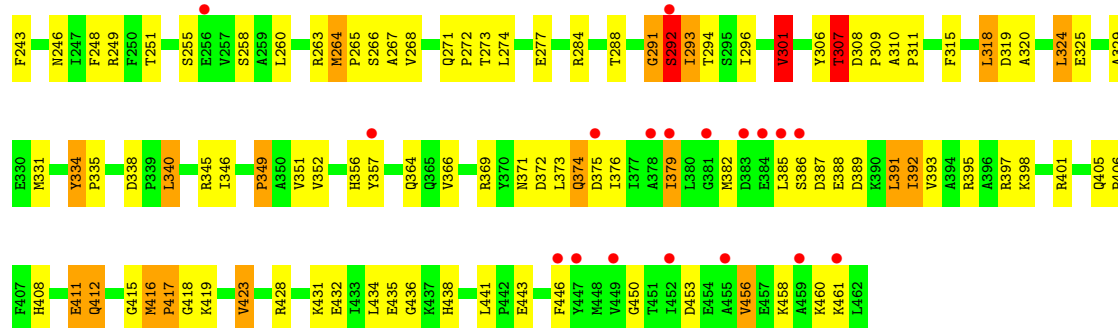


• Molecule 1: ATP synthase subunit alpha

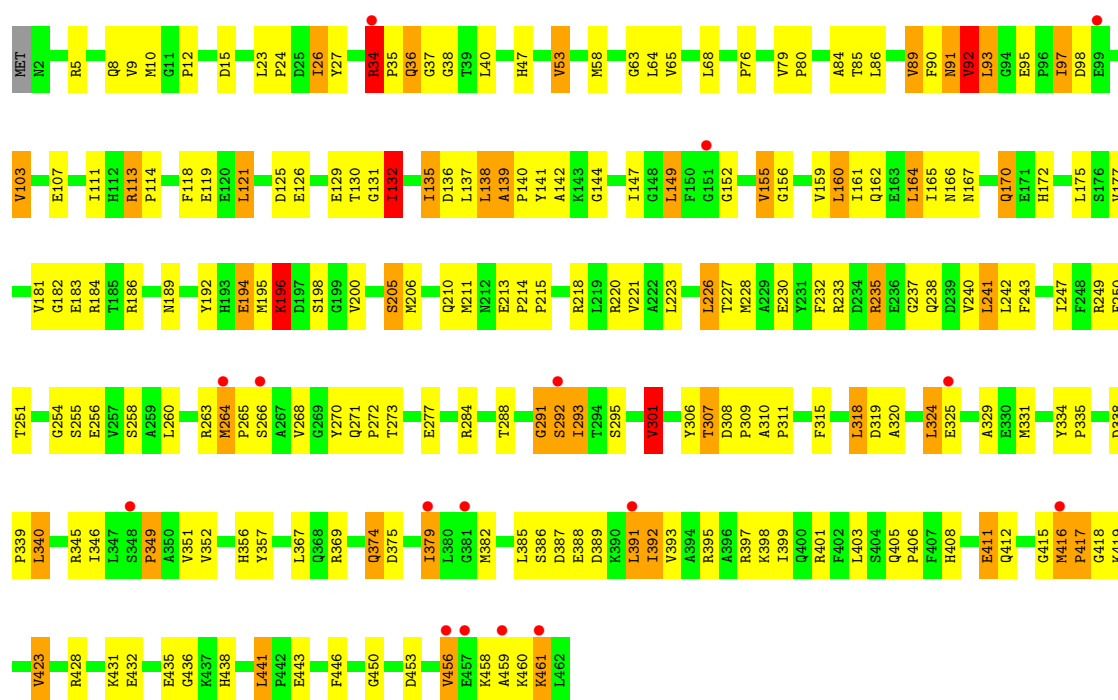


• Molecule 2: ATP synthase subunit beta

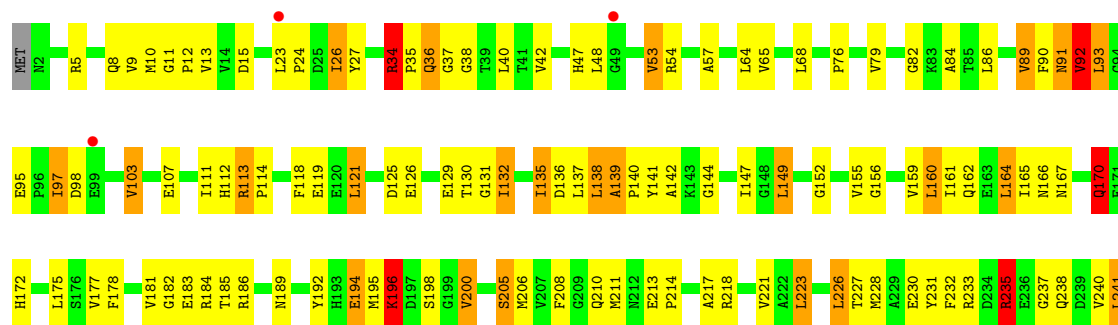


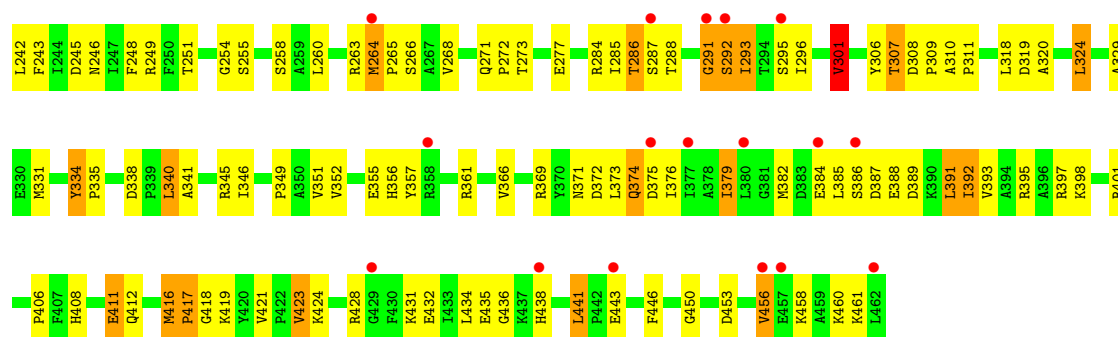


• Molecule 2: ATP synthase subunit beta

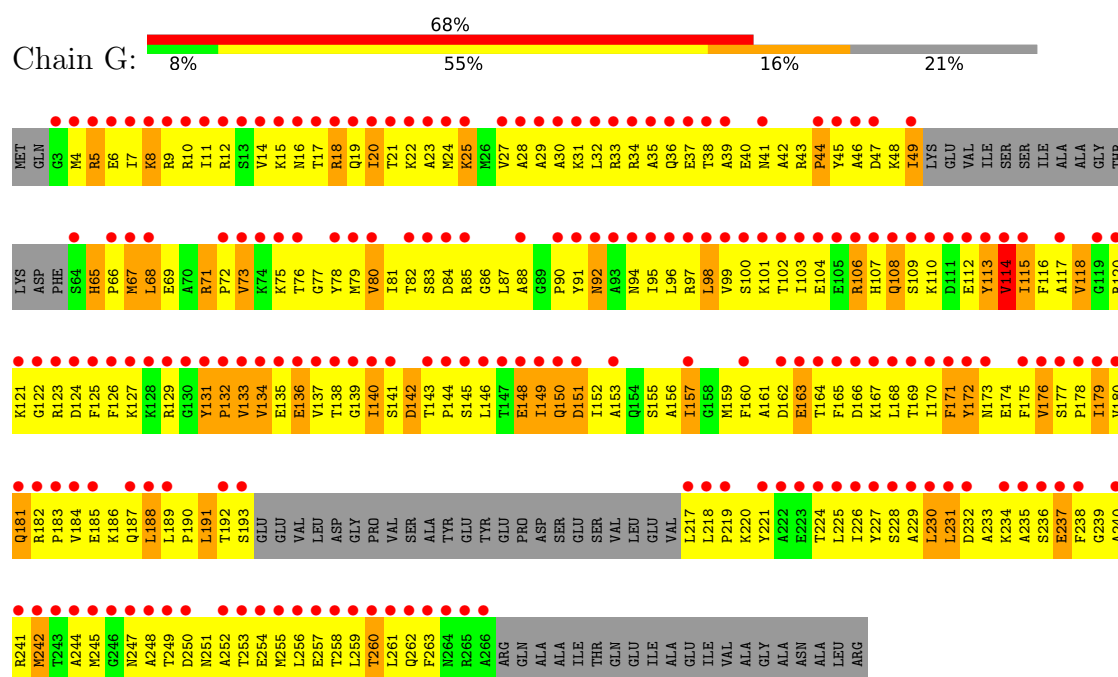


• Molecule 2: ATP synthase subunit beta

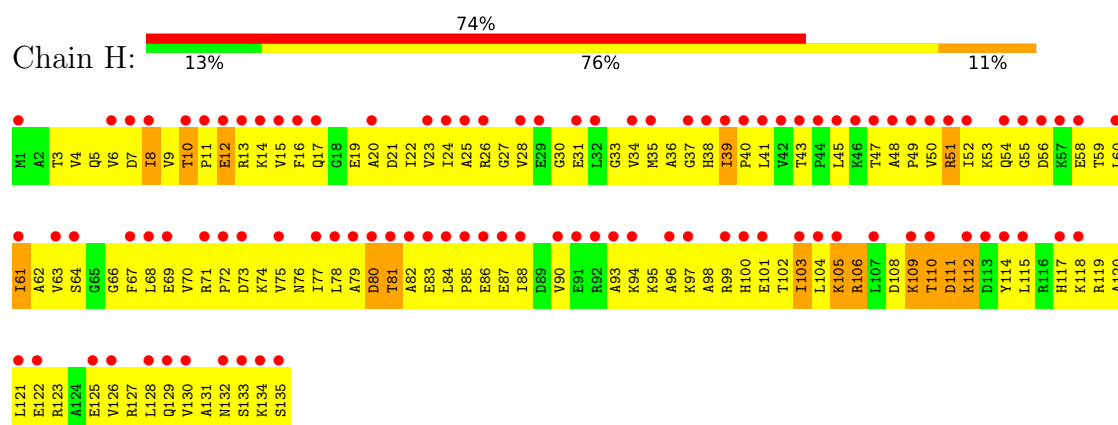




• Molecule 3: ATP synthase subunit gamma



• Molecule 4: ATP synthase subunit epsilon



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	123.21Å 173.02Å 218.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.06 40.00 – 3.06	Depositor EDS
% Data completeness (in resolution range)	94.6 (40.00-3.06) 94.6 (40.00-3.06)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 2.81Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.252 , 0.306 0.244 , 0.304	Depositor DCC
R_{free} test set	2577 reflections (2.50%)	wwPDB-VP
Wilson B-factor (Å ²)	63.9	Xtriage
Anisotropy	0.477	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 122.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	30018	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.81% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.62	0/3699	1.00	11/5006 (0.2%)
1	B	0.63	1/3699 (0.0%)	1.00	18/5006 (0.4%)
1	C	0.62	0/3699	0.99	14/5006 (0.3%)
2	D	0.61	0/3582	0.98	18/4852 (0.4%)
2	E	0.71	0/3582	1.02	17/4852 (0.4%)
2	F	0.69	0/3582	1.03	21/4852 (0.4%)
3	G	0.22	0/5460	0.52	0/7344
4	H	0.18	0/3183	0.45	0/4287
All	All	0.56	1/30486 (0.0%)	0.89	99/41205 (0.2%)

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
2	D	0	1
2	E	0	1
2	F	0	1
3	G	0	2
4	H	0	1
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	330	ILE	CA-CB	-5.54	1.51	1.54

All (99) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	276	LEU	N-CA-C	-8.38	101.38	111.69
2	F	293	ILE	N-CA-C	7.79	119.44	108.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	191	VAL	N-CA-C	7.57	118.71	108.11
2	F	334	TYR	CA-C-N	-7.52	110.44	119.84
2	F	334	TYR	C-N-CA	-7.52	110.44	119.84
1	B	276	LEU	N-CA-C	-7.47	102.50	111.69
2	E	293	ILE	N-CA-C	7.36	118.94	109.30
2	E	139	ALA	CA-C-N	7.31	127.36	119.90
2	E	139	ALA	C-N-CA	7.31	127.36	119.90
2	D	293	ILE	N-CA-C	7.28	118.76	108.93
1	A	276	LEU	N-CA-C	-7.24	102.78	111.69
2	F	235	ARG	N-CA-C	-7.05	101.23	110.53
2	F	23	LEU	CA-C-N	6.89	126.65	119.76
2	F	23	LEU	C-N-CA	6.89	126.65	119.76
2	E	23	LEU	CA-C-N	6.73	126.49	119.76
2	E	23	LEU	C-N-CA	6.73	126.49	119.76
2	D	23	LEU	CA-C-N	6.70	126.46	119.76
2	D	23	LEU	C-N-CA	6.70	126.46	119.76
1	A	406	THR	CB-CA-C	-6.65	106.83	116.54
2	E	235	ARG	N-CA-C	-6.62	101.61	110.55
2	F	196	LYS	N-CA-C	-6.58	105.08	113.23
2	D	334	TYR	CA-C-N	-6.52	111.69	119.84
2	D	334	TYR	C-N-CA	-6.52	111.69	119.84
1	B	406	THR	CB-CA-C	-6.43	107.16	116.54
1	C	406	THR	CB-CA-C	-6.40	107.19	116.54
2	D	235	ARG	N-CA-C	-6.38	101.94	110.55
1	A	113	GLN	CA-C-N	6.36	126.12	119.76
1	A	113	GLN	C-N-CA	6.36	126.12	119.76
1	B	363	VAL	N-CA-C	6.34	118.27	108.44
2	E	335	PRO	N-CA-C	-6.29	99.51	112.47
1	A	494	PHE	N-CA-C	-6.28	106.25	114.04
2	D	349	PRO	N-CA-C	-6.20	106.11	113.86
2	D	335	PRO	N-CA-C	-6.18	99.75	112.47
2	D	139	ALA	CA-C-N	6.15	126.17	119.90
2	D	139	ALA	C-N-CA	6.15	126.17	119.90
2	F	139	ALA	CA-C-N	6.15	126.17	119.90
2	F	139	ALA	C-N-CA	6.15	126.17	119.90
2	F	79	VAL	CA-C-N	6.13	126.14	119.89
2	F	79	VAL	C-N-CA	6.13	126.14	119.89
1	C	494	PHE	N-CA-C	-6.11	106.46	114.04
2	D	301	VAL	CA-C-N	6.08	126.25	119.32
2	D	301	VAL	C-N-CA	6.08	126.25	119.32
2	E	301	VAL	CA-C-N	6.03	126.19	119.32
2	E	301	VAL	C-N-CA	6.03	126.19	119.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	191	VAL	N-CA-C	6.03	116.80	108.12
1	C	363	VAL	N-CA-C	6.00	117.73	108.44
1	A	299	GLU	N-CA-C	-5.92	106.06	113.28
1	B	494	PHE	N-CA-C	-5.89	106.74	114.04
1	C	113	GLN	CA-C-N	5.82	125.58	119.76
1	C	113	GLN	C-N-CA	5.82	125.58	119.76
2	F	132	ILE	N-CA-C	5.82	116.58	109.30
2	F	92	VAL	CB-CA-C	-5.81	103.57	112.05
1	B	252	LYS	N-CA-C	-5.78	106.27	113.38
2	D	196	LYS	N-CA-C	-5.78	105.33	112.90
2	E	198	SER	N-CA-C	-5.76	105.91	113.17
1	A	363	VAL	N-CA-C	5.76	117.37	108.44
2	D	198	SER	N-CA-C	-5.75	105.92	113.17
2	F	301	VAL	CA-C-N	5.73	125.41	119.05
2	F	301	VAL	C-N-CA	5.73	125.41	119.05
2	F	335	PRO	N-CA-C	-5.70	100.73	112.47
2	E	132	ILE	N-CA-C	5.70	116.42	109.30
1	C	230	GLU	CA-C-N	5.67	125.60	119.76
1	C	230	GLU	C-N-CA	5.67	125.60	119.76
2	F	198	SER	N-CA-C	-5.67	106.02	113.17
1	B	286	TYR	CA-C-N	5.66	126.92	119.84
1	B	286	TYR	C-N-CA	5.66	126.92	119.84
2	E	92	VAL	CB-CA-C	-5.64	104.65	112.04
2	E	307	THR	N-CA-C	-5.58	106.52	113.38
2	D	79	VAL	CA-C-N	5.57	125.52	119.78
2	D	79	VAL	C-N-CA	5.57	125.52	119.78
1	C	481	LEU	CA-C-N	5.50	126.71	119.84
1	C	481	LEU	C-N-CA	5.50	126.71	119.84
1	A	252	LYS	N-CA-C	-5.49	106.75	113.50
2	E	459	ALA	N-CA-C	-5.48	106.62	113.15
1	C	190	ASP	N-CA-C	-5.47	106.44	113.23
2	F	208	PHE	N-CA-C	5.47	117.33	108.41
1	C	263	LEU	N-CA-C	-5.46	106.46	113.01
1	B	131	SER	CA-C-N	5.41	125.36	119.78
1	B	131	SER	C-N-CA	5.41	125.36	119.78
2	F	421	VAL	CA-C-N	5.38	125.39	119.90
2	F	421	VAL	C-N-CA	5.38	125.39	119.90
1	B	149	GLY	N-CA-C	-5.34	108.72	115.08
2	E	349	PRO	N-CA-C	-5.34	107.18	113.86
1	B	230	GLU	CA-C-N	5.28	125.20	119.76
1	B	230	GLU	C-N-CA	5.28	125.20	119.76
1	C	486	GLU	N-CA-C	-5.28	105.61	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	361	ARG	N-CA-C	-5.26	105.97	112.38
1	B	481	LEU	CA-C-N	5.22	126.37	119.84
1	B	481	LEU	C-N-CA	5.22	126.37	119.84
1	B	190	ASP	N-CA-C	-5.22	106.76	113.23
1	B	486	GLU	N-CA-C	-5.21	105.68	111.36
1	B	113	GLN	CA-C-N	5.13	124.89	119.76
1	B	113	GLN	C-N-CA	5.13	124.89	119.76
1	A	481	LEU	CA-C-N	5.09	126.20	119.84
1	A	481	LEU	C-N-CA	5.09	126.20	119.84
2	E	58	MET	N-CA-C	-5.08	106.00	113.61
2	D	307	THR	N-CA-C	-5.06	107.16	113.38
2	D	292	SER	N-CA-C	5.05	121.56	110.80
2	E	196	LYS	N-CA-C	-5.05	106.29	112.90

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	334	TYR	Peptide
2	E	334	TYR	Peptide
2	F	334	TYR	Peptide
3	G	171[B]	PHE	Peptide
3	G	171[C]	PHE	Peptide
4	H	111[C]	ASP	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3640	0	3675	269	0
1	B	3640	0	3675	268	0
1	C	3640	0	3675	260	0
2	D	3522	0	3530	223	1
2	E	3522	0	3530	216	0
2	F	3522	0	3530	219	0
3	G	5382	0	5529	644	0
4	H	3150	0	3331	292	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	30018	0	30475	2253	1

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 37.

All (2253) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:371:ASN:CB	3:G:10[B]:ARG:NH1	1.78	1.45
2:F:371:ASN:HB3	3:G:10[B]:ARG:NH1	1.03	1.35
1:B:83:ARG:HB2	2:E:47:HIS:CE1	1.64	1.31
3:G:28[C]:ALA:HA	3:G:238[C]:PHE:HD1	1.04	1.17
1:A:275:LEU:HD22	2:D:264:MET:HA	1.28	1.15
4:H:110[C]:THR:O	4:H:112[C]:LYS:HG3	1.45	1.12
1:B:106:ARG:HH11	1:B:106:ARG:HG2	1.03	1.12
1:C:106:ARG:HG2	1:C:106:ARG:HH11	1.13	1.10
3:G:32[C]:LEU:CG	3:G:238[C]:PHE:HB2	1.82	1.09
3:G:71[B]:ARG:HG3	3:G:71[B]:ARG:HH11	1.01	1.09
2:F:371:ASN:CB	3:G:10[B]:ARG:HH12	1.44	1.09
1:B:354:ARG:HH11	1:B:354:ARG:CG	1.68	1.07
1:A:106:ARG:HG2	1:A:106:ARG:HH11	1.16	1.06
3:G:32[C]:LEU:HG	3:G:238[C]:PHE:HB2	1.37	1.06
1:A:354:ARG:CG	1:A:354:ARG:HH11	1.69	1.06
3:G:84[C]:ASP:HB3	3:G:120[C]:ARG:H	1.08	1.06
1:A:440:VAL:HG12	1:A:445:MET:HE3	1.32	1.05
1:B:62:MET:HE3	1:B:95:MET:HE3	1.39	1.05
1:B:275:LEU:HB3	2:E:264:MET:CG	1.87	1.05
3:G:28[C]:ALA:HA	3:G:238[C]:PHE:CD1	1.91	1.04
1:A:462:SER:HA	1:A:465:ARG:NH1	1.72	1.04
1:C:354:ARG:HH11	1:C:354:ARG:CG	1.68	1.04
3:G:4[A]:MET:HG3	3:G:5[A]:ARG:NH1	1.73	1.03
4:H:110[C]:THR:HB	4:H:112[C]:LYS:HE2	1.40	1.03
1:B:151:LYS:H	1:B:422:GLN:HE22	1.06	1.03
1:B:440:VAL:HG12	1:B:445:MET:HE3	1.41	1.03
3:G:32[C]:LEU:HD23	3:G:238[C]:PHE:CG	1.92	1.03
1:B:106:ARG:HH11	1:B:106:ARG:CG	1.71	1.03
1:C:440:VAL:HG12	1:C:445:MET:HE3	1.40	1.03
1:A:62:MET:HE3	1:A:95:MET:HE3	1.41	1.02
1:B:275:LEU:HD22	2:E:264:MET:HA	1.40	1.02
3:G:32[C]:LEU:CB	3:G:238[C]:PHE:HB2	1.90	1.02
3:G:80[A]:VAL:HA	3:G:171[A]:PHE:HB2	1.38	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:462:SER:HA	1:C:465:ARG:NH1	1.73	1.01
1:B:462:SER:HA	1:B:465:ARG:NH1	1.76	1.00
3:G:38[C]:THR:HA	4:H:13[C]:ARG:NH2	1.77	0.99
1:C:354:ARG:HH11	1:C:354:ARG:HG3	1.26	0.99
3:G:32[C]:LEU:HB2	3:G:238[C]:PHE:CB	1.93	0.98
2:F:371:ASN:CG	3:G:10[B]:ARG:NH1	2.21	0.98
1:B:275:LEU:HB3	2:E:264:MET:HG3	1.43	0.98
1:A:492:GLU:HA	1:A:495:LYS:HB2	1.45	0.98
3:G:48[C]:LYS:HD3	4:H:78[C]:LEU:HD22	1.46	0.98
1:A:151:LYS:H	1:A:422:GLN:HE22	1.03	0.97
1:C:106:ARG:HH11	1:C:106:ARG:CG	1.78	0.97
3:G:71[A]:ARG:CG	3:G:71[A]:ARG:HH11	1.77	0.97
4:H:61[B]:ILE:HG22	4:H:84[B]:LEU:HA	1.43	0.96
1:B:492:GLU:HA	1:B:495:LYS:HB2	1.44	0.96
1:C:171:ARG:HH11	1:C:171:ARG:CG	1.78	0.96
4:H:13[B]:ARG:HH11	4:H:13[B]:ARG:HG3	1.27	0.96
1:C:492:GLU:HA	1:C:495:LYS:HB2	1.44	0.96
3:G:32[C]:LEU:HB2	3:G:238[C]:PHE:HB2	1.43	0.96
3:G:72[C]:PRO:HA	3:G:73[C]:VAL:HG13	1.48	0.96
1:A:415:ARG:HH11	1:A:415:ARG:CG	1.78	0.96
1:C:62:MET:HE3	1:C:95:MET:HE3	1.44	0.96
1:B:354:ARG:HH11	1:B:354:ARG:HG3	1.27	0.96
1:C:275:LEU:HD22	2:F:264:MET:HA	1.43	0.96
1:A:354:ARG:HH11	1:A:354:ARG:HG3	1.30	0.96
1:C:415:ARG:HH11	1:C:415:ARG:CG	1.78	0.95
1:C:137:MET:HG3	2:D:98:ASP:HA	1.48	0.95
1:B:415:ARG:CG	1:B:415:ARG:HH11	1.78	0.95
1:C:83:ARG:HB2	2:F:47:HIS:CE1	1.99	0.95
1:C:284:GLU:HG3	1:C:329:TYR:CG	2.01	0.95
1:A:171:ARG:HH11	1:A:171:ARG:HG3	1.30	0.95
1:C:365:ARG:HH21	2:D:186:ARG:HH22	1.14	0.94
3:G:71[B]:ARG:HG3	3:G:71[B]:ARG:NH1	1.79	0.94
3:G:87[C]:LEU:N	3:G:241[C]:ARG:HH21	1.64	0.94
3:G:162[A]:ASP:HA	3:G:163[A]:GLU:HB2	1.50	0.94
1:C:365:ARG:HH21	2:D:186:ARG:NH2	1.65	0.93
3:G:86[C]:GLY:HA2	3:G:241[C]:ARG:HH22	1.31	0.93
1:A:156:MET:HE3	1:A:383:ARG:HA	1.50	0.93
1:C:435:ILE:HD13	1:C:464:MET:HE2	1.51	0.92
3:G:146[C]:LEU:HA	3:G:227[C]:TYR:OH	1.69	0.92
2:E:264:MET:HE3	2:E:272:PRO:HB3	1.51	0.92
3:G:238[C]:PHE:CE2	3:G:241[C]:ARG:NH1	2.36	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:GLU:HG3	1:A:329:TYR:CG	2.05	0.92
1:B:83:ARG:HB2	2:E:47:HIS:HE1	1.33	0.92
1:B:156:MET:HE3	1:B:383:ARG:HA	1.52	0.92
3:G:168[A]:LEU:HB3	3:G:189[A]:LEU:HB2	1.50	0.92
1:C:151:LYS:H	1:C:422:GLN:HE22	1.00	0.91
2:D:175:LEU:H	2:D:238:GLN:HE21	1.17	0.91
1:B:284:GLU:HG3	1:B:329:TYR:CG	2.06	0.91
3:G:162[C]:ASP:HA	3:G:163[C]:GLU:HB2	1.52	0.91
4:H:6[C]:VAL:HG21	4:H:23[C]:VAL:HG21	1.51	0.91
3:G:43[A]:ARG:HB2	3:G:44[A]:PRO:HD3	1.52	0.91
1:A:171:ARG:HH11	1:A:171:ARG:CG	1.83	0.90
1:A:365:ARG:HH21	2:E:186:ARG:HH22	1.20	0.90
1:A:106:ARG:HH11	1:A:106:ARG:CG	1.84	0.90
1:C:171:ARG:HH11	1:C:171:ARG:HG3	1.33	0.90
3:G:32[B]:LEU:HG	3:G:238[B]:PHE:CB	2.01	0.90
3:G:65[C]:HIS:HD2	3:G:69[C]:GLU:HB2	1.37	0.90
2:D:213:GLU:HG3	2:D:214:PRO:HD2	1.54	0.90
3:G:84[C]:ASP:HB2	3:G:120[C]:ARG:HB3	1.54	0.89
3:G:86[C]:GLY:HA2	3:G:241[C]:ARG:NH2	1.85	0.89
2:D:89:VAL:HG22	2:D:98:ASP:HB3	1.54	0.89
3:G:172[C]:TYR:HB3	3:G:184[C]:VAL:HG12	1.52	0.89
4:H:100[A]:HIS:HB2	4:H:121[A]:LEU:HG	1.54	0.89
2:D:264:MET:HE3	2:D:272:PRO:HB3	1.53	0.88
4:H:110[C]:THR:C	4:H:112[C]:LYS:HG3	1.98	0.88
1:B:171:ARG:HH11	1:B:171:ARG:CG	1.86	0.88
1:A:106:ARG:HG2	1:A:106:ARG:NH1	1.85	0.88
1:B:435:ILE:HD13	1:B:464:MET:HE2	1.56	0.88
2:E:268:VAL:HG11	2:E:309:PRO:HG2	1.54	0.88
2:F:264:MET:HB3	2:F:265:PRO:HA	1.53	0.88
1:B:106:ARG:HG2	1:B:106:ARG:NH1	1.73	0.87
1:C:474:HIS:NE2	1:C:482:PRO:HD2	1.89	0.87
1:B:171:ARG:HH11	1:B:171:ARG:HG3	1.39	0.87
2:E:264:MET:CB	2:E:272:PRO:HG3	2.05	0.87
3:G:160[A]:PHE:HB2	3:G:189[A]:LEU:HD21	1.55	0.87
4:H:66[C]:GLY:HA3	4:H:79[C]:ALA:HA	1.53	0.87
1:C:83:ARG:HB2	2:F:47:HIS:HE1	1.36	0.87
1:B:83:ARG:CB	2:E:47:HIS:CE1	2.54	0.87
2:D:268:VAL:HG11	2:D:309:PRO:HG2	1.57	0.87
4:H:5[B]:GLN:HA	4:H:19[B]:GLU:HA	1.56	0.87
3:G:38[C]:THR:HA	4:H:13[C]:ARG:HH22	1.36	0.86
1:C:66:LEU:HB3	2:D:66:ARG:HD3	1.56	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:371:ASN:CB	3:G:10[B]:ARG:HH11	1.65	0.86
3:G:29[C]:ALA:HB2	3:G:242[C]:MET:SD	2.14	0.86
3:G:131[C]:TYR:H	3:G:132[C]:PRO:HA	1.40	0.86
4:H:110[C]:THR:HB	4:H:112[C]:LYS:CE	2.05	0.86
2:D:130:THR:HG21	2:D:135:ILE:HD11	1.55	0.86
1:A:83:ARG:HB2	2:D:47:HIS:CE1	2.10	0.86
1:B:275:LEU:C	2:E:264:MET:HE2	2.01	0.86
2:E:89:VAL:HG22	2:E:98:ASP:HB3	1.56	0.86
2:F:175:LEU:H	2:F:238:GLN:HE21	1.21	0.86
1:A:164:ARG:HH22	2:E:184:ARG:HD3	1.38	0.86
2:F:268:VAL:HG11	2:F:309:PRO:HG2	1.57	0.86
1:C:480:GLU:C	1:C:482:PRO:HD3	2.01	0.85
2:F:264:MET:HE3	2:F:272:PRO:HB3	1.57	0.85
2:D:264:MET:HB3	2:D:265:PRO:HA	1.55	0.85
4:H:90[C]:VAL:HG22	4:H:131[C]:ALA:HB1	1.59	0.85
2:F:213:GLU:HG3	2:F:214:PRO:HD2	1.58	0.85
2:D:34:ARG:HG3	2:D:35:PRO:HA	1.58	0.85
3:G:72[C]:PRO:HB2	3:G:73[C]:VAL:HG22	1.58	0.85
1:A:474:HIS:NE2	1:A:482:PRO:HD2	1.90	0.85
1:B:480:GLU:C	1:B:482:PRO:HD3	2.02	0.85
2:E:175:LEU:H	2:E:238:GLN:HE21	1.21	0.84
4:H:8[A]:ILE:HA	4:H:77[A]:ILE:HG12	1.60	0.84
3:G:32[A]:LEU:HD12	3:G:35[A]:ALA:HB2	1.58	0.84
1:C:156:MET:HE3	1:C:383:ARG:HA	1.55	0.84
2:E:34:ARG:HG3	2:E:35:PRO:HA	1.59	0.84
4:H:51[C]:ARG:HG2	4:H:60[C]:LEU:HA	1.57	0.84
1:A:480:GLU:C	1:A:482:PRO:HD3	2.01	0.84
2:E:264:MET:HB3	2:E:265:PRO:HA	1.57	0.84
2:F:130:THR:HG21	2:F:135:ILE:HD11	1.58	0.84
4:H:50[C]:VAL:H	4:H:61[C]:ILE:HG12	1.42	0.84
3:G:32[B]:LEU:HG	3:G:238[B]:PHE:HB2	1.59	0.84
3:G:45[C]:TYR:HA	3:G:48[C]:LYS:HD2	1.58	0.84
2:F:89:VAL:HG22	2:F:98:ASP:HB3	1.58	0.84
1:B:474:HIS:NE2	1:B:482:PRO:HD2	1.92	0.83
2:F:371:ASN:HB3	3:G:10[B]:ARG:HH11	1.03	0.83
3:G:148[A]:GLU:HG2	3:G:149[A]:ILE:HG13	1.59	0.83
2:D:175:LEU:H	2:D:238:GLN:NE2	1.76	0.83
2:F:34:ARG:HG3	2:F:35:PRO:HA	1.61	0.83
1:A:435:ILE:HD13	1:A:464:MET:HE2	1.60	0.83
1:A:79:TYR:HE1	2:D:26:ILE:HD11	1.44	0.83
3:G:188[A]:LEU:HD21	3:G:225[A]:LEU:HB3	1.59	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:103[B]:ILE:HD11	4:H:117[B]:HIS:CD2	2.14	0.83
2:F:371:ASN:CA	3:G:10[B]:ARG:HH12	1.93	0.82
4:H:47[A]:THR:HG21	4:H:122[A]:GLU:HB3	1.62	0.82
2:D:264:MET:CB	2:D:272:PRO:HG3	2.10	0.82
1:B:415:ARG:HH11	1:B:415:ARG:HG2	1.45	0.81
3:G:84[C]:ASP:CB	3:G:120[C]:ARG:H	1.91	0.81
1:A:66:LEU:HD12	2:E:9:VAL:HB	1.63	0.81
2:E:398:LYS:HD3	2:E:446:PHE:CE1	2.14	0.81
3:G:142[B]:ASP:HA	3:G:234[B]:LYS:NZ	1.95	0.81
2:E:264:MET:HB3	2:E:272:PRO:HG3	1.62	0.81
3:G:71[A]:ARG:HH11	3:G:71[A]:ARG:HG2	1.45	0.81
1:B:275:LEU:CB	2:E:264:MET:HG3	2.11	0.81
2:F:264:MET:CB	2:F:272:PRO:HG3	2.10	0.81
3:G:170[C]:ILE:HD11	3:G:186[C]:LYS:HB2	1.62	0.81
3:G:189[A]:LEU:HB3	3:G:190[A]:PRO:HD3	1.63	0.81
1:C:106:ARG:HG2	1:C:106:ARG:NH1	1.80	0.81
4:H:25[B]:ALA:HB2	4:H:50[B]:VAL:HG13	1.61	0.81
1:A:415:ARG:HH11	1:A:415:ARG:HG2	1.46	0.80
2:F:175:LEU:H	2:F:238:GLN:NE2	1.79	0.80
3:G:72[A]:PRO:HB3	3:G:73[A]:VAL:HB	1.61	0.80
1:B:66:LEU:HD12	2:F:9:VAL:HB	1.62	0.80
3:G:45[C]:TYR:HE2	3:G:224[C]:THR:HG21	1.45	0.80
4:H:26[B]:ARG:HA	4:H:31[B]:GLU:HG2	1.63	0.80
2:E:130:THR:HG21	2:E:135:ILE:HD11	1.62	0.80
3:G:120[B]:ARG:HD3	3:G:123[B]:ARG:HH21	1.44	0.80
4:H:60[C]:LEU:HD12	4:H:130[C]:VAL:HA	1.62	0.80
1:C:354:ARG:HG3	1:C:354:ARG:NH1	1.95	0.80
1:C:440:VAL:HA	1:C:445:MET:HG3	1.64	0.80
1:B:275:LEU:HB3	2:E:264:MET:SD	2.20	0.80
3:G:71[B]:ARG:HH11	3:G:71[B]:ARG:CG	1.91	0.80
3:G:120[B]:ARG:CD	3:G:123[B]:ARG:HH21	1.95	0.80
3:G:96[A]:LEU:HA	3:G:99[A]:VAL:HG12	1.64	0.79
3:G:118[C]:VAL:HA	3:G:137[C]:VAL:HG13	1.64	0.79
3:G:220[C]:LYS:O	3:G:224[C]:THR:HG23	1.82	0.79
4:H:110[C]:THR:O	4:H:112[C]:LYS:CG	2.29	0.79
3:G:72[B]:PRO:HB3	3:G:73[B]:VAL:HB	1.64	0.79
3:G:261[B]:LEU:HD12	3:G:262[B]:GLN:HG3	1.63	0.79
4:H:5[A]:GLN:HG2	4:H:19[A]:GLU:HG2	1.62	0.79
1:B:345:GLU:HB2	1:B:348:LEU:HD22	1.65	0.79
4:H:103[B]:ILE:HA	4:H:106[B]:ARG:HG3	1.64	0.79
1:A:275:LEU:HG	1:A:278:ARG:HA	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:72[C]:PRO:CA	3:G:73[C]:VAL:HG13	2.14	0.78
3:G:32[A]:LEU:HB2	3:G:238[A]:PHE:HB2	1.63	0.78
3:G:85[C]:ARG:HD2	3:G:85[C]:ARG:O	1.84	0.78
4:H:13[B]:ARG:HH11	4:H:13[B]:ARG:CG	1.96	0.78
1:C:345:GLU:HB2	1:C:348:LEU:HD22	1.63	0.78
1:C:499:THR:N	1:C:500:PRO:HD3	1.99	0.78
3:G:65[C]:HIS:CD2	3:G:69[C]:GLU:HB2	2.19	0.78
2:E:175:LEU:H	2:E:238:GLN:NE2	1.82	0.78
3:G:68[C]:LEU:H	3:G:68[C]:LEU:HD22	1.49	0.78
1:B:83:ARG:HB2	2:E:47:HIS:ND1	1.97	0.78
3:G:71[B]:ARG:NH2	3:G:163[B]:GLU:HG2	1.99	0.78
2:E:213:GLU:HG3	2:E:214:PRO:HD2	1.64	0.77
1:C:151:LYS:N	1:C:422:GLN:HE22	1.81	0.77
4:H:110[C]:THR:CB	4:H:112[C]:LYS:HE2	2.13	0.77
3:G:76[C]:THR:HB	3:G:167[C]:LYS:HG2	1.67	0.77
3:G:149[C]:ILE:C	3:G:151[C]:ASP:H	1.91	0.77
3:G:84[C]:ASP:HB3	3:G:120[C]:ARG:N	1.94	0.77
3:G:87[C]:LEU:H	3:G:241[C]:ARG:NH2	1.83	0.77
1:A:354:ARG:HH11	1:A:354:ARG:HG2	1.50	0.77
3:G:170[C]:ILE:HG13	3:G:188[C]:LEU:HD11	1.66	0.77
1:C:415:ARG:HH11	1:C:415:ARG:HG3	1.49	0.77
3:G:32[A]:LEU:HB2	3:G:238[A]:PHE:CB	2.16	0.76
4:H:97[C]:LYS:HE3	4:H:128[C]:LEU:HD12	1.67	0.76
2:F:408:HIS:ND1	2:F:418:GLY:HA3	2.00	0.76
1:B:275:LEU:HG	1:B:278:ARG:HA	1.67	0.76
1:C:79:TYR:HE1	2:F:26:ILE:HD11	1.49	0.76
3:G:72[B]:PRO:CA	3:G:73[B]:VAL:HB	2.15	0.76
1:C:415:ARG:HH11	1:C:415:ARG:HG2	1.51	0.76
1:A:354:ARG:HG3	1:A:354:ARG:NH1	1.99	0.76
3:G:78[B]:TYR:HD1	3:G:115[B]:ILE:HG22	1.51	0.76
1:B:48:MET:HE3	1:B:94:ILE:HG23	1.68	0.76
1:A:275:LEU:HB3	2:D:264:MET:CG	2.16	0.76
1:A:345:GLU:HB2	1:A:348:LEU:HD22	1.68	0.76
2:E:379:ILE:HD12	3:G:252[A]:ALA:HB2	1.68	0.75
3:G:81[B]:ILE:HA	3:G:118[B]:VAL:HG13	1.68	0.75
3:G:170[B]:ILE:HD11	3:G:186[B]:LYS:HB2	1.67	0.75
1:B:354:ARG:HG3	1:B:354:ARG:NH1	1.97	0.75
1:B:328:ALA:O	1:B:332:THR:HG23	1.86	0.75
4:H:34[A]:VAL:HA	4:H:38[A]:HIS:CE1	2.22	0.75
4:H:117[C]:HIS:HA	4:H:120[C]:ALA:HB3	1.68	0.75
1:B:440:VAL:HA	1:B:445:MET:HG3	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:275:LEU:HG	1:C:278:ARG:HA	1.67	0.75
3:G:25[C]:LYS:HG2	3:G:245[C]:MET:HB2	1.69	0.75
1:B:62:MET:HB2	1:B:95:MET:HE1	1.69	0.75
3:G:241[B]:ARG:HB2	3:G:241[B]:ARG:HH11	1.51	0.75
1:B:275:LEU:CB	2:E:264:MET:SD	2.75	0.74
1:A:499:THR:N	1:A:500:PRO:HD3	2.02	0.74
1:A:462:SER:CA	1:A:465:ARG:NH1	2.50	0.74
3:G:40[B]:GLU:O	3:G:44[B]:PRO:HD3	1.87	0.74
2:D:419:LYS:HE2	2:D:450:GLY:HA3	1.69	0.74
3:G:65[C]:HIS:HD2	3:G:69[C]:GLU:CB	2.00	0.74
3:G:118[C]:VAL:HA	3:G:137[C]:VAL:CG1	2.18	0.74
3:G:5[A]:ARG:NH1	3:G:5[A]:ARG:HB3	2.02	0.74
3:G:87[C]:LEU:H	3:G:241[C]:ARG:HH21	1.34	0.74
3:G:146[B]:LEU:HA	3:G:227[B]:TYR:OH	1.88	0.74
1:B:136:VAL:O	2:F:189:ASN:HB2	1.87	0.74
2:D:264:MET:HB3	2:D:272:PRO:HG3	1.70	0.74
4:H:47[B]:THR:HG21	4:H:122[B]:GLU:HB3	1.68	0.74
1:C:481:LEU:N	1:C:482:PRO:HD3	2.02	0.73
3:G:91[B]:TYR:CD2	3:G:240[B]:ALA:HB1	2.23	0.73
1:B:298:LEU:HD12	1:B:317:PRO:HG3	1.70	0.73
1:B:354:ARG:CG	1:B:354:ARG:NH1	2.40	0.73
2:E:310:ALA:HB3	2:E:311:PRO:HD3	1.70	0.73
3:G:32[C]:LEU:HB2	3:G:238[C]:PHE:HB3	1.69	0.73
3:G:72[A]:PRO:CA	3:G:73[A]:VAL:HB	2.18	0.73
1:B:79:TYR:HE1	2:E:26:ILE:HD11	1.51	0.73
1:B:499:THR:N	1:B:500:PRO:HD3	2.02	0.73
1:B:354:ARG:HH11	1:B:354:ARG:HG2	1.51	0.73
3:G:43[C]:ARG:HA	3:G:46[C]:ALA:HB3	1.68	0.73
4:H:100[A]:HIS:CD2	4:H:120[A]:ALA:HB1	2.23	0.73
1:B:44:LEU:HB3	1:B:47:VAL:HG13	1.70	0.73
1:C:328:ALA:O	1:C:332:THR:HG23	1.88	0.73
2:F:255:SER:HA	2:F:271:GLN:HG3	1.70	0.73
1:C:44:LEU:HB3	1:C:47:VAL:HG13	1.69	0.73
2:D:175:LEU:HG	2:D:238:GLN:HE22	1.53	0.73
3:G:71[A]:ARG:HH11	3:G:71[A]:ARG:HG3	1.53	0.73
1:C:354:ARG:HH11	1:C:354:ARG:HG2	1.53	0.73
2:D:374:GLN:HE21	2:D:374:GLN:HA	1.54	0.73
2:D:401:ARG:HD3	2:D:443:GLU:O	1.88	0.73
3:G:172[B]:TYR:CE1	3:G:229[B]:ALA:HA	2.24	0.73
2:E:136:ASP:HB3	2:E:423:VAL:HG13	1.70	0.73
2:F:419:LYS:HE2	2:F:450:GLY:HA3	1.68	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:72[A]:PRO:CB	3:G:73[A]:VAL:HB	2.18	0.73
4:H:9[C]:VAL:HG13	4:H:14[C]:LYS:HA	1.71	0.73
1:C:365:ARG:NH2	2:D:186:ARG:HH22	1.87	0.72
3:G:140[C]:ILE:HD12	3:G:234[C]:LYS:NZ	2.04	0.72
2:F:264:MET:HB2	2:F:272:PRO:HG3	1.71	0.72
3:G:72[B]:PRO:CB	3:G:73[B]:VAL:HB	2.19	0.72
3:G:4[A]:MET:HE3	3:G:5[A]:ARG:NH2	2.04	0.72
3:G:45[C]:TYR:CB	4:H:11[C]:PRO:HA	2.19	0.72
3:G:92[C]:ASN:HD21	3:G:121[C]:LYS:HB3	1.54	0.72
3:G:107[C]:HIS:C	3:G:109[C]:SER:H	1.95	0.72
4:H:103[A]:ILE:HA	4:H:106[A]:ARG:HB2	1.70	0.72
2:D:255:SER:HA	2:D:271:GLN:HG3	1.71	0.72
3:G:80[B]:VAL:HB	3:G:171[B]:PHE:HD1	1.54	0.72
3:G:172[B]:TYR:HE1	3:G:229[B]:ALA:HA	1.53	0.72
4:H:104[C]:LEU:HD13	4:H:118[C]:LYS:HG2	1.70	0.72
2:D:310:ALA:HB3	2:D:311:PRO:HD3	1.72	0.72
2:E:156:GLY:O	2:E:159:VAL:HG12	1.90	0.72
3:G:98[C]:LEU:O	3:G:102[C]:THR:HG23	1.89	0.72
1:C:438:TYR:HA	1:C:441:THR:HG22	1.70	0.72
2:D:301:VAL:HG13	2:D:306:TYR:HE1	1.54	0.72
3:G:72[C]:PRO:CB	3:G:73[C]:VAL:HG22	2.19	0.72
1:C:326:VAL:HG11	1:C:343:PHE:HE2	1.55	0.72
1:C:390:ARG:HH21	1:C:391:GLU:HG2	1.54	0.72
1:A:415:ARG:HH11	1:A:415:ARG:HG3	1.53	0.71
1:B:415:ARG:HH11	1:B:415:ARG:HG3	1.54	0.71
2:F:136:ASP:HB3	2:F:423:VAL:HG13	1.71	0.71
1:A:440:VAL:HA	1:A:445:MET:HG3	1.71	0.71
2:E:175:LEU:HG	2:E:238:GLN:HE22	1.54	0.71
3:G:32[A]:LEU:HD23	3:G:238[A]:PHE:CG	2.26	0.71
3:G:131[A]:TYR:H	3:G:132[A]:PRO:HA	1.54	0.71
2:E:142:ALA:HB2	2:E:346:ILE:HD13	1.73	0.71
2:E:268:VAL:HG22	2:E:268:VAL:O	1.89	0.71
2:E:301:VAL:HG13	2:E:306:TYR:HE1	1.55	0.71
2:E:416:MET:H	2:E:417:PRO:HA	1.55	0.71
1:A:44:LEU:HB3	1:A:47:VAL:HG13	1.71	0.71
3:G:144[B]:PRO:O	3:G:145[B]:SER:HB2	1.90	0.71
3:G:176[C]:VAL:HB	3:G:180[C]:VAL:HG23	1.71	0.71
1:A:390:ARG:HH21	1:A:391:GLU:HG2	1.56	0.71
1:A:438:TYR:HA	1:A:441:THR:HG22	1.72	0.71
2:F:268:VAL:O	2:F:268:VAL:HG22	1.91	0.71
1:A:137:MET:HG3	2:E:98:ASP:HA	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:298:LEU:HD22	1:B:298:LEU:H	1.56	0.71
2:D:136:ASP:HB3	2:D:423:VAL:HG13	1.73	0.71
3:G:32[B]:LEU:CD2	3:G:238[B]:PHE:HB3	2.20	0.71
4:H:6[B]:VAL:HG11	4:H:23[B]:VAL:HG21	1.72	0.71
1:A:342:ILE:HA	1:A:362:SER:OG	1.91	0.71
1:B:151:LYS:N	1:B:422:GLN:HE22	1.85	0.71
1:C:342:ILE:HA	1:C:362:SER:OG	1.90	0.70
2:E:255:SER:HA	2:E:271:GLN:HG3	1.71	0.70
2:F:374:GLN:HA	2:F:374:GLN:HE21	1.56	0.70
3:G:71[B]:ARG:HH21	3:G:163[B]:GLU:HG2	1.54	0.70
1:A:151:LYS:N	1:A:422:GLN:HE22	1.83	0.70
1:C:462:SER:CA	1:C:465:ARG:NH1	2.53	0.70
3:G:131[B]:TYR:H	3:G:132[B]:PRO:HA	1.56	0.70
3:G:5[A]:ARG:HH11	3:G:5[A]:ARG:H	1.38	0.70
2:F:401:ARG:HD3	2:F:443:GLU:O	1.92	0.70
3:G:32[A]:LEU:HD23	3:G:238[A]:PHE:CD2	2.27	0.70
1:C:298:LEU:HD12	1:C:317:PRO:HG3	1.72	0.70
2:D:226:LEU:HD11	2:D:284:ARG:HB2	1.74	0.70
3:G:132[C]:PRO:O	3:G:133[C]:VAL:HB	1.91	0.70
1:C:171:ARG:CG	1:C:171:ARG:NH1	2.48	0.70
2:D:264:MET:HB2	2:D:272:PRO:HG3	1.74	0.70
2:F:301:VAL:HG13	2:F:306:TYR:HE1	1.56	0.70
4:H:22[C]:ILE:HG13	4:H:53[C]:LYS:HD2	1.72	0.70
4:H:100[B]:HIS:HD2	4:H:117[B]:HIS:HD2	1.40	0.70
1:B:62:MET:HB2	1:B:95:MET:CE	2.22	0.70
2:F:137:LEU:HG	2:F:138:LEU:HD13	1.74	0.70
1:B:326:VAL:HG11	1:B:343:PHE:HE2	1.57	0.69
4:H:35[B]:MET:HE3	4:H:36[B]:ALA:H	1.56	0.69
1:A:326:VAL:HG11	1:A:343:PHE:HE2	1.57	0.69
2:F:310:ALA:HB3	2:F:311:PRO:HD3	1.74	0.69
1:A:343:PHE:CD1	1:A:361:ILE:HG13	2.27	0.69
2:D:65:VAL:O	2:D:68:LEU:HG	1.93	0.69
4:H:14[B]:LYS:HZ2	4:H:17[B]:GLN:HG2	1.55	0.69
3:G:77[C]:GLY:HA3	3:G:165[C]:PHE:CZ	2.28	0.69
1:C:343:PHE:CD1	1:C:361:ILE:HG13	2.28	0.69
2:E:419:LYS:HE2	2:E:450:GLY:HA3	1.73	0.69
3:G:48[A]:LYS:HG3	3:G:49[A]:ILE:H	1.56	0.69
1:B:388:GLN:HG3	1:B:409:LYS:NZ	2.08	0.69
1:A:275:LEU:HB3	2:D:264:MET:HG3	1.74	0.69
1:B:438:TYR:HA	1:B:441:THR:HG22	1.74	0.69
2:E:264:MET:HB2	2:E:272:PRO:HG3	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:374:GLN:HA	2:E:374:GLN:HE21	1.57	0.69
2:F:264:MET:HB3	2:F:265:PRO:CA	2.22	0.69
4:H:27[A]:GLY:H	4:H:31[A]:GLU:HA	1.57	0.69
1:C:151:LYS:H	1:C:422:GLN:NE2	1.84	0.69
1:C:401:ASP:HB3	1:C:406:THR:HG22	1.74	0.69
2:E:125:ASP:CG	2:E:345:ARG:HH22	2.01	0.69
2:E:408:HIS:ND1	2:E:418:GLY:HA3	2.08	0.69
3:G:8[B]:LYS:HD2	3:G:263[B]:PHE:CE1	2.28	0.69
4:H:20[A]:ALA:HA	4:H:54[A]:GLN:HB3	1.75	0.69
1:B:48:MET:CE	1:B:94:ILE:HG23	2.23	0.69
1:A:48:MET:HB3	2:E:63:GLY:HA2	1.75	0.69
2:D:398:LYS:HD3	2:D:446:PHE:CE1	2.27	0.69
3:G:172[A]:TYR:HD1	3:G:173[A]:ASN:H	1.41	0.69
1:C:48:MET:HE3	1:C:94:ILE:HG23	1.73	0.68
2:D:408:HIS:ND1	2:D:418:GLY:HA3	2.08	0.68
2:E:416:MET:N	2:E:417:PRO:HA	2.08	0.68
1:A:438:TYR:CE1	1:A:487:LEU:HD12	2.27	0.68
1:B:164:ARG:HH22	2:F:184:ARG:HD3	1.59	0.68
2:F:264:MET:HB3	2:F:272:PRO:HG3	1.73	0.68
3:G:66[C]:PRO:O	3:G:67[C]:MET:HB3	1.92	0.68
3:G:148[C]:GLU:HG2	3:G:149[C]:ILE:HG13	1.75	0.68
4:H:66[C]:GLY:CA	4:H:79[C]:ALA:HA	2.24	0.68
1:B:390:ARG:HH21	1:B:391:GLU:HG2	1.58	0.68
3:G:143[A]:THR:H	3:G:144[A]:PRO:HA	1.57	0.68
3:G:80[C]:VAL:HG11	3:G:126[C]:PHE:CE2	2.28	0.68
3:G:172[C]:TYR:HE1	3:G:232[C]:ASP:HB3	1.58	0.68
3:G:176[C]:VAL:HG12	3:G:177[C]:SER:N	2.08	0.68
4:H:9[A]:VAL:HG22	4:H:14[A]:LYS:HE3	1.75	0.68
1:A:415:ARG:HG2	1:A:415:ARG:NH1	2.08	0.68
1:B:481:LEU:N	1:B:482:PRO:HD3	2.09	0.68
3:G:45[C]:TYR:CG	4:H:11[C]:PRO:HA	2.29	0.68
3:G:72[B]:PRO:HA	3:G:73[B]:VAL:HB	1.75	0.68
3:G:90[B]:PRO:HB2	3:G:94[B]:ASN:HD22	1.58	0.68
4:H:24[C]:ILE:HD11	4:H:51[C]:ARG:HB2	1.76	0.68
2:F:8:GLN:HB2	2:F:15:ASP:HB2	1.76	0.68
1:B:79:TYR:CE1	2:E:26:ILE:HD11	2.28	0.68
1:B:342:ILE:HA	1:B:362:SER:OG	1.93	0.68
2:D:162:GLN:HE22	2:D:194:GLU:HG2	1.57	0.68
3:G:68[A]:LEU:HA	3:G:160[A]:PHE:HE2	1.59	0.68
3:G:253[C]:THR:HG22	3:G:254[C]:GLU:N	2.08	0.68
2:D:156:GLY:O	2:D:159:VAL:HG12	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:156:GLY:O	2:F:159:VAL:HG12	1.94	0.68
2:F:398:LYS:HD3	2:F:446:PHE:CE1	2.29	0.68
1:A:354:ARG:CG	1:A:354:ARG:NH1	2.40	0.67
2:D:137:LEU:HG	2:D:138:LEU:HD13	1.75	0.67
3:G:144[A]:PRO:HG2	3:G:230[A]:LEU:CD1	2.24	0.67
1:C:48:MET:CE	1:C:94:ILE:HG23	2.24	0.67
1:C:161:ARG:HH12	1:C:190:ASP:HB3	1.59	0.67
2:F:91:ASN:HD21	2:F:95:GLU:H	1.42	0.67
1:A:481:LEU:N	1:A:482:PRO:HD3	2.08	0.67
1:B:275:LEU:CD2	2:E:264:MET:HA	2.21	0.67
3:G:104[C]:GLU:HA	3:G:107[C]:HIS:HD1	1.60	0.67
1:A:328:ALA:O	1:A:332:THR:HG23	1.94	0.67
1:B:415:ARG:HG2	1:B:415:ARG:NH1	2.08	0.67
2:D:125:ASP:CG	2:D:345:ARG:HH22	2.02	0.67
1:B:401:ASP:HB3	1:B:406:THR:HG22	1.74	0.67
4:H:4[B]:VAL:HG21	4:H:37[B]:GLY:H	1.60	0.67
1:B:275:LEU:CA	2:E:264:MET:HE2	2.25	0.67
2:F:384:GLU:OE2	3:G:87[B]:LEU:HA	1.95	0.67
3:G:123[B]:ARG:HG3	3:G:136[B]:GLU:OE2	1.95	0.67
2:D:152:GLY:H	2:D:155:VAL:CG2	2.08	0.67
2:E:8:GLN:HB2	2:E:15:ASP:HB2	1.75	0.67
2:E:135:ILE:HD12	2:E:141:TYR:CZ	2.30	0.67
2:F:135:ILE:HD12	2:F:141:TYR:CZ	2.29	0.67
3:G:66[A]:PRO:HD2	3:G:68[A]:LEU:HD23	1.77	0.67
3:G:113[B]:TYR:O	3:G:114[B]:VAL:HG22	1.95	0.67
1:A:388:GLN:HG3	1:A:409:LYS:NZ	2.10	0.67
2:E:137:LEU:HG	2:E:138:LEU:HD13	1.77	0.67
3:G:79[C]:MET:O	3:G:170[C]:ILE:HA	1.95	0.67
3:G:92[A]:ASN:O	3:G:95[A]:ILE:HG22	1.95	0.67
4:H:81[B]:THR:HG21	4:H:127[B]:ARG:HH21	1.58	0.67
1:A:401:ASP:HB3	1:A:406:THR:HG22	1.76	0.67
1:B:129:ILE:HD11	1:B:237:LEU:HD22	1.77	0.67
3:G:96[C]:LEU:HD13	3:G:125[C]:PHE:CD1	2.29	0.67
4:H:24[B]:ILE:HG22	4:H:33[B]:GLY:HA2	1.75	0.67
1:B:44:LEU:HB3	1:B:47:VAL:CG1	2.26	0.66
3:G:85[C]:ARG:HH12	3:G:238[C]:PHE:HZ	1.41	0.66
1:C:114:PRO:HG3	1:C:121:ILE:HD12	1.78	0.66
1:B:386:LEU:HD23	1:B:386:LEU:H	1.60	0.66
1:C:140:LYS:HE2	1:C:143:HIS:CE1	2.30	0.66
2:D:379:ILE:HD11	3:G:17[C]:THR:CG2	2.25	0.66
2:F:175:LEU:HG	2:F:238:GLN:HE22	1.59	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:86[B]:GLY:HA2	3:G:241[B]:ARG:HH22	1.61	0.66
1:B:294:HIS:O	1:B:298:LEU:HD22	1.95	0.66
2:D:308:ASP:O	2:D:311:PRO:HD2	1.96	0.66
3:G:32[C]:LEU:HD23	3:G:238[C]:PHE:CD2	2.29	0.66
3:G:142[B]:ASP:HA	3:G:234[B]:LYS:HZ3	1.61	0.66
1:A:151:LYS:H	1:A:422:GLN:NE2	1.86	0.66
2:D:142:ALA:HB2	2:D:346:ILE:HD13	1.76	0.66
2:F:226:LEU:HD11	2:F:284:ARG:HB2	1.76	0.66
1:A:83:ARG:HB2	2:D:47:HIS:HE1	1.56	0.66
1:B:52:LEU:O	1:B:91:THR:HB	1.96	0.66
2:D:91:ASN:HD21	2:D:95:GLU:H	1.44	0.66
2:F:416:MET:N	2:F:417:PRO:HA	2.11	0.66
3:G:160[C]:PHE:CB	3:G:189[C]:LEU:HD23	2.26	0.66
1:A:62:MET:HB2	1:A:95:MET:HE1	1.78	0.66
1:B:161:ARG:HH12	1:B:190:ASP:HB3	1.61	0.66
1:C:44:LEU:HB3	1:C:47:VAL:CG1	2.26	0.66
3:G:33[B]:ARG:C	3:G:35[B]:ALA:H	2.04	0.66
3:G:80[B]:VAL:HA	3:G:171[B]:PHE:HB2	1.78	0.66
3:G:87[C]:LEU:N	3:G:241[C]:ARG:NH2	2.36	0.66
4:H:60[C]:LEU:HB2	4:H:130[C]:VAL:HG13	1.76	0.66
1:A:52:LEU:O	1:A:91:THR:HB	1.96	0.66
3:G:152[C]:ILE:H	3:G:152[C]:ILE:HD12	1.61	0.66
4:H:22[B]:ILE:HG13	4:H:53[B]:LYS:HD2	1.77	0.66
1:B:275:LEU:HD22	2:E:264:MET:CA	2.22	0.65
1:C:480:GLU:O	1:C:481:LEU:HB3	1.95	0.65
1:A:262:ASP:H	1:A:318:PHE:HB2	1.60	0.65
2:D:264:MET:HB3	2:D:265:PRO:CA	2.26	0.65
3:G:32[B]:LEU:CG	3:G:238[B]:PHE:CB	2.74	0.65
2:E:144:GLY:HA2	2:E:293:ILE:O	1.97	0.65
3:G:67[C]:MET:C	3:G:69[C]:GLU:H	2.03	0.65
1:A:298:LEU:HD12	1:A:317:PRO:HG3	1.77	0.65
1:A:449:PRO:HB2	1:A:452:ASP:HB2	1.79	0.65
1:B:343:PHE:CD1	1:B:361:ILE:HG13	2.31	0.65
2:D:8:GLN:HB2	2:D:15:ASP:HB2	1.79	0.65
1:A:365:ARG:HH21	2:E:186:ARG:NH2	1.92	0.65
2:D:416:MET:H	2:D:417:PRO:HA	1.60	0.65
2:E:65:VAL:O	2:E:68:LEU:HG	1.97	0.65
3:G:113[A]:TYR:O	3:G:114[A]:VAL:HG22	1.97	0.65
4:H:14[B]:LYS:NZ	4:H:17[B]:GLN:HG2	2.11	0.65
1:A:62:MET:HB2	1:A:95:MET:CE	2.26	0.65
3:G:65[C]:HIS:HD2	3:G:69[C]:GLU:CA	2.10	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:79[B]:MET:HG3	3:G:116[B]:PHE:HB2	1.79	0.65
4:H:9[C]:VAL:HG21	4:H:14[C]:LYS:HD2	1.78	0.65
4:H:39[A]:ILE:H	4:H:39[A]:ILE:HD13	1.61	0.65
1:A:140:LYS:HE2	1:A:143:HIS:CE1	2.31	0.65
1:A:44:LEU:HB3	1:A:47:VAL:CG1	2.27	0.65
1:C:449:PRO:HB2	1:C:452:ASP:HB2	1.78	0.65
1:C:419:ILE:HG21	1:C:440:VAL:HG11	1.78	0.65
3:G:32[B]:LEU:CG	3:G:238[B]:PHE:HB2	2.26	0.65
3:G:79[C]:MET:HE3	3:G:152[C]:ILE:HG22	1.78	0.65
2:D:416:MET:N	2:D:417:PRO:HA	2.11	0.64
2:E:195:MET:HE2	2:E:206:MET:SD	2.37	0.64
1:B:462:SER:CA	1:B:465:ARG:NH1	2.56	0.64
4:H:13[B]:ARG:HG3	4:H:13[B]:ARG:NH1	2.08	0.64
3:G:66[C]:PRO:HD2	3:G:68[C]:LEU:HD23	1.80	0.64
3:G:91[A]:TYR:CD2	3:G:240[A]:ALA:HB1	2.31	0.64
3:G:149[C]:ILE:C	3:G:151[C]:ASP:N	2.55	0.64
3:G:244[C]:ALA:C	3:G:245[C]:MET:HE2	2.21	0.64
1:A:114:PRO:HG3	1:A:121:ILE:HD12	1.79	0.64
1:B:140:LYS:HE2	1:B:143:HIS:CE1	2.32	0.64
2:E:226:LEU:HD11	2:E:284:ARG:HB2	1.79	0.64
2:F:416:MET:H	2:F:417:PRO:HA	1.60	0.64
3:G:4[A]:MET:HE3	3:G:5[A]:ARG:HH22	1.60	0.64
2:F:162:GLN:HE22	2:F:194:GLU:HG2	1.62	0.64
4:H:51[B]:ARG:HE	4:H:60[B]:LEU:HD21	1.62	0.64
1:B:438:TYR:CE1	1:B:487:LEU:HD12	2.33	0.64
2:D:379:ILE:HD11	3:G:17[C]:THR:HG21	1.78	0.64
3:G:82[B]:THR:HG22	3:G:95[B]:ILE:HD13	1.78	0.64
3:G:91[B]:TYR:CG	3:G:240[B]:ALA:HB1	2.32	0.64
3:G:107[C]:HIS:C	3:G:109[C]:SER:N	2.54	0.64
1:C:52:LEU:O	1:C:91:THR:HB	1.96	0.64
1:C:62:MET:HB2	1:C:95:MET:CE	2.28	0.64
2:F:125:ASP:CG	2:F:345:ARG:HH22	2.05	0.64
3:G:146[A]:LEU:HD12	4:H:81[A]:THR:HB	1.78	0.64
1:A:100:GLY:HA2	1:A:248:TYR:CE2	2.33	0.64
2:D:135:ILE:HD12	2:D:141:TYR:CZ	2.32	0.64
2:E:162:GLN:HE22	2:E:194:GLU:HG2	1.63	0.64
3:G:184[A]:VAL:HG22	3:G:185[A]:GLU:H	1.61	0.64
1:A:48:MET:HE3	1:A:94:ILE:HG23	1.79	0.63
1:C:66:LEU:HB3	2:D:66:ARG:CD	2.26	0.63
2:E:291:GLY:O	2:E:292:SER:HB2	1.98	0.63
4:H:8[B]:ILE:CG1	4:H:15[B]:VAL:HB	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:8[C]:ILE:HG13	4:H:15[C]:VAL:HB	1.78	0.63
3:G:16[C]:ASN:O	3:G:19[C]:GLN:HB2	1.98	0.63
3:G:41[C]:ASN:HB3	4:H:13[C]:ARG:HE	1.63	0.63
3:G:77[A]:GLY:O	3:G:168[A]:LEU:HA	1.98	0.63
1:C:156:MET:CE	1:C:383:ARG:HA	2.29	0.63
2:F:65:VAL:O	2:F:68:LEU:HG	1.98	0.63
2:D:291:GLY:O	2:D:292:SER:HB2	1.98	0.63
4:H:41[C]:LEU:HB2	4:H:70[C]:VAL:HB	1.80	0.63
1:C:388:GLN:HG3	1:C:409:LYS:NZ	2.14	0.63
1:A:161:ARG:HH12	1:A:190:ASP:HB3	1.62	0.63
1:A:275:LEU:CA	2:D:264:MET:HE2	2.29	0.63
1:A:462:SER:HB3	1:A:465:ARG:HH12	1.63	0.63
1:B:46:LYS:NZ	1:B:46:LYS:HB2	2.14	0.63
1:B:156:MET:CE	1:B:383:ARG:HA	2.27	0.63
2:D:90:PHE:HE2	2:D:103:VAL:HG21	1.63	0.63
2:E:152:GLY:H	2:E:155:VAL:CG2	2.12	0.63
2:F:308:ASP:O	2:F:311:PRO:HD2	1.98	0.63
4:H:45[C]:LEU:HG	4:H:68[C]:LEU:HG	1.80	0.63
2:F:460:LYS:O	2:F:461:LYS:HD2	1.97	0.63
4:H:13[C]:ARG:HD2	4:H:13[C]:ARG:N	2.13	0.63
1:B:136:VAL:HG12	2:F:185:THR:HG23	1.80	0.63
1:C:62:MET:HB2	1:C:95:MET:HE1	1.79	0.63
1:C:298:LEU:H	1:C:298:LEU:HD22	1.64	0.63
4:H:21[B]:ASP:HB2	4:H:22[B]:ILE:HD13	1.80	0.63
1:B:449:PRO:HB2	1:B:452:ASP:HB2	1.80	0.62
3:G:153[C]:ALA:O	3:G:157[C]:ILE:HD12	1.99	0.62
3:G:238[A]:PHE:CE2	3:G:241[A]:ARG:NH1	2.66	0.62
2:D:268:VAL:O	2:D:268:VAL:HG22	1.98	0.62
3:G:32[B]:LEU:HG	3:G:238[B]:PHE:HB3	1.81	0.62
4:H:100[C]:HIS:HD2	4:H:117[C]:HIS:CD2	2.17	0.62
1:B:448:ILE:HG23	1:B:449:PRO:HD2	1.81	0.62
1:C:415:ARG:HG2	1:C:415:ARG:NH1	2.12	0.62
2:D:213:GLU:HG3	2:D:214:PRO:CD	2.28	0.62
2:F:152:GLY:H	2:F:155:VAL:CG2	2.11	0.62
4:H:108[C]:ASP:C	4:H:109[C]:LYS:HD2	2.24	0.62
2:E:264:MET:HB3	2:E:265:PRO:CA	2.29	0.62
4:H:45[A]:LEU:HD21	4:H:68[A]:LEU:HD11	1.80	0.62
1:C:475:ILE:HG12	1:C:481:LEU:HA	1.81	0.62
2:E:90:PHE:HE2	2:E:103:VAL:HG21	1.64	0.62
3:G:104[C]:GLU:HA	3:G:107[C]:HIS:ND1	2.15	0.62
4:H:86[C]:GLU:HG2	4:H:134[C]:LYS:HB3	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:LYS:HB2	1:A:46:LYS:NZ	2.15	0.62
1:C:47:VAL:HG21	1:C:71:VAL:HG21	1.81	0.62
1:C:390:ARG:NH2	1:C:391:GLU:HG2	2.13	0.62
2:D:125:ASP:OD2	2:D:345:ARG:NH2	2.32	0.62
2:D:233:ARG:O	2:D:237:GLY:HA2	1.99	0.62
3:G:104[B]:GLU:HA	3:G:107[B]:HIS:ND1	2.13	0.62
4:H:4[A]:VAL:HG23	4:H:36[A]:ALA:HA	1.81	0.62
4:H:109[B]:LYS:HB2	4:H:109[B]:LYS:NZ	2.14	0.62
4:H:109[C]:LYS:O	4:H:112[C]:LYS:HE3	2.00	0.62
3:G:67[B]:MET:SD	3:G:161[B]:ALA:HA	2.39	0.62
3:G:142[B]:ASP:HA	3:G:234[B]:LYS:HZ1	1.62	0.62
2:F:395:ARG:NH2	2:F:436:GLY:HA3	2.14	0.62
3:G:81[A]:ILE:HG21	3:G:230[A]:LEU:HD23	1.82	0.62
3:G:177[B]:SER:HB3	3:G:180[B]:VAL:HG13	1.81	0.62
4:H:110[C]:THR:HB	4:H:112[C]:LYS:NZ	2.14	0.62
1:A:386:LEU:HD23	1:A:386:LEU:H	1.63	0.62
1:B:358:ASN:O	1:B:362:SER:HB2	1.99	0.62
2:F:371:ASN:CG	3:G:10[B]:ARG:HH11	1.96	0.62
3:G:5[A]:ARG:HH11	3:G:5[A]:ARG:N	1.97	0.61
3:G:221[C]:TYR:CE2	3:G:225[C]:LEU:HD11	2.36	0.61
4:H:84[B]:LEU:HB3	4:H:85[B]:PRO:CD	2.30	0.61
2:E:301:VAL:HG13	2:E:306:TYR:CE1	2.36	0.61
3:G:15[B]:LYS:HZ3	3:G:256[B]:LEU:HD21	1.64	0.61
3:G:112[C]:GLU:O	3:G:114[C]:VAL:N	2.33	0.61
3:G:176[C]:VAL:HG12	3:G:177[C]:SER:H	1.65	0.61
4:H:84[B]:LEU:HB3	4:H:85[B]:PRO:HD2	1.81	0.61
1:A:358:ASN:O	1:A:362:SER:HB2	2.00	0.61
1:B:345:GLU:HG2	1:B:358:ASN:HB2	1.83	0.61
3:G:91[A]:TYR:O	3:G:92[A]:ASN:HB2	2.01	0.61
3:G:168[B]:LEU:HB3	3:G:189[B]:LEU:HB2	1.82	0.61
4:H:21[B]:ASP:O	4:H:35[B]:MET:HE1	2.01	0.61
4:H:108[C]:ASP:O	4:H:112[C]:LYS:HE3	2.00	0.61
1:A:345:GLU:HG2	1:A:358:ASN:HB2	1.83	0.61
1:A:448:ILE:HG23	1:A:449:PRO:HD2	1.82	0.61
1:B:275:LEU:HA	1:B:278:ARG:N	2.16	0.61
1:C:435:ILE:CD1	1:C:464:MET:HE2	2.28	0.61
2:F:233:ARG:O	2:F:237:GLY:HA2	1.99	0.61
3:G:28[A]:ALA:HA	3:G:238[A]:PHE:CD1	2.35	0.61
3:G:71[A]:ARG:HG3	3:G:71[A]:ARG:NH1	2.15	0.61
3:G:116[C]:PHE:HD1	3:G:152[C]:ILE:HG23	1.65	0.61
1:B:440:VAL:HA	1:B:445:MET:CG	2.31	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:100:GLY:HA2	1:C:248:TYR:CE2	2.36	0.61
1:C:462:SER:HB3	1:C:465:ARG:HH12	1.65	0.61
2:E:398:LYS:HD3	2:E:446:PHE:CZ	2.36	0.61
4:H:110[B]:THR:HB	4:H:112[B]:LYS:HG3	1.81	0.61
2:E:375:ASP:O	2:E:379:ILE:HG23	2.01	0.61
3:G:135[C]:GLU:OE1	3:G:152[C]:ILE:HG13	2.00	0.61
3:G:218[C]:LEU:O	3:G:218[C]:LEU:HD23	2.01	0.61
1:A:79:TYR:CE1	2:D:26:ILE:HD11	2.31	0.61
1:A:475:ILE:HG12	1:A:481:LEU:HA	1.83	0.61
1:B:275:LEU:CB	2:E:264:MET:CG	2.72	0.61
3:G:31[B]:LYS:C	3:G:32[B]:LEU:HD22	2.26	0.61
3:G:38[A]:THR:CG2	4:H:13[A]:ARG:HH21	2.13	0.61
3:G:143[B]:THR:HB	3:G:144[B]:PRO:C	2.25	0.61
1:A:480:GLU:O	1:A:481:LEU:HB3	2.00	0.61
1:B:475:ILE:HG12	1:B:481:LEU:HA	1.82	0.61
1:C:386:LEU:HD23	1:C:386:LEU:H	1.65	0.61
2:E:125:ASP:OD2	2:E:345:ARG:NH2	2.33	0.61
3:G:72[A]:PRO:HA	3:G:73[A]:VAL:HB	1.80	0.61
4:H:40[C]:PRO:HA	4:H:70[C]:VAL:O	2.00	0.61
1:C:345:GLU:HG2	1:C:358:ASN:HB2	1.81	0.60
2:E:401:ARG:HD3	2:E:443:GLU:O	2.01	0.60
2:F:91:ASN:ND2	2:F:95:GLU:H	1.97	0.60
1:A:275:LEU:HD13	2:D:264:MET:HG3	1.83	0.60
1:A:390:ARG:NH2	1:A:391:GLU:HG2	2.16	0.60
1:C:354:ARG:CG	1:C:354:ARG:NH1	2.40	0.60
1:C:481:LEU:N	1:C:482:PRO:CD	2.65	0.60
1:A:41:VAL:HG21	1:A:88:VAL:HG21	1.83	0.60
1:C:440:VAL:HA	1:C:445:MET:CG	2.29	0.60
3:G:175[B]:PHE:HD1	3:G:236[B]:SER:HA	1.65	0.60
3:G:255[C]:MET:HA	3:G:258[C]:THR:HG23	1.81	0.60
1:C:294:HIS:O	1:C:298:LEU:HD22	2.00	0.60
2:F:149:LEU:HD21	2:F:324:LEU:HD22	1.84	0.60
1:A:156:MET:C	1:A:157:ILE:HG13	2.25	0.60
3:G:68[C]:LEU:HD22	3:G:68[C]:LEU:N	2.15	0.60
4:H:119[B]:ARG:HA	4:H:122[B]:GLU:CD	2.26	0.60
1:B:114:PRO:HG3	1:B:121:ILE:HD12	1.84	0.60
2:D:460:LYS:O	2:D:461:LYS:HD2	2.02	0.60
2:E:91:ASN:HD21	2:E:95:GLU:H	1.48	0.60
2:F:226:LEU:O	2:F:230:GLU:HG3	2.02	0.60
4:H:100[C]:HIS:HD2	4:H:117[C]:HIS:HD2	1.50	0.60
1:B:47:VAL:HG21	1:B:71:VAL:HG21	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:419:ILE:HG21	1:B:440:VAL:HG11	1.82	0.60
2:D:91:ASN:ND2	2:D:95:GLU:H	1.99	0.60
3:G:17[B]:THR:O	3:G:17[B]:THR:HG22	2.02	0.60
3:G:131[C]:TYR:N	3:G:132[C]:PRO:HA	2.09	0.60
1:A:140:LYS:CE	1:A:143:HIS:CE1	2.85	0.60
1:A:143:HIS:CD2	1:A:144:GLU:HG2	2.37	0.60
1:A:419:ILE:HG21	1:A:440:VAL:HG11	1.82	0.60
3:G:78[B]:TYR:CD1	3:G:115[B]:ILE:HG22	2.37	0.60
4:H:49[B]:PRO:HG3	4:H:130[B]:VAL:HG22	1.84	0.60
1:B:365:ARG:HH21	2:F:186:ARG:HH22	1.47	0.60
1:C:275:LEU:HB3	2:F:264:MET:CG	2.32	0.60
1:C:440:VAL:CA	1:C:445:MET:HG3	2.32	0.60
2:D:144:GLY:HA2	2:D:293:ILE:O	2.02	0.60
2:F:291:GLY:O	2:F:292:SER:HB2	2.02	0.60
3:G:87[A]:LEU:HG	3:G:245[A]:MET:HE1	1.82	0.60
4:H:121[B]:LEU:HD22	4:H:125[B]:GLU:OE2	2.02	0.60
2:F:213:GLU:HG3	2:F:214:PRO:CD	2.31	0.60
3:G:11[A]:ILE:O	3:G:15[A]:LYS:HG3	2.02	0.60
3:G:113[C]:TYR:O	3:G:114[C]:VAL:HG22	2.02	0.60
3:G:120[B]:ARG:HD3	3:G:123[B]:ARG:NH2	2.14	0.60
4:H:100[C]:HIS:CD2	4:H:117[C]:HIS:HD2	2.20	0.60
1:B:298:LEU:HD21	1:B:337:ILE:HG21	1.83	0.59
3:G:28[C]:ALA:HB3	3:G:242[C]:MET:HB3	1.83	0.59
3:G:31[A]:LYS:HG2	3:G:32[A]:LEU:HD22	1.83	0.59
3:G:101[C]:LYS:HD2	3:G:101[C]:LYS:C	2.27	0.59
4:H:23[C]:VAL:HB	4:H:34[C]:VAL:HB	1.84	0.59
1:A:252:LYS:HD3	1:A:254:LYS:HE2	1.84	0.59
1:A:298:LEU:HD21	1:A:337:ILE:HG21	1.84	0.59
1:B:390:ARG:NH2	1:B:391:GLU:HG2	2.17	0.59
1:C:140:LYS:CE	1:C:143:HIS:CE1	2.85	0.59
2:F:144:GLY:HA2	2:F:293:ILE:O	2.02	0.59
4:H:45[A]:LEU:HD11	4:H:68[A]:LEU:HD21	1.84	0.59
1:A:272:GLU:CD	2:D:273:THR:HG22	2.27	0.59
3:G:129[C]:ARG:O	3:G:131[C]:TYR:HD1	1.86	0.59
3:G:234[C]:LYS:O	3:G:235[C]:ALA:C	2.44	0.59
1:C:358:ASN:O	1:C:362:SER:HB2	2.01	0.59
2:D:149:LEU:HD21	2:D:324:LEU:HD22	1.84	0.59
2:E:416:MET:HB2	2:E:417:PRO:O	2.02	0.59
2:E:438:HIS:HB3	2:E:441:LEU:HD22	1.85	0.59
3:G:15[B]:LYS:HG3	3:G:256[B]:LEU:HD11	1.84	0.59
4:H:110[C]:THR:C	4:H:112[C]:LYS:HE2	2.26	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:412:ARG:NH2	1:A:443:GLY:N	2.50	0.59
2:E:395:ARG:NH2	2:E:436:GLY:HA3	2.17	0.59
4:H:22[A]:ILE:HD11	4:H:53[A]:LYS:HD2	1.83	0.59
1:A:435:ILE:HD12	1:A:472:LEU:HD21	1.84	0.59
3:G:48[C]:LYS:HD3	4:H:78[C]:LEU:CD2	2.27	0.59
3:G:91[A]:TYR:CG	3:G:240[A]:ALA:HB1	2.37	0.59
3:G:241[C]:ARG:O	3:G:245[C]:MET:HG2	2.02	0.59
1:A:164:ARG:NH2	2:E:184:ARG:HD3	2.12	0.59
3:G:256[B]:LEU:HD23	3:G:256[B]:LEU:O	2.03	0.59
4:H:111[C]:ASP:O	4:H:112[C]:LYS:HB2	2.03	0.59
1:B:36:ASP:OD2	2:E:263:ARG:HD3	2.01	0.59
1:B:156:MET:C	1:B:157:ILE:HG13	2.28	0.59
2:D:266:SER:OG	2:D:268:VAL:HG12	2.03	0.59
3:G:144[C]:PRO:HG2	3:G:230[C]:LEU:HD13	1.85	0.59
3:G:177[C]:SER:OG	3:G:180[C]:VAL:HG22	2.03	0.59
4:H:110[C]:THR:CA	4:H:112[C]:LYS:HE2	2.33	0.59
1:A:156:MET:CE	1:A:383:ARG:HA	2.29	0.59
2:D:182:GLY:H	2:D:210:GLN:H	1.51	0.59
3:G:29[A]:ALA:HB2	3:G:242[A]:MET:SD	2.43	0.59
4:H:8[B]:ILE:HG13	4:H:15[B]:VAL:HB	1.85	0.59
1:C:188:GLY:O	1:C:189:GLN:HB2	2.03	0.59
1:C:438:TYR:CE1	1:C:487:LEU:HD12	2.37	0.59
2:F:266:SER:OG	2:F:268:VAL:HG12	2.02	0.58
3:G:71[C]:ARG:NH2	3:G:163[C]:GLU:HG3	2.18	0.58
3:G:123[B]:ARG:HD2	3:G:124[B]:ASP:OD2	2.03	0.58
1:C:354:ARG:HA	1:C:355:PRO:C	2.28	0.58
2:E:40:LEU:HD23	2:E:64:LEU:HD11	1.85	0.58
3:G:18[C]:ARG:NH1	3:G:253[C]:THR:OG1	2.32	0.58
3:G:114[C]:VAL:HB	3:G:134[C]:VAL:HG13	1.84	0.58
3:G:160[C]:PHE:HB3	3:G:189[C]:LEU:HD23	1.85	0.58
4:H:34[A]:VAL:HG13	4:H:38[A]:HIS:ND1	2.19	0.58
4:H:51[C]:ARG:CG	4:H:60[C]:LEU:HA	2.31	0.58
1:C:31:VAL:HG11	1:C:34:VAL:HG22	1.85	0.58
2:E:139:ALA:N	2:E:140:PRO:HD3	2.18	0.58
4:H:60[A]:LEU:HD13	4:H:130[A]:VAL:HA	1.84	0.58
2:D:301:VAL:HG13	2:D:306:TYR:CE1	2.36	0.58
2:F:226:LEU:HD11	2:F:284:ARG:CB	2.33	0.58
3:G:28[A]:ALA:HA	3:G:238[A]:PHE:HD1	1.68	0.58
3:G:45[C]:TYR:CE2	3:G:224[C]:THR:HG21	2.33	0.58
4:H:49[A]:PRO:HA	4:H:61[A]:ILE:O	2.03	0.58
1:B:412:ARG:NH2	1:B:443:GLY:N	2.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:95[B]:ILE:O	3:G:99[B]:VAL:HG13	2.04	0.58
3:G:189[B]:LEU:HB3	3:G:190[B]:PRO:HD3	1.85	0.58
4:H:103[B]:ILE:HD11	4:H:117[B]:HIS:NE2	2.19	0.58
1:B:382:LEU:O	1:B:386:LEU:HD23	2.03	0.58
2:D:91:ASN:HD22	2:D:91:ASN:C	2.11	0.58
3:G:126[B]:PHE:HB3	3:G:132[B]:PRO:O	2.04	0.58
3:G:177[B]:SER:CB	3:G:180[B]:VAL:HG13	2.34	0.58
3:G:94[C]:ASN:HB3	3:G:97[C]:ARG:NH1	2.19	0.58
4:H:50[B]:VAL:HG23	4:H:63[B]:VAL:HG21	1.85	0.58
1:A:275:LEU:CB	2:D:264:MET:HG3	2.34	0.58
2:D:395:ARG:NH2	2:D:436:GLY:HA3	2.18	0.58
2:E:40:LEU:CD2	2:E:64:LEU:HD11	2.33	0.58
2:E:91:ASN:C	2:E:91:ASN:HD22	2.12	0.58
2:F:90:PHE:HE2	2:F:103:VAL:HG21	1.68	0.58
3:G:84[C]:ASP:CB	3:G:120[C]:ARG:HB3	2.30	0.58
1:A:382:LEU:O	1:A:386:LEU:HD23	2.04	0.58
2:D:232:PHE:HB2	2:D:240:VAL:HG21	1.86	0.58
3:G:76[A]:THR:HA	3:G:167[A]:LYS:HD3	1.86	0.58
3:G:140[C]:ILE:HD12	3:G:234[C]:LYS:HZ3	1.68	0.58
3:G:166[C]:ASP:C	3:G:167[C]:LYS:HD2	2.29	0.58
1:B:31:VAL:HG11	1:B:34:VAL:HG22	1.86	0.57
1:B:140:LYS:CE	1:B:143:HIS:CE1	2.87	0.57
3:G:43[C]:ARG:CA	3:G:46[C]:ALA:HB3	2.34	0.57
3:G:68[B]:LEU:HD13	3:G:160[B]:PHE:CE2	2.38	0.57
1:C:275:LEU:HB3	2:F:264:MET:HG3	1.85	0.57
2:F:182:GLY:H	2:F:210:GLN:H	1.50	0.57
2:F:416:MET:HB2	2:F:417:PRO:O	2.04	0.57
3:G:78[B]:TYR:OH	3:G:106[B]:ARG:HD2	2.04	0.57
3:G:144[C]:PRO:HG2	3:G:230[C]:LEU:CD1	2.34	0.57
1:A:275:LEU:C	2:D:264:MET:HE2	2.29	0.57
1:C:412:ARG:NH2	1:C:443:GLY:N	2.53	0.57
1:C:499:THR:H	1:C:500:PRO:HD3	1.69	0.57
2:F:111:ILE:HA	2:F:227:THR:OG1	2.05	0.57
3:G:81[A]:ILE:HA	3:G:118[A]:VAL:HG13	1.85	0.57
3:G:230[C]:LEU:O	3:G:230[C]:LEU:HD22	2.03	0.57
2:D:375:ASP:O	2:D:379:ILE:HG23	2.04	0.57
3:G:112[C]:GLU:OE2	3:G:112[C]:GLU:HA	2.03	0.57
1:B:354:ARG:HA	1:B:355:PRO:C	2.28	0.57
2:F:301:VAL:HG13	2:F:306:TYR:CE1	2.39	0.57
3:G:85[B]:ARG:NH2	3:G:241[B]:ARG:HH21	2.03	0.57
3:G:86[A]:GLY:HA3	3:G:121[A]:LYS:HD2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:149[B]:ILE:HD12	3:G:150[B]:GLN:N	2.19	0.57
1:A:188:GLY:O	1:A:189:GLN:HB2	2.04	0.57
1:C:275:LEU:CG	1:C:278:ARG:HA	2.34	0.57
2:E:131:GLY:HA3	2:E:167:ASN:ND2	2.19	0.57
3:G:38[A]:THR:HG21	4:H:13[A]:ARG:HH21	1.70	0.57
4:H:49[B]:PRO:HG3	4:H:130[B]:VAL:CG2	2.33	0.57
1:C:382:LEU:O	1:C:386:LEU:HD23	2.04	0.57
3:G:80[C]:VAL:HG11	3:G:126[C]:PHE:HE2	1.65	0.57
3:G:86[A]:GLY:O	3:G:87[A]:LEU:HB2	2.03	0.57
3:G:92[C]:ASN:ND2	3:G:121[C]:LYS:HB3	2.18	0.57
3:G:261[C]:LEU:HD12	3:G:262[C]:GLN:HG3	1.87	0.57
4:H:100[B]:HIS:HD2	4:H:117[B]:HIS:CD2	2.23	0.57
1:A:109:ASN:OD1	1:A:113:GLN:HG2	2.05	0.57
1:A:136:VAL:O	2:E:189:ASN:HB2	2.05	0.57
1:A:354:ARG:HA	1:A:355:PRO:C	2.30	0.57
1:B:275:LEU:CG	1:B:278:ARG:HA	2.33	0.57
1:C:252:LYS:HD3	1:C:254:LYS:HE2	1.87	0.57
2:F:131:GLY:HA3	2:F:167:ASN:ND2	2.19	0.57
4:H:8[B]:ILE:HA	4:H:77[B]:ILE:HG12	1.87	0.57
1:A:275:LEU:CG	1:A:278:ARG:HA	2.33	0.57
1:A:440:VAL:HA	1:A:445:MET:CG	2.34	0.57
4:H:114[C]:TYR:O	4:H:118[C]:LYS:HB2	2.04	0.57
1:C:79:TYR:CE1	2:F:26:ILE:HD11	2.35	0.57
3:G:91[C]:TYR:CD1	3:G:181[C]:GLN:HG2	2.39	0.57
3:G:187[C]:GLN:C	3:G:188[C]:LEU:HD23	2.29	0.57
1:A:415:ARG:CG	1:A:415:ARG:NH1	2.49	0.56
1:B:462:SER:HB3	1:B:465:ARG:HH12	1.69	0.56
2:E:388:GLU:O	2:E:392:ILE:HG23	2.05	0.56
2:F:205:SER:HB2	2:F:228:MET:HE1	1.87	0.56
2:F:349:PRO:HG3	2:F:357:TYR:CD2	2.40	0.56
3:G:4[A]:MET:O	3:G:8[A]:LYS:HE3	2.04	0.56
4:H:12[C]:GLU:C	4:H:13[C]:ARG:HD2	2.30	0.56
1:B:480:GLU:O	1:B:481:LEU:HB3	2.02	0.56
1:C:140:LYS:NZ	1:C:143:HIS:HE1	2.02	0.56
2:D:181:VAL:HG22	2:D:221:VAL:HG13	1.86	0.56
2:D:241:LEU:HD23	2:D:243:PHE:CZ	2.40	0.56
3:G:140[B]:ILE:O	3:G:141[B]:SER:HB3	2.05	0.56
3:G:140[C]:ILE:HD12	3:G:234[C]:LYS:HZ1	1.71	0.56
4:H:5[A]:GLN:HB2	4:H:74[A]:LYS:HG2	1.87	0.56
4:H:117[C]:HIS:O	4:H:121[C]:LEU:HG	2.05	0.56
1:B:298:LEU:H	1:B:298:LEU:CD2	2.19	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:440:VAL:CA	1:B:445:MET:HG3	2.35	0.56
1:C:156:MET:C	1:C:157:ILE:HG13	2.30	0.56
1:C:248:TYR:O	1:C:252:LYS:HB2	2.05	0.56
1:C:292:TYR:O	1:C:296:ARG:HB3	2.05	0.56
2:D:131:GLY:HA3	2:D:167:ASN:ND2	2.21	0.56
2:E:213:GLU:HG3	2:E:214:PRO:CD	2.35	0.56
2:E:369:ARG:HG2	2:E:392:ILE:HD11	1.87	0.56
2:F:125:ASP:OD2	2:F:345:ARG:NH2	2.38	0.56
2:F:288:THR:HG23	2:F:291:GLY:H	1.70	0.56
3:G:6[B]:GLU:O	3:G:10[B]:ARG:HG3	2.05	0.56
3:G:42[C]:ALA:O	3:G:43[C]:ARG:C	2.47	0.56
3:G:47[C]:ASP:O	3:G:48[C]:LYS:C	2.47	0.56
3:G:126[B]:PHE:HD1	3:G:131[B]:TYR:CD1	2.23	0.56
3:G:148[B]:GLU:CD	3:G:149[B]:ILE:HG13	2.30	0.56
3:G:149[B]:ILE:HD11	3:G:227[B]:TYR:CE2	2.40	0.56
4:H:13[B]:ARG:CG	4:H:13[B]:ARG:NH1	2.60	0.56
4:H:49[A]:PRO:HG3	4:H:126[A]:VAL:HG13	1.87	0.56
1:A:31:VAL:HG11	1:A:34:VAL:HG22	1.88	0.56
1:A:238:ALA:HB3	1:A:239:PRO:HD3	1.86	0.56
1:B:252:LYS:HD3	1:B:254:LYS:HE2	1.85	0.56
3:G:41[C]:ASN:O	3:G:44[C]:PRO:HD2	2.06	0.56
3:G:80[C]:VAL:CG1	3:G:126[C]:PHE:HE2	2.19	0.56
3:G:104[B]:GLU:HA	3:G:107[B]:HIS:CE1	2.40	0.56
4:H:119[B]:ARG:HA	4:H:122[B]:GLU:OE1	2.04	0.56
1:B:171:ARG:CG	1:B:171:ARG:NH1	2.55	0.56
3:G:43[C]:ARG:HB2	3:G:44[C]:PRO:HD3	1.88	0.56
3:G:95[B]:ILE:HG23	3:G:96[B]:LEU:N	2.20	0.56
3:G:230[B]:LEU:O	3:G:234[B]:LYS:HB2	2.05	0.56
4:H:12[A]:GLU:C	4:H:13[A]:ARG:HD2	2.31	0.56
4:H:93[B]:ALA:HB3	4:H:128[B]:LEU:HG	1.88	0.56
1:B:188:GLY:O	1:B:189:GLN:HB2	2.04	0.56
1:B:435:ILE:HD12	1:B:472:LEU:HD21	1.88	0.56
1:C:495:LYS:O	1:C:496:LYS:HB2	2.06	0.56
2:E:241:LEU:HD23	2:E:243:PHE:CZ	2.40	0.56
2:F:388:GLU:O	2:F:392:ILE:HG23	2.06	0.56
3:G:5[A]:ARG:HB3	3:G:5[A]:ARG:HH11	1.70	0.56
3:G:72[C]:PRO:HA	3:G:73[C]:VAL:CG1	2.29	0.56
3:G:148[C]:GLU:N	3:G:148[C]:GLU:OE1	2.38	0.56
3:G:170[C]:ILE:HD12	3:G:170[C]:ILE:H	1.70	0.56
1:A:294:HIS:O	1:A:298:LEU:HD22	2.05	0.56
1:B:34:VAL:HG13	1:B:39:ALA:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:129:ILE:HD11	1:C:237:LEU:HD22	1.88	0.56
2:D:226:LEU:HD11	2:D:284:ARG:CB	2.35	0.56
2:E:233:ARG:O	2:E:237:GLY:HA2	2.05	0.56
2:E:460:LYS:O	2:E:461:LYS:HD2	2.06	0.56
4:H:24[C]:ILE:HA	4:H:33[C]:GLY:HA2	1.86	0.56
4:H:103[B]:ILE:HD11	4:H:117[B]:HIS:CG	2.41	0.56
2:D:352:VAL:HG21	2:D:356:HIS:CD2	2.41	0.56
1:B:261:ASP:O	1:B:262:ASP:HB2	2.05	0.56
1:C:41:VAL:HG21	1:C:88:VAL:HG21	1.87	0.56
1:C:435:ILE:HD12	1:C:472:LEU:HD21	1.88	0.56
2:D:416:MET:HB2	2:D:417:PRO:O	2.06	0.56
2:F:142:ALA:HB2	2:F:346:ILE:HD13	1.86	0.56
2:F:371:ASN:ND2	3:G:10[B]:ARG:HH11	2.04	0.56
3:G:17[B]:THR:HA	3:G:20[B]:ILE:HD12	1.87	0.56
3:G:83[A]:SER:HB3	3:G:237[A]:GLU:HG2	1.88	0.56
3:G:86[C]:GLY:CA	3:G:241[C]:ARG:NH2	2.64	0.56
4:H:86[A]:GLU:HG2	4:H:134[A]:LYS:HB3	1.88	0.56
1:A:140:LYS:NZ	1:A:143:HIS:HE1	2.03	0.56
1:A:431:GLU:HG2	1:A:432:GLU:H	1.71	0.56
1:B:305:SER:OG	1:B:308:LYS:HG2	2.06	0.56
1:A:129:ILE:HD11	1:A:237:LEU:HD22	1.86	0.55
2:E:182:GLY:H	2:E:210:GLN:H	1.53	0.55
3:G:5[A]:ARG:H	3:G:5[A]:ARG:HD2	1.70	0.55
3:G:45[B]:TYR:CZ	4:H:11[B]:PRO:HG3	2.41	0.55
1:B:106:ARG:CG	1:B:106:ARG:NH1	2.44	0.55
1:C:262:ASP:H	1:C:318:PHE:HB2	1.71	0.55
3:G:172[C]:TYR:HD2	3:G:186[C]:LYS:HG2	1.71	0.55
1:C:114:PRO:HG3	1:C:121:ILE:CD1	2.36	0.55
2:D:113:ARG:HD3	2:D:114:PRO:O	2.06	0.55
2:E:205:SER:HB2	2:E:228:MET:HE1	1.87	0.55
3:G:21[A]:THR:HG21	3:G:248[A]:ALA:HB3	1.88	0.55
3:G:152[C]:ILE:HD12	3:G:152[C]:ILE:N	2.21	0.55
4:H:39[A]:ILE:HB	4:H:40[A]:PRO:HD2	1.87	0.55
4:H:68[B]:LEU:HD23	4:H:77[B]:ILE:HG22	1.88	0.55
4:H:88[A]:ILE:HD11	4:H:131[A]:ALA:HA	1.88	0.55
1:A:481:LEU:N	1:A:482:PRO:CD	2.70	0.55
1:C:298:LEU:HD21	1:C:337:ILE:HG21	1.86	0.55
3:G:17[B]:THR:HA	3:G:20[B]:ILE:CD1	2.37	0.55
3:G:104[C]:GLU:CD	3:G:107[C]:HIS:HE1	2.15	0.55
1:C:156:MET:SD	1:C:359:VAL:HG11	2.47	0.55
2:D:12:PRO:HD2	2:D:260:LEU:HD22	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:96[C]:LEU:HD11	3:G:122[C]:GLY:HA2	1.88	0.55
4:H:47[B]:THR:CG2	4:H:122[B]:GLU:HB3	2.36	0.55
1:A:382:LEU:HD11	1:A:416:THR:HG23	1.88	0.55
1:B:481:LEU:N	1:B:482:PRO:CD	2.70	0.55
1:B:495:LYS:HE3	1:B:496:LYS:H	1.72	0.55
1:C:384:LEU:O	1:C:388:GLN:HG2	2.07	0.55
2:F:395:ARG:HH21	2:F:436:GLY:HA3	1.71	0.55
2:F:416:MET:HE2	2:F:416:MET:HA	1.88	0.55
2:F:438:HIS:HB3	2:F:441:LEU:HD22	1.89	0.55
3:G:39[B]:ALA:HA	3:G:231[B]:LEU:HD21	1.88	0.55
3:G:104[C]:GLU:HA	3:G:107[C]:HIS:CE1	2.41	0.55
4:H:100[A]:HIS:CB	4:H:121[A]:LEU:HG	2.31	0.55
1:B:355:PRO:HB2	1:B:357:VAL:HG23	1.87	0.55
3:G:84[C]:ASP:HB2	3:G:120[C]:ARG:CB	2.33	0.55
3:G:120[B]:ARG:HG3	3:G:123[B]:ARG:HE	1.71	0.55
3:G:120[C]:ARG:HG2	3:G:120[C]:ARG:O	2.06	0.55
3:G:170[B]:ILE:HD12	3:G:186[B]:LYS:H	1.70	0.55
1:B:32:ILE:HG12	1:B:40:ARG:O	2.07	0.55
1:B:456:PHE:HZ	1:B:495:LYS:HD2	1.72	0.55
1:C:32:ILE:HG12	1:C:40:ARG:O	2.07	0.55
2:F:397:ARG:O	2:F:401:ARG:HD2	2.07	0.55
3:G:5[B]:ARG:NH1	3:G:5[B]:ARG:HB2	2.22	0.55
3:G:68[C]:LEU:H	3:G:68[C]:LEU:CD2	2.17	0.55
4:H:6[B]:VAL:HG12	4:H:75[B]:VAL:HB	1.89	0.55
1:B:365:ARG:HH21	2:F:186:ARG:NH2	2.04	0.55
3:G:77[B]:GLY:O	3:G:168[B]:LEU:HG	2.06	0.55
3:G:94[A]:ASN:HB3	3:G:97[A]:ARG:NH1	2.22	0.55
3:G:96[B]:LEU:O	3:G:99[B]:VAL:HG22	2.06	0.55
4:H:93[A]:ALA:HB3	4:H:128[A]:LEU:HD21	1.89	0.55
4:H:108[A]:ASP:HA	4:H:114[A]:TYR:HE1	1.72	0.55
1:B:41:VAL:HG21	1:B:88:VAL:HG21	1.88	0.55
1:B:129:ILE:CD1	1:B:237:LEU:HD22	2.37	0.55
1:B:440:VAL:HB	1:B:445:MET:HG3	1.88	0.55
1:C:495:LYS:HE3	1:C:496:LYS:H	1.72	0.55
2:D:397:ARG:O	2:D:401:ARG:HD2	2.07	0.55
3:G:36[B]:GLN:HA	3:G:39[B]:ALA:HB3	1.89	0.55
3:G:79[A]:MET:HE1	3:G:226[A]:ILE:HD12	1.89	0.55
3:G:129[B]:ARG:HB2	3:G:131[B]:TYR:HE1	1.71	0.55
3:G:260[B]:THR:HG22	3:G:260[B]:THR:O	2.07	0.55
1:C:261:ASP:O	1:C:262:ASP:HB2	2.06	0.54
2:E:266:SER:OG	2:E:268:VAL:HG12	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:374:GLN:HA	2:E:374:GLN:NE2	2.22	0.54
3:G:170[C]:ILE:HG13	3:G:188[C]:LEU:HD21	1.87	0.54
3:G:221[C]:TYR:O	3:G:225[C]:LEU:HG	2.07	0.54
4:H:9[B]:VAL:HG22	4:H:14[B]:LYS:HD2	1.89	0.54
4:H:69[C]:GLU:OE1	4:H:76[C]:ASN:HB2	2.07	0.54
1:A:275:LEU:HA	1:A:278:ARG:N	2.22	0.54
1:A:384:LEU:O	1:A:388:GLN:HG2	2.07	0.54
1:B:157:ILE:HG21	1:B:342:ILE:HG12	1.89	0.54
2:D:288:THR:HG23	2:D:291:GLY:H	1.72	0.54
3:G:4[A]:MET:HG3	3:G:5[A]:ARG:HH11	1.68	0.54
3:G:116[B]:PHE:HZ	3:G:159[B]:MET:HG3	1.72	0.54
1:A:456:PHE:HZ	1:A:495:LYS:HD2	1.73	0.54
1:A:481:LEU:O	1:A:482:PRO:O	2.25	0.54
2:D:393:VAL:O	2:D:397:ARG:HG3	2.06	0.54
3:G:17[C]:THR:O	3:G:21[C]:THR:HG23	2.07	0.54
3:G:24[C]:MET:HE1	3:G:87[C]:LEU:HD23	1.87	0.54
4:H:28[B]:VAL:C	4:H:30[B]:GLY:H	2.15	0.54
1:C:275:LEU:CD1	1:C:281:PRO:HD3	2.37	0.54
2:D:453:ASP:O	2:D:456:VAL:HG23	2.07	0.54
2:E:12:PRO:HD2	2:E:260:LEU:HD22	1.89	0.54
3:G:25[C]:LYS:HG2	3:G:245[C]:MET:CB	2.37	0.54
1:A:495:LYS:O	1:A:496:LYS:HB2	2.08	0.54
1:C:171:ARG:HG3	1:C:171:ARG:NH1	2.13	0.54
1:C:262:ASP:OD1	1:C:264:SER:HB2	2.07	0.54
1:B:275:LEU:CG	2:E:264:MET:HG3	2.37	0.54
1:B:275:LEU:HB2	2:E:264:MET:SD	2.47	0.54
1:B:384:LEU:O	1:B:388:GLN:HG2	2.08	0.54
1:B:419:ILE:HD13	1:B:440:VAL:HG11	1.89	0.54
1:C:284:GLU:HG3	1:C:329:TYR:CB	2.38	0.54
3:G:41[B]:ASN:O	3:G:44[B]:PRO:HD2	2.08	0.54
3:G:107[C]:HIS:C	3:G:107[C]:HIS:CD2	2.86	0.54
3:G:255[A]:MET:HG3	3:G:259[A]:LEU:HD23	1.90	0.54
2:E:319:ASP:OD2	2:E:345:ARG:HD3	2.07	0.54
2:E:352:VAL:HG21	2:E:356:HIS:CD2	2.43	0.54
2:F:371:ASN:HB3	3:G:10[B]:ARG:HH12	1.02	0.54
3:G:77[B]:GLY:HA3	3:G:165[B]:PHE:CE2	2.42	0.54
3:G:117[A]:ALA:O	3:G:136[A]:GLU:HA	2.07	0.54
1:B:248:TYR:O	1:B:252:LYS:HB2	2.08	0.54
1:B:418:GLU:OE2	1:B:421:LYS:HE2	2.08	0.54
2:E:226:LEU:HD11	2:E:284:ARG:CB	2.37	0.54
3:G:37[C]:GLU:C	3:G:39[C]:ALA:H	2.15	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:122[B]:GLY:O	3:G:126[B]:PHE:HB2	2.07	0.54
4:H:120[B]:ALA:C	4:H:122[B]:GLU:H	2.16	0.54
1:B:275:LEU:HA	1:B:278:ARG:H	1.72	0.54
1:C:305:SER:OG	1:C:308:LYS:HG2	2.07	0.54
2:F:40:LEU:HD23	2:F:64:LEU:HD11	1.89	0.54
3:G:114[C]:VAL:HB	3:G:134[C]:VAL:CG1	2.38	0.54
4:H:10[C]:THR:OG1	4:H:11[C]:PRO:HD2	2.07	0.54
4:H:21[B]:ASP:OD2	4:H:21[B]:ASP:N	2.40	0.54
4:H:63[A]:VAL:HG13	4:H:79[A]:ALA:HB1	1.88	0.54
1:A:495:LYS:HE3	1:A:496:LYS:H	1.72	0.54
1:C:382:LEU:HD11	1:C:416:THR:HG23	1.90	0.54
2:D:26:ILE:O	2:D:27:TYR:HB2	2.08	0.54
2:D:372:ASP:OD2	3:G:9[C]:ARG:NH1	2.39	0.54
3:G:91[C]:TYR:CD2	3:G:240[C]:ALA:HB1	2.43	0.54
3:G:95[C]:ILE:CD1	3:G:171[C]:PHE:HB3	2.38	0.54
1:A:407:GLN:HA	1:A:411:ASN:HB2	1.91	0.53
1:C:32:ILE:HG13	1:C:33:GLN:HG3	1.90	0.53
2:D:205:SER:HB2	2:D:228:MET:HE1	1.90	0.53
2:E:111:ILE:HA	2:E:227:THR:OG1	2.08	0.53
2:F:139:ALA:N	2:F:140:PRO:HD3	2.23	0.53
3:G:32[C]:LEU:CD2	3:G:238[C]:PHE:CG	2.80	0.53
3:G:72[C]:PRO:CB	3:G:73[C]:VAL:HG13	2.37	0.53
3:G:132[C]:PRO:O	3:G:133[C]:VAL:CB	2.56	0.53
3:G:244[C]:ALA:O	3:G:248[C]:ALA:HB2	2.07	0.53
1:B:262:ASP:H	1:B:318:PHE:HB2	1.73	0.53
1:B:499:THR:H	1:B:500:PRO:HD3	1.73	0.53
2:D:97:ILE:O	2:D:97:ILE:HG12	2.07	0.53
1:A:292:TYR:O	1:A:296:ARG:HB3	2.09	0.53
1:B:100:GLY:HA2	1:B:248:TYR:CE2	2.42	0.53
1:B:140:LYS:NZ	1:B:143:HIS:HE1	2.05	0.53
1:C:47:VAL:HG12	1:C:90:ARG:HG2	1.91	0.53
2:D:111:ILE:HA	2:D:227:THR:OG1	2.07	0.53
2:D:438:HIS:HB3	2:D:441:LEU:HD22	1.89	0.53
2:E:393:VAL:O	2:E:397:ARG:HG3	2.07	0.53
2:E:395:ARG:HH21	2:E:436:GLY:HA3	1.74	0.53
2:F:384:GLU:HG2	3:G:121[B]:LYS:NZ	2.24	0.53
3:G:68[A]:LEU:HA	3:G:160[A]:PHE:CE2	2.41	0.53
3:G:143[B]:THR:HB	3:G:144[B]:PRO:CA	2.39	0.53
4:H:51[C]:ARG:HG2	4:H:60[C]:LEU:CA	2.34	0.53
4:H:100[A]:HIS:CD2	4:H:120[A]:ALA:CB	2.90	0.53
1:B:109:ASN:HB2	1:B:110:PRO:CD	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:275:LEU:HA	1:C:278:ARG:N	2.23	0.53
2:E:288:THR:HG23	2:E:291:GLY:H	1.74	0.53
3:G:84[B]:ASP:HB2	3:G:120[B]:ARG:CZ	2.39	0.53
3:G:170[C]:ILE:HD11	3:G:188[C]:LEU:HD21	1.90	0.53
3:G:188[C]:LEU:HD23	3:G:188[C]:LEU:N	2.24	0.53
4:H:51[B]:ARG:HG2	4:H:60[B]:LEU:HD23	1.90	0.53
1:A:34:VAL:HG13	1:A:39:ALA:HB2	1.90	0.53
1:A:271:ARG:NH1	1:A:285:ALA:CB	2.72	0.53
1:A:418:GLU:OE2	1:A:421:LYS:HE2	2.08	0.53
1:A:440:VAL:CA	1:A:445:MET:HG3	2.36	0.53
1:A:449:PRO:HG2	1:A:452:ASP:OD1	2.09	0.53
1:C:456:PHE:HZ	1:C:495:LYS:HD2	1.73	0.53
2:F:393:VAL:O	2:F:397:ARG:HG3	2.08	0.53
3:G:32[A]:LEU:CB	3:G:238[A]:PHE:HB2	2.37	0.53
1:A:298:LEU:HD22	1:A:298:LEU:H	1.72	0.53
1:A:388:GLN:HG3	1:A:409:LYS:HZ1	1.71	0.53
1:A:456:PHE:O	1:A:460:LEU:HB2	2.09	0.53
1:C:106:ARG:HH11	1:C:106:ARG:CB	2.20	0.53
1:C:275:LEU:HD12	1:C:281:PRO:HD3	1.91	0.53
1:C:418:GLU:OE2	1:C:421:LYS:HE2	2.08	0.53
2:D:369:ARG:HG2	2:D:392:ILE:HD11	1.91	0.53
2:D:416:MET:HE2	2:D:416:MET:HA	1.90	0.53
3:G:43[C]:ARG:O	3:G:47[C]:ASP:N	2.42	0.53
3:G:118[C]:VAL:HB	3:G:137[C]:VAL:HG11	1.89	0.53
1:A:157:ILE:N	1:A:158:PRO:CD	2.71	0.53
1:B:275:LEU:HA	1:B:278:ARG:CA	2.39	0.53
1:B:284:GLU:HG3	1:B:329:TYR:CB	2.39	0.53
1:B:415:ARG:NH1	1:B:450:VAL:HG22	2.23	0.53
1:C:46:LYS:HB2	1:C:46:LYS:NZ	2.23	0.53
2:F:375:ASP:O	2:F:379:ILE:HG23	2.08	0.53
2:F:458:LYS:C	2:F:460:LYS:H	2.16	0.53
3:G:255[B]:MET:C	3:G:257[B]:GLU:H	2.16	0.53
2:D:374:GLN:HA	2:D:374:GLN:NE2	2.21	0.53
2:D:382:MET:HG3	2:D:385:LEU:HD22	1.90	0.53
3:G:7[B]:ILE:HA	3:G:10[B]:ARG:HB2	1.91	0.53
3:G:72[C]:PRO:HB3	3:G:73[C]:VAL:HG13	1.91	0.53
3:G:131[B]:TYR:N	3:G:132[B]:PRO:HA	2.21	0.53
3:G:238[C]:PHE:HA	3:G:241[C]:ARG:HB3	1.90	0.53
4:H:97[A]:LYS:NZ	4:H:125[A]:GLU:HG2	2.23	0.53
1:A:284:GLU:HG3	1:A:329:TYR:CB	2.39	0.53
1:B:48:MET:HG3	1:B:51:GLU:OE2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:109:ASN:OD1	1:C:113:GLN:HG2	2.09	0.53
1:C:157:ILE:HG21	1:C:342:ILE:HG12	1.90	0.53
2:D:398:LYS:HD3	2:D:446:PHE:CZ	2.44	0.53
3:G:75[C]:LYS:HB2	3:G:75[C]:LYS:NZ	2.24	0.53
3:G:129[B]:ARG:HB2	3:G:131[B]:TYR:CE1	2.44	0.53
1:A:47:VAL:HG21	1:A:71:VAL:HG21	1.90	0.53
1:C:419:ILE:HD13	1:C:440:VAL:HG11	1.91	0.53
2:E:315:PHE:HA	2:E:318:LEU:HD22	1.90	0.53
3:G:94[C]:ASN:HA	3:G:97[C]:ARG:HB3	1.90	0.53
3:G:238[A]:PHE:O	3:G:242[A]:MET:HB3	2.08	0.53
4:H:88[B]:ILE:HD11	4:H:131[B]:ALA:HA	1.91	0.53
4:H:110[C]:THR:O	4:H:112[C]:LYS:HE2	2.09	0.53
1:A:275:LEU:CD2	2:D:264:MET:HA	2.20	0.52
1:C:171:ARG:HH11	1:C:171:ARG:HG2	1.69	0.52
1:C:407:GLN:HA	1:C:411:ASN:HB2	1.91	0.52
2:D:162:GLN:NE2	2:D:194:GLU:HG2	2.24	0.52
2:D:395:ARG:HH21	2:D:436:GLY:HA3	1.74	0.52
2:F:241:LEU:HD23	2:F:243:PHE:CZ	2.44	0.52
2:F:428:ARG:O	2:F:432:GLU:HG3	2.09	0.52
3:G:43[C]:ARG:HB2	3:G:44[C]:PRO:CD	2.39	0.52
3:G:84[A]:ASP:OD2	3:G:139[A]:GLY:HA2	2.08	0.52
4:H:101[B]:GLU:CD	4:H:121[B]:LEU:HD21	2.34	0.52
4:H:109[C]:LYS:O	4:H:112[C]:LYS:CE	2.58	0.52
4:H:119[C]:ARG:HA	4:H:122[C]:GLU:CD	2.34	0.52
2:D:301:VAL:O	2:D:301:VAL:HG22	2.09	0.52
3:G:15[B]:LYS:NZ	3:G:256[B]:LEU:HD21	2.24	0.52
3:G:71[B]:ARG:NH1	3:G:71[B]:ARG:CG	2.57	0.52
1:C:440:VAL:HG12	1:C:445:MET:CE	2.28	0.52
1:C:440:VAL:HB	1:C:445:MET:HG3	1.91	0.52
2:D:356:HIS:CD2	2:D:356:HIS:C	2.88	0.52
3:G:38[C]:THR:HA	4:H:13[C]:ARG:HH21	1.71	0.52
3:G:79[A]:MET:HA	3:G:115[A]:ILE:O	2.08	0.52
3:G:159[B]:MET:HB3	3:G:165[B]:PHE:CD1	2.44	0.52
2:F:129:GLU:O	2:F:172:HIS:HE1	1.92	0.52
3:G:77[C]:GLY:HA3	3:G:165[C]:PHE:CE2	2.45	0.52
3:G:86[C]:GLY:C	3:G:241[C]:ARG:HH21	2.15	0.52
3:G:131[B]:TYR:H	3:G:132[B]:PRO:CA	2.22	0.52
3:G:170[C]:ILE:CG1	3:G:188[C]:LEU:HD21	2.39	0.52
1:A:48:MET:CE	1:A:94:ILE:HG23	2.39	0.52
1:A:412:ARG:HG3	1:A:446:ASP:OD1	2.09	0.52
1:B:456:PHE:O	1:B:460:LEU:HB2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:275:LEU:HD12	1:C:279:ARG:O	2.09	0.52
2:D:84:ALA:HB1	2:D:103:VAL:HG12	1.91	0.52
2:F:12:PRO:HD2	2:F:260:LEU:HD22	1.91	0.52
3:G:19[A]:GLN:HA	3:G:22[A]:LYS:HG2	1.91	0.52
3:G:79[A]:MET:HE2	3:G:170[A]:ILE:HG21	1.91	0.52
3:G:88[B]:ALA:CB	3:G:241[B]:ARG:HA	2.40	0.52
3:G:146[B]:LEU:HA	3:G:227[B]:TYR:HH	1.73	0.52
1:A:142:VAL:HG22	1:A:161:ARG:O	2.10	0.52
1:A:271:ARG:NH1	1:A:285:ALA:HB1	2.25	0.52
2:E:382:MET:HG3	2:E:385:LEU:HD22	1.91	0.52
2:F:181:VAL:HG22	2:F:221:VAL:HG13	1.92	0.52
3:G:65[C]:HIS:CD2	3:G:69[C]:GLU:CA	2.93	0.52
3:G:184[C]:VAL:HG11	3:G:186[C]:LYS:HE3	1.92	0.52
1:A:171:ARG:CG	1:A:171:ARG:NH1	2.53	0.52
1:B:106:ARG:HH11	1:B:106:ARG:CB	2.22	0.52
2:D:35:PRO:HD2	2:D:36:GLN:OE1	2.09	0.52
3:G:8[C]:LYS:HA	3:G:11[C]:ILE:HB	1.92	0.52
3:G:67[A]:MET:SD	3:G:161[A]:ALA:HA	2.49	0.52
4:H:118[C]:LYS:HA	4:H:121[C]:LEU:HG	1.92	0.52
1:A:305:SER:OG	1:A:308:LYS:HG2	2.10	0.52
1:B:238:ALA:HB3	1:B:239:PRO:HD3	1.92	0.52
1:B:382:LEU:HD11	1:B:416:THR:HG23	1.92	0.52
2:F:195:MET:HE2	2:F:206:MET:SD	2.50	0.52
1:A:462:SER:CA	1:A:465:ARG:HH12	2.21	0.52
1:B:275:LEU:HD13	2:E:264:MET:HG3	1.91	0.52
1:B:440:VAL:CB	1:B:445:MET:HG3	2.40	0.52
2:E:91:ASN:ND2	2:E:95:GLU:H	2.08	0.52
3:G:68[A]:LEU:HD22	3:G:68[A]:LEU:H	1.75	0.52
4:H:3[C]:THR:OG1	4:H:19[C]:GLU:HB3	2.10	0.52
1:A:275:LEU:HD12	1:A:279:ARG:O	2.10	0.51
3:G:48[C]:LYS:HZ1	4:H:9[C]:VAL:CG1	2.24	0.51
3:G:85[C]:ARG:O	3:G:85[C]:ARG:CD	2.57	0.51
4:H:7[C]:ASP:HA	4:H:16[C]:PHE:O	2.10	0.51
4:H:53[A]:LYS:HE2	4:H:58[A]:GLU:HG2	1.92	0.51
1:A:157:ILE:HG21	1:A:342:ILE:HG12	1.93	0.51
1:B:108:VAL:HG13	1:B:109:ASN:O	2.10	0.51
1:B:495:LYS:O	1:B:496:LYS:HB2	2.09	0.51
1:C:41:VAL:CG2	1:C:88:VAL:HG21	2.40	0.51
1:C:440:VAL:CB	1:C:445:MET:HG3	2.41	0.51
2:E:84:ALA:HB1	2:E:103:VAL:HG12	1.92	0.51
2:F:386:SER:HB3	2:F:389:ASP:OD1	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:257[C]:GLU:O	3:G:257[C]:GLU:HG2	2.08	0.51
1:A:440:VAL:HB	1:A:445:MET:HG3	1.90	0.51
1:C:238:ALA:HB3	1:C:239:PRO:HD3	1.93	0.51
2:F:382:MET:HG3	2:F:385:LEU:HD22	1.92	0.51
3:G:15[C]:LYS:O	3:G:18[C]:ARG:HB3	2.09	0.51
1:C:275:LEU:HD13	2:F:264:MET:HG3	1.92	0.51
1:C:456:PHE:O	1:C:460:LEU:HB2	2.11	0.51
2:D:85:THR:O	2:D:205:SER:HB3	2.11	0.51
2:F:40:LEU:CD2	2:F:64:LEU:HD11	2.40	0.51
3:G:32[B]:LEU:CG	3:G:238[B]:PHE:HB3	2.37	0.51
3:G:86[A]:GLY:HA2	3:G:241[A]:ARG:NH2	2.26	0.51
4:H:63[C]:VAL:HG13	4:H:79[C]:ALA:HB1	1.93	0.51
4:H:114[C]:TYR:HB3	4:H:118[C]:LYS:HE2	1.93	0.51
1:C:143:HIS:CD2	1:C:144:GLU:HG2	2.46	0.51
2:E:226:LEU:O	2:E:230:GLU:HG3	2.11	0.51
4:H:14[B]:LYS:NZ	4:H:14[B]:LYS:HB3	2.25	0.51
1:A:261:ASP:O	1:A:262:ASP:HB2	2.11	0.51
1:B:109:ASN:OD1	1:B:113:GLN:HG2	2.10	0.51
1:C:106:ARG:CG	1:C:106:ARG:NH1	2.48	0.51
1:C:137:MET:HG3	2:D:97:ILE:O	2.11	0.51
1:C:271:ARG:NH1	1:C:285:ALA:CB	2.74	0.51
2:D:226:LEU:O	2:D:230:GLU:HG3	2.10	0.51
2:D:246:ASN:OD1	2:D:248:PHE:HB3	2.11	0.51
2:E:453:ASP:O	2:E:456:VAL:HG23	2.11	0.51
2:F:113:ARG:HD3	2:F:114:PRO:O	2.11	0.51
3:G:115[C]:ILE:HD11	3:G:133[C]:VAL:HB	1.92	0.51
3:G:155[B]:SER:O	3:G:159[B]:MET:HG2	2.10	0.51
3:G:244[B]:ALA:C	3:G:245[B]:MET:HE2	2.35	0.51
1:B:407:GLN:HA	1:B:411:ASN:HB2	1.92	0.51
1:C:140:LYS:HE2	1:C:143:HIS:ND1	2.26	0.51
2:E:411:GLU:OE2	2:E:417:PRO:HB3	2.11	0.51
2:F:91:ASN:C	2:F:91:ASN:HD22	2.17	0.51
2:F:131:GLY:HA3	2:F:167:ASN:HD22	1.76	0.51
3:G:77[B]:GLY:HA3	3:G:165[B]:PHE:CZ	2.46	0.51
3:G:170[C]:ILE:CD1	3:G:188[C]:LEU:HD21	2.41	0.51
2:E:129:GLU:O	2:E:172:HIS:HE1	1.93	0.51
2:E:183:GLU:C	2:E:211:MET:HE3	2.36	0.51
3:G:238[C]:PHE:C	3:G:241[C]:ARG:H	2.19	0.51
4:H:8[B]:ILE:HD13	4:H:61[B]:ILE:HD12	1.92	0.51
4:H:48[B]:ALA:O	4:H:63[B]:VAL:HB	2.10	0.51
1:A:140:LYS:HE2	1:A:143:HIS:ND1	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:449:PRO:HG2	1:B:452:ASP:OD1	2.09	0.51
1:C:355:PRO:HB2	1:C:357:VAL:HG23	1.92	0.51
4:H:8[B]:ILE:HD11	4:H:15[B]:VAL:HB	1.93	0.51
1:A:184:ILE:HG22	1:A:427:PRO:HG2	1.91	0.51
1:B:164:ARG:NH2	2:F:184:ARG:HD3	2.23	0.51
2:D:139:ALA:N	2:D:140:PRO:HD3	2.25	0.51
3:G:14[A]:VAL:CG1	3:G:256[A]:LEU:HG	2.41	0.51
3:G:32[C]:LEU:CD2	3:G:238[C]:PHE:HB2	2.41	0.51
3:G:101[C]:LYS:HD2	3:G:101[C]:LYS:O	2.11	0.51
3:G:177[C]:SER:O	3:G:180[C]:VAL:O	2.29	0.51
3:G:217[C]:LEU:C	3:G:219[C]:PRO:HD3	2.36	0.51
4:H:39[A]:ILE:HB	4:H:40[A]:PRO:CD	2.41	0.51
1:B:481:LEU:O	1:B:482:PRO:O	2.28	0.50
1:C:275:LEU:CA	2:F:264:MET:HE2	2.41	0.50
2:D:428:ARG:O	2:D:432:GLU:HG3	2.12	0.50
2:E:131:GLY:HA3	2:E:167:ASN:HD22	1.75	0.50
2:E:416:MET:HE2	2:E:416:MET:HA	1.93	0.50
3:G:48[C]:LYS:NZ	4:H:9[C]:VAL:HB	2.26	0.50
1:A:275:LEU:HA	1:A:278:ARG:H	1.77	0.50
1:A:407:GLN:CA	1:A:411:ASN:HB2	2.42	0.50
2:D:129:GLU:O	2:D:172:HIS:HE1	1.94	0.50
2:E:428:ARG:O	2:E:432:GLU:HG3	2.11	0.50
3:G:102[B]:THR:C	3:G:104[B]:GLU:H	2.19	0.50
3:G:149[C]:ILE:O	3:G:151[C]:ASP:N	2.44	0.50
1:C:407:GLN:HB3	1:C:411:ASN:HB2	1.93	0.50
2:D:388:GLU:O	2:D:392:ILE:HG23	2.10	0.50
2:E:26:ILE:O	2:E:27:TYR:HB2	2.10	0.50
2:F:301:VAL:CG1	2:F:306:TYR:HE1	2.24	0.50
3:G:244[C]:ALA:O	3:G:245[C]:MET:HE2	2.11	0.50
1:A:440:VAL:CB	1:A:445:MET:HG3	2.42	0.50
1:A:462:SER:CB	1:A:465:ARG:HH12	2.23	0.50
1:B:157:ILE:N	1:B:158:PRO:CD	2.75	0.50
1:C:136:VAL:HG12	2:D:185:THR:HG23	1.92	0.50
1:C:157:ILE:N	1:C:158:PRO:CD	2.74	0.50
1:C:407:GLN:CA	1:C:411:ASN:HB2	2.42	0.50
2:E:301:VAL:CG1	2:E:306:TYR:HE1	2.21	0.50
2:E:386:SER:HB3	2:E:389:ASP:OD1	2.11	0.50
2:E:458:LYS:C	2:E:460:LYS:H	2.18	0.50
3:G:113[C]:TYR:O	3:G:114[C]:VAL:HG13	2.10	0.50
4:H:22[C]:ILE:HG22	4:H:35[C]:MET:HE1	1.93	0.50
4:H:50[C]:VAL:H	4:H:61[C]:ILE:CG1	2.21	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:68[C]:LEU:HD23	4:H:77[C]:ILE:HG22	1.93	0.50
1:A:355:PRO:HB2	1:A:357:VAL:HG23	1.92	0.50
1:B:32:ILE:HG13	1:B:33:GLN:HG3	1.93	0.50
1:B:151:LYS:H	1:B:422:GLN:NE2	1.89	0.50
1:C:449:PRO:HG2	1:C:452:ASP:OD1	2.12	0.50
2:D:386:SER:HB3	2:D:389:ASP:OD1	2.11	0.50
2:E:181:VAL:HG22	2:E:221:VAL:HG13	1.94	0.50
2:E:273:THR:O	2:E:277:GLU:HG3	2.12	0.50
3:G:149[B]:ILE:HD11	3:G:227[B]:TYR:CZ	2.47	0.50
1:C:448:ILE:HG23	1:C:449:PRO:HD2	1.93	0.50
2:D:160:LEU:HD22	2:D:164:LEU:HD22	1.94	0.50
2:D:349:PRO:HG3	2:D:357:TYR:CD2	2.46	0.50
3:G:31[B]:LYS:HE3	3:G:142[B]:ASP:CG	2.36	0.50
3:G:80[B]:VAL:HB	3:G:171[B]:PHE:CD1	2.39	0.50
3:G:132[C]:PRO:CG	3:G:133[C]:VAL:H	2.25	0.50
3:G:155[C]:SER:O	3:G:159[C]:MET:HG3	2.12	0.50
3:G:182[A]:ARG:HA	3:G:182[A]:ARG:NE	2.27	0.50
4:H:10[A]:THR:HA	4:H:79[A]:ALA:O	2.12	0.50
4:H:114[C]:TYR:HA	4:H:118[C]:LYS:HG3	1.93	0.50
1:A:48:MET:CB	2:E:63:GLY:HA2	2.40	0.50
1:A:248:TYR:O	1:A:252:LYS:HB2	2.11	0.50
2:D:161:ILE:HG23	2:D:243:PHE:CE1	2.47	0.50
2:D:325:GLU:CG	2:D:338:ASP:HB2	2.42	0.50
3:G:107[C]:HIS:HB2	3:G:113[C]:TYR:OH	2.11	0.50
3:G:174[A]:GLU:HA	3:G:232[A]:ASP:OD2	2.11	0.50
1:A:143:HIS:NE2	1:A:144:GLU:HG2	2.27	0.50
1:B:412:ARG:HG3	1:B:446:ASP:OD1	2.11	0.50
1:C:481:LEU:O	1:C:482:PRO:O	2.29	0.50
2:E:349:PRO:HG3	2:E:357:TYR:CD2	2.46	0.50
2:F:162:GLN:NE2	2:F:194:GLU:HG2	2.27	0.50
2:F:264:MET:HG2	2:F:265:PRO:O	2.11	0.50
2:F:374:GLN:HA	2:F:374:GLN:NE2	2.23	0.50
2:F:453:ASP:O	2:F:456:VAL:HG23	2.11	0.50
3:G:96[A]:LEU:HD22	3:G:125[A]:PHE:CD1	2.47	0.50
4:H:83[C]:GLU:HB2	4:H:87[C]:GLU:HB3	1.94	0.50
4:H:97[A]:LYS:HZ3	4:H:125[A]:GLU:HG2	1.77	0.50
1:B:395:PHE:CD2	1:B:395:PHE:N	2.80	0.50
1:C:438:TYR:HA	1:C:441:THR:CG2	2.39	0.50
2:E:241:LEU:O	2:E:242:LEU:HB3	2.12	0.50
2:F:386:SER:HB3	2:F:389:ASP:HB2	1.94	0.50
1:A:48:MET:HG3	1:A:51:GLU:OE2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:10[C]:ARG:HB3	3:G:259[C]:LEU:HD11	1.93	0.49
3:G:172[A]:TYR:HD1	3:G:173[A]:ASN:N	2.09	0.49
4:H:9[C]:VAL:HA	4:H:15[C]:VAL:HG23	1.94	0.49
4:H:47[C]:THR:HA	4:H:64[C]:SER:HA	1.93	0.49
1:A:48:MET:HB3	2:E:63:GLY:CA	2.42	0.49
1:A:275:LEU:HD12	1:A:281:PRO:HD3	1.94	0.49
1:A:275:LEU:CD1	1:A:281:PRO:HD3	2.41	0.49
1:B:275:LEU:CD1	1:B:281:PRO:HD3	2.42	0.49
2:D:329:ALA:C	2:D:331:MET:H	2.20	0.49
3:G:96[A]:LEU:HD13	3:G:125[A]:PHE:CG	2.47	0.49
4:H:7[B]:ASP:HA	4:H:16[B]:PHE:O	2.12	0.49
4:H:50[C]:VAL:N	4:H:61[C]:ILE:HG12	2.20	0.49
4:H:79[B]:ALA:HB3	4:H:82[B]:ALA:HB2	1.94	0.49
2:D:411:GLU:OE2	2:D:417:PRO:HB3	2.12	0.49
2:E:308:ASP:O	2:E:311:PRO:HD2	2.12	0.49
2:E:386:SER:HB3	2:E:389:ASP:HB2	1.94	0.49
3:G:27[A]:VAL:O	3:G:31[A]:LYS:HB2	2.11	0.49
4:H:62[A]:ALA:N	4:H:130[A]:VAL:HG21	2.27	0.49
4:H:86[A]:GLU:HG2	4:H:134[A]:LYS:HD3	1.94	0.49
4:H:118[C]:LYS:HA	4:H:121[C]:LEU:HB2	1.93	0.49
1:B:275:LEU:HD12	1:B:279:ARG:O	2.13	0.49
1:C:275:LEU:HA	1:C:278:ARG:CA	2.41	0.49
2:D:147:ILE:HA	2:D:320:ALA:O	2.12	0.49
3:G:32[C]:LEU:HD23	3:G:238[C]:PHE:CB	2.41	0.49
3:G:95[C]:ILE:HD11	3:G:171[C]:PHE:HB3	1.94	0.49
3:G:220[C]:LYS:HB3	3:G:220[C]:LYS:NZ	2.28	0.49
3:G:236[A]:SER:O	3:G:240[A]:ALA:N	2.37	0.49
4:H:26[C]:ARG:HB2	4:H:48[C]:ALA:CB	2.42	0.49
1:A:205:VAL:O	1:A:209:VAL:HG23	2.13	0.49
1:A:415:ARG:NH1	1:A:450:VAL:HG22	2.27	0.49
2:E:160:LEU:HD22	2:E:164:LEU:HD22	1.95	0.49
2:E:431:LYS:HE3	2:E:435:GLU:OE2	2.12	0.49
2:F:398:LYS:HD3	2:F:446:PHE:CZ	2.46	0.49
3:G:38[B]:THR:HG22	4:H:13[B]:ARG:HE	1.77	0.49
4:H:94[B]:LYS:HG3	4:H:128[B]:LEU:HD11	1.92	0.49
1:C:411:ASN:O	1:C:415:ARG:NH1	2.45	0.49
3:G:33[B]:ARG:C	3:G:35[B]:ALA:N	2.70	0.49
4:H:88[B]:ILE:HD13	4:H:130[B]:VAL:HG12	1.94	0.49
1:A:275:LEU:HB3	2:D:264:MET:SD	2.52	0.49
1:A:407:GLN:HB3	1:A:411:ASN:HB2	1.94	0.49
1:B:407:GLN:HB3	1:B:411:ASN:HB2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:95:MET:CA	1:C:95:MET:HE2	2.42	0.49
1:C:388:GLN:HG3	1:C:409:LYS:HZ1	1.78	0.49
2:E:406:PRO:HB3	2:E:416:MET:HG3	1.94	0.49
3:G:7[C]:ILE:HD12	3:G:262[C]:GLN:HB3	1.95	0.49
3:G:14[A]:VAL:HG12	3:G:256[A]:LEU:HG	1.95	0.49
3:G:118[C]:VAL:HB	3:G:137[C]:VAL:CG1	2.43	0.49
4:H:119[B]:ARG:O	4:H:122[B]:GLU:HB2	2.13	0.49
1:A:46:LYS:HB2	1:A:46:LYS:HZ2	1.76	0.49
2:F:268:VAL:O	2:F:268:VAL:CG2	2.59	0.49
3:G:32[B]:LEU:HA	3:G:35[B]:ALA:HB2	1.93	0.49
3:G:45[B]:TYR:O	3:G:49[B]:ILE:HG12	2.12	0.49
4:H:43[C]:THR:H	4:H:68[C]:LEU:HB2	1.78	0.49
4:H:103[B]:ILE:HD11	4:H:117[B]:HIS:CE1	2.48	0.49
1:A:419:ILE:HD13	1:A:440:VAL:HG11	1.95	0.49
1:A:499:THR:H	1:A:500:PRO:HD3	1.73	0.49
1:B:286:TYR:HB3	1:B:287:PRO:HD2	1.95	0.49
1:B:386:LEU:HD22	1:B:416:THR:HG21	1.94	0.49
2:E:346:ILE:HB	2:E:351:VAL:HG11	1.95	0.49
2:E:411:GLU:CD	2:E:417:PRO:HB3	2.38	0.49
3:G:22[C]:LYS:HB3	3:G:249[C]:THR:OG1	2.13	0.49
3:G:32[C]:LEU:CD2	3:G:238[C]:PHE:CD2	2.94	0.49
3:G:45[C]:TYR:HB3	4:H:11[C]:PRO:HA	1.94	0.49
3:G:68[C]:LEU:HD12	3:G:189[C]:LEU:HG	1.95	0.49
3:G:79[B]:MET:HA	3:G:115[B]:ILE:O	2.13	0.49
3:G:143[C]:THR:HB	3:G:144[C]:PRO:HA	1.94	0.49
4:H:103[A]:ILE:HD13	4:H:103[A]:ILE:H	1.78	0.49
2:D:130:THR:CG2	2:D:135:ILE:HD11	2.36	0.49
2:D:411:GLU:CD	2:D:417:PRO:HB3	2.38	0.49
2:F:379:ILE:HG13	2:F:379:ILE:O	2.13	0.49
3:G:96[A]:LEU:CA	3:G:99[A]:VAL:HG12	2.40	0.49
4:H:63[A]:VAL:HG12	4:H:64[A]:SER:N	2.28	0.49
4:H:64[B]:SER:HB2	4:H:123[B]:ARG:HG2	1.95	0.49
4:H:66[C]:GLY:HA3	4:H:79[C]:ALA:CA	2.35	0.49
4:H:101[A]:GLU:HG2	4:H:104[A]:LEU:HD12	1.94	0.49
1:A:114:PRO:HG3	1:A:121:ILE:CD1	2.43	0.48
2:D:264:MET:HG2	2:D:265:PRO:O	2.13	0.48
3:G:84[C]:ASP:OD1	3:G:140[C]:ILE:HG12	2.13	0.48
3:G:143[C]:THR:HB	3:G:144[C]:PRO:CA	2.43	0.48
4:H:71[C]:ARG:HB3	4:H:72[C]:PRO:HD2	1.95	0.48
1:B:298:LEU:CD2	1:B:298:LEU:N	2.76	0.48
2:D:458:LYS:C	2:D:460:LYS:H	2.20	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:113:ARG:HD3	2:E:114:PRO:O	2.13	0.48
2:F:161:ILE:HG23	2:F:243:PHE:CE1	2.48	0.48
2:F:166:ASN:O	2:F:170:GLN:HB2	2.13	0.48
3:G:35[C]:ALA:HA	3:G:38[C]:THR:OG1	2.13	0.48
3:G:132[C]:PRO:CD	3:G:133[C]:VAL:H	2.25	0.48
1:C:34:VAL:HG13	1:C:39:ALA:HB2	1.94	0.48
2:E:107:GLU:CD	2:E:235:ARG:HH12	2.22	0.48
2:E:268:VAL:O	2:E:268:VAL:CG2	2.58	0.48
2:F:329:ALA:C	2:F:331:MET:H	2.20	0.48
2:F:411:GLU:OE2	2:F:417:PRO:HB3	2.13	0.48
3:G:32[B]:LEU:HD21	3:G:238[B]:PHE:HB3	1.93	0.48
3:G:94[A]:ASN:HA	3:G:97[A]:ARG:HB3	1.95	0.48
4:H:62[A]:ALA:O	4:H:82[A]:ALA:HA	2.13	0.48
1:A:411:ASN:O	1:A:415:ARG:NH1	2.46	0.48
1:A:471:LEU:HD13	1:A:487:LEU:HD22	1.95	0.48
1:C:462:SER:CB	1:C:465:ARG:HH12	2.26	0.48
2:D:379:ILE:HA	3:G:251[C]:ASN:HB3	1.95	0.48
2:E:166:ASN:O	2:E:170:GLN:HB2	2.13	0.48
2:E:379:ILE:HG13	2:E:379:ILE:O	2.12	0.48
2:F:48:LEU:HD11	2:F:54:ARG:HB2	1.95	0.48
3:G:12[B]:ARG:HB3	3:G:12[B]:ARG:NH1	2.28	0.48
1:A:41:VAL:CG2	1:A:88:VAL:HG21	2.42	0.48
1:A:176:THR:O	1:A:180:ILE:HG12	2.13	0.48
1:B:456:PHE:CZ	1:B:495:LYS:HD2	2.49	0.48
2:D:301:VAL:CG1	2:D:306:TYR:HE1	2.23	0.48
2:E:397:ARG:O	2:E:401:ARG:HD2	2.13	0.48
2:F:97:ILE:O	2:F:97:ILE:HG12	2.13	0.48
2:F:340:LEU:HD12	2:F:340:LEU:HA	1.67	0.48
2:F:406:PRO:HB3	2:F:416:MET:HG3	1.95	0.48
3:G:27[C]:VAL:HA	3:G:30[C]:ALA:HB3	1.96	0.48
3:G:41[B]:ASN:C	3:G:44[B]:PRO:HD2	2.38	0.48
3:G:127[C]:LYS:C	3:G:127[C]:LYS:HD3	2.39	0.48
3:G:178[A]:PRO:HB3	3:G:242[A]:MET:HE2	1.95	0.48
1:B:172:GLN:NE2	2:E:345:ARG:HB3	2.28	0.48
1:C:326:VAL:HG11	1:C:343:PHE:CE2	2.42	0.48
2:D:91:ASN:ND2	2:D:91:ASN:C	2.71	0.48
2:E:356:HIS:CD2	2:E:356:HIS:C	2.91	0.48
2:E:416:MET:N	2:E:417:PRO:CA	2.76	0.48
2:F:129:GLU:O	2:F:172:HIS:CE1	2.66	0.48
3:G:31[C]:LYS:HB3	3:G:32[C]:LEU:HD22	1.94	0.48
1:B:205:VAL:O	1:B:209:VAL:HG23	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:264:MET:HE3	2:D:272:PRO:CB	2.37	0.48
1:B:83:ARG:CB	2:E:47:HIS:HE1	2.12	0.48
1:B:284:GLU:HG3	1:B:329:TYR:HB2	1.96	0.48
1:C:462:SER:CA	1:C:465:ARG:HH12	2.27	0.48
2:D:386:SER:HB3	2:D:389:ASP:HB2	1.95	0.48
2:E:232:PHE:HB2	2:E:240:VAL:HG21	1.94	0.48
4:H:88[C]:ILE:HD12	4:H:131[C]:ALA:HA	1.95	0.48
1:A:275:LEU:HB3	2:D:264:MET:HE2	1.96	0.48
1:B:187:LYS:C	1:B:189:GLN:HG2	2.39	0.48
1:B:407:GLN:CA	1:B:411:ASN:HB2	2.43	0.48
1:C:333:ASN:O	1:C:337:ILE:HG13	2.13	0.48
1:C:471:LEU:HD13	1:C:487:LEU:HD22	1.95	0.48
2:D:142:ALA:HB2	2:D:346:ILE:HG21	1.96	0.48
2:E:35:PRO:HD2	2:E:36:GLN:OE1	2.14	0.48
3:G:167[C]:LYS:HD2	3:G:167[C]:LYS:N	2.28	0.48
1:B:388:GLN:HG3	1:B:409:LYS:HZ2	1.77	0.48
3:G:85[C]:ARG:CA	3:G:120[C]:ARG:NH2	2.77	0.48
3:G:238[C]:PHE:O	3:G:241[C]:ARG:N	2.46	0.48
4:H:22[A]:ILE:HG22	4:H:35[A]:MET:SD	2.54	0.48
4:H:90[B]:VAL:HG13	4:H:128[B]:LEU:HD21	1.95	0.48
1:B:65:ASN:HB3	2:F:10:MET:HE3	1.96	0.47
1:C:475:ILE:O	1:C:479:GLY:HA3	2.14	0.47
2:D:23:LEU:HA	2:D:24:PRO:HD3	1.75	0.47
3:G:31[B]:LYS:HG2	3:G:32[B]:LEU:HD22	1.95	0.47
3:G:65[B]:HIS:HB3	3:G:68[B]:LEU:HB2	1.96	0.47
3:G:238[B]:PHE:CD1	3:G:241[B]:ARG:HD2	2.49	0.47
1:A:326:VAL:O	1:A:326:VAL:HG12	2.13	0.47
1:A:460:LEU:O	1:A:464:MET:HG2	2.14	0.47
1:B:431:GLU:HG2	1:B:432:GLU:H	1.77	0.47
1:C:108:VAL:HG13	1:C:109:ASN:O	2.14	0.47
2:E:165:ILE:HG21	2:E:200:VAL:HG13	1.95	0.47
2:F:356:HIS:C	2:F:356:HIS:CD2	2.92	0.47
2:F:369:ARG:HG2	2:F:392:ILE:HD11	1.96	0.47
3:G:5[A]:ARG:HG2	3:G:6[A]:GLU:HG2	1.95	0.47
3:G:27[B]:VAL:HG12	3:G:28[B]:ALA:N	2.28	0.47
4:H:14[B]:LYS:HZ2	4:H:14[B]:LYS:HB3	1.79	0.47
4:H:49[B]:PRO:HA	4:H:61[B]:ILE:O	2.14	0.47
1:A:456:PHE:CZ	1:A:495:LYS:HD2	2.49	0.47
1:B:326:VAL:HG11	1:B:343:PHE:CE2	2.44	0.47
1:C:167:ILE:HD11	1:C:316:LEU:HD13	1.95	0.47
1:C:298:LEU:H	1:C:298:LEU:CD2	2.27	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:415:ARG:NH1	1:C:450:VAL:HG22	2.29	0.47
3:G:4[A]:MET:HG3	3:G:5[A]:ARG:HH12	1.73	0.47
3:G:87[C]:LEU:HD12	3:G:87[C]:LEU:HA	1.51	0.47
3:G:153[B]:ALA:O	3:G:157[B]:ILE:HG12	2.13	0.47
3:G:160[C]:PHE:HA	3:G:165[C]:PHE:HB2	1.95	0.47
3:G:168[B]:LEU:CB	3:G:189[B]:LEU:HB2	2.43	0.47
1:A:32:ILE:HG13	1:A:33:GLN:HG3	1.96	0.47
1:B:411:ASN:O	1:B:415:ARG:NH1	2.48	0.47
2:F:232:PHE:HB2	2:F:240:VAL:HG21	1.95	0.47
2:F:233:ARG:HD3	2:F:292:SER:HB3	1.95	0.47
3:G:14[B]:VAL:HG12	3:G:256[B]:LEU:HD12	1.96	0.47
4:H:4[B]:VAL:HG21	4:H:36[B]:ALA:HA	1.96	0.47
4:H:100[B]:HIS:CD2	4:H:117[B]:HIS:HD2	2.28	0.47
4:H:126[C]:VAL:O	4:H:130[C]:VAL:HB	2.14	0.47
1:C:275:LEU:HB3	2:F:264:MET:HE2	1.96	0.47
2:E:149:LEU:HD21	2:E:324:LEU:HD22	1.95	0.47
3:G:11[C]:ILE:HG13	3:G:259[C]:LEU:HD12	1.96	0.47
3:G:25[C]:LYS:HD2	3:G:25[C]:LYS:O	2.14	0.47
3:G:108[B]:GLN:NE2	3:G:108[B]:GLN:H	2.12	0.47
4:H:96[C]:ALA:CB	4:H:100[C]:HIS:ND1	2.77	0.47
4:H:119[C]:ARG:HA	4:H:122[C]:GLU:OE2	2.15	0.47
1:A:330:ILE:HB	1:A:331:PRO:HD3	1.95	0.47
1:A:386:LEU:HD22	1:A:416:THR:HG21	1.97	0.47
1:B:179:ALA:HB2	1:B:318:PHE:HZ	1.79	0.47
1:C:275:LEU:HG	1:C:278:ARG:CA	2.42	0.47
2:E:329:ALA:C	2:E:331:MET:H	2.22	0.47
2:F:264:MET:CB	2:F:265:PRO:CA	2.90	0.47
3:G:95[C]:ILE:O	3:G:95[C]:ILE:HD13	2.15	0.47
1:A:210:GLU:HB2	2:D:123:THR:HB	1.96	0.47
1:A:431:GLU:HB2	1:A:472:LEU:HD22	1.97	0.47
1:B:140:LYS:HE2	1:B:143:HIS:ND1	2.30	0.47
1:B:146:LEU:HD21	1:B:257:LEU:HD13	1.96	0.47
1:B:481:LEU:C	1:B:481:LEU:HD22	2.39	0.47
1:C:151:LYS:HD2	1:C:419:ILE:O	2.14	0.47
2:D:264:MET:CB	2:D:265:PRO:CA	2.92	0.47
2:D:406:PRO:HB3	2:D:416:MET:HG3	1.97	0.47
2:E:233:ARG:HD3	2:E:292:SER:HB3	1.97	0.47
2:F:352:VAL:HG21	2:F:356:HIS:CD2	2.49	0.47
3:G:72[B]:PRO:HA	3:G:73[B]:VAL:CB	2.41	0.47
3:G:85[C]:ARG:HA	3:G:120[C]:ARG:NH2	2.30	0.47
3:G:95[C]:ILE:O	3:G:99[C]:VAL:HG13	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:168[C]:LEU:HD22	3:G:189[C]:LEU:HD22	1.97	0.47
3:G:181[A]:GLN:O	3:G:183[A]:PRO:HD3	2.15	0.47
4:H:41[C]:LEU:HD12	4:H:70[C]:VAL:HG11	1.96	0.47
4:H:60[A]:LEU:HB2	4:H:130[A]:VAL:HG13	1.96	0.47
4:H:101[B]:GLU:HB3	4:H:121[B]:LEU:HD21	1.97	0.47
1:A:99:VAL:CG1	1:A:248:TYR:CD1	2.98	0.47
1:A:435:ILE:CD1	1:A:464:MET:HE2	2.37	0.47
1:B:31:VAL:CG1	1:B:34:VAL:HG22	2.45	0.47
1:B:271:ARG:NH1	1:B:285:ALA:CB	2.78	0.47
1:B:471:LEU:HD13	1:B:487:LEU:HD22	1.96	0.47
2:F:254:GLY:HA3	2:F:271:GLN:HE21	1.80	0.47
3:G:71[C]:ARG:HH22	3:G:163[C]:GLU:HG3	1.79	0.47
3:G:150[B]:GLN:O	3:G:150[B]:GLN:HG2	2.15	0.47
3:G:168[C]:LEU:HB2	3:G:189[C]:LEU:HB2	1.97	0.47
3:G:175[C]:PHE:HB2	3:G:236[C]:SER:OG	2.14	0.47
3:G:245[B]:MET:C	3:G:247[B]:ASN:H	2.21	0.47
1:C:31:VAL:CG1	1:C:34:VAL:HG22	2.44	0.47
1:C:99:VAL:CG1	1:C:248:TYR:CD1	2.98	0.47
1:C:271:ARG:NH1	1:C:285:ALA:HB1	2.29	0.47
2:E:441:LEU:HD21	2:E:456:VAL:HG13	1.96	0.47
2:F:411:GLU:CD	2:F:417:PRO:HB3	2.40	0.47
3:G:168[B]:LEU:H	3:G:190[B]:PRO:HD3	1.80	0.47
3:G:185[C]:GLU:HG3	3:G:185[C]:GLU:O	2.15	0.47
4:H:9[C]:VAL:HG22	4:H:14[C]:LYS:HA	1.96	0.47
4:H:85[A]:PRO:HA	4:H:130[A]:VAL:HG12	1.97	0.47
1:B:47:VAL:HG12	1:B:90:ARG:HG2	1.95	0.47
1:C:66:LEU:HD13	2:D:66:ARG:HG3	1.97	0.47
1:C:386:LEU:HD22	1:C:416:THR:HG21	1.97	0.47
1:C:460:LEU:O	1:C:464:MET:HG2	2.15	0.47
1:C:462:SER:HA	1:C:465:ARG:HH12	1.72	0.47
2:D:48:LEU:HD11	2:D:54:ARG:HB2	1.97	0.47
2:F:65:VAL:HB	2:F:68:LEU:HD21	1.97	0.47
2:F:84:ALA:HB1	2:F:103:VAL:HG12	1.96	0.47
4:H:4[A]:VAL:HG13	4:H:73[A]:ASP:O	2.15	0.47
4:H:123[B]:ARG:O	4:H:127[B]:ARG:HG3	2.14	0.47
1:A:106:ARG:CG	1:A:106:ARG:NH1	2.55	0.46
1:A:337:ILE:O	2:E:184:ARG:NE	2.47	0.46
1:C:286:TYR:HB3	1:C:287:PRO:HD2	1.96	0.46
1:C:499:THR:N	1:C:500:PRO:CD	2.76	0.46
2:D:65:VAL:HB	2:D:68:LEU:HD21	1.98	0.46
2:D:129:GLU:O	2:D:172:HIS:CE1	2.67	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:247:ILE:O	2:E:250:PHE:HB3	2.14	0.46
2:E:254:GLY:HA3	2:E:271:GLN:NE2	2.30	0.46
2:F:34:ARG:CG	2:F:35:PRO:HA	2.39	0.46
3:G:43[C]:ARG:O	3:G:44[C]:PRO:C	2.58	0.46
3:G:79[A]:MET:HE1	3:G:226[A]:ILE:HG23	1.97	0.46
3:G:95[B]:ILE:HG23	3:G:96[B]:LEU:H	1.80	0.46
3:G:140[C]:ILE:HG13	3:G:141[C]:SER:N	2.31	0.46
3:G:249[B]:THR:O	3:G:250[B]:ASP:C	2.57	0.46
1:A:275:LEU:HA	1:A:278:ARG:CA	2.45	0.46
1:B:143:HIS:CD2	1:B:144:GLU:HG2	2.50	0.46
1:B:184:ILE:HG22	1:B:427:PRO:HG2	1.96	0.46
1:C:275:LEU:C	1:C:278:ARG:H	2.24	0.46
1:C:431:GLU:HG2	1:C:432:GLU:H	1.78	0.46
3:G:29[B]:ALA:HA	3:G:242[B]:MET:SD	2.55	0.46
3:G:32[C]:LEU:CG	3:G:238[C]:PHE:CB	2.75	0.46
1:A:95:MET:HE2	1:A:95:MET:CA	2.45	0.46
1:B:275:LEU:C	1:B:278:ARG:H	2.24	0.46
1:C:284:GLU:HG3	1:C:329:TYR:CD1	2.48	0.46
2:D:264:MET:HG2	2:D:265:PRO:C	2.40	0.46
2:E:125:ASP:CG	2:E:345:ARG:NH2	2.68	0.46
3:G:68[A]:LEU:HD22	3:G:68[A]:LEU:N	2.30	0.46
3:G:170[A]:ILE:O	3:G:185[A]:GLU:HB2	2.15	0.46
3:G:217[A]:LEU:O	3:G:219[A]:PRO:HD3	2.16	0.46
4:H:8[C]:ILE:HG13	4:H:8[C]:ILE:O	2.15	0.46
4:H:130[B]:VAL:C	4:H:132[B]:ASN:H	2.24	0.46
1:A:275:LEU:CB	2:D:264:MET:SD	3.03	0.46
1:B:41:VAL:CG2	1:B:88:VAL:HG21	2.44	0.46
1:B:275:LEU:HA	1:B:278:ARG:HA	1.98	0.46
1:B:354:ARG:NH1	1:B:354:ARG:HG2	2.22	0.46
2:E:27:TYR:O	2:E:76:PRO:HA	2.15	0.46
2:E:97:ILE:O	2:E:97:ILE:HG12	2.14	0.46
2:E:301:VAL:O	2:E:301:VAL:HG22	2.13	0.46
2:E:340:LEU:HD12	2:E:340:LEU:HA	1.62	0.46
3:G:116[C]:PHE:HE2	3:G:165[C]:PHE:HZ	1.62	0.46
1:B:99:VAL:CG1	1:B:248:TYR:CD1	2.99	0.46
1:C:456:PHE:CZ	1:C:495:LYS:HD2	2.50	0.46
2:D:233:ARG:HD3	2:D:292:SER:HB3	1.98	0.46
2:D:441:LEU:HD21	2:D:456:VAL:HG13	1.97	0.46
3:G:27[C]:VAL:O	3:G:28[C]:ALA:C	2.59	0.46
4:H:20[C]:ALA:HA	4:H:53[C]:LYS:O	2.16	0.46
1:A:31:VAL:CG1	1:A:34:VAL:HG22	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:209:VAL:HG21	2:D:118:PHE:HZ	1.80	0.46
1:A:284:GLU:HG3	1:A:329:TYR:HB2	1.97	0.46
2:E:162:GLN:NE2	2:E:194:GLU:HG2	2.29	0.46
2:E:175:LEU:HG	2:E:238:GLN:NE2	2.27	0.46
3:G:88[B]:ALA:HB1	3:G:241[B]:ARG:HA	1.96	0.46
4:H:9[A]:VAL:HG13	4:H:14[A]:LYS:HE3	1.97	0.46
1:C:184:ILE:HG22	1:C:427:PRO:HG2	1.98	0.46
1:C:188:GLY:O	1:C:189:GLN:CB	2.64	0.46
1:C:284:GLU:HG3	1:C:329:TYR:CD2	2.48	0.46
1:C:477:GLN:O	1:C:478:THR:C	2.59	0.46
2:E:241:LEU:HD12	2:E:241:LEU:HA	1.70	0.46
2:F:346:ILE:HB	2:F:351:VAL:HG11	1.98	0.46
3:G:76[C]:THR:HB	3:G:167[C]:LYS:CG	2.40	0.46
3:G:170[B]:ILE:HD12	3:G:170[B]:ILE:O	2.14	0.46
1:A:395:PHE:CD2	1:A:395:PHE:N	2.82	0.46
1:B:44:LEU:HD23	1:B:44:LEU:HA	1.77	0.46
1:C:395:PHE:N	1:C:395:PHE:CD2	2.82	0.46
1:C:438:TYR:CA	1:C:441:THR:HG22	2.42	0.46
2:D:131:GLY:HA3	2:D:167:ASN:HD22	1.77	0.46
2:E:264:MET:CB	2:E:265:PRO:CA	2.93	0.46
2:F:27:TYR:O	2:F:76:PRO:HA	2.15	0.46
2:F:292:SER:OG	2:F:293:ILE:N	2.46	0.46
3:G:65[C]:HIS:CD2	3:G:69[C]:GLU:HA	2.51	0.46
3:G:175[B]:PHE:HA	3:G:236[B]:SER:HB2	1.98	0.46
1:B:95:MET:HE2	1:B:95:MET:CA	2.45	0.46
1:B:292:TYR:O	1:B:296:ARG:HB3	2.16	0.46
1:B:388:GLN:HG3	1:B:409:LYS:HZ1	1.78	0.46
2:D:373:LEU:HA	2:D:376:ILE:HG12	1.98	0.46
2:D:416:MET:N	2:D:417:PRO:CA	2.79	0.46
2:E:292:SER:OG	2:E:293:ILE:N	2.46	0.46
2:F:235:ARG:O	2:F:237:GLY:N	2.48	0.46
2:F:246:ASN:OD1	2:F:248:PHE:HB3	2.15	0.46
3:G:75[A]:LYS:HD2	3:G:164[A]:THR:HG22	1.98	0.46
3:G:75[A]:LYS:HD2	3:G:164[A]:THR:O	2.16	0.46
3:G:192[B]:THR:O	3:G:193[B]:SER:C	2.59	0.46
1:A:109:ASN:HD21	1:A:113:GLN:CG	2.29	0.46
2:D:34:ARG:CG	2:D:35:PRO:HA	2.38	0.46
2:D:241:LEU:HD12	2:D:241:LEU:HA	1.64	0.46
2:D:346:ILE:HB	2:D:351:VAL:HG11	1.97	0.46
2:E:24:PRO:HD2	2:E:53:VAL:HG11	1.98	0.46
2:E:34:ARG:CG	2:E:35:PRO:HA	2.37	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:264:MET:CB	2:E:265:PRO:HA	2.39	0.46
2:F:107:GLU:CD	2:F:235:ARG:HH12	2.23	0.46
3:G:38[C]:THR:O	3:G:231[C]:LEU:HD21	2.15	0.46
3:G:76[A]:THR:HB	3:G:78[A]:TYR:CE1	2.51	0.46
3:G:152[C]:ILE:H	3:G:152[C]:ILE:CD1	2.28	0.46
3:G:189[A]:LEU:HB3	3:G:190[A]:PRO:CD	2.40	0.46
4:H:38[B]:HIS:NE2	4:H:41[B]:LEU:CD1	2.79	0.46
4:H:49[C]:PRO:HB3	4:H:61[C]:ILE:H	1.81	0.46
1:A:109:ASN:HB2	1:A:110:PRO:CD	2.46	0.45
1:A:354:ARG:HG2	1:A:354:ARG:NH1	2.20	0.45
1:A:477:GLN:O	1:A:478:THR:C	2.58	0.45
1:B:275:LEU:HD12	1:B:281:PRO:HD3	1.97	0.45
1:C:298:LEU:HD12	1:C:317:PRO:CG	2.44	0.45
2:D:291:GLY:O	2:D:292:SER:CB	2.63	0.45
2:D:308:ASP:C	2:D:311:PRO:HD2	2.40	0.45
2:D:379:ILE:O	2:D:379:ILE:HG13	2.16	0.45
2:E:65:VAL:HB	2:E:68:LEU:HD21	1.98	0.45
2:F:12:PRO:HG2	2:F:260:LEU:HD11	1.97	0.45
2:F:308:ASP:C	2:F:311:PRO:HD2	2.41	0.45
3:G:164[C]:THR:O	3:G:165[C]:PHE:HD1	1.99	0.45
3:G:189[C]:LEU:HA	3:G:189[C]:LEU:HD12	1.12	0.45
4:H:64[C]:SER:OG	4:H:81[C]:THR:HG23	2.16	0.45
4:H:114[C]:TYR:HD2	4:H:118[C]:LYS:HD3	1.81	0.45
1:A:275:LEU:HG	1:A:278:ARG:CA	2.42	0.45
1:A:286:TYR:HB3	1:A:287:PRO:HD2	1.98	0.45
1:A:333:ASN:O	1:A:337:ILE:HG13	2.15	0.45
1:B:188:GLY:O	1:B:189:GLN:CB	2.65	0.45
1:C:233:PRO:O	1:C:237:LEU:HG	2.16	0.45
1:C:243:CYS:HB2	1:C:260:TYR:OH	2.16	0.45
2:D:27:TYR:O	2:D:76:PRO:HA	2.17	0.45
2:F:92:VAL:HG21	2:F:217:ALA:HB1	1.98	0.45
3:G:32[C]:LEU:HD12	3:G:234[C]:LYS:C	2.41	0.45
3:G:49[B]:ILE:O	3:G:49[B]:ILE:HG13	2.15	0.45
3:G:86[B]:GLY:CA	3:G:241[B]:ARG:HH22	2.26	0.45
3:G:220[B]:LYS:HD3	3:G:220[B]:LYS:HA	1.72	0.45
4:H:95[C]:LYS:HA	4:H:95[C]:LYS:HD2	1.63	0.45
4:H:97[C]:LYS:HE3	4:H:128[C]:LEU:CD1	2.42	0.45
1:B:93:ARG:HD3	1:B:96:GLU:OE2	2.17	0.45
1:C:284:GLU:HG3	1:C:329:TYR:HB2	1.98	0.45
2:D:125:ASP:CG	2:D:345:ARG:NH2	2.72	0.45
2:E:89:VAL:HG23	2:E:97:ILE:CG2	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:160:LEU:HD22	2:F:164:LEU:HD22	1.97	0.45
3:G:123[C]:ARG:CG	3:G:136[C]:GLU:HB2	2.45	0.45
4:H:100[A]:HIS:HB2	4:H:121[A]:LEU:CG	2.36	0.45
1:C:275:LEU:CB	2:F:264:MET:HG3	2.46	0.45
2:E:135:ILE:HD12	2:E:141:TYR:CE2	2.51	0.45
2:E:254:GLY:HA3	2:E:271:GLN:HE21	1.81	0.45
2:E:387:ASP:O	2:E:391:LEU:HB2	2.17	0.45
2:F:12:PRO:HD2	2:F:260:LEU:CD2	2.47	0.45
2:F:183:GLU:C	2:F:211:MET:HE3	2.42	0.45
2:F:218:ARG:O	2:F:221:VAL:HG12	2.16	0.45
3:G:23[C]:ALA:O	3:G:27[C]:VAL:HG23	2.16	0.45
3:G:86[A]:GLY:CA	3:G:121[A]:LYS:HD2	2.47	0.45
3:G:131[A]:TYR:N	3:G:132[A]:PRO:HA	2.25	0.45
4:H:88[A]:ILE:HD11	4:H:131[A]:ALA:CA	2.47	0.45
1:A:492:GLU:CA	1:A:495:LYS:HB2	2.33	0.45
1:B:157:ILE:HG21	1:B:342:ILE:CG1	2.46	0.45
1:B:419:ILE:HD13	1:B:440:VAL:CG1	2.47	0.45
1:B:448:ILE:HG23	1:B:449:PRO:CD	2.47	0.45
1:B:462:SER:CA	1:B:465:ARG:HH12	2.30	0.45
1:C:179:ALA:HB2	1:C:318:PHE:HZ	1.82	0.45
2:D:387:ASP:O	2:D:391:LEU:HB2	2.17	0.45
2:F:135:ILE:HD12	2:F:141:TYR:CE2	2.50	0.45
3:G:184[C]:VAL:CG1	3:G:186[C]:LYS:HE3	2.47	0.45
1:A:151:LYS:HE2	1:A:428:MET:CE	2.46	0.45
1:B:389:TYR:CD1	1:B:413:GLY:HA3	2.51	0.45
1:B:435:ILE:CD1	1:B:464:MET:HE2	2.35	0.45
1:B:477:GLN:O	1:B:478:THR:C	2.60	0.45
1:C:65:ASN:HB3	2:D:10:MET:HE3	1.97	0.45
1:C:205:VAL:O	1:C:209:VAL:HG23	2.17	0.45
2:D:92:VAL:HG21	2:D:217:ALA:HB1	1.99	0.45
2:D:135:ILE:HD12	2:D:141:TYR:CE2	2.52	0.45
2:D:166:ASN:O	2:D:170:GLN:HB2	2.16	0.45
2:D:307:THR:O	2:D:307:THR:HG23	2.16	0.45
2:D:419:LYS:CE	2:D:450:GLY:HA3	2.42	0.45
2:F:397:ARG:NH1	2:F:443:GLU:OE2	2.49	0.45
2:F:423:VAL:O	2:F:424:LYS:C	2.58	0.45
4:H:96[C]:ALA:HB1	4:H:100[C]:HIS:ND1	2.31	0.45
1:A:194:ILE:CD1	1:A:222:ILE:HD12	2.46	0.45
1:B:167:ILE:HD11	1:B:316:LEU:HD13	1.99	0.45
1:B:232:ALA:N	1:B:233:PRO:CD	2.79	0.45
1:B:330:ILE:HB	1:B:331:PRO:HD3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:176:THR:O	1:C:180:ILE:HG12	2.17	0.45
1:C:187:LYS:C	1:C:189:GLN:HG2	2.41	0.45
1:C:319:ILE:HD13	1:C:319:ILE:HA	1.75	0.45
1:C:450:VAL:C	1:C:452:ASP:H	2.25	0.45
2:E:264:MET:HG2	2:E:265:PRO:C	2.41	0.45
2:F:35:PRO:HD2	2:F:36:GLN:OE1	2.17	0.45
2:F:149:LEU:CD2	2:F:324:LEU:HD22	2.47	0.45
2:F:416:MET:N	2:F:417:PRO:CA	2.78	0.45
4:H:8[B]:ILE:CD1	4:H:15[B]:VAL:HB	2.46	0.45
1:B:262:ASP:OD1	1:B:264:SER:HB2	2.17	0.45
1:C:109:ASN:HB3	1:C:115:LEU:HD11	1.99	0.45
1:C:481:LEU:C	1:C:481:LEU:HD22	2.42	0.45
2:D:165:ILE:HG21	2:D:200:VAL:HG13	1.99	0.45
2:D:241:LEU:O	2:D:242:LEU:HB3	2.16	0.45
2:D:461:LYS:HE2	2:D:461:LYS:HB3	1.71	0.45
2:E:177:VAL:O	2:E:242:LEU:HA	2.16	0.45
2:F:264:MET:HG2	2:F:265:PRO:C	2.42	0.45
3:G:255[C]:MET:CA	3:G:258[C]:THR:HG23	2.46	0.45
4:H:97[C]:LYS:HG3	4:H:128[C]:LEU:HD11	1.99	0.45
1:A:326:VAL:HG11	1:A:343:PHE:CE2	2.45	0.45
1:C:412:ARG:HG3	1:C:446:ASP:OD1	2.17	0.45
2:D:40:LEU:HD23	2:D:64:LEU:HD11	1.98	0.45
2:F:387:ASP:O	2:F:391:LEU:HB2	2.17	0.45
3:G:32[C]:LEU:HG	3:G:238[C]:PHE:CB	2.27	0.45
3:G:113[C]:TYR:C	3:G:114[C]:VAL:HG13	2.42	0.45
1:A:47:VAL:HG12	1:A:90:ARG:HG2	1.97	0.45
1:A:121:ILE:HG22	1:A:123:THR:HG22	1.99	0.45
1:A:144:GLU:O	1:A:161:ARG:HG3	2.17	0.45
1:B:275:LEU:HG	1:B:278:ARG:CA	2.43	0.45
1:C:480:GLU:HG3	1:C:482:PRO:CD	2.47	0.45
2:D:195:MET:HE2	2:D:206:MET:SD	2.57	0.45
3:G:96[C]:LEU:HD13	3:G:125[C]:PHE:CG	2.52	0.45
3:G:144[C]:PRO:HD3	3:G:231[C]:LEU:CD1	2.47	0.45
3:G:219[C]:PRO:C	3:G:221[C]:TYR:N	2.75	0.45
3:G:234[C]:LYS:HD2	3:G:234[C]:LYS:HA	1.61	0.45
4:H:71[B]:ARG:HB2	4:H:74[B]:LYS:O	2.17	0.45
4:H:102[C]:THR:C	4:H:105[C]:LYS:HE2	2.41	0.45
1:A:157:ILE:N	1:A:158:PRO:HD2	2.32	0.44
1:A:179:ALA:HB2	1:A:318:PHE:HZ	1.82	0.44
1:A:183:ILE:HG12	1:A:193:CYS:HB3	1.99	0.44
1:A:188:GLY:O	1:A:189:GLN:CB	2.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:495:LYS:HE3	1:A:495:LYS:HB3	1.45	0.44
1:C:275:LEU:HA	1:C:278:ARG:H	1.82	0.44
2:F:82:GLY:HA2	2:F:231:TYR:CE2	2.52	0.44
2:F:177:VAL:O	2:F:242:LEU:HA	2.17	0.44
3:G:65[C]:HIS:CD2	3:G:68[C]:LEU:O	2.69	0.44
3:G:82[C]:THR:HG21	3:G:96[C]:LEU:HD21	1.98	0.44
3:G:103[C]:ILE:C	3:G:103[C]:ILE:HD12	2.43	0.44
3:G:114[B]:VAL:HB	3:G:134[B]:VAL:HG13	2.00	0.44
3:G:132[C]:PRO:HD2	3:G:133[C]:VAL:H	1.81	0.44
3:G:233[B]:ALA:C	3:G:235[B]:ALA:H	2.25	0.44
4:H:35[A]:MET:H	4:H:38[A]:HIS:CE1	2.34	0.44
1:C:48:MET:HA	2:D:65:VAL:HG22	2.00	0.44
1:C:275:LEU:C	2:F:264:MET:HE2	2.42	0.44
2:D:79:VAL:HG11	2:D:224:THR:HG23	1.99	0.44
2:D:288:THR:HG23	2:D:291:GLY:N	2.32	0.44
3:G:48[A]:LYS:CG	3:G:49[A]:ILE:H	2.26	0.44
3:G:68[B]:LEU:HD22	3:G:68[B]:LEU:N	2.32	0.44
3:G:71[C]:ARG:NH1	3:G:166[C]:ASP:HA	2.32	0.44
3:G:139[C]:GLY:O	3:G:141[C]:SER:N	2.50	0.44
4:H:8[A]:ILE:HG13	4:H:16[A]:PHE:H	1.83	0.44
4:H:8[C]:ILE:O	4:H:15[C]:VAL:HB	2.17	0.44
4:H:35[B]:MET:HE3	4:H:36[B]:ALA:N	2.29	0.44
4:H:125[A]:GLU:O	4:H:129[A]:GLN:HG3	2.17	0.44
1:A:157:ILE:HG21	1:A:342:ILE:CG1	2.46	0.44
1:C:183:ILE:HG12	1:C:193:CYS:HB3	1.98	0.44
2:E:161:ILE:HG23	2:E:243:PHE:CE1	2.53	0.44
2:F:273:THR:O	2:F:277:GLU:HG3	2.18	0.44
2:F:285:ILE:HD13	2:F:295:SER:HB2	2.00	0.44
3:G:72[B]:PRO:CA	3:G:73[B]:VAL:CB	2.89	0.44
3:G:131[A]:TYR:HB2	3:G:132[A]:PRO:O	2.18	0.44
3:G:141[B]:SER:OG	3:G:144[B]:PRO:HA	2.17	0.44
3:G:159[A]:MET:HB3	3:G:165[A]:PHE:CG	2.52	0.44
1:A:275:LEU:CB	2:D:264:MET:HE2	2.47	0.44
1:A:475:ILE:O	1:A:479:GLY:HA3	2.18	0.44
1:A:495:LYS:HB3	1:A:496:LYS:H	1.58	0.44
1:B:462:SER:HA	1:B:465:ARG:HH12	1.75	0.44
1:B:480:GLU:HG3	1:B:482:PRO:HD3	1.99	0.44
1:B:499:THR:N	1:B:500:PRO:CD	2.78	0.44
1:C:181:ASP:OD1	1:C:425:HIS:HA	2.17	0.44
1:C:275:LEU:HA	1:C:278:ARG:HA	1.98	0.44
2:D:315:PHE:HA	2:D:318:LEU:HD22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:264:MET:HG2	2:E:265:PRO:O	2.17	0.44
2:E:419:LYS:CE	2:E:450:GLY:HA3	2.43	0.44
2:F:192:TYR:O	2:F:196:LYS:HB3	2.17	0.44
2:F:301:VAL:O	2:F:301:VAL:HG22	2.16	0.44
2:F:441:LEU:HD21	2:F:456:VAL:HG13	1.99	0.44
3:G:170[C]:ILE:HD12	3:G:170[C]:ILE:N	2.33	0.44
3:G:177[B]:SER:HB3	3:G:180[B]:VAL:CG1	2.47	0.44
4:H:110[C]:THR:C	4:H:112[C]:LYS:CG	2.81	0.44
1:A:142:VAL:CG1	1:A:160:GLY:HA3	2.48	0.44
1:A:187:LYS:C	1:A:189:GLN:HG2	2.42	0.44
1:A:232:ALA:N	1:A:233:PRO:CD	2.81	0.44
1:A:298:LEU:HD21	1:A:337:ILE:CG2	2.47	0.44
1:B:99:VAL:HG11	1:B:248:TYR:HB2	1.99	0.44
1:B:176:THR:O	1:B:180:ILE:HG12	2.17	0.44
2:D:177:VAL:O	2:D:242:LEU:HA	2.18	0.44
2:E:85:THR:O	2:E:205:SER:HB3	2.17	0.44
2:E:218:ARG:O	2:E:221:VAL:HG12	2.17	0.44
2:F:307:THR:O	2:F:307:THR:HG23	2.16	0.44
3:G:67[C]:MET:C	3:G:69[C]:GLU:N	2.71	0.44
3:G:86[A]:GLY:HA3	3:G:121[A]:LYS:CD	2.48	0.44
3:G:174[B]:GLU:O	3:G:174[B]:GLU:HG3	2.17	0.44
4:H:71[B]:ARG:C	4:H:73[B]:ASP:H	2.24	0.44
1:B:183:ILE:HG12	1:B:193:CYS:HB3	2.00	0.44
2:D:379:ILE:HD11	3:G:17[C]:THR:HG22	1.96	0.44
2:F:165:ILE:HG21	2:F:200:VAL:HG13	2.00	0.44
3:G:11[B]:ILE:HD11	3:G:259[B]:LEU:O	2.18	0.44
3:G:49[C]:ILE:HD13	3:G:49[C]:ILE:HA	1.68	0.44
3:G:184[A]:VAL:HG22	3:G:185[A]:GLU:N	2.29	0.44
3:G:252[C]:ALA:O	3:G:253[C]:THR:C	2.60	0.44
4:H:93[A]:ALA:HA	4:H:96[A]:ALA:HB3	1.99	0.44
1:A:31:VAL:HG12	1:A:84:GLU:HA	1.99	0.44
1:A:389:TYR:CD1	1:A:413:GLY:HA3	2.53	0.44
1:A:448:ILE:HG23	1:A:449:PRO:CD	2.48	0.44
1:B:95:MET:O	1:B:128:PRO:HA	2.17	0.44
1:C:46:LYS:HB2	1:C:46:LYS:HZ2	1.83	0.44
2:D:12:PRO:HD2	2:D:260:LEU:CD2	2.48	0.44
2:D:366:VAL:HG21	2:D:434:LEU:CD2	2.48	0.44
2:E:91:ASN:C	2:E:91:ASN:ND2	2.73	0.44
2:E:288:THR:O	2:E:291:GLY:HA2	2.17	0.44
3:G:28[C]:ALA:CA	3:G:238[C]:PHE:HD1	1.98	0.44
3:G:36[B]:GLN:HA	3:G:39[B]:ALA:CB	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:45[A]:TYR:HE1	4:H:9[A]:VAL:HG12	1.83	0.44
3:G:79[B]:MET:HG3	3:G:116[B]:PHE:CB	2.46	0.44
3:G:132[C]:PRO:CD	3:G:133[C]:VAL:N	2.80	0.44
4:H:9[C]:VAL:CG2	4:H:14[C]:LYS:HD2	2.47	0.44
4:H:52[A]:ILE:HD11	4:H:59[A]:THR:HB	2.00	0.44
4:H:71[B]:ARG:C	4:H:73[B]:ASP:N	2.76	0.44
4:H:117[B]:HIS:O	4:H:120[B]:ALA:HB3	2.18	0.44
1:B:94:ILE:HD12	1:B:94:ILE:O	2.18	0.44
1:B:415:ARG:CG	1:B:415:ARG:NH1	2.49	0.44
1:C:71:VAL:HG23	2:D:66:ARG:NH2	2.32	0.44
1:C:91:THR:HG22	1:C:93:ARG:CG	2.48	0.44
2:D:107:GLU:CD	2:D:235:ARG:HH12	2.26	0.44
2:D:340:LEU:HD12	2:D:340:LEU:HA	1.67	0.44
3:G:102[A]:THR:O	3:G:106[A]:ARG:HB2	2.18	0.44
3:G:149[B]:ILE:O	3:G:153[B]:ALA:HB3	2.18	0.44
3:G:172[A]:TYR:HB2	3:G:185[A]:GLU:HA	1.99	0.44
4:H:80[C]:ASP:HB3	4:H:81[C]:THR:H	1.60	0.44
1:B:460:LEU:O	1:B:463:PHE:HB3	2.18	0.44
1:B:480:GLU:HG3	1:B:482:PRO:CD	2.47	0.44
3:G:65[C]:HIS:C	3:G:67[C]:MET:N	2.73	0.44
3:G:85[B]:ARG:HH22	3:G:241[B]:ARG:HE	1.66	0.44
3:G:101[C]:LYS:NZ	3:G:102[C]:THR:HG22	2.33	0.44
4:H:71[C]:ARG:HB3	4:H:72[C]:PRO:CD	2.48	0.44
1:A:438:TYR:HA	1:A:441:THR:CG2	2.44	0.43
1:C:171:ARG:NH1	1:C:171:ARG:HG2	2.27	0.43
1:C:328:ALA:HB3	1:C:331:PRO:HG2	2.00	0.43
2:E:147:ILE:HA	2:E:320:ALA:O	2.17	0.43
2:E:338:ASP:HA	2:E:339:PRO:HD3	1.92	0.43
3:G:148[B]:GLU:HG2	3:G:149[B]:ILE:HG23	2.00	0.43
3:G:192[C]:THR:O	3:G:193[C]:SER:C	2.60	0.43
3:G:261[C]:LEU:HD12	3:G:262[C]:GLN:N	2.33	0.43
4:H:23[B]:VAL:HG22	4:H:52[B]:ILE:HG22	2.00	0.43
1:C:95:MET:O	1:C:128:PRO:HA	2.18	0.43
2:E:164:LEU:HD12	2:E:164:LEU:HA	1.82	0.43
2:F:419:LYS:CE	2:F:450:GLY:HA3	2.43	0.43
3:G:112[C]:GLU:C	3:G:113[C]:TYR:CG	2.95	0.43
3:G:143[A]:THR:HB	3:G:144[A]:PRO:CA	2.48	0.43
3:G:238[C]:PHE:O	3:G:239[C]:GLY:C	2.61	0.43
4:H:104[C]:LEU:HD21	4:H:117[C]:HIS:HB2	1.99	0.43
1:B:462:SER:CB	1:B:465:ARG:HH12	2.31	0.43
1:C:194:ILE:HD13	1:C:222:ILE:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:258:SER:OG	2:E:263:ARG:HB2	2.19	0.43
3:G:94[B]:ASN:OD1	3:G:183[B]:PRO:HG3	2.18	0.43
3:G:162[A]:ASP:CA	3:G:163[A]:GLU:HB2	2.35	0.43
4:H:117[A]:HIS:HA	4:H:120[A]:ALA:CB	2.48	0.43
1:A:186:GLN:HB2	1:A:220:TYR:CE1	2.54	0.43
2:E:192:TYR:O	2:E:196:LYS:HB3	2.17	0.43
2:F:24:PRO:HD2	2:F:53:VAL:HG11	1.99	0.43
2:F:371:ASN:ND2	3:G:10[B]:ARG:NH1	2.64	0.43
3:G:16[B]:ASN:C	3:G:18[B]:ARG:H	2.26	0.43
3:G:39[A]:ALA:C	3:G:41[A]:ASN:H	2.26	0.43
3:G:218[C]:LEU:HD12	4:H:67[C]:PHE:CE1	2.53	0.43
3:G:227[C]:TYR:O	3:G:228[C]:SER:C	2.59	0.43
4:H:51[C]:ARG:NE	4:H:60[C]:LEU:CD2	2.81	0.43
4:H:59[B]:THR:HB	4:H:85[B]:PRO:HG2	2.00	0.43
1:A:151:LYS:HD2	1:A:419:ILE:O	2.19	0.43
1:B:114:PRO:HG3	1:B:121:ILE:CD1	2.48	0.43
1:B:460:LEU:O	1:B:464:MET:HG2	2.17	0.43
2:D:292:SER:OG	2:D:293:ILE:N	2.47	0.43
2:E:129:GLU:O	2:E:172:HIS:CE1	2.70	0.43
3:G:5[A]:ARG:HH11	3:G:5[A]:ARG:CB	2.30	0.43
3:G:37[C]:GLU:C	3:G:39[C]:ALA:N	2.76	0.43
3:G:48[C]:LYS:CD	4:H:78[C]:LEU:HD22	2.34	0.43
4:H:55[C]:GLY:O	4:H:56[C]:ASP:HB2	2.18	0.43
1:A:234:LEU:HD12	1:A:234:LEU:HA	1.84	0.43
1:A:271:ARG:HH11	1:A:285:ALA:HB1	1.83	0.43
1:B:137:MET:HG3	2:F:98:ASP:HA	1.98	0.43
1:B:284:GLU:HG3	1:B:329:TYR:CD2	2.49	0.43
1:B:431:GLU:HB2	1:B:472:LEU:HD22	2.00	0.43
1:C:113:GLN:HA	1:C:114:PRO:HD3	1.79	0.43
1:C:460:LEU:O	1:C:463:PHE:HB3	2.17	0.43
2:D:192:TYR:O	2:D:196:LYS:HB3	2.19	0.43
2:F:223:LEU:HD12	2:F:223:LEU:HA	1.79	0.43
2:F:288:THR:HG23	2:F:291:GLY:N	2.32	0.43
3:G:33[B]:ARG:HG2	3:G:34[B]:ARG:N	2.33	0.43
1:A:106:ARG:HH11	1:A:106:ARG:CB	2.29	0.43
1:A:481:LEU:HD22	1:A:481:LEU:C	2.43	0.43
1:B:171:ARG:HG3	1:B:171:ARG:NH1	2.19	0.43
2:D:325:GLU:HG3	2:D:338:ASP:HB2	1.99	0.43
2:E:86:LEU:HD11	2:E:175:LEU:HD13	2.00	0.43
2:E:132:ILE:H	2:E:132:ILE:HG12	1.47	0.43
2:F:147:ILE:HA	2:F:320:ALA:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:87[A]:LEU:N	3:G:241[A]:ARG:HH21	2.15	0.43
3:G:120[B]:ARG:HG2	3:G:120[B]:ARG:O	2.19	0.43
4:H:96[B]:ALA:HA	4:H:99[B]:ARG:HB2	2.01	0.43
4:H:123[A]:ARG:O	4:H:127[A]:ARG:HG3	2.18	0.43
1:A:95:MET:O	1:A:128:PRO:HA	2.19	0.43
1:A:113:GLN:HA	1:A:114:PRO:HD3	1.80	0.43
1:A:262:ASP:OD1	1:A:264:SER:HB2	2.18	0.43
1:B:144:GLU:O	1:B:161:ARG:HG3	2.19	0.43
1:B:233:PRO:O	1:B:237:LEU:HG	2.18	0.43
1:C:31:VAL:HG12	1:C:84:GLU:HA	2.01	0.43
1:C:48:MET:HE1	1:C:94:ILE:HG23	1.99	0.43
1:C:480:GLU:HG3	1:C:482:PRO:HD3	2.00	0.43
2:D:296:ILE:HD12	2:D:296:ILE:N	2.34	0.43
2:F:118:PHE:HA	2:F:121:LEU:HD22	2.01	0.43
2:F:254:GLY:HA3	2:F:271:GLN:NE2	2.33	0.43
2:F:324:LEU:HD12	2:F:324:LEU:HA	1.81	0.43
2:F:373:LEU:HA	2:F:376:ILE:HG12	2.01	0.43
3:G:4[A]:MET:HE3	3:G:5[A]:ARG:CZ	2.49	0.43
4:H:51[C]:ARG:NE	4:H:60[C]:LEU:HD22	2.33	0.43
1:A:276:LEU:HD23	1:A:276:LEU:HA	1.87	0.43
1:B:156:MET:SD	1:B:359:VAL:HG11	2.58	0.43
2:D:233:ARG:CD	2:D:292:SER:HB3	2.49	0.43
2:E:291:GLY:O	2:E:292:SER:CB	2.65	0.43
3:G:149[B]:ILE:C	3:G:151[B]:ASP:N	2.74	0.43
3:G:162[C]:ASP:HA	3:G:163[C]:GLU:CB	2.33	0.43
3:G:241[A]:ARG:O	3:G:245[A]:MET:HG2	2.19	0.43
4:H:85[C]:PRO:O	4:H:134[C]:LYS:HG2	2.18	0.43
1:A:44:LEU:HD23	1:A:44:LEU:HA	1.78	0.43
1:A:271:ARG:HH11	1:A:285:ALA:CB	2.31	0.43
1:A:285:ALA:HA	2:D:267:ALA:HB3	2.01	0.43
1:A:491:ILE:HG22	1:A:495:LYS:HG3	2.00	0.43
1:B:44:LEU:O	1:B:47:VAL:HG22	2.19	0.43
1:B:140:LYS:NZ	1:B:143:HIS:CE1	2.87	0.43
1:C:91:THR:HG22	1:C:93:ARG:H	1.84	0.43
2:E:385:LEU:O	2:E:386:SER:C	2.62	0.43
2:F:26:ILE:O	2:F:27:TYR:HB2	2.19	0.43
2:F:142:ALA:HB2	2:F:346:ILE:HG21	2.01	0.43
3:G:80[C]:VAL:HG11	3:G:126[C]:PHE:CZ	2.53	0.43
3:G:107[C]:HIS:CD2	3:G:107[C]:HIS:O	2.72	0.43
3:G:115[A]:ILE:HD13	3:G:115[A]:ILE:N	2.33	0.43
3:G:133[B]:VAL:HG22	3:G:134[B]:VAL:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:148[B]:GLU:OE1	3:G:149[B]:ILE:HG13	2.19	0.43
3:G:151[C]:ASP:O	3:G:155[C]:SER:N	2.41	0.43
4:H:47[B]:THR:HG21	4:H:122[B]:GLU:CB	2.43	0.43
1:B:275:LEU:H	2:E:264:MET:CE	2.32	0.42
1:B:333:ASN:O	1:B:337:ILE:HG13	2.20	0.42
1:B:386:LEU:HA	1:B:389:TYR:HB3	2.01	0.42
1:B:411:ASN:HD22	1:B:411:ASN:HA	1.59	0.42
1:C:99:VAL:HG13	1:C:248:TYR:CG	2.54	0.42
2:D:388:GLU:O	2:D:391:LEU:HB3	2.19	0.42
3:G:144[B]:PRO:HG2	3:G:230[B]:LEU:CD1	2.48	0.42
3:G:225[C]:LEU:O	3:G:228[C]:SER:HB2	2.19	0.42
4:H:26[A]:ARG:HA	4:H:31[A]:GLU:HB3	2.01	0.42
4:H:40[B]:PRO:HA	4:H:70[B]:VAL:HB	2.00	0.42
1:B:94:ILE:O	1:B:95:MET:C	2.62	0.42
1:C:121:ILE:HG22	1:C:123:THR:HG22	2.02	0.42
2:D:91:ASN:ND2	2:D:91:ASN:H	2.17	0.42
2:D:218:ARG:O	2:D:221:VAL:HG12	2.19	0.42
2:F:91:ASN:ND2	2:F:91:ASN:H	2.17	0.42
3:G:32[B]:LEU:CD1	3:G:238[B]:PHE:HB2	2.49	0.42
3:G:245[C]:MET:HE2	3:G:245[C]:MET:HA	2.02	0.42
4:H:8[A]:ILE:HD11	4:H:15[A]:VAL:HB	2.00	0.42
4:H:111[C]:ASP:C	4:H:112[C]:LYS:CG	2.92	0.42
4:H:118[C]:LYS:C	4:H:121[C]:LEU:H	2.26	0.42
1:A:194:ILE:HD13	1:A:222:ILE:HD12	2.01	0.42
1:A:440:VAL:HG22	1:A:441:THR:N	2.34	0.42
1:A:462:SER:HA	1:A:465:ARG:HH12	1.69	0.42
1:B:161:ARG:HH12	1:B:190:ASP:CB	2.30	0.42
1:C:431:GLU:HB2	1:C:472:LEU:HD22	2.02	0.42
2:D:258:SER:OG	2:D:263:ARG:HB2	2.18	0.42
2:D:371:ASN:HB3	3:G:10[C]:ARG:HD2	2.02	0.42
2:E:367:LEU:HD21	2:E:399:ILE:HG22	2.01	0.42
2:F:258:SER:OG	2:F:263:ARG:HB2	2.19	0.42
2:F:288:THR:O	2:F:291:GLY:HA2	2.19	0.42
2:F:372:ASP:O	2:F:376:ILE:HG12	2.19	0.42
3:G:104[C]:GLU:CA	3:G:107[C]:HIS:HD1	2.28	0.42
4:H:61[B]:ILE:O	4:H:63[B]:VAL:HG23	2.20	0.42
4:H:114[A]:TYR:O	4:H:118[A]:LYS:HE2	2.20	0.42
1:A:99:VAL:HG13	1:A:248:TYR:CG	2.54	0.42
1:A:110:PRO:HG3	1:A:238:ALA:HA	2.01	0.42
1:A:189:GLN:HE22	1:A:220:TYR:HB3	1.85	0.42
1:A:480:GLU:HG3	1:A:482:PRO:CD	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:140:LYS:NZ	1:C:143:HIS:CE1	2.86	0.42
1:C:194:ILE:CD1	1:C:222:ILE:HD12	2.49	0.42
1:C:419:ILE:HD13	1:C:440:VAL:CG1	2.49	0.42
2:D:308:ASP:CG	2:D:309:PRO:HD2	2.45	0.42
2:D:385:LEU:O	2:D:386:SER:C	2.62	0.42
2:E:142:ALA:CB	2:E:346:ILE:HD13	2.46	0.42
3:G:15[B]:LYS:HG3	3:G:256[B]:LEU:CD1	2.47	0.42
3:G:32[C]:LEU:HD13	3:G:35[C]:ALA:HB2	2.01	0.42
3:G:39[C]:ALA:O	3:G:42[C]:ALA:N	2.50	0.42
3:G:107[C]:HIS:HB2	3:G:113[C]:TYR:CE1	2.54	0.42
3:G:179[A]:ILE:HG23	3:G:180[A]:VAL:HG13	2.02	0.42
3:G:225[A]:LEU:HD23	3:G:225[A]:LEU:HA	1.95	0.42
4:H:51[B]:ARG:NE	4:H:60[B]:LEU:HD21	2.32	0.42
4:H:110[C]:THR:O	4:H:112[C]:LYS:CD	2.66	0.42
1:A:475:ILE:HA	1:A:479:GLY:HA2	2.00	0.42
1:B:66:LEU:HD12	2:F:9:VAL:CB	2.42	0.42
1:B:439:ALA:HB1	1:B:445:MET:HE2	2.01	0.42
1:B:492:GLU:CA	1:B:495:LYS:HB2	2.33	0.42
2:F:42:VAL:HG12	2:F:57:ALA:HA	2.02	0.42
2:F:137:LEU:CG	2:F:138:LEU:HD13	2.47	0.42
3:G:18[B]:ARG:O	3:G:18[B]:ARG:HG2	2.18	0.42
3:G:65[A]:HIS:HD2	3:G:69[A]:GLU:OE2	2.02	0.42
3:G:82[A]:THR:HG21	3:G:122[A]:GLY:HA3	2.01	0.42
1:A:91:THR:HG22	1:A:93:ARG:CG	2.49	0.42
1:A:171:ARG:HG3	1:A:171:ARG:NH1	2.13	0.42
1:A:365:ARG:NH2	2:E:186:ARG:HH22	2.01	0.42
1:A:402:LEU:C	1:A:406:THR:HG21	2.45	0.42
1:B:46:LYS:HB2	1:B:46:LYS:HZ3	1.84	0.42
1:B:113:GLN:HA	1:B:114:PRO:HD3	1.85	0.42
1:B:194:ILE:CD1	1:B:222:ILE:HD12	2.50	0.42
1:B:471:LEU:HD21	1:B:486:GLU:OE1	2.20	0.42
2:D:164:LEU:HD12	2:D:164:LEU:HA	1.75	0.42
2:D:273:THR:O	2:D:274:LEU:C	2.63	0.42
2:F:286:THR:OG1	2:F:287:SER:N	2.51	0.42
3:G:8[B]:LYS:CD	3:G:263[B]:PHE:CE1	3.00	0.42
3:G:43[B]:ARG:N	3:G:44[B]:PRO:CD	2.83	0.42
3:G:78[B]:TYR:O	3:G:116[B]:PHE:HD2	2.02	0.42
3:G:82[B]:THR:CG2	3:G:95[B]:ILE:HD13	2.48	0.42
3:G:144[A]:PRO:O	3:G:145[A]:SER:HB2	2.18	0.42
3:G:217[A]:LEU:HG	3:G:218[A]:LEU:N	2.34	0.42
4:H:111[C]:ASP:OD2	4:H:115[C]:LEU:HD11	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:271:ARG:NH1	1:A:285:ALA:HB3	2.35	0.42
1:B:187:LYS:O	1:B:189:GLN:HG2	2.19	0.42
1:B:275:LEU:CD1	2:E:264:MET:HG3	2.50	0.42
1:C:94:ILE:O	1:C:95:MET:C	2.62	0.42
2:D:93:LEU:HD12	2:D:93:LEU:HA	1.73	0.42
2:F:89:VAL:HG23	2:F:97:ILE:CG2	2.50	0.42
2:F:178:PHE:CZ	2:F:245:ASP:HB2	2.54	0.42
2:F:385:LEU:O	2:F:386:SER:C	2.62	0.42
3:G:115[A]:ILE:O	3:G:116[A]:PHE:C	2.62	0.42
4:H:10[A]:THR:HG23	4:H:13[A]:ARG:O	2.19	0.42
4:H:22[B]:ILE:HG22	4:H:35[B]:MET:SD	2.59	0.42
1:A:99:VAL:HG11	1:A:248:TYR:HB2	2.01	0.42
1:A:140:LYS:HB3	1:A:305:SER:HA	2.01	0.42
1:C:275:LEU:CB	2:F:264:MET:HE2	2.50	0.42
1:C:483:ASP:O	1:C:486:GLU:HB3	2.19	0.42
2:D:235:ARG:O	2:D:237:GLY:N	2.52	0.42
3:G:32[C]:LEU:HD12	3:G:235[C]:ALA:N	2.34	0.42
3:G:169[A]:THR:HG23	3:G:186[A]:LYS:O	2.20	0.42
3:G:191[C]:LEU:HD12	3:G:191[C]:LEU:HA	1.86	0.42
4:H:90[B]:VAL:HA	4:H:128[B]:LEU:HD21	2.02	0.42
4:H:115[B]:LEU:O	4:H:119[B]:ARG:HG3	2.20	0.42
1:A:480:GLU:HG3	1:A:482:PRO:HD3	2.01	0.42
1:B:271:ARG:NH1	1:B:285:ALA:HB1	2.34	0.42
1:B:319:ILE:HD13	1:B:319:ILE:HA	1.74	0.42
1:C:62:MET:HB2	1:C:95:MET:HE3	2.00	0.42
1:C:109:ASN:OD1	1:C:109:ASN:C	2.63	0.42
1:C:271:ARG:HH11	1:C:285:ALA:CB	2.33	0.42
2:D:80:PRO:HG3	2:D:108:ARG:NH1	2.35	0.42
2:D:239:ASP:HA	2:D:292:SER:HA	2.02	0.42
2:D:412:GLN:HE21	2:D:412:GLN:HB2	1.52	0.42
3:G:112[A]:GLU:C	3:G:113[A]:TYR:CG	2.98	0.42
3:G:148[C]:GLU:CG	3:G:149[C]:ILE:HG13	2.47	0.42
3:G:175[B]:PHE:CD1	3:G:236[B]:SER:HA	2.48	0.42
1:A:499:THR:N	1:A:500:PRO:CD	2.78	0.42
1:B:52:LEU:O	1:B:53:LEU:HD23	2.19	0.42
1:B:166:LEU:HB3	1:B:341:GLN:HB3	2.01	0.42
1:B:171:ARG:HH11	1:B:171:ARG:HG2	1.78	0.42
1:B:187:LYS:O	1:B:189:GLN:CG	2.68	0.42
1:B:402:LEU:C	1:B:406:THR:HG21	2.44	0.42
1:B:483:ASP:O	1:B:486:GLU:HB3	2.20	0.42
1:C:232:ALA:N	1:C:233:PRO:CD	2.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:42:VAL:HG12	2:D:57:ALA:HA	2.02	0.42
2:D:86:LEU:HD11	2:D:175:LEU:HD13	2.02	0.42
2:E:205:SER:HB2	2:E:228:MET:CE	2.48	0.42
3:G:45[B]:TYR:CE2	3:G:49[B]:ILE:HD11	2.55	0.42
3:G:124[A]:ASP:C	3:G:126[A]:PHE:H	2.28	0.42
3:G:144[C]:PRO:O	3:G:145[C]:SER:HB2	2.19	0.42
1:A:275:LEU:C	1:A:278:ARG:H	2.28	0.41
1:B:191:VAL:HA	1:B:255:HIS:O	2.20	0.41
1:C:271:ARG:NH1	1:C:285:ALA:HB3	2.35	0.41
1:C:354:ARG:NH1	1:C:354:ARG:HG2	2.23	0.41
1:C:440:VAL:HG22	1:C:441:THR:N	2.35	0.41
2:D:183:GLU:C	2:D:211:MET:HE3	2.45	0.41
2:E:91:ASN:ND2	2:E:91:ASN:H	2.17	0.41
2:E:242:LEU:O	2:E:295:SER:HA	2.20	0.41
3:G:81[C]:ILE:HA	3:G:118[C]:VAL:HG13	2.02	0.41
3:G:143[A]:THR:N	3:G:144[A]:PRO:HA	2.25	0.41
3:G:182[A]:ARG:NH2	3:G:183[A]:PRO:HD2	2.35	0.41
3:G:217[B]:LEU:HG	3:G:218[B]:LEU:N	2.35	0.41
4:H:22[B]:ILE:CG1	4:H:53[B]:LYS:HD2	2.46	0.41
4:H:117[C]:HIS:HA	4:H:120[C]:ALA:CB	2.46	0.41
1:A:236:TYR:HE1	1:A:293:LEU:CD1	2.34	0.41
1:A:284:GLU:HG3	1:A:329:TYR:CD1	2.52	0.41
1:A:386:LEU:HA	1:A:389:TYR:HB3	2.02	0.41
1:B:460:LEU:HG	1:B:494:PHE:CE2	2.55	0.41
1:C:109:ASN:HB2	1:C:110:PRO:CD	2.49	0.41
1:C:167:ILE:O	1:C:318:PHE:HA	2.20	0.41
2:D:233:ARG:HB2	2:D:292:SER:CB	2.50	0.41
2:E:401:ARG:C	2:E:403:LEU:H	2.28	0.41
2:F:205:SER:HB2	2:F:228:MET:CE	2.50	0.41
3:G:18[C]:ARG:HH12	3:G:253[C]:THR:CB	2.33	0.41
3:G:72[A]:PRO:HA	3:G:73[A]:VAL:CB	2.44	0.41
3:G:79[A]:MET:HB3	3:G:170[A]:ILE:HB	2.01	0.41
3:G:149[B]:ILE:C	3:G:151[B]:ASP:H	2.28	0.41
3:G:167[A]:LYS:N	3:G:167[A]:LYS:HD2	2.35	0.41
3:G:239[B]:GLY:O	3:G:242[B]:MET:HG2	2.21	0.41
4:H:4[B]:VAL:CG2	4:H:36[B]:ALA:HA	2.50	0.41
1:A:167:ILE:HD11	1:A:316:LEU:HD13	2.03	0.41
1:A:217:ALA:HA	1:A:220:TYR:CE2	2.56	0.41
1:A:275:LEU:HA	1:A:278:ARG:HA	2.02	0.41
1:B:121:ILE:HG22	1:B:123:THR:HG22	2.02	0.41
1:C:439:ALA:HB1	1:C:445:MET:HE2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:24:PRO:HD2	2:D:53:VAL:HG11	2.01	0.41
2:F:11:GLY:C	2:F:13:VAL:H	2.27	0.41
2:F:91:ASN:ND2	2:F:91:ASN:C	2.76	0.41
2:F:93:LEU:HD12	2:F:93:LEU:HA	1.72	0.41
2:F:233:ARG:CD	2:F:292:SER:HB3	2.50	0.41
2:F:416:MET:HA	2:F:416:MET:CE	2.50	0.41
3:G:79[C]:MET:HG3	3:G:116[C]:PHE:HB2	2.03	0.41
3:G:84[A]:ASP:OD1	3:G:140[A]:ILE:HG12	2.20	0.41
3:G:115[A]:ILE:HD11	3:G:126[A]:PHE:CE1	2.55	0.41
4:H:22[C]:ILE:CG1	4:H:53[C]:LYS:HD2	2.47	0.41
4:H:27[C]:GLY:HA2	4:H:45[C]:LEU:HD23	2.02	0.41
4:H:38[B]:HIS:NE2	4:H:41[B]:LEU:HD12	2.35	0.41
1:A:440:VAL:HG12	1:A:445:MET:CE	2.24	0.41
1:B:65:ASN:HB3	2:F:10:MET:CE	2.49	0.41
2:D:12:PRO:HG2	2:D:260:LEU:HD11	2.03	0.41
2:E:93:LEU:HD12	2:E:93:LEU:HA	1.59	0.41
2:E:218:ARG:HH11	2:E:218:ARG:HD2	1.74	0.41
2:E:397:ARG:NH1	2:E:443:GLU:OE2	2.53	0.41
2:F:291:GLY:O	2:F:292:SER:CB	2.68	0.41
3:G:71[B]:ARG:HA	3:G:72[B]:PRO:HD3	1.87	0.41
3:G:98[A]:LEU:HD22	3:G:98[A]:LEU:HA	1.83	0.41
3:G:168[B]:LEU:HD23	3:G:169[B]:THR:N	2.36	0.41
3:G:188[A]:LEU:CD2	3:G:225[A]:LEU:HB3	2.41	0.41
4:H:9[C]:VAL:HG11	4:H:14[C]:LYS:HD3	2.02	0.41
1:A:62:MET:HB2	1:A:95:MET:HE3	1.98	0.41
1:C:330:ILE:HB	1:C:331:PRO:HD3	2.01	0.41
1:C:389:TYR:CD1	1:C:413:GLY:HA3	2.54	0.41
2:E:118:PHE:HA	2:E:121:LEU:HD22	2.02	0.41
2:E:270:TYR:CZ	2:E:310:ALA:HB2	2.55	0.41
2:F:241:LEU:O	2:F:242:LEU:HB3	2.20	0.41
3:G:17[B]:THR:O	3:G:17[B]:THR:CG2	2.67	0.41
3:G:83[C]:SER:O	3:G:121[C]:LYS:HB2	2.21	0.41
3:G:99[B]:VAL:CG2	3:G:100[B]:SER:N	2.82	0.41
3:G:184[B]:VAL:HG21	3:G:186[B]:LYS:HE3	2.03	0.41
4:H:5[B]:GLN:HG2	4:H:19[B]:GLU:HG2	2.01	0.41
4:H:8[C]:ILE:HD13	4:H:61[C]:ILE:HD12	2.02	0.41
4:H:59[C]:THR:OG1	4:H:85[C]:PRO:HB3	2.21	0.41
4:H:86[A]:GLU:CG	4:H:134[A]:LYS:HB3	2.51	0.41
4:H:133[B]:SER:C	4:H:135[B]:SER:H	2.29	0.41
1:A:429:PRO:O	1:A:430:VAL:C	2.63	0.41
1:A:498:PHE:CD1	1:A:499:THR:HG22	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:271:ARG:HH11	1:C:285:ALA:HB1	1.86	0.41
1:C:402:LEU:C	1:C:406:THR:HG21	2.46	0.41
2:D:241:LEU:O	2:D:294:THR:O	2.38	0.41
2:E:288:THR:HG23	2:E:291:GLY:N	2.35	0.41
2:E:411:GLU:HA	2:E:415:GLY:HA2	2.02	0.41
2:F:241:LEU:HA	2:F:241:LEU:HD12	1.59	0.41
2:F:296:ILE:HD12	2:F:296:ILE:N	2.36	0.41
3:G:5[C]:ARG:O	3:G:8[C]:LYS:HB2	2.20	0.41
3:G:71[C]:ARG:HA	3:G:72[C]:PRO:HD3	1.81	0.41
3:G:79[B]:MET:HB2	3:G:168[B]:LEU:HD21	2.01	0.41
3:G:86[B]:GLY:C	3:G:241[B]:ARG:NH2	2.79	0.41
4:H:9[A]:VAL:HG13	4:H:14[A]:LYS:CD	2.51	0.41
4:H:38[B]:HIS:CD2	4:H:39[B]:ILE:H	2.38	0.41
1:A:99:VAL:CG1	1:A:248:TYR:HB2	2.51	0.41
1:C:67:GLU:HB2	1:C:70:ASN:O	2.19	0.41
1:C:69:ASP:OD1	1:C:69:ASP:N	2.53	0.41
3:G:79[A]:MET:H	3:G:170[A]:ILE:HA	1.85	0.41
3:G:114[A]:VAL:HB	3:G:134[A]:VAL:HG13	2.02	0.41
3:G:120[C]:ARG:O	3:G:120[C]:ARG:CG	2.67	0.41
4:H:6[B]:VAL:HA	4:H:75[B]:VAL:O	2.20	0.41
4:H:48[A]:ALA:HA	4:H:49[A]:PRO:HD3	1.98	0.41
4:H:109[A]:LYS:HE3	4:H:109[A]:LYS:HB2	1.94	0.41
1:A:94:ILE:H	1:A:94:ILE:HG13	1.59	0.41
1:A:275:LEU:CB	2:D:264:MET:CG	2.94	0.41
1:B:438:TYR:HA	1:B:441:THR:CG2	2.45	0.41
1:B:450:VAL:C	1:B:452:ASP:H	2.29	0.41
1:B:459:GLU:HA	1:B:462:SER:OG	2.21	0.41
1:C:140:LYS:HB3	1:C:305:SER:HA	2.03	0.41
1:C:278:ARG:HE	1:C:278:ARG:HB3	1.68	0.41
1:C:411:ASN:HD22	1:C:411:ASN:HA	1.60	0.41
1:C:460:LEU:HG	1:C:494:PHE:CE2	2.55	0.41
2:D:181:VAL:HG22	2:D:221:VAL:CG1	2.49	0.41
2:F:366:VAL:HG21	2:F:434:LEU:CD2	2.51	0.41
3:G:80[A]:VAL:HG11	3:G:126[A]:PHE:CZ	2.55	0.41
3:G:86[B]:GLY:O	3:G:87[B]:LEU:HB2	2.19	0.41
3:G:116[C]:PHE:HE2	3:G:165[C]:PHE:CZ	2.38	0.41
3:G:160[B]:PHE:HB2	3:G:189[B]:LEU:HD21	2.03	0.41
1:A:48:MET:HB3	2:E:63:GLY:C	2.45	0.41
1:B:206:ALA:HA	2:E:118:PHE:CZ	2.56	0.41
1:B:491:ILE:HG22	1:B:495:LYS:HG3	2.02	0.41
1:B:495:LYS:HB3	1:B:496:LYS:H	1.58	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:144:GLU:O	1:C:161:ARG:HG3	2.21	0.41
2:D:40:LEU:CD2	2:D:64:LEU:HD11	2.50	0.41
2:D:149:LEU:CD2	2:D:324:LEU:HD22	2.51	0.41
2:D:240:VAL:HG12	2:D:241:LEU:N	2.36	0.41
2:D:325:GLU:HG2	2:D:338:ASP:HB2	2.02	0.41
2:E:92:VAL:HG11	2:E:220:ARG:HB2	2.03	0.41
2:E:325:GLU:CG	2:E:338:ASP:HB2	2.51	0.41
2:E:395:ARG:NH2	2:E:436:GLY:CA	2.83	0.41
2:F:338:ASP:HB3	2:F:341:ALA:HB3	2.03	0.41
3:G:38[B]:THR:O	3:G:231[B]:LEU:HD21	2.21	0.41
3:G:91[A]:TYR:O	3:G:92[A]:ASN:CB	2.66	0.41
3:G:175[B]:PHE:CZ	3:G:177[B]:SER:O	2.74	0.41
3:G:234[C]:LYS:O	3:G:237[C]:GLU:N	2.52	0.41
4:H:39[B]:ILE:CG2	4:H:40[B]:PRO:HD2	2.51	0.41
4:H:103[B]:ILE:HG22	4:H:106[B]:ARG:NE	2.36	0.41
4:H:128[C]:LEU:HD23	4:H:128[C]:LEU:HA	1.91	0.41
1:A:161:ARG:HH12	1:A:190:ASP:CB	2.29	0.41
1:B:91:THR:HG22	1:B:93:ARG:CG	2.50	0.41
1:C:497:GLY:O	1:C:498:PHE:CG	2.74	0.41
2:D:77:ILE:O	2:D:111:ILE:HG23	2.20	0.41
2:D:268:VAL:O	2:D:268:VAL:CG2	2.67	0.41
2:E:264:MET:HE3	2:E:272:PRO:CB	2.36	0.41
2:E:419:LYS:HD2	2:E:419:LYS:HA	1.88	0.41
2:F:458:LYS:C	2:F:460:LYS:N	2.79	0.41
3:G:12[B]:ARG:CZ	3:G:12[B]:ARG:CB	2.99	0.41
3:G:48[C]:LYS:HZ1	4:H:9[C]:VAL:HB	1.86	0.41
3:G:83[B]:SER:HB3	3:G:92[B]:ASN:ND2	2.35	0.41
1:A:94:ILE:O	1:A:95:MET:C	2.63	0.40
1:A:419:ILE:HD13	1:A:440:VAL:CG1	2.51	0.40
1:C:161:ARG:HH12	1:C:190:ASP:CB	2.30	0.40
1:C:386:LEU:HA	1:C:389:TYR:HB3	2.02	0.40
1:C:491:ILE:HG22	1:C:495:LYS:HG3	2.02	0.40
2:D:235:ARG:C	2:D:237:GLY:H	2.29	0.40
2:D:319:ASP:OD2	2:D:345:ARG:HD3	2.21	0.40
2:D:411:GLU:HA	2:D:415:GLY:HA2	2.02	0.40
2:D:431:LYS:HE3	2:D:435:GLU:OE2	2.20	0.40
2:E:215:PRO:HB3	2:E:256:GLU:HB2	2.03	0.40
3:G:75[A]:LYS:CD	3:G:164[A]:THR:HG22	2.51	0.40
3:G:132[C]:PRO:HD2	3:G:133[C]:VAL:N	2.37	0.40
3:G:156[C]:ALA:HB1	3:G:168[C]:LEU:HD11	2.04	0.40
3:G:169[A]:THR:HG23	3:G:186[A]:LYS:C	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:261[C]:LEU:CD1	3:G:262[C]:GLN:HG3	2.48	0.40
4:H:45[C]:LEU:HD11	4:H:68[C]:LEU:HD21	2.02	0.40
4:H:121[B]:LEU:C	4:H:122[B]:GLU:HG3	2.46	0.40
1:A:459:GLU:HA	1:A:462:SER:OG	2.20	0.40
1:B:56:GLU:HG3	1:B:87:GLN:HB2	2.03	0.40
1:B:271:ARG:HH11	1:B:285:ALA:CB	2.34	0.40
1:C:83:ARG:CB	2:F:47:HIS:CE1	2.88	0.40
2:E:308:ASP:CG	2:E:309:PRO:HD2	2.46	0.40
2:F:86:LEU:HD11	2:F:175:LEU:HD13	2.03	0.40
2:F:264:MET:HE3	2:F:272:PRO:CB	2.39	0.40
3:G:37[B]:GLU:C	3:G:39[B]:ALA:H	2.30	0.40
3:G:165[A]:PHE:HE2	3:G:168[A]:LEU:HD13	1.86	0.40
4:H:15[C]:VAL:HG12	4:H:16[C]:PHE:CD1	2.57	0.40
4:H:64[C]:SER:HB2	4:H:123[C]:ARG:HE	1.86	0.40
4:H:101[B]:GLU:HB3	4:H:121[B]:LEU:HG	2.02	0.40
4:H:111[C]:ASP:N	4:H:112[C]:LYS:HG3	2.35	0.40
1:A:284:GLU:HG3	1:A:329:TYR:CD2	2.52	0.40
1:B:475:ILE:HA	1:B:479:GLY:HA2	2.03	0.40
1:C:471:LEU:HD21	1:C:486:GLU:OE1	2.21	0.40
2:E:79:VAL:HA	2:E:80:PRO:HD3	1.95	0.40
2:F:27:TYR:HB3	2:F:112:HIS:CD2	2.57	0.40
2:F:235:ARG:HA	2:F:235:ARG:HD3	1.89	0.40
2:F:319:ASP:OD2	2:F:345:ARG:HD3	2.22	0.40
2:F:431:LYS:HE3	2:F:435:GLU:OE2	2.20	0.40
3:G:32[A]:LEU:HB2	3:G:238[A]:PHE:HB3	2.00	0.40
4:H:50[A]:VAL:HG23	4:H:63[A]:VAL:HG21	2.04	0.40
4:H:100[B]:HIS:HB3	4:H:120[B]:ALA:HB3	2.03	0.40
1:A:460:LEU:O	1:A:463:PHE:HB3	2.20	0.40
1:B:142:VAL:CG1	1:B:160:GLY:HA3	2.52	0.40
1:C:44:LEU:HD23	1:C:44:LEU:HA	1.79	0.40
2:D:167:ASN:OD1	2:D:408:HIS:HD2	2.04	0.40
2:D:288:THR:C	2:D:291:GLY:H	2.30	0.40
2:E:233:ARG:CG	2:E:292:SER:HB3	2.51	0.40
2:E:318:LEU:HD12	2:E:318:LEU:HA	1.87	0.40
3:G:91[B]:TYR:O	3:G:92[B]:ASN:HB2	2.20	0.40
3:G:176[C]:VAL:CG1	3:G:177[C]:SER:N	2.76	0.40
3:G:179[B]:ILE:O	3:G:179[B]:ILE:HG23	2.21	0.40
3:G:255[C]:MET:HA	3:G:258[C]:THR:CG2	2.50	0.40
1:A:483:ASP:O	1:A:486:GLU:HB3	2.21	0.40
1:B:31:VAL:HG12	1:B:84:GLU:HA	2.04	0.40
2:D:273:THR:O	2:D:277:GLU:HG3	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:288:THR:C	2:E:291:GLY:H	2.29	0.40
2:F:355:GLU:O	2:F:356:HIS:C	2.64	0.40
3:G:45[A]:TYR:CE1	4:H:9[A]:VAL:HG12	2.57	0.40
3:G:179[C]:ILE:HG22	3:G:180[C]:VAL:HG13	2.04	0.40
4:H:38[C]:HIS:O	4:H:72[C]:PRO:HA	2.22	0.40
4:H:90[B]:VAL:O	4:H:128[B]:LEU:HD21	2.21	0.40

All (1) 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)
2:D:37:GLY:O	4:H:111[C]:ASP:O[2_454]	2.11	0.09

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	472/502 (94%)	418 (89%)	44 (9%)	10 (2%)	5	21
1	B	472/502 (94%)	417 (88%)	44 (9%)	11 (2%)	5	19
1	C	472/502 (94%)	417 (88%)	44 (9%)	11 (2%)	5	19
2	D	459/462 (99%)	406 (88%)	44 (10%)	9 (2%)	6	21
2	E	459/462 (99%)	408 (89%)	43 (9%)	8 (2%)	7	25
2	F	459/462 (99%)	407 (89%)	43 (9%)	9 (2%)	6	21
3	G	663/286 (232%)	468 (71%)	141 (21%)	54 (8%)	1	3
4	H	399/135 (296%)	294 (74%)	78 (20%)	27 (7%)	1	4
All	All	3855/3313 (116%)	3235 (84%)	481 (12%)	139 (4%)	4	12

All (139) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	189	GLN
1	A	396	ALA
1	A	404	LYS
1	A	481	LEU
1	A	482	PRO
1	B	189	GLN
1	B	262	ASP
1	B	396	ALA
1	B	404	LYS
1	B	481	LEU
1	B	482	PRO
1	C	189	GLN
1	C	262	ASP
1	C	396	ALA
1	C	404	LYS
1	C	481	LEU
1	C	482	PRO
2	D	264	MET
2	D	292	SER
2	E	264	MET
2	E	292	SER
2	F	264	MET
2	F	292	SER
3	G	67[A]	MET
3	G	67[B]	MET
3	G	67[C]	MET
3	G	73[A]	VAL
3	G	73[B]	VAL
3	G	73[C]	VAL
3	G	92[A]	ASN
3	G	92[B]	ASN
3	G	92[C]	ASN
3	G	106[A]	ARG
3	G	106[B]	ARG
3	G	106[C]	ARG
3	G	132[A]	PRO
3	G	132[B]	PRO
3	G	132[C]	PRO
3	G	133[A]	VAL
3	G	133[B]	VAL
3	G	133[C]	VAL
3	G	138[A]	THR
3	G	138[B]	THR

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Mol	Chain	Res	Type
3	G	138[C]	THR
3	G	140[A]	ILE
3	G	140[B]	ILE
3	G	140[C]	ILE
3	G	150[A]	GLN
3	G	150[B]	GLN
3	G	150[C]	GLN
3	G	163[A]	GLU
3	G	163[B]	GLU
3	G	163[C]	GLU
3	G	172[A]	TYR
3	G	172[B]	TYR
3	G	172[C]	TYR
3	G	176[A]	VAL
3	G	176[B]	VAL
3	G	176[C]	VAL
4	H	105[A]	LYS
4	H	105[B]	LYS
4	H	105[C]	LYS
4	H	112[A]	LYS
4	H	112[B]	LYS
4	H	112[C]	LYS
1	A	262	ASP
1	A	495	LYS
1	B	495	LYS
1	C	449	PRO
1	C	495	LYS
3	G	113[A]	TYR
3	G	113[B]	TYR
3	G	113[C]	TYR
3	G	114[A]	VAL
3	G	114[B]	VAL
3	G	114[C]	VAL
4	H	51[A]	ARG
4	H	51[B]	ARG
4	H	51[C]	ARG
4	H	80[A]	ASP
4	H	80[B]	ASP
4	H	80[C]	ASP
4	H	106[A]	ARG
4	H	106[B]	ARG
4	H	106[C]	ARG

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Mol	Chain	Res	Type
4	H	109[A]	LYS
4	H	109[B]	LYS
4	H	109[C]	LYS
1	A	449	PRO
1	B	449	PRO
3	G	44[A]	PRO
3	G	44[B]	PRO
3	G	44[C]	PRO
3	G	131[A]	TYR
3	G	131[B]	TYR
3	G	131[C]	TYR
4	H	110[A]	THR
4	H	110[B]	THR
4	H	110[C]	THR
1	A	402	LEU
1	A	478	THR
1	B	402	LEU
1	B	478	THR
1	C	402	LEU
1	C	478	THR
2	D	38	GLY
2	D	170	GLN
2	D	301	VAL
2	E	301	VAL
2	F	170	GLN
2	F	301	VAL
2	D	37	GLY
3	G	191[A]	LEU
3	G	191[B]	LEU
3	G	191[C]	LEU
4	H	98[A]	ALA
4	H	98[B]	ALA
4	H	98[C]	ALA
1	B	329	TYR
2	E	34	ARG
2	E	38	GLY
2	F	34	ARG
4	H	12[A]	GLU
4	H	12[B]	GLU
4	H	12[C]	GLU
1	C	157	ILE
2	D	34	ARG

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Mol	Chain	Res	Type
2	E	37	GLY
2	D	291	GLY
2	F	37	GLY
2	F	291	GLY
3	G	65[A]	HIS
3	G	65[B]	HIS
3	G	65[C]	HIS
2	E	291	GLY
2	F	38	GLY
2	F	417	PRO
2	D	417	PRO
2	E	417	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	388/413 (94%)	341 (88%)	47 (12%)	5	17
1	B	388/413 (94%)	339 (87%)	49 (13%)	4	16
1	C	388/413 (94%)	342 (88%)	46 (12%)	5	18
2	D	375/376 (100%)	328 (88%)	47 (12%)	4	16
2	E	375/376 (100%)	326 (87%)	49 (13%)	4	15
2	F	375/376 (100%)	327 (87%)	48 (13%)	4	15
3	G	576/239 (241%)	486 (84%)	90 (16%)	2	10
4	H	339/113 (300%)	321 (95%)	18 (5%)	20	47
All	All	3204/2719 (118%)	2810 (88%)	394 (12%)	4	16

All (394) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	THR
1	A	34	VAL
1	A	38	ILE

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Mol	Chain	Res	Type
1	A	46	LYS
1	A	52	LEU
1	A	87	GLN
1	A	88	VAL
1	A	91	THR
1	A	93	ARG
1	A	94	ILE
1	A	99	VAL
1	A	106	ARG
1	A	108	VAL
1	A	121	ILE
1	A	136	VAL
1	A	144	GLU
1	A	157	ILE
1	A	171	ARG
1	A	177	THR
1	A	187	LYS
1	A	189	GLN
1	A	191	VAL
1	A	194	ILE
1	A	262	ASP
1	A	274	SER
1	A	275	LEU
1	A	278	ARG
1	A	279	ARG
1	A	298	LEU
1	A	319	ILE
1	A	335	ILE
1	A	341	GLN
1	A	344	LEU
1	A	354	ARG
1	A	362	SER
1	A	381	THR
1	A	397	GLN
1	A	411	ASN
1	A	415	ARG
1	A	430	VAL
1	A	440	VAL
1	A	448	ILE
1	A	460	LEU
1	A	468	LYS
1	A	481	LEU

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Mol	Chain	Res	Type
1	A	485	LYS
1	A	499	THR
1	B	30	THR
1	B	34	VAL
1	B	38	ILE
1	B	46	LYS
1	B	52	LEU
1	B	80	THR
1	B	87	GLN
1	B	88	VAL
1	B	91	THR
1	B	93	ARG
1	B	94	ILE
1	B	99	VAL
1	B	106	ARG
1	B	108	VAL
1	B	121	ILE
1	B	136	VAL
1	B	144	GLU
1	B	157	ILE
1	B	171	ARG
1	B	177	THR
1	B	187	LYS
1	B	189	GLN
1	B	191	VAL
1	B	194	ILE
1	B	262	ASP
1	B	274	SER
1	B	275	LEU
1	B	278	ARG
1	B	279	ARG
1	B	298	LEU
1	B	319	ILE
1	B	335	ILE
1	B	341	GLN
1	B	344	LEU
1	B	354	ARG
1	B	362	SER
1	B	381	THR
1	B	397	GLN
1	B	411	ASN
1	B	415	ARG

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Mol	Chain	Res	Type
1	B	430	VAL
1	B	440	VAL
1	B	448	ILE
1	B	460	LEU
1	B	462	SER
1	B	468	LYS
1	B	481	LEU
1	B	485	LYS
1	B	499	THR
1	C	28	VAL
1	C	30	THR
1	C	34	VAL
1	C	38	ILE
1	C	46	LYS
1	C	52	LEU
1	C	87	GLN
1	C	88	VAL
1	C	91	THR
1	C	93	ARG
1	C	94	ILE
1	C	99	VAL
1	C	106	ARG
1	C	108	VAL
1	C	121	ILE
1	C	136	VAL
1	C	157	ILE
1	C	171	ARG
1	C	177	THR
1	C	187	LYS
1	C	189	GLN
1	C	191	VAL
1	C	194	ILE
1	C	262	ASP
1	C	274	SER
1	C	275	LEU
1	C	278	ARG
1	C	279	ARG
1	C	298	LEU
1	C	319	ILE
1	C	341	GLN
1	C	344	LEU
1	C	354	ARG

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Mol	Chain	Res	Type
1	C	362	SER
1	C	381	THR
1	C	397	GLN
1	C	411	ASN
1	C	415	ARG
1	C	430	VAL
1	C	440	VAL
1	C	448	ILE
1	C	460	LEU
1	C	468	LYS
1	C	481	LEU
1	C	485	LYS
1	C	499	THR
2	D	5	ARG
2	D	26	ILE
2	D	34	ARG
2	D	36	GLN
2	D	53	VAL
2	D	89	VAL
2	D	91	ASN
2	D	92	VAL
2	D	93	LEU
2	D	97	ILE
2	D	103	VAL
2	D	113	ARG
2	D	119	GLU
2	D	121	LEU
2	D	126	GLU
2	D	132	ILE
2	D	135	ILE
2	D	138	LEU
2	D	149	LEU
2	D	155	VAL
2	D	160	LEU
2	D	164	LEU
2	D	170	GLN
2	D	194	GLU
2	D	196	LYS
2	D	200	VAL
2	D	223	LEU
2	D	226	LEU
2	D	241	LEU

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Mol	Chain	Res	Type
2	D	249	ARG
2	D	251	THR
2	D	301	VAL
2	D	307	THR
2	D	318	LEU
2	D	324	LEU
2	D	340	LEU
2	D	364	GLN
2	D	374	GLN
2	D	379	ILE
2	D	391	LEU
2	D	392	ILE
2	D	405	GLN
2	D	411	GLU
2	D	412	GLN
2	D	416	MET
2	D	423	VAL
2	D	456	VAL
2	E	5	ARG
2	E	10	MET
2	E	26	ILE
2	E	34	ARG
2	E	36	GLN
2	E	53	VAL
2	E	89	VAL
2	E	91	ASN
2	E	92	VAL
2	E	93	LEU
2	E	97	ILE
2	E	103	VAL
2	E	113	ARG
2	E	119	GLU
2	E	121	LEU
2	E	126	GLU
2	E	132	ILE
2	E	135	ILE
2	E	138	LEU
2	E	149	LEU
2	E	155	VAL
2	E	160	LEU
2	E	164	LEU
2	E	170	GLN

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Mol	Chain	Res	Type
2	E	194	GLU
2	E	196	LYS
2	E	205	SER
2	E	223	LEU
2	E	226	LEU
2	E	241	LEU
2	E	249	ARG
2	E	251	THR
2	E	301	VAL
2	E	307	THR
2	E	318	LEU
2	E	324	LEU
2	E	340	LEU
2	E	374	GLN
2	E	379	ILE
2	E	391	LEU
2	E	392	ILE
2	E	405	GLN
2	E	411	GLU
2	E	412	GLN
2	E	416	MET
2	E	423	VAL
2	E	441	LEU
2	E	456	VAL
2	E	461	LYS
2	F	5	ARG
2	F	26	ILE
2	F	34	ARG
2	F	36	GLN
2	F	53	VAL
2	F	89	VAL
2	F	91	ASN
2	F	92	VAL
2	F	93	LEU
2	F	97	ILE
2	F	103	VAL
2	F	113	ARG
2	F	119	GLU
2	F	121	LEU
2	F	126	GLU
2	F	132	ILE
2	F	135	ILE

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Mol	Chain	Res	Type
2	F	138	LEU
2	F	149	LEU
2	F	160	LEU
2	F	164	LEU
2	F	170	GLN
2	F	194	GLU
2	F	196	LYS
2	F	200	VAL
2	F	205	SER
2	F	223	LEU
2	F	226	LEU
2	F	235	ARG
2	F	241	LEU
2	F	249	ARG
2	F	251	THR
2	F	286	THR
2	F	301	VAL
2	F	307	THR
2	F	318	LEU
2	F	324	LEU
2	F	340	LEU
2	F	374	GLN
2	F	379	ILE
2	F	391	LEU
2	F	392	ILE
2	F	411	GLU
2	F	412	GLN
2	F	416	MET
2	F	423	VAL
2	F	441	LEU
2	F	456	VAL
3	G	5[A]	ARG
3	G	5[B]	ARG
3	G	5[C]	ARG
3	G	8[A]	LYS
3	G	8[B]	LYS
3	G	8[C]	LYS
3	G	18[A]	ARG
3	G	18[B]	ARG
3	G	18[C]	ARG
3	G	20[A]	ILE
3	G	20[B]	ILE

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Mol	Chain	Res	Type
3	G	20[C]	ILE
3	G	25[A]	LYS
3	G	25[B]	LYS
3	G	25[C]	LYS
3	G	49[A]	ILE
3	G	49[B]	ILE
3	G	49[C]	ILE
3	G	68[A]	LEU
3	G	68[B]	LEU
3	G	68[C]	LEU
3	G	71[A]	ARG
3	G	71[B]	ARG
3	G	71[C]	ARG
3	G	80[A]	VAL
3	G	80[B]	VAL
3	G	80[C]	VAL
3	G	98[A]	LEU
3	G	98[B]	LEU
3	G	98[C]	LEU
3	G	108[A]	GLN
3	G	108[B]	GLN
3	G	108[C]	GLN
3	G	110[A]	LYS
3	G	110[B]	LYS
3	G	110[C]	LYS
3	G	114[A]	VAL
3	G	114[B]	VAL
3	G	114[C]	VAL
3	G	115[A]	ILE
3	G	115[B]	ILE
3	G	115[C]	ILE
3	G	118[A]	VAL
3	G	118[B]	VAL
3	G	118[C]	VAL
3	G	134[A]	VAL
3	G	134[B]	VAL
3	G	134[C]	VAL
3	G	136[A]	GLU
3	G	136[B]	GLU
3	G	136[C]	GLU
3	G	142[A]	ASP
3	G	142[B]	ASP

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Mol	Chain	Res	Type
3	G	142[C]	ASP
3	G	148[A]	GLU
3	G	148[B]	GLU
3	G	148[C]	GLU
3	G	149[A]	ILE
3	G	149[B]	ILE
3	G	149[C]	ILE
3	G	151[A]	ASP
3	G	151[B]	ASP
3	G	151[C]	ASP
3	G	157[A]	ILE
3	G	157[B]	ILE
3	G	157[C]	ILE
3	G	179[A]	ILE
3	G	179[B]	ILE
3	G	179[C]	ILE
3	G	181[A]	GLN
3	G	181[B]	GLN
3	G	181[C]	GLN
3	G	188[A]	LEU
3	G	188[B]	LEU
3	G	188[C]	LEU
3	G	230[A]	LEU
3	G	230[B]	LEU
3	G	230[C]	LEU
3	G	231[A]	LEU
3	G	231[B]	LEU
3	G	231[C]	LEU
3	G	237[A]	GLU
3	G	237[B]	GLU
3	G	237[C]	GLU
3	G	242[A]	MET
3	G	242[B]	MET
3	G	242[C]	MET
3	G	260[A]	THR
3	G	260[B]	THR
3	G	260[C]	THR
4	H	8[A]	ILE
4	H	8[B]	ILE
4	H	8[C]	ILE
4	H	10[A]	THR
4	H	10[B]	THR

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Mol	Chain	Res	Type
4	H	10[C]	THR
4	H	39[A]	ILE
4	H	39[B]	ILE
4	H	39[C]	ILE
4	H	61[A]	ILE
4	H	61[B]	ILE
4	H	61[C]	ILE
4	H	81[A]	THR
4	H	81[B]	THR
4	H	81[C]	THR
4	H	103[A]	ILE
4	H	103[B]	ILE
4	H	103[C]	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (78) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	64	GLN
1	A	87	GLN
1	A	113	GLN
1	A	143	HIS
1	A	147	GLN
1	A	189	GLN
1	A	215	HIS
1	A	333	ASN
1	A	341	GLN
1	A	411	ASN
1	A	422	GLN
1	A	477	GLN
1	B	64	GLN
1	B	87	GLN
1	B	113	GLN
1	B	143	HIS
1	B	147	GLN
1	B	189	GLN
1	B	215	HIS
1	B	333	ASN
1	B	341	GLN
1	B	411	ASN
1	B	422	GLN
1	B	477	GLN
1	C	64	GLN

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Mol	Chain	Res	Type
1	C	87	GLN
1	C	113	GLN
1	C	143	HIS
1	C	147	GLN
1	C	189	GLN
1	C	215	HIS
1	C	333	ASN
1	C	411	ASN
1	C	422	GLN
1	C	477	GLN
2	D	2	ASN
2	D	8	GLN
2	D	36	GLN
2	D	91	ASN
2	D	162	GLN
2	D	166	ASN
2	D	172	HIS
2	D	238	GLN
2	D	280	GLN
2	D	323	ASN
2	D	356	HIS
2	D	374	GLN
2	D	408	HIS
2	D	412	GLN
2	D	438	HIS
2	E	2	ASN
2	E	36	GLN
2	E	91	ASN
2	E	162	GLN
2	E	166	ASN
2	E	172	HIS
2	E	189	ASN
2	E	238	GLN
2	E	280	GLN
2	E	323	ASN
2	E	356	HIS
2	E	374	GLN
2	E	408	HIS
2	E	412	GLN
2	E	438	HIS
2	F	2	ASN
2	F	36	GLN

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Mol	Chain	Res	Type
2	F	91	ASN
2	F	162	GLN
2	F	172	HIS
2	F	238	GLN
2	F	280	GLN
2	F	323	ASN
2	F	356	HIS
2	F	371	ASN
2	F	374	GLN
2	F	412	GLN
2	F	438	HIS

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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	474/502 (94%)	0.40	26 (5%)	30 16	44, 69, 152, 234	0
1	B	474/502 (94%)	0.36	35 (7%)	20 10	38, 61, 167, 246	0
1	C	474/502 (94%)	0.44	24 (5%)	33 17	45, 67, 128, 185	0
2	D	461/462 (99%)	0.49	24 (5%)	33 16	43, 76, 129, 174	0
2	E	461/462 (99%)	0.20	16 (3%)	47 26	36, 55, 113, 170	0
2	F	461/462 (99%)	0.32	20 (4%)	40 21	40, 62, 124, 173	0
3	G	227/286 (79%)	3.63	195 (85%)	0 0	3, 17, 34, 47	227 (100%)
4	H	135/135 (100%)	3.20	100 (74%)	0 0	27, 44, 65, 71	135 (100%)
All	All	3167/3313 (95%)	0.73	440 (13%)	6 4	3, 62, 136, 246	362 (11%)

All (440) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	G	223[A]	GLU	13.2
3	G	143[A]	THR	10.1
3	G	145[A]	SER	9.8
3	G	132[A]	PRO	9.1
3	G	227[A]	TYR	8.0
3	G	103[A]	ILE	8.0
3	G	168[A]	LEU	7.9
3	G	188[A]	LEU	7.7
3	G	113[A]	TYR	7.6
4	H	129[A]	GLN	7.5
3	G	146[A]	LEU	7.4
4	H	79[A]	ALA	7.4
3	G	4[A]	MET	7.2
4	H	78[A]	LEU	7.2
4	H	16[A]	PHE	7.0
4	H	125[A]	GLU	7.0

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Mol	Chain	Res	Type	RSRZ
3	G	14[A]	VAL	6.9
3	G	170[A]	ILE	6.6
4	H	90[A]	VAL	6.6
4	H	82[A]	ALA	6.3
4	H	94[A]	LYS	6.3
4	H	68[A]	LEU	6.2
3	G	19[A]	GLN	6.1
3	G	90[A]	PRO	6.1
3	G	107[A]	HIS	6.1
3	G	21[A]	THR	6.1
2	D	379	ILE	6.1
3	G	130[A]	GLY	6.1
4	H	55[A]	GLY	6.0
3	G	102[A]	THR	5.9
3	G	78[A]	TYR	5.9
3	G	229[A]	ALA	5.9
1	A	405	ALA	5.9
3	G	222[A]	ALA	5.9
3	G	91[A]	TYR	5.8
4	H	6[A]	VAL	5.8
4	H	29[A]	GLU	5.7
4	H	91[A]	GLU	5.7
3	G	20[A]	ILE	5.7
3	G	9[A]	ARG	5.7
1	B	101	GLU	5.6
4	H	67[A]	PHE	5.6
3	G	112[A]	GLU	5.5
3	G	92[A]	ASN	5.5
3	G	99[A]	VAL	5.5
3	G	189[A]	LEU	5.5
4	H	25[A]	ALA	5.5
3	G	13[A]	SER	5.5
3	G	17[A]	THR	5.5
3	G	266[A]	ALA	5.5
3	G	7[A]	ILE	5.4
3	G	33[A]	ARG	5.4
4	H	12[A]	GLU	5.4
4	H	132[A]	ASN	5.4
4	H	135[A]	SER	5.3
1	C	498	PHE	5.2
3	G	124[A]	ASP	5.2
3	G	250[A]	ASP	5.2

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Mol	Chain	Res	Type	RSRZ
3	G	115[A]	ILE	5.1
3	G	262[A]	GLN	5.0
3	G	16[A]	ASN	5.0
3	G	117[A]	ALA	5.0
4	H	134[A]	LYS	5.0
3	G	261[A]	LEU	5.0
3	G	176[A]	VAL	5.0
4	H	14[A]	LYS	4.9
3	G	66[A]	PRO	4.9
3	G	125[A]	PHE	4.9
4	H	13[A]	ARG	4.8
4	H	130[A]	VAL	4.8
3	G	147[A]	THR	4.8
4	H	11[A]	PRO	4.8
2	D	384	GLU	4.7
4	H	97[A]	LYS	4.7
3	G	180[A]	VAL	4.7
3	G	75[A]	LYS	4.7
4	H	115[A]	LEU	4.7
3	G	5[A]	ARG	4.7
3	G	263[A]	PHE	4.7
2	E	416	MET	4.7
4	H	77[A]	ILE	4.6
3	G	133[A]	VAL	4.6
4	H	44[A]	PRO	4.6
3	G	177[A]	SER	4.6
3	G	179[A]	ILE	4.6
4	H	8[A]	ILE	4.6
3	G	74[A]	LYS	4.6
2	D	292	SER	4.6
4	H	133[A]	SER	4.6
3	G	138[A]	THR	4.6
3	G	148[A]	GLU	4.5
3	G	257[A]	GLU	4.5
3	G	6[A]	GLU	4.5
3	G	139[A]	GLY	4.5
3	G	85[A]	ARG	4.5
4	H	87[A]	GLU	4.5
4	H	85[A]	PRO	4.5
3	G	253[A]	THR	4.4
3	G	173[A]	ASN	4.4
3	G	178[A]	PRO	4.4

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Mol	Chain	Res	Type	RSRZ
3	G	230[A]	LEU	4.4
1	A	452	ASP	4.4
1	A	189	GLN	4.3
3	G	12[A]	ARG	4.3
4	H	126[A]	VAL	4.3
4	H	26[A]	ARG	4.3
3	G	175[A]	PHE	4.3
3	G	226[A]	ILE	4.3
3	G	97[A]	ARG	4.2
4	H	56[A]	ASP	4.2
3	G	10[A]	ARG	4.2
1	B	275	LEU	4.2
4	H	32[A]	LEU	4.2
3	G	149[A]	ILE	4.2
3	G	258[A]	THR	4.1
3	G	104[A]	GLU	4.1
3	G	171[A]	PHE	4.1
2	D	455	ALA	4.1
3	G	246[A]	GLY	4.1
4	H	41[A]	LEU	4.0
4	H	121[A]	LEU	4.0
3	G	110[A]	LYS	4.0
3	G	237[A]	GLU	4.0
3	G	11[A]	ILE	4.0
3	G	193[A]	SER	4.0
3	G	129[A]	ARG	4.0
1	C	499	THR	4.0
3	G	221[A]	TYR	4.0
3	G	231[A]	LEU	4.0
3	G	101[A]	LYS	3.9
3	G	131[A]	TYR	3.9
3	G	224[A]	THR	3.9
3	G	122[A]	GLY	3.9
3	G	23[A]	ALA	3.9
3	G	265[A]	ARG	3.9
4	H	80[A]	ASP	3.9
3	G	80[A]	VAL	3.9
3	G	29[A]	ALA	3.9
3	G	34[A]	ARG	3.9
3	G	73[A]	VAL	3.9
4	H	81[A]	THR	3.9
1	C	43	GLY	3.9

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Mol	Chain	Res	Type	RSRZ
3	G	38[A]	THR	3.8
3	G	22[A]	LYS	3.8
3	G	31[A]	LYS	3.8
3	G	234[A]	LYS	3.8
3	G	8[A]	LYS	3.8
4	H	100[A]	HIS	3.8
3	G	24[A]	MET	3.8
3	G	141[A]	SER	3.7
3	G	144[A]	PRO	3.7
3	G	182[A]	ARG	3.7
4	H	20[A]	ALA	3.6
4	H	122[A]	GLU	3.6
3	G	140[A]	ILE	3.6
4	H	31[A]	GLU	3.6
3	G	82[A]	THR	3.6
4	H	49[A]	PRO	3.6
1	A	88	VAL	3.6
2	F	292	SER	3.6
3	G	37[A]	GLU	3.6
3	G	111[A]	ASP	3.6
3	G	232[A]	ASP	3.6
4	H	43[A]	THR	3.6
1	A	275	LEU	3.6
4	H	104[A]	LEU	3.6
3	G	255[A]	MET	3.5
4	H	42[A]	VAL	3.5
3	G	254[A]	GLU	3.5
1	B	405	ALA	3.5
3	G	219[A]	PRO	3.5
4	H	63[A]	VAL	3.5
4	H	101[A]	GLU	3.4
3	G	238[A]	PHE	3.4
3	G	256[A]	LEU	3.4
4	H	60[A]	LEU	3.4
4	H	50[A]	VAL	3.4
3	G	157[A]	ILE	3.4
1	B	284	GLU	3.4
3	G	225[A]	LEU	3.4
1	B	283	ARG	3.4
1	B	460	LEU	3.4
4	H	61[A]	ILE	3.4
3	G	27[A]	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
4	H	92[A]	ARG	3.3
2	D	153	ALA	3.3
2	D	381	GLY	3.3
3	G	121[A]	LYS	3.3
3	G	172[A]	TYR	3.3
4	H	24[A]	ILE	3.3
3	G	136[A]	GLU	3.3
1	C	496	LYS	3.3
1	C	345	GLU	3.3
3	G	88[A]	ALA	3.3
4	H	84[A]	LEU	3.3
4	H	58[A]	GLU	3.3
3	G	259[A]	LEU	3.2
3	G	169[A]	THR	3.2
3	G	119[A]	GLY	3.2
4	H	73[A]	ASP	3.2
2	D	5	ARG	3.2
1	A	471	LEU	3.2
4	H	40[A]	PRO	3.2
2	E	264	MET	3.2
3	G	39[A]	ALA	3.2
4	H	37[A]	GLY	3.2
3	G	35[A]	ALA	3.2
3	G	252[A]	ALA	3.2
3	G	162[A]	ASP	3.1
1	A	350	TYR	3.1
2	D	461	LYS	3.1
1	A	87	GLN	3.1
3	G	32[A]	LEU	3.1
4	H	47[A]	THR	3.1
1	C	497	GLY	3.1
1	C	28	VAL	3.1
1	A	467	ASN	3.1
3	G	95[A]	ILE	3.1
3	G	18[A]	ARG	3.1
3	G	120[A]	ARG	3.1
1	A	500	PRO	3.1
3	G	93[A]	ALA	3.1
3	G	217[A]	LEU	3.1
4	H	57[A]	LYS	3.1
1	B	190	ASP	3.1
4	H	93[A]	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
2	F	295	SER	3.0
3	G	84[A]	ASP	3.0
4	H	17[A]	GLN	3.0
4	H	105[A]	LYS	3.0
3	G	160[A]	PHE	3.0
1	B	400	SER	3.0
3	G	100[A]	SER	3.0
3	G	109[A]	SER	3.0
3	G	151[A]	ASP	3.0
4	H	118[A]	LYS	3.0
1	B	67	GLU	3.0
3	G	163[A]	GLU	3.0
4	H	71[A]	ARG	3.0
1	B	499	THR	3.0
1	B	461	LEU	3.0
3	G	187[A]	GLN	3.0
1	B	456	PHE	3.0
4	H	10[A]	THR	3.0
1	C	63	ALA	2.9
3	G	244[A]	ALA	2.9
3	G	248[A]	ALA	2.9
3	G	28[A]	ALA	2.9
4	H	15[A]	VAL	2.9
1	A	453	VAL	2.9
1	B	498	PHE	2.9
3	G	64[A]	SER	2.9
1	B	491	ILE	2.9
3	G	68[A]	LEU	2.9
3	G	79[A]	MET	2.9
3	G	106[A]	ARG	2.9
1	B	447	ASP	2.9
4	H	110[A]	THR	2.9
2	F	386	SER	2.9
3	G	98[A]	LEU	2.9
3	G	108[A]	GLN	2.9
3	G	235[A]	ALA	2.9
3	G	260[A]	THR	2.9
2	F	456	VAL	2.9
3	G	164[A]	THR	2.8
3	G	218[A]	LEU	2.8
1	A	387	ALA	2.8
2	E	459	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
4	H	7[A]	ASP	2.8
3	G	94[A]	ASN	2.8
3	G	264[A]	ASN	2.8
2	D	452	ILE	2.8
2	D	459	ALA	2.8
3	G	236[A]	SER	2.8
1	A	478	THR	2.8
3	G	137[A]	VAL	2.8
1	B	446	ASP	2.8
4	H	52[A]	ILE	2.8
4	H	88[A]	ILE	2.8
4	H	117[A]	HIS	2.8
3	G	181[A]	GLN	2.8
3	G	105[A]	GLU	2.8
3	G	135[A]	GLU	2.8
1	C	439	ALA	2.7
1	A	481	LEU	2.7
2	F	462	LEU	2.7
3	G	126[A]	PHE	2.7
3	G	192[A]	THR	2.7
2	D	375	ASP	2.7
4	H	34[A]	VAL	2.7
3	G	44[A]	PRO	2.7
1	C	483	ASP	2.7
4	H	113[A]	ASP	2.7
4	H	107[A]	LEU	2.7
3	G	241[A]	ARG	2.7
3	G	128[A]	LYS	2.7
1	C	136	VAL	2.7
1	C	275	LEU	2.7
3	G	242[A]	MET	2.7
3	G	249[A]	THR	2.7
2	F	375	ASP	2.7
3	G	15[A]	LYS	2.6
4	H	75[A]	VAL	2.6
3	G	183[A]	PRO	2.6
4	H	1[A]	MET	2.6
2	D	256	GLU	2.6
3	G	123[A]	ARG	2.6
3	G	30[A]	ALA	2.6
3	G	127[A]	LYS	2.6
3	G	72[A]	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
3	G	228[A]	SER	2.6
1	A	403	ASP	2.6
3	G	3[A]	GLY	2.6
3	G	134[A]	VAL	2.6
3	G	153[A]	ALA	2.6
2	F	380	LEU	2.5
2	E	151	GLY	2.5
4	H	64[A]	SER	2.5
1	A	404	LYS	2.5
3	G	114[A]	VAL	2.5
4	H	28[A]	VAL	2.5
3	G	96[A]	LEU	2.5
1	B	92	GLY	2.5
4	H	51[A]	ARG	2.5
1	B	493	GLU	2.5
4	H	86[A]	GLU	2.5
3	G	41[A]	ASN	2.5
1	A	365	ARG	2.5
1	C	396	ALA	2.5
1	B	181	ASP	2.5
3	G	25[A]	LYS	2.5
4	H	114[A]	TYR	2.5
1	B	413	GLY	2.5
1	B	464	MET	2.4
2	E	325	GLU	2.4
1	C	452	ASP	2.4
3	G	36[A]	GLN	2.4
3	G	240[A]	ALA	2.4
4	H	103[A]	ILE	2.4
2	F	384	GLU	2.4
1	B	455	ARG	2.4
4	H	46[A]	LYS	2.4
1	B	262	ASP	2.4
2	E	456	VAL	2.4
2	F	358	ARG	2.4
3	G	184[A]	VAL	2.4
2	E	379	ILE	2.4
2	E	292	SER	2.4
2	D	449	VAL	2.4
1	C	85	GLY	2.4
3	G	247[A]	ASN	2.4
3	G	167[A]	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
2	D	206	MET	2.4
1	B	494	PHE	2.4
2	E	391	LEU	2.3
1	B	412	ARG	2.3
2	F	377	ILE	2.3
4	H	38[A]	HIS	2.3
3	G	47[A]	ASP	2.3
3	G	166[A]	ASP	2.3
2	D	446	PHE	2.3
2	F	23	LEU	2.3
1	B	457	GLU	2.3
2	E	348	SER	2.3
4	H	54[A]	GLN	2.3
1	B	254	LYS	2.3
3	G	45[A]	TYR	2.3
2	D	383	ASP	2.3
4	H	112[A]	LYS	2.3
1	A	417	VAL	2.3
2	F	443	GLU	2.3
2	F	49	GLY	2.3
2	E	381	GLY	2.2
3	G	46[A]	ALA	2.2
3	G	245[A]	MET	2.2
1	C	392	LEU	2.2
2	D	447	TYR	2.2
3	G	83[A]	SER	2.2
1	C	45	GLU	2.2
4	H	39[A]	ILE	2.2
1	A	399	GLY	2.2
1	B	497	GLY	2.2
4	H	45[A]	LEU	2.2
3	G	76[A]	THR	2.2
2	E	99	GLU	2.2
1	C	399	GLY	2.2
1	B	389	TYR	2.2
2	D	81	VAL	2.2
3	G	150[A]	GLN	2.2
2	F	99	GLU	2.2
2	F	429	GLY	2.2
2	E	266	SER	2.2
1	B	481	LEU	2.2
3	G	67[A]	MET	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	387	ALA	2.2
1	C	413	GLY	2.2
2	F	291	GLY	2.2
1	A	306	ASP	2.2
1	B	478	THR	2.1
3	G	49[A]	ILE	2.1
4	H	48[A]	ALA	2.1
4	H	69[A]	GLU	2.1
1	A	280	PRO	2.1
4	H	99[A]	ARG	2.1
3	G	165[A]	PHE	2.1
1	A	475	ILE	2.1
1	C	350	TYR	2.1
1	B	409	LYS	2.1
2	D	385	LEU	2.1
4	H	109[A]	LYS	2.1
1	A	455	ARG	2.1
4	H	96[A]	ALA	2.1
1	B	122	GLU	2.1
2	D	131	GLY	2.1
2	F	287	SER	2.1
1	C	190	ASP	2.1
1	C	262	ASP	2.1
4	H	23[A]	VAL	2.1
1	A	497	GLY	2.1
3	G	185[A]	GLU	2.1
4	H	72[A]	PRO	2.1
2	E	34	ARG	2.1
3	G	243[A]	THR	2.1
1	C	445	MET	2.1
2	F	264	MET	2.1
1	B	289	ASP	2.1
2	D	378	ALA	2.1
1	A	457	GLU	2.1
2	F	457	GLU	2.1
2	E	461	LYS	2.0
1	A	227	SER	2.0
2	D	386	SER	2.0
4	H	128[A]	LEU	2.0
4	H	35[A]	MET	2.0
2	D	213	GLU	2.0
1	B	70	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
2	F	438	HIS	2.0
2	D	357	TYR	2.0
2	E	457	GLU	2.0
4	H	83[A]	GLU	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.