



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:32 PM UTC

PDB ID : 3HOX / pdb_00003hox
Title : Complete RNA polymerase II elongation complex V
Authors : Sydow, J.F.; Brueckner, F.; Cheung, A.C.M.; Damsma, G.E.; Dengl, S.;
Lehmann, E.; Vassylyev, D.; Cramer, P.
Deposited on : 2009-06-03
Resolution : 3.65 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
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

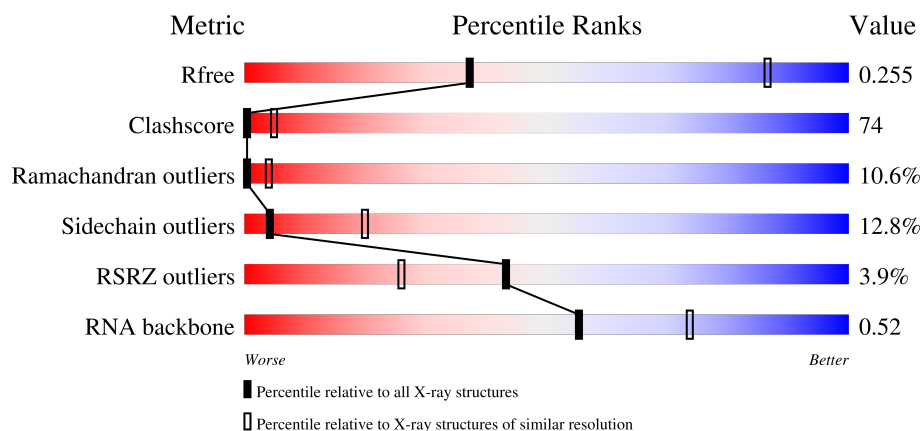
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.65 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	1062 (3.78-3.54)
Clashscore	190562	1009 (3.76-3.56)
Ramachandran outliers	187476	1054 (3.78-3.54)
Sidechain outliers	187428	1052 (3.78-3.54)
RSRZ outliers	180081	1061 (3.78-3.54)
RNA backbone	3983	1027 (4.26-3.06)

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	1733	
2	B	1224	
3	C	347	
4	D	221	

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Mol	Chain	Length	Quality of chain
5	E	215	
6	F	155	
7	G	171	
8	H	146	
9	I	122	
10	J	70	
11	K	120	
12	L	70	
13	N	12	
14	T	26	
15	P	18	

2 Entry composition [i](#)

There are 17 unique types of molecules in this entry. The entry contains 31918 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 DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1417	Total	C	N	O	S	0	0	0
			11151	7027	1950	2112	62			

- Molecule 2 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1113	Total	C	N	O	S	0	0	0
			8847	5600	1552	1640	55			

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	266	Total	C	N	O	S	0	0	0
			2095	1317	348	417	13			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-28	MET	-	expression tag	UNP P16370
C	-27	GLY	-	expression tag	UNP P16370
C	-26	SER	-	expression tag	UNP P16370
C	-25	HIS	-	expression tag	UNP P16370
C	-24	HIS	-	expression tag	UNP P16370
C	-23	HIS	-	expression tag	UNP P16370
C	-22	HIS	-	expression tag	UNP P16370
C	-21	HIS	-	expression tag	UNP P16370
C	-20	HIS	-	expression tag	UNP P16370
C	-19	SER	-	expression tag	UNP P16370
C	-18	ASN	-	expression tag	UNP P16370
C	-17	SER	-	expression tag	UNP P16370
C	-16	GLY	-	expression tag	UNP P16370
C	-15	LEU	-	expression tag	UNP P16370

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-14	ASN	-	expression tag	UNP P16370
C	-13	ASP	-	expression tag	UNP P16370
C	-12	ILE	-	expression tag	UNP P16370
C	-11	PHE	-	expression tag	UNP P16370
C	-10	GLU	-	expression tag	UNP P16370
C	-9	ALA	-	expression tag	UNP P16370
C	-8	GLN	-	expression tag	UNP P16370
C	-7	LYS	-	expression tag	UNP P16370
C	-6	ILE	-	expression tag	UNP P16370
C	-5	GLU	-	expression tag	UNP P16370
C	-4	TRP	-	expression tag	UNP P16370
C	-3	HIS	-	expression tag	UNP P16370
C	-2	GLU	-	expression tag	UNP P16370
C	-1	ASP	-	expression tag	UNP P16370
C	0	THR	-	expression tag	UNP P16370
C	1	GLY	-	expression tag	UNP P16370

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	178	Total	C	N	O	S	0	0	0
			1434	887	257	288	2			

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	214	Total	C	N	O	S	0	0	0
			1752	1111	309	321	11			

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	87	Total	C	N	O	S	0	0	0
			705	451	119	132	3			

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	171	Total	C	N	O	S	0	0	0
			1340	861	222	249	8			

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	135	Total	C	N	O	S	0	0	0
			1081	680	183	214	4			

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	119	Total	C	N	O	S	0	0	0
			971	596	179	186	10			

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	65	Total	C	N	O	S	0	0	0
			532	339	93	94	6			

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	114	Total	C	N	O	S	0	0	0
			919	590	156	171	2			

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	46	Total	C	N	O	S	0	0	0
			363	224	72	63	4			

- Molecule 13 is a DNA chain called 5'-D(*AP*CP*TP*AP*CP*TP*TP*GP*AP*GP*CP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	N	7	Total	C	N	O	P	0	0	0
			137	68	22	41	6			

- Molecule 14 is a DNA chain called 5'-D(*AP*GP*CP*TP*C*AP*AP*GP*TP*AP*GP*TP*TP*AP*AP*GP*CP*CP*(BRU)P*GP*GP*TP*CP*AP*TP*T)-3'.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
14	T	18	Total	Br	C	N	O	P	0	0	0
			369	1	176	69	106	17			

- Molecule 15 is a RNA chain called 5'-R(*UP*GP*CP*AP*UP*UP*U*CP*AP*AP*CP*CP

*AP*GP*GP*CP*UP*U)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	P	11	Total	C	N	O	P	0	0	0
			213	95	39	69	10			

- Molecule 16 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	A	2	Total	Zn	0	0
			2	2		
16	B	1	Total	Zn	0	0
			1	1		
16	C	1	Total	Zn	0	0
			1	1		
16	I	2	Total	Zn	0	0
			2	2		
16	J	1	Total	Zn	0	0
			1	1		
16	L	1	Total	Zn	0	0
			1	1		

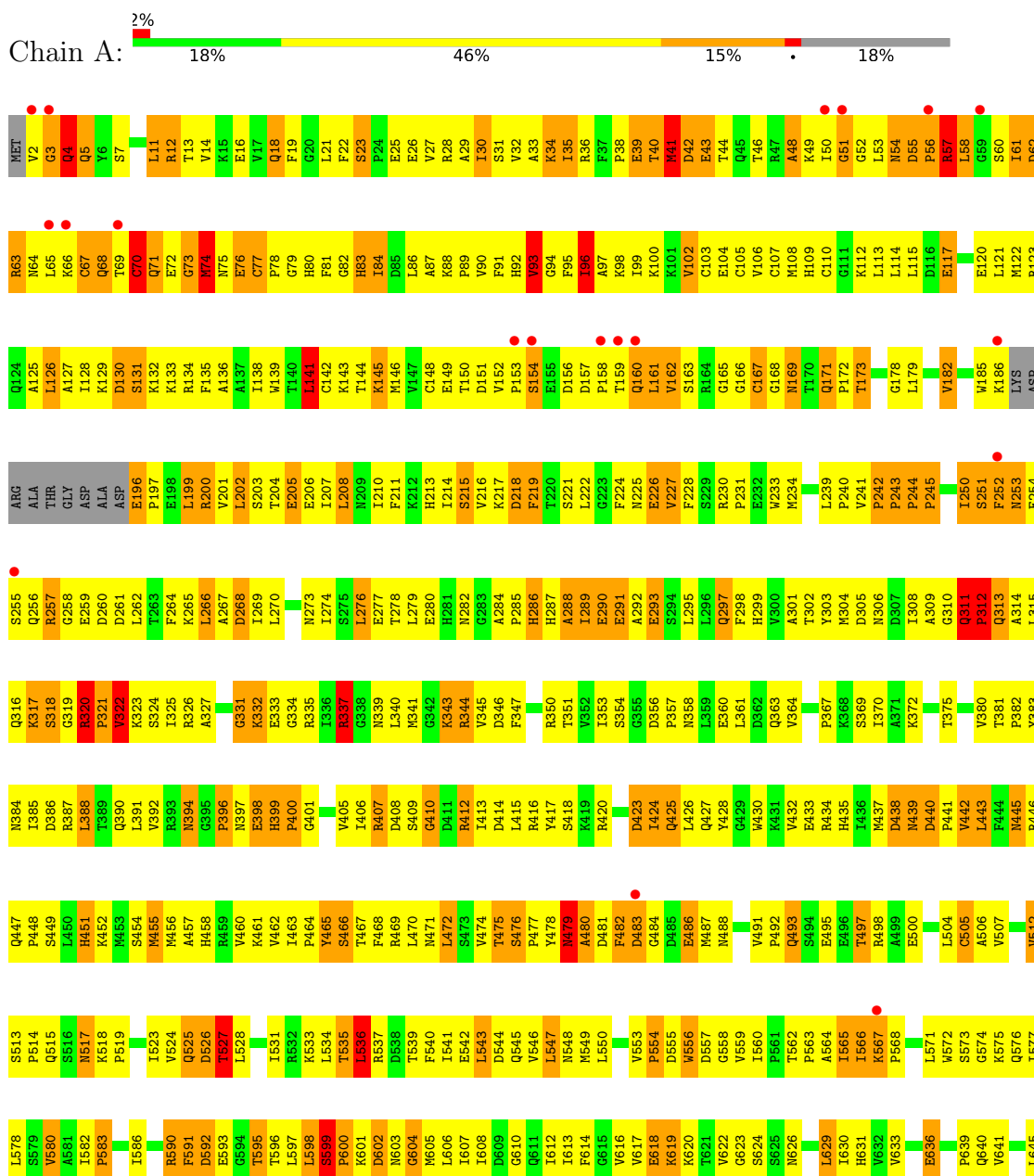
- Molecule 17 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	1	Total	Mg	0	0
			1	1		

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

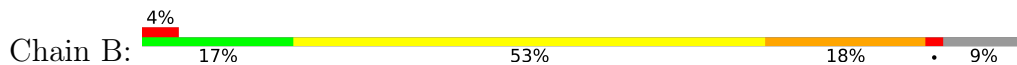
• Molecule 1: DNA-directed RNA polymerase II subunit RPB1



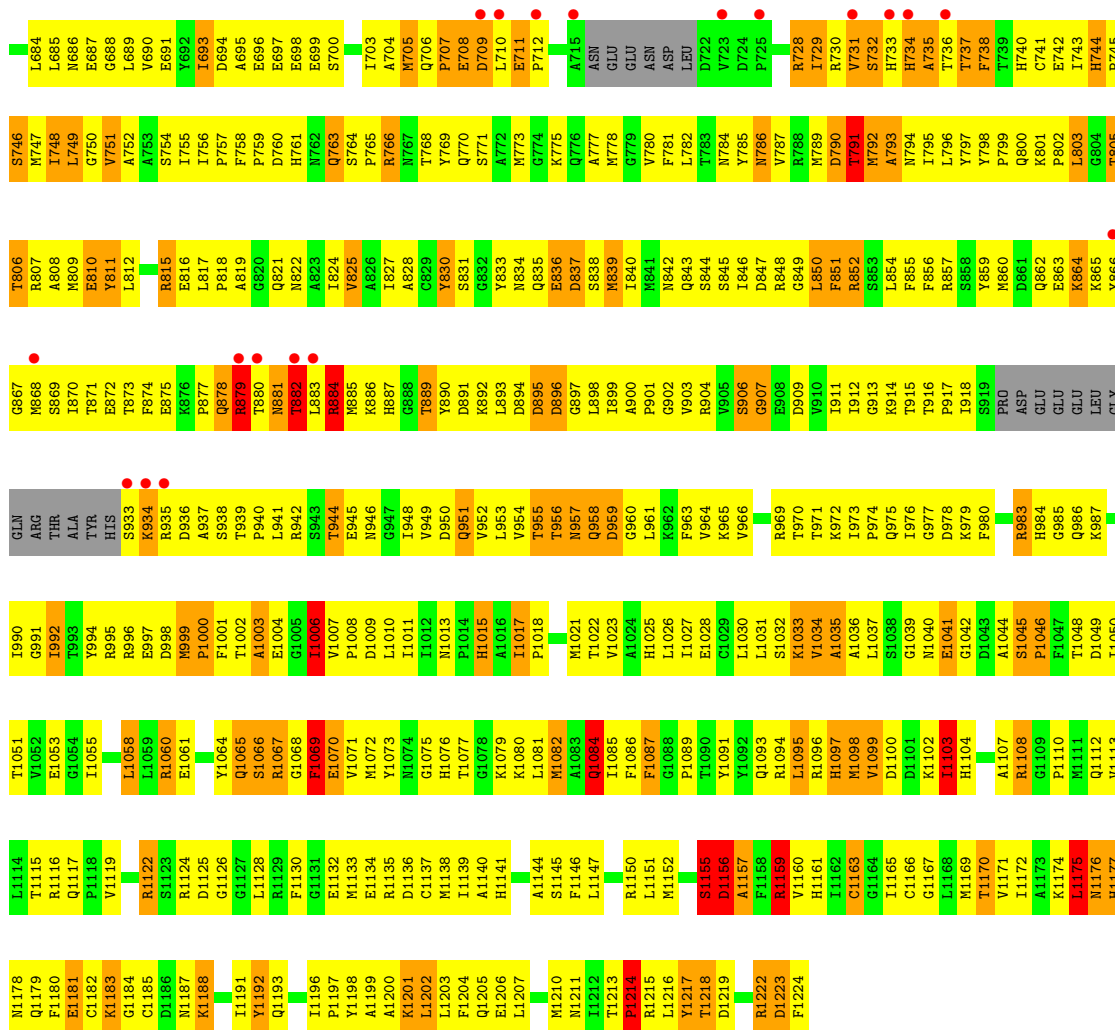


[illegible]

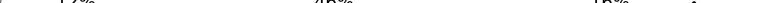
- Molecule 2: DNA-directed RNA polymerase II subunit RPB2

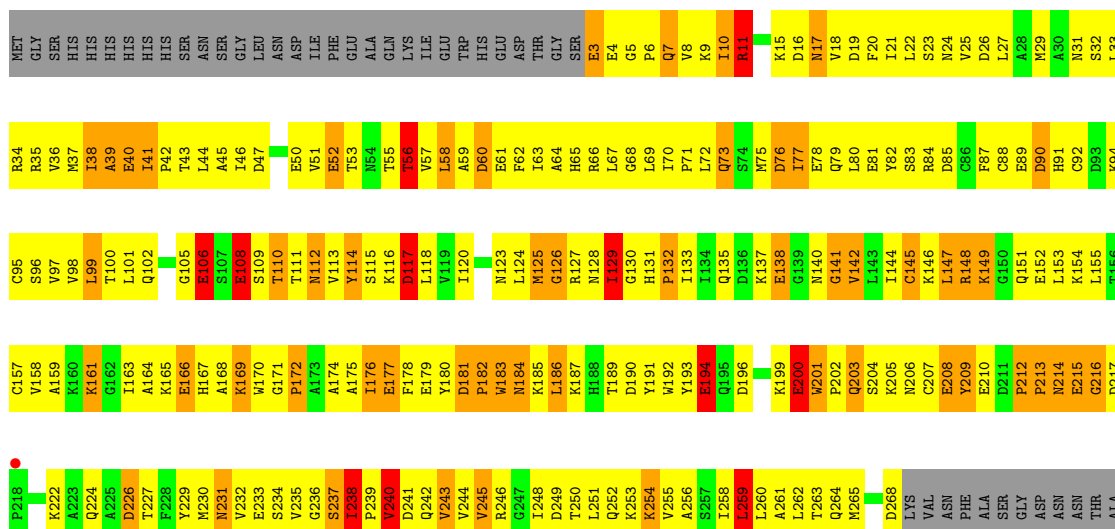


E621	E622	E623	E624	G625	G626	F627	F628	A629	G630	G631	G632	G633	G634	G635	P636	L637	F638	F639	G640	E641	E642	D643	D644	S645	L646	G647	H648	E649	E650	L651	G652	G653	G654	G655	G656	H657		L661	M662	A663		TLE	GLU	GLY	GLY	PHE	GLU	ASP	VAL	GLU	E678	G679	T680	E681								
R496	R497	R498	R499	P501	P502	F503	G503	R504	R505	G506	G507	L508	L509	A509	R510	P511	R512	G513	L514	H515	R516	G517	H518	G519	G520		E526	F527	P528	L529	G530	Q531	A532	R535	L536	R537	N538	L539	S540	L541	M542	S543	R544	R545	G546	G547	T549	D550	P551	P552	G553	L554	M555	T556	R557	D558	L559	P560				
V661	G662	M663	E664	P665	L666	E667	D668	V669	V670	P671	H672	Q673	S674	A675	R676	D677	A678	E679	L680	F681	G682	H683	G684	V685	H686	H687	G688	H689	E690	R691	P692	P693	A694	R695	L696	M697	E698		L661	M662	A663		TLE	GLU	GLY	GLY	PHE	GLU	ASP	VAL	GLU	E678	G679	T680	E681							
R434	T435	E437	GLU	ALA	HIS	ASP	PHE	ASN	MET	LYS	L446	L447	T448	R449	K450	A451	A452	A453	T454	S455	G456	L457	K458	A459	L461	A462	T463	G464	M465	A466	A467	A468	A469	K470	K471	A472	M473	S474	S475	R476	C477	G478	V479	S480	A481	V482	L483	M484	R485	A486	T487	L488	T489	L490		L495						
K374	A375	F376	F377	L378	G379	Y380	M381	L382	N383	R384	L385	L386	C387	C388	A389	L390	A391	D392	K393	D394	L395	D396	Q397	R398	D399	H400	F401	GLY	ALA	L406	D407	L408	A409	G410	P411	L412	L413	L414	Q415	L416	F417	K418	T419	L420	F421	K422	K423	L424	T425	K426	D427	L428	F429	R430	A431		L495					
L311	E312	M313	L314	K315	P316	C317	V318		V323	L324	Q325	D326	R327	C328	T329	A330	L331	D332	F333	L334	G335	R336	ARG	GLY	THR	ALA	GLY	ALA	GLY	L346	L347	R348	T349	Q350	P351	A352	K353	D354	L355	L356	Q357	K358	E359	F360	L361	P362	H363	L364	T365	Q366	L367	E368	G369	F370	E371	S372	R373					
S248	R249	F250	L251	S252	T253	L254	Q255	V256	K257	L258	Y259	G260	R261	C262	G263	S264	Y265	S266	A267	T268		T272	L273	F274	Y275	L276	K277	Q278	D279	E280	P281	T282	V283	L284	L285	F286	A287	L288	K289	G290	L291	L292	P293	D294	G295	E296	L297	E298	E299	L300		Y303	R304	N305	D307	K308	G309	R310				
T185	Y124	F125	G126	S127	L128	F129	L190	T191	L192	K193	E194	C195	ARG		M199	G200	G201	Y202	F203	L204	T205	N206	G207	S208	E209	K210	V211	L212		Q215	E216	R217	S218	L219	G220	N221	L222	V225	F226	M101	Y102	K164	L165	P166	S167	G168	G169	L170	H110	A111	M172	L173	R174	Y175	Q115		R118	L119	Y180	E245	K246	C247
D61	L62	E163	C64	E65	D66	S67	T68	L69	D131	V132	K133	K134	THR	THR		GLN	ALA	HIS	THR	VAL	GLY	ASP	GLY	ARG	GLY	LEU	SER	LEU	ILE	S91	X31	F92		Y96	Y97	Y98	K99	P100	M101	Y102	M103	E104	S105	D106	G107	V108	L109	H110	A111	L112	L113	P114	Q115			L118	L119	R180	E245	K246	C247	



- Molecule 3: DNA-directed RNA polymerase II subunit RPB3

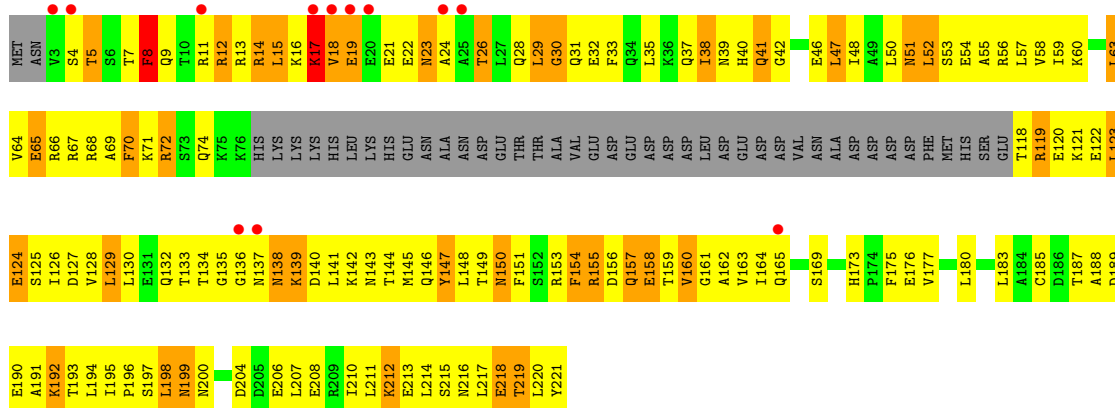
Chain C:  12% 46% 16% 1% 23%



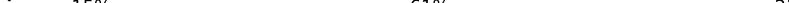
SER	ASN	ASN	MET	LEU	GLY	SER	ASN	GLU	ASP	VAL	MET	MET	THR	GLY	ALA	GLU	GLN	ASP	PRO	TYR	SER	SER	ASN	ALA	SER	SER	GLN	MET	GLY	ASN	THR	GLY	SER	GLY	GLY	TYR	ASP	ASN	ALA	TRP
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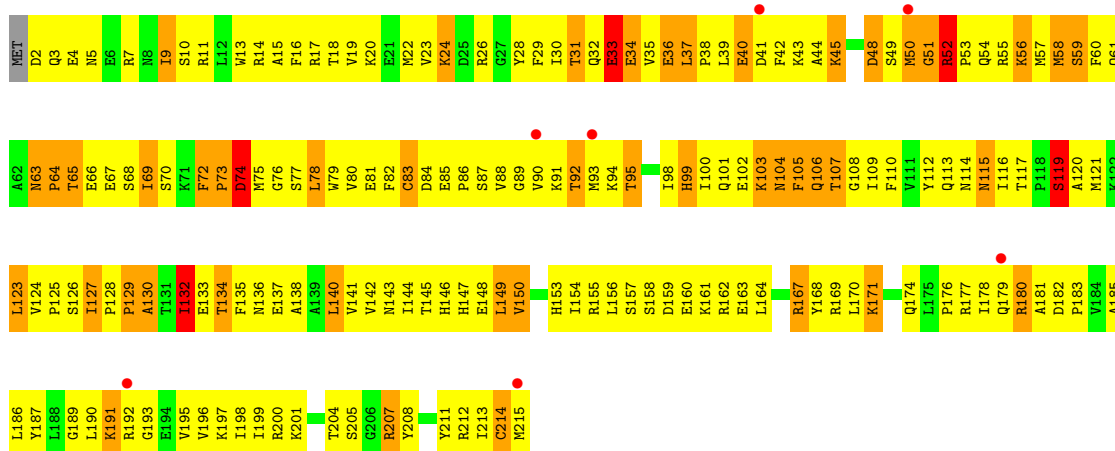
- Molecule 4: DNA-directed RNA polymerase II subunit RPB4

Chain D: 5% 17% 46% 17% 19%

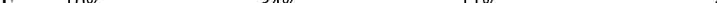


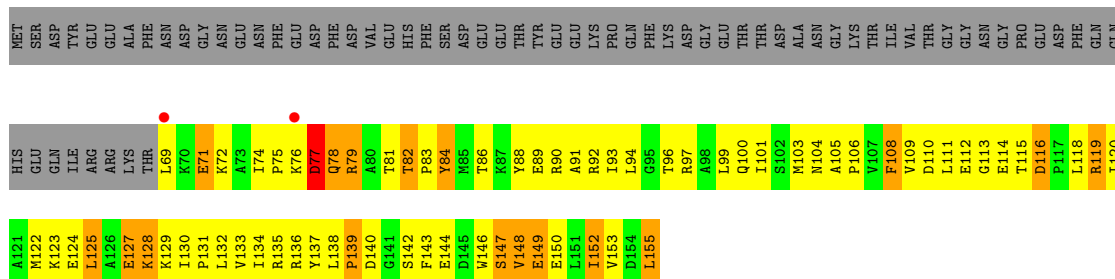
- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

Chain E:  3% 15% 61% 21%

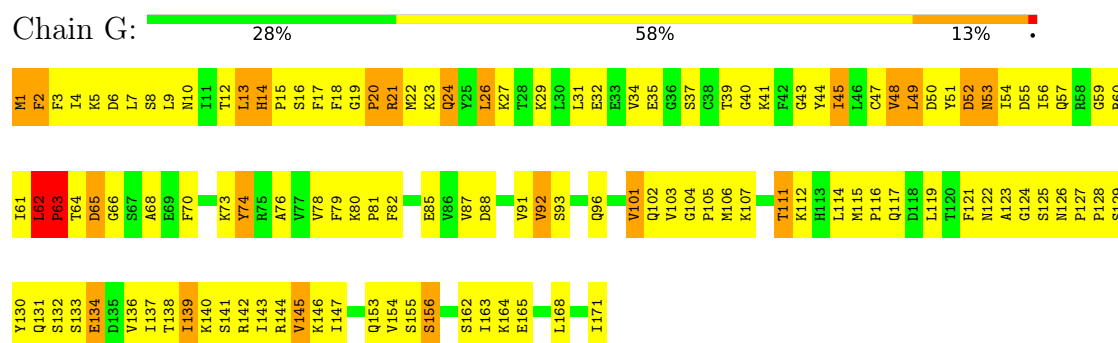


- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2

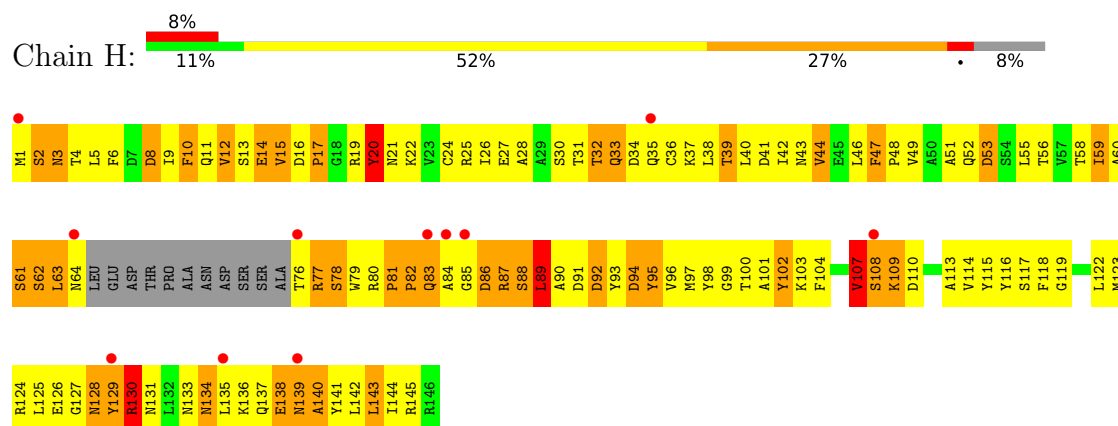
Chain F:  10% 34% 11% 44%



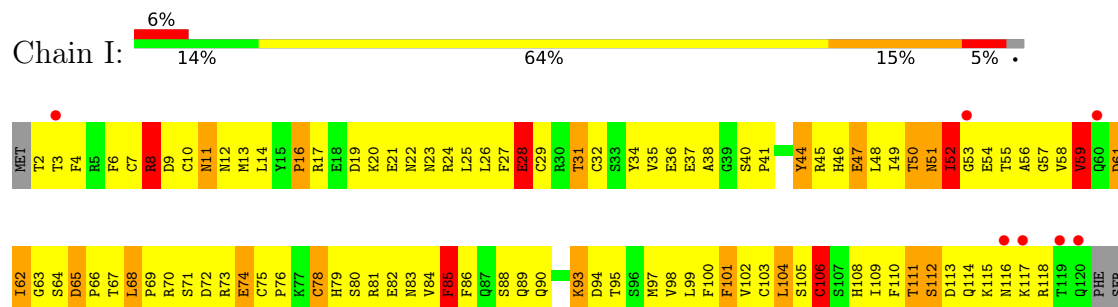
- Molecule 7: DNA-directed RNA polymerase II subunit RPB7



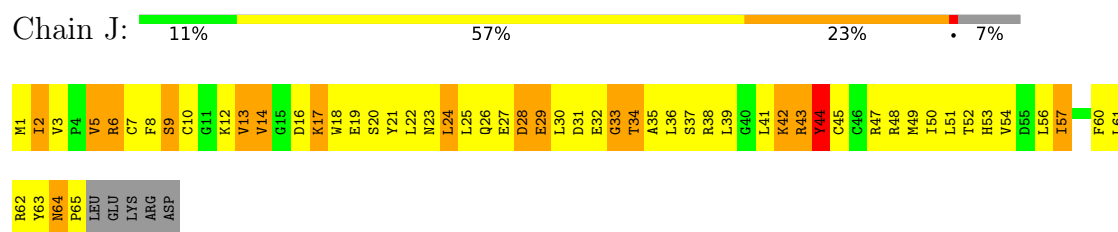
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3



- Molecule 9: DNA-directed RNA polymerase II subunit RPB9



- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5



- Molecule 11: DNA-directed RNA polymerase II subunit RPB11





- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4



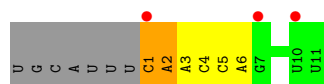
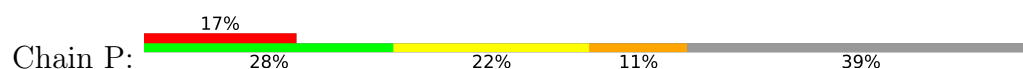
- Molecule 13: 5'-D(*AP*CP*TP*AP*CP*TP*TP*GP*AP*GP*CP*T)-3'



- Molecule 14: 5'-D(*AP*GP*CP*TP*C*AP*AP*GP*TP*AP*GP*TP*TP*AP*AP*GP*CP*C
P*(BRU)P*GP*GP*TP*CP*AP*TP*T)-3'



- Molecule 15: 5'-R(*UP*GP*CP*AP*UP*UP*U*CP*AP*AP*CP*CP*AP*GP*GP*CP*UP*U
) -3'



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	221.62Å 393.72Å 282.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.65 50.00 – 3.65	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-3.65) 99.9 (50.00-3.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.64 (at 3.67Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.212 , 0.250 0.214 , 0.255	Depositor DCC
R_{free} test set	2686 reflections (1.97%)	wwPDB-VP
Wilson B-factor (Å ²)	86.1	Xtriage
Anisotropy	0.065	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 100.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.015 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.021 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	31918	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.00% 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 ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: BRU, ZN, MG

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	0.69	2/11351 (0.0%)	1.19	117/15350 (0.8%)
2	B	0.64	0/9019	1.12	63/12160 (0.5%)
3	C	0.69	0/2133	1.20	32/2891 (1.1%)
4	D	0.59	0/1444	1.19	13/1935 (0.7%)
5	E	0.60	0/1788	1.19	24/2406 (1.0%)
6	F	0.80	0/717	1.34	10/967 (1.0%)
7	G	0.67	0/1368	1.22	11/1844 (0.6%)
8	H	0.57	0/1099	1.12	9/1488 (0.6%)
9	I	0.59	0/989	1.18	11/1331 (0.8%)
10	J	0.64	0/541	1.13	3/727 (0.4%)
11	K	0.60	0/937	1.08	3/1265 (0.2%)
12	L	0.72	0/365	1.23	4/485 (0.8%)
13	N	0.54	0/152	0.98	0/232
14	T	0.49	0/391	0.82	0/600
15	P	0.53	0/237	0.90	0/368
All	All	0.65	2/32531 (0.0%)	1.16	300/44049 (0.7%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	2
14	T	0	3
All	All	0	5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	55	ASP	CA-C	-5.32	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1424	VAL	CA-CB	-5.27	1.48	1.54

All (300) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	56	PRO	N-CA-C	-17.16	94.50	114.92
4	D	26	THR	N-CA-C	-14.68	92.33	112.30
6	F	71	GLU	N-CA-C	-12.72	97.14	113.17
2	B	1185	CYS	N-CA-C	-12.22	98.55	114.31
5	E	5	ASN	N-CA-C	-11.78	98.89	113.97
7	G	62	LEU	CA-C-N	-11.66	105.26	119.84
7	G	62	LEU	C-N-CA	-11.66	105.26	119.84
1	A	3	GLY	N-CA-C	-10.89	100.16	115.30
5	E	171	LYS	N-CA-C	-10.80	96.59	110.53
1	A	1243	VAL	N-CA-C	10.31	123.71	108.45
2	B	427	ASP	N-CA-C	-10.19	99.63	113.18
2	B	1184	GLY	N-CA-C	-9.93	102.96	113.58
1	A	629	LEU	N-CA-C	-9.67	100.59	111.71
3	C	39	ALA	N-CA-C	9.31	127.06	114.12
9	I	61	ASP	N-CA-C	-9.27	101.23	114.12
7	G	40	GLY	N-CA-C	-9.26	103.17	114.66
1	A	40	THR	N-CA-C	-9.22	100.79	111.03
1	A	289	ILE	N-CA-C	-9.06	102.03	110.82
4	D	41	GLN	N-CA-C	-8.85	101.80	112.59
2	B	606	LYS	N-CA-C	-8.71	102.57	113.55
9	I	112	SER	N-CA-C	-8.71	100.04	111.71
2	B	473	MET	N-CA-C	-8.62	102.47	113.16
1	A	117	GLU	N-CA-C	-8.54	102.77	113.01
12	L	68	GLU	N-CA-C	-8.41	98.64	110.50
6	F	82	THR	CA-C-N	8.41	128.10	119.19
6	F	82	THR	C-N-CA	8.41	128.10	119.19
2	B	363	HIS	N-CA-C	-8.38	96.72	109.79
1	A	513	SER	CA-C-N	8.35	128.08	119.64
1	A	513	SER	C-N-CA	8.35	128.08	119.64
2	B	934	LYS	N-CA-C	8.35	121.49	109.71
1	A	291	GLU	N-CA-C	-8.34	103.11	113.20
1	A	710	LEU	N-CA-C	-8.33	101.23	111.40
1	A	1386	ARG	N-CA-C	-8.32	102.39	112.54
4	D	188	ALA	N-CA-C	-8.32	102.23	112.38
2	B	628	THR	N-CA-C	-8.27	103.32	113.41
4	D	31	GLN	N-CA-C	-8.25	102.37	111.36
6	F	148	VAL	N-CA-C	-8.16	101.32	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	681	TRP	N-CA-C	-8.12	100.76	111.24
2	B	1201	LYS	N-CA-C	-8.10	102.45	111.28
3	C	108	GLU	N-CA-C	-8.08	103.43	113.20
1	A	1244	ARG	N-CA-C	7.93	127.33	109.81
1	A	602	ASP	N-CA-C	-7.85	100.68	111.28
2	B	526	GLU	N-CA-C	7.80	121.65	108.23
1	A	983	ILE	N-CA-C	-7.79	102.86	112.76
2	B	851	PHE	N-CA-C	7.78	122.36	112.86
4	D	72	ARG	N-CA-C	-7.73	102.86	111.82
1	A	1207	LEU	N-CA-C	7.65	121.59	109.50
2	B	296	GLU	N-CA-C	-7.62	102.31	111.69
1	A	1311	VAL	N-CA-C	7.56	118.70	108.11
5	E	103	LYS	N-CA-C	-7.55	104.20	113.19
2	B	1177	HIS	N-CA-C	-7.54	102.04	112.30
2	B	680	THR	N-CA-C	7.52	119.99	109.31
1	A	964	ILE	N-CA-C	-7.49	105.83	111.90
1	A	311	GLN	N-CA-C	7.48	126.34	109.81
3	C	238	ILE	CA-C-N	7.42	127.69	119.90
3	C	238	ILE	C-N-CA	7.42	127.69	119.90
10	J	5	VAL	N-CA-C	-7.37	99.18	109.21
1	A	861	GLY	N-CA-C	-7.34	105.70	115.40
8	H	34	ASP	N-CA-C	-7.32	104.30	112.57
1	A	1421	CYS	N-CA-C	-7.30	102.13	111.92
1	A	71	GLN	CB-CA-C	-7.29	108.16	116.54
4	D	38	ILE	N-CA-C	7.29	118.98	109.58
1	A	293	GLU	N-CA-C	-7.28	103.43	111.36
1	A	1104	ILE	N-CA-C	7.26	117.78	110.23
2	B	510	LYS	N-CA-C	-7.24	104.21	113.77
1	A	598	LEU	N-CA-C	-7.24	101.34	112.99
2	B	1015	HIS	N-CA-C	7.19	119.98	111.71
4	D	8	PHE	N-CA-C	7.17	126.08	110.80
6	F	127	GLU	N-CA-C	-7.08	101.88	111.87
12	L	58	LYS	N-CA-C	7.08	122.02	112.88
1	A	998	LEU	N-CA-C	7.04	120.51	109.96
10	J	9	SER	N-CA-C	6.99	118.79	111.03
1	A	553	VAL	CA-C-N	6.99	128.58	119.84
1	A	553	VAL	C-N-CA	6.99	128.58	119.84
1	A	636	GLU	N-CA-C	6.96	120.26	111.69
1	A	1241	ARG	N-CA-C	6.93	121.41	112.12
1	A	266	LEU	N-CA-C	-6.91	103.36	111.03
1	A	23	SER	N-CA-C	-6.91	101.36	110.07
9	I	85	PHE	N-CA-C	6.91	119.88	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	564	ALA	N-CA-C	-6.90	103.84	111.36
9	I	65	ASP	CA-C-N	6.84	126.81	119.28
9	I	65	ASP	C-N-CA	6.84	126.81	119.28
1	A	539	THR	N-CA-C	6.80	119.21	108.67
1	A	320	ARG	CA-C-N	6.78	128.32	119.84
1	A	320	ARG	C-N-CA	6.78	128.32	119.84
1	A	398	GLU	N-CA-C	-6.78	102.07	110.41
1	A	4	GLN	N-CA-C	6.75	125.18	110.80
1	A	805	LEU	N-CA-C	-6.73	103.87	111.14
12	L	62	LYS	N-CA-C	-6.68	103.81	112.23
5	E	63	ASN	N-CA-C	6.68	120.10	108.82
7	G	65	ASP	N-CA-C	-6.64	100.14	110.17
2	B	366	GLN	N-CA-C	-6.64	104.81	113.17
2	B	896	ASP	N-CA-C	-6.57	105.12	113.01
9	I	31	THR	N-CA-C	-6.56	105.90	114.04
5	E	150	VAL	CA-C-N	6.55	126.73	120.31
5	E	150	VAL	C-N-CA	6.55	126.73	120.31
8	H	16	ASP	N-CA-C	6.54	119.86	109.40
1	A	542	GLU	N-CA-C	6.53	120.46	109.76
1	A	829	VAL	N-CA-C	-6.51	105.36	111.48
2	B	732	SER	N-CA-C	6.49	117.14	108.38
2	B	645	SER	N-CA-C	-6.47	105.45	113.15
5	E	33	GLU	N-CA-C	-6.46	104.32	111.36
2	B	550	ASP	CA-C-N	6.43	125.86	118.85
2	B	550	ASP	C-N-CA	6.43	125.86	118.85
6	F	108	PHE	N-CA-C	6.41	120.11	112.93
2	B	172	ILE	N-CA-C	6.39	117.50	108.36
8	H	130	ARG	N-CA-C	-6.37	104.06	112.72
1	A	30	ILE	CB-CA-C	-6.35	103.75	111.88
3	C	96	SER	N-CA-C	6.34	118.49	108.79
1	A	513	SER	N-CA-C	6.33	118.04	110.07
4	D	12	ARG	N-CA-C	6.32	119.15	110.24
7	G	14	HIS	CA-C-N	-6.31	112.50	119.19
7	G	14	HIS	C-N-CA	-6.31	112.50	119.19
6	F	74	ILE	CA-C-N	6.31	126.25	119.76
6	F	74	ILE	C-N-CA	6.31	126.25	119.76
2	B	1066	SER	N-CA-C	6.30	119.13	111.82
2	B	102	VAL	N-CA-C	6.30	117.83	107.24
1	A	966	ASN	N-CA-C	-6.30	103.55	111.11
2	B	99	LYS	N-CA-C	-6.29	101.41	110.08
2	B	1045	SER	CA-C-N	6.22	127.61	119.84
2	B	1045	SER	C-N-CA	6.22	127.61	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1076	ALA	N-CA-C	-6.21	105.53	113.23
2	B	516	ASN	N-CA-C	-6.18	103.86	111.40
2	B	471	LYS	N-CA-C	-6.15	106.14	113.21
2	B	66	ASP	N-CA-C	-6.15	104.39	113.61
1	A	102	VAL	N-CA-C	-6.13	104.77	110.53
2	B	882	THR	N-CA-C	6.13	123.86	110.80
2	B	1009	ASP	N-CA-C	-6.13	105.93	113.41
4	D	51	ASN	N-CA-C	-6.12	100.31	110.17
1	A	227	VAL	N-CA-C	6.12	116.86	111.90
1	A	1422	ARG	N-CA-C	-6.11	105.87	113.38
1	A	218	ASP	N-CA-C	-6.11	104.31	110.97
2	B	1033	LYS	N-CA-C	-6.11	104.62	111.28
3	C	135	GLN	N-CA-C	-6.08	104.50	113.61
2	B	195	CYS	CA-C-N	6.07	126.24	119.32
2	B	195	CYS	C-N-CA	6.07	126.24	119.32
1	A	243	PRO	CA-C-N	6.06	126.62	120.38
1	A	243	PRO	C-N-CA	6.06	126.62	120.38
1	A	1155	ASP	CA-C-N	6.06	125.68	119.56
1	A	1155	ASP	C-N-CA	6.06	125.68	119.56
1	A	996	ASN	N-CA-C	6.05	121.41	113.30
1	A	1445	ILE	CB-CA-C	-6.05	104.00	111.08
1	A	171	GLN	CA-C-N	6.04	126.35	119.83
1	A	171	GLN	C-N-CA	6.04	126.35	119.83
5	E	180	ARG	N-CA-C	-6.03	105.18	112.54
2	B	616	ILE	N-CA-C	6.03	116.81	108.12
5	E	63	ASN	CA-C-N	6.00	127.34	119.84
5	E	63	ASN	C-N-CA	6.00	127.34	119.84
3	C	212	PRO	CA-C-N	5.98	127.32	119.84
3	C	212	PRO	C-N-CA	5.98	127.32	119.84
4	D	18	VAL	N-CA-C	5.97	116.52	108.17
1	A	81	PHE	N-CA-C	5.96	118.65	110.24
1	A	566	ILE	N-CA-C	-5.96	106.43	111.56
7	G	145	VAL	N-CA-C	5.96	117.94	108.89
1	A	1319	VAL	N-CA-C	5.96	115.51	108.96
1	A	535	THR	N-CA-C	5.95	120.61	112.04
3	C	222	LYS	N-CA-C	-5.95	105.98	113.18
3	C	204	SER	N-CA-C	5.94	119.31	110.52
1	A	582	ILE	CA-C-N	5.94	127.26	119.84
1	A	582	ILE	C-N-CA	5.94	127.26	119.84
2	B	1217	TYR	N-CA-C	5.94	118.63	109.07
1	A	1404	GLU	N-CA-C	5.90	119.54	112.93
1	A	466	SER	N-CA-C	5.90	123.37	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	292	ILE	N-CA-C	5.89	121.59	108.88
1	A	227	VAL	CB-CA-C	-5.88	105.66	111.30
3	C	4	GLU	N-CA-C	5.88	120.00	112.12
2	B	1159	ARG	N-CA-C	5.88	118.31	108.02
1	A	388	LEU	N-CA-C	5.83	118.41	111.71
4	D	212	LYS	N-CA-C	-5.83	104.84	111.07
1	A	682	THR	N-CA-C	-5.80	105.09	111.82
1	A	1169	ILE	N-CA-C	5.80	121.40	109.34
1	A	242	PRO	CA-C-N	5.79	126.34	120.38
1	A	242	PRO	C-N-CA	5.79	126.34	120.38
5	E	9	ILE	N-CA-C	-5.79	106.17	111.67
7	G	52	ASP	N-CA-C	5.78	119.42	112.38
1	A	1102	LYS	N-CA-C	-5.77	104.90	111.07
1	A	1339	LEU	N-CA-C	5.76	120.31	113.28
2	B	434	ARG	N-CA-C	-5.76	107.25	114.56
2	B	112	LEU	N-CA-C	5.75	117.71	110.24
3	C	52	GLU	N-CA-C	-5.73	106.83	113.88
1	A	646	PHE	N-CA-C	-5.73	104.03	111.02
5	E	58	MET	N-CA-C	5.72	118.46	111.82
9	I	28	GLU	N-CA-C	5.71	116.82	108.14
1	A	860	LEU	N-CA-C	-5.69	105.68	113.30
1	A	143	LYS	N-CA-C	-5.69	105.06	112.23
1	A	1190	PRO	N-CA-C	-5.69	106.28	114.18
2	B	803	LEU	N-CA-C	-5.68	104.73	111.03
5	E	132	ILE	N-CA-C	5.67	116.05	108.11
3	C	106	GLU	N-CA-C	-5.67	105.39	112.93
1	A	83	HIS	N-CA-C	5.66	115.76	108.34
1	A	847	ASP	N-CA-C	5.65	122.83	110.80
1	A	1322	ILE	CB-CA-C	-5.64	104.02	111.70
3	C	201	TRP	CA-C-N	5.62	125.64	119.90
3	C	201	TRP	C-N-CA	5.62	125.64	119.90
2	B	1070	GLU	N-CA-C	-5.62	100.39	108.60
1	A	990	VAL	N-CA-C	-5.62	104.89	110.62
8	H	109	LYS	CB-CA-C	-5.62	110.11	116.63
2	B	1170	THR	N-CA-C	5.60	117.83	111.11
12	L	44	ASP	N-CA-C	-5.59	105.15	112.41
1	A	482	PHE	N-CA-C	5.58	119.40	112.59
2	B	472	ALA	N-CA-C	5.58	118.68	107.41
1	A	1403	GLU	N-CA-C	5.58	122.68	110.80
1	A	337	ARG	N-CA-C	5.56	118.06	111.33
9	I	68	LEU	CA-C-N	5.56	126.03	120.14
9	I	68	LEU	C-N-CA	5.56	126.03	120.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	55	ASP	N-CA-CB	5.55	120.25	110.37
8	H	88	SER	N-CA-C	-5.54	103.59	110.41
4	D	70	PHE	N-CA-C	-5.54	105.72	113.37
9	I	52	ILE	N-CA-C	5.54	116.34	107.98
7	G	153	GLN	N-CA-C	5.52	117.09	107.49
3	C	259	LEU	N-CA-C	-5.49	105.21	111.14
2	B	361	LEU	CA-C-N	5.48	126.69	119.84
2	B	361	LEU	C-N-CA	5.48	126.69	119.84
1	A	259	GLU	N-CA-C	5.48	117.37	110.24
1	A	916	GLY	N-CA-C	5.48	120.71	113.37
1	A	590	ARG	N-CA-C	5.47	117.51	108.48
2	B	1013	ASN	N-CA-C	5.47	117.52	109.42
2	B	650	GLU	N-CA-C	5.47	117.57	108.99
1	A	467	THR	N-CA-C	5.44	118.42	109.72
2	B	479	VAL	N-CA-C	-5.43	104.07	110.21
1	A	1005	GLU	N-CA-C	5.42	117.27	111.36
5	E	39	LEU	N-CA-C	5.41	116.87	110.97
3	C	200	GLU	N-CA-C	5.41	117.25	111.36
3	C	171	GLY	CA-C-N	-5.40	113.09	119.84
3	C	171	GLY	C-N-CA	-5.40	113.09	119.84
1	A	251	SER	N-CA-C	5.40	118.05	110.23
1	A	505	CYS	N-CA-C	5.39	117.78	110.88
2	B	208	SER	N-CA-C	5.39	118.71	110.20
1	A	288	ALA	N-CA-C	-5.38	99.33	110.80
2	B	763	GLN	N-CA-C	-5.38	102.08	110.10
1	A	927	VAL	N-CA-C	-5.38	105.84	110.74
1	A	440	ASP	N-CA-C	-5.36	101.49	109.42
10	J	44	TYR	N-CA-C	5.36	122.21	110.80
2	B	836	GLU	N-CA-C	5.35	119.21	111.56
2	B	791	THR	N-CA-C	-5.34	102.14	110.10
2	B	395	GLN	N-CA-C	-5.33	103.49	110.53
5	E	56	LYS	N-CA-C	-5.33	105.87	112.38
6	F	152	ILE	CB-CA-C	-5.33	105.73	111.59
1	A	580	VAL	N-CA-C	-5.30	106.11	113.00
1	A	480	ALA	N-CA-C	5.28	118.15	109.76
1	A	950	GLY	N-CA-C	-5.28	107.25	114.64
3	C	194	GLU	N-CA-C	-5.28	104.90	112.13
2	B	609	ILE	N-CA-C	-5.27	100.89	108.48
1	A	980	ASP	N-CA-C	-5.27	104.02	110.61
1	A	769	SER	N-CA-C	5.27	117.08	109.07
3	C	38	ILE	N-CA-C	5.26	115.88	110.36
9	I	104	LEU	N-CA-C	-5.23	105.64	112.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	343	LYS	N-CA-C	5.22	116.22	108.60
1	A	217	LYS	N-CA-C	-5.22	106.17	112.54
3	C	40	GLU	CA-C-N	-5.20	118.84	122.59
3	C	40	GLU	C-N-CA	-5.20	118.84	122.59
1	A	809	THR	N-CA-C	-5.19	103.60	110.40
1	A	1138	ILE	CB-CA-C	-5.19	106.32	111.30
4	D	176	GLU	N-CA-C	-5.18	105.54	111.14
5	E	200	ARG	N-CA-C	5.18	117.55	109.52
1	A	472	LEU	N-CA-C	5.18	119.68	112.90
1	A	56	PRO	CA-C-N	5.17	131.41	121.54
1	A	56	PRO	C-N-CA	5.17	131.41	121.54
3	C	41	ILE	CA-C-N	5.17	125.08	119.76
3	C	41	ILE	C-N-CA	5.17	125.08	119.76
1	A	698	GLN	N-CA-C	-5.16	106.83	113.23
2	B	665	GLU	N-CA-C	-5.16	105.54	111.07
5	E	52	ARG	CA-C-N	5.16	125.08	119.76
5	E	52	ARG	C-N-CA	5.16	125.08	119.76
3	C	181	ASP	CA-C-N	5.15	126.28	119.84
3	C	181	ASP	C-N-CA	5.15	126.28	119.84
1	A	12	ARG	N-CA-C	5.15	115.84	108.74
2	B	1084	GLN	N-CA-C	-5.15	100.65	109.24
3	C	254	LYS	N-CA-C	-5.13	105.38	110.97
1	A	1368	MET	N-CA-C	-5.13	105.69	111.28
11	K	87	LEU	N-CA-C	-5.12	105.38	110.97
6	F	77	ASP	N-CA-C	-5.12	101.36	109.76
3	C	114	TYR	N-CA-C	5.12	117.64	109.81
7	G	104	GLY	CA-C-N	5.11	124.77	119.56
7	G	104	GLY	C-N-CA	5.11	124.77	119.56
1	A	1101	LEU	N-CA-C	-5.11	105.71	111.28
11	K	68	PHE	N-CA-C	5.10	117.29	109.07
3	C	201	TRP	N-CA-C	5.09	117.59	108.47
8	H	20	TYR	N-CA-C	5.09	118.42	108.18
1	A	970	THR	N-CA-C	-5.09	105.92	111.82
8	H	87	ARG	N-CA-C	-5.09	101.72	108.74
1	A	833	GLU	N-CA-C	-5.08	105.82	111.36
8	H	16	ASP	CA-C-N	5.08	126.19	119.84
8	H	16	ASP	C-N-CA	5.08	126.19	119.84
1	A	1358	SER	N-CA-C	-5.08	105.75	111.28
5	E	119	SER	N-CA-C	-5.07	106.78	113.12
2	B	233	PRO	N-CA-C	-5.07	107.53	113.86
11	K	2	ASN	N-CA-C	-5.06	106.95	112.72
2	B	852	ARG	N-CA-C	-5.05	104.02	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	183	TRP	N-CA-C	-5.05	98.36	107.75
5	E	105	PHE	CB-CA-C	-5.04	109.81	117.07
1	A	1405	THR	N-CA-C	5.03	121.52	110.80
1	A	827	THR	N-CA-C	-5.03	105.80	111.28
5	E	149	LEU	CA-C-N	-5.03	117.79	123.02
5	E	149	LEU	C-N-CA	-5.03	117.79	123.02
3	C	112	ASN	N-CA-C	5.01	117.13	109.07
1	A	74	MET	N-CA-C	5.01	121.47	110.80
2	B	760	ASP	N-CA-C	-5.00	105.91	112.72
5	E	105	PHE	CA-C-O	5.00	120.84	117.94
5	E	214	CYS	N-CA-C	5.00	117.97	109.76

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	1192	TYR	Sidechain
2	B	431	TYR	Sidechain
14	T	14	DA	Sidechain
14	T	16	DT	Sidechain
14	T	21	DC	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	11151	0	11226	1688	0
2	B	8847	0	8884	1444	0
3	C	2095	0	2051	369	0
4	D	1434	0	1460	227	0
5	E	1752	0	1776	283	0
6	F	705	0	731	118	0
7	G	1340	0	1357	188	0
8	H	1081	0	1051	213	0
9	I	971	0	929	158	0
10	J	532	0	542	120	0
11	K	919	0	929	127	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	L	363	0	388	98	0
13	N	137	0	82	10	0
14	T	369	0	202	27	0
15	P	213	0	110	19	0
16	A	2	0	0	0	0
16	B	1	0	0	0	0
16	C	1	0	0	0	0
16	I	2	0	0	0	0
16	J	1	0	0	0	0
16	L	1	0	0	0	0
17	A	1	0	0	0	0
All	All	31918	0	31718	4698	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 74.

All (4698) 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:B:559:SER:HA	2:B:563:MET:HB3	1.20	1.16
2:B:1072:MET:HE3	2:B:1085:ILE:HB	1.28	1.13
12:L:55:ILE:HG12	12:L:56:LEU:H	0.97	1.12
12:L:55:ILE:CG1	12:L:56:LEU:H	1.59	1.12
3:C:43:THR:HG22	3:C:44:LEU:H	1.07	1.12
1:A:53:LEU:HD23	1:A:54:ASN:N	1.65	1.10
1:A:899:VAL:HB	1:A:929:LEU:HD11	1.12	1.10
10:J:1:MET:N	10:J:57:ILE:H	1.50	1.09
5:E:56:LYS:HE2	5:E:84:ASP:HB2	1.33	1.07
2:B:577:ALA:HB1	2:B:589:VAL:HG11	1.35	1.07
8:H:4:THR:HA	8:H:60:ALA:HB2	1.23	1.07
2:B:278:GLN:HG2	2:B:279:ASP:H	1.17	1.06
5:E:78:LEU:HD21	5:E:80:VAL:HG23	1.31	1.06
5:E:94:LYS:HE2	5:E:98:ILE:HD11	1.32	1.06
3:C:66:ARG:NH1	10:J:2:ILE:HG21	1.70	1.06
1:A:901:LEU:N	1:A:926:GLN:HE21	1.53	1.05
1:A:1208:THR:HB	1:A:1211:GLN:HG3	1.30	1.05
2:B:597:MET:HA	2:B:597:MET:HE3	1.38	1.04
1:A:399:HIS:HB3	1:A:400:PRO:HD3	1.39	1.04
1:A:541:ILE:HD13	1:A:549:MET:HE1	1.39	1.04
2:B:483:LEU:HD11	2:B:491:THR:HG23	1.33	1.04
2:B:642:ASP:HA	2:B:649:LYS:HA	1.39	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:62:LEU:HD13	7:G:63:PRO:HD2	1.40	1.04
8:H:100:THR:HG23	8:H:138:GLU:HA	1.39	1.04
1:A:1364:ASN:OD1	1:A:1366:ARG:HG2	1.58	1.03
2:B:615:MET:HB3	2:B:626:ILE:HG12	1.40	1.03
10:J:16:ASP:OD1	10:J:17:LYS:HD2	1.57	1.02
1:A:1444:MET:HG2	7:G:60:ARG:HA	1.41	1.01
2:B:1112:GLN:HA	15:P:1:C:H5'	1.39	1.01
7:G:26:LEU:HD12	7:G:56:ILE:HD11	1.38	1.01
1:A:244:PRO:HB2	1:A:245:PRO:HD3	1.40	1.01
5:E:40:GLU:HA	5:E:43:LYS:HE2	1.43	1.01
8:H:17:PRO:HB3	8:H:24:CYS:SG	2.00	1.00
1:A:913:LEU:HD12	1:A:914:GLU:H	1.23	1.00
8:H:130:ARG:HH11	8:H:130:ARG:HB2	1.24	1.00
1:A:768:GLN:HG2	1:A:816:HIS:HA	1.43	1.00
1:A:779:PHE:CE1	1:A:785:PRO:HD3	1.96	1.00
3:C:73:GLN:HE22	3:C:75:MET:HB2	1.27	0.99
2:B:806:THR:HG22	2:B:809:MET:HG2	1.41	0.99
5:E:22:MET:HE3	5:E:26:ARG:HE	1.25	0.99
1:A:14:VAL:H	1:A:1432:GLN:HE22	1.01	0.99
6:F:77:ASP:O	6:F:78:GLN:HB2	1.58	0.99
2:B:652:LYS:HB3	2:B:689:LEU:HD23	1.43	0.99
1:A:901:LEU:H	1:A:926:GLN:NE2	1.59	0.99
1:A:40:THR:HG22	1:A:41:MET:HG3	1.44	0.98
7:G:15:PRO:HA	7:G:18:PHE:CD1	1.96	0.98
2:B:261:ARG:HH11	2:B:261:ARG:HB3	1.27	0.98
9:I:93:LYS:H	9:I:93:LYS:HD3	1.25	0.98
1:A:337:ARG:HE	1:A:839:ARG:NH2	1.62	0.98
1:A:225:ASN:HD22	1:A:228:PHE:H	1.01	0.97
5:E:30:ILE:HG23	5:E:34:GLU:HG2	1.44	0.97
1:A:145:LYS:HA	1:A:145:LYS:HE3	1.46	0.97
1:A:858:ASN:ND2	1:A:860:LEU:H	1.63	0.97
2:B:999:MET:HA	2:B:999:MET:HE3	1.46	0.97
10:J:64:ASN:HB3	10:J:65:PRO:CD	1.94	0.97
1:A:1063:MET:SD	1:A:1436:ILE:HG12	2.04	0.97
7:G:112:LYS:HA	7:G:115:MET:HE3	1.47	0.97
2:B:744:HIS:HD2	2:B:745:PRO:HD2	1.30	0.96
2:B:1065:GLN:HE21	2:B:1067:ARG:H	1.07	0.96
10:J:36:LEU:HB2	10:J:47:ARG:HH12	1.30	0.96
2:B:168:GLY:H	2:B:450:ALA:HB1	1.28	0.96
2:B:292:ILE:HD11	2:B:327:ARG:H	1.29	0.96
10:J:1:MET:H2	10:J:57:ILE:N	1.62	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:GLU:HG3	1:A:46:THR:HB	1.47	0.96
12:L:55:ILE:HG12	12:L:56:LEU:N	1.75	0.96
11:K:47:ARG:HB3	11:K:47:ARG:HH11	1.29	0.96
1:A:1223:ASP:HA	1:A:1243:VAL:HG22	1.47	0.96
2:B:1201:LYS:HE2	2:B:1205:GLN:OE1	1.65	0.96
3:C:43:THR:HG22	3:C:44:LEU:N	1.80	0.96
2:B:282:ILE:HD12	2:B:382:ILE:HD13	1.48	0.95
4:D:154:PHE:CD1	4:D:163:VAL:HG21	2.00	0.95
6:F:93:ILE:HD11	6:F:134:ILE:HD11	1.46	0.95
1:A:754:SER:H	1:A:757:ASN:ND2	1.64	0.95
1:A:53:LEU:HD23	1:A:54:ASN:H	1.29	0.95
6:F:128:LYS:HG2	6:F:149:GLU:HA	1.49	0.95
2:B:37:PHE:CE1	2:B:41:LYS:HG3	2.01	0.95
2:B:579:ARG:HB2	2:B:586:TRP:HE1	1.31	0.95
1:A:639:PRO:HG2	1:A:640:GLN:NE2	1.82	0.94
2:B:885:MET:HA	2:B:936:ASP:HB3	1.48	0.94
1:A:855:THR:HG21	1:A:857:ARG:HE	1.30	0.94
2:B:62:ILE:HG23	2:B:418:LYS:HG2	1.45	0.94
1:A:779:PHE:HE1	1:A:785:PRO:HD3	1.32	0.94
5:E:207:ARG:HB3	5:E:207:ARG:HH11	1.29	0.94
15:P:1:C:H4'	15:P:2:A:H5''	1.48	0.94
2:B:515:HIS:HD2	2:B:516:ASN:H	1.07	0.94
10:J:5:VAL:HG12	10:J:6:ARG:HG3	1.48	0.94
2:B:778:MET:HE1	2:B:1094:ARG:HD3	1.46	0.94
1:A:107:CYS:HA	1:A:171:GLN:NE2	1.82	0.93
10:J:3:VAL:HG21	10:J:18:TRP:HB2	1.47	0.93
5:E:117:THR:HG22	5:E:119:SER:H	1.31	0.93
1:A:41:MET:CB	1:A:49:LYS:HA	1.96	0.93
7:G:165:GLU:HB2	7:G:168:LEU:HD12	1.48	0.93
1:A:341:MET:HE2	1:A:843:LYS:NZ	1.81	0.93
1:A:567:LYS:HB2	1:A:568:PRO:HD2	1.51	0.93
1:A:741:ASN:HD22	1:A:744:LYS:H	1.09	0.93
14:T:15:DG:C8	14:T:16:DT:H72	2.04	0.93
9:I:105:SER:O	9:I:106:CYS:HB3	1.68	0.93
2:B:642:ASP:HB3	2:B:649:LYS:HD2	1.50	0.92
3:C:69:LEU:H	3:C:69:LEU:HD12	1.34	0.92
9:I:6:PHE:HB3	9:I:12:ASN:O	1.70	0.92
1:A:536:LEU:HD23	1:A:536:LEU:H	1.35	0.92
2:B:1113:VAL:H	15:P:1:C:H5''	1.33	0.92
2:B:238:ALA:HB3	2:B:256:VAL:HB	1.51	0.92
1:A:1445:ILE:H	1:A:1445:ILE:HD12	1.32	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:130:ARG:HD3	8:H:130:ARG:N	1.83	0.92
1:A:831:THR:HG23	1:A:832:ALA:H	1.34	0.92
2:B:866:TYR:HB2	2:B:870:ILE:HB	1.52	0.92
1:A:682:THR:HG23	1:A:728:LYS:HE3	1.48	0.91
3:C:177:GLU:HG3	3:C:231:ASN:HD22	1.34	0.91
2:B:806:THR:HG23	2:B:808:ALA:H	1.33	0.91
1:A:108:MET:HA	1:A:210:ILE:HD13	1.51	0.91
2:B:882:THR:HG21	2:B:935:ARG:HA	1.52	0.91
2:B:842:ASN:HD22	2:B:845:SER:H	1.17	0.91
2:B:217:ARG:HE	2:B:405:ARG:HB2	1.33	0.91
2:B:516:ASN:HD22	2:B:516:ASN:N	1.69	0.91
1:A:41:MET:HB3	1:A:49:LYS:HA	1.51	0.90
1:A:754:SER:H	1:A:757:ASN:HD22	0.93	0.90
2:B:278:GLN:CG	2:B:279:ASP:H	1.82	0.90
1:A:1259:MET:HA	1:A:1262:LYS:HD2	1.50	0.90
1:A:535:THR:HG21	1:A:616:VAL:HA	1.52	0.90
12:L:60:ARG:HG2	12:L:61:THR:H	1.36	0.90
2:B:515:HIS:CD2	2:B:516:ASN:H	1.89	0.90
3:C:66:ARG:HH12	10:J:2:ILE:HG21	1.32	0.90
1:A:1261:LYS:O	1:A:1264:GLU:HB3	1.72	0.90
1:A:1116:LEU:N	1:A:1308:THR:HG22	1.87	0.90
2:B:995:ARG:HH12	3:C:165:LYS:HG2	1.35	0.90
2:B:953:LEU:HD21	2:B:965:LYS:HB2	1.51	0.89
4:D:71:LYS:HA	4:D:74:GLN:HB2	1.54	0.89
10:J:12:LYS:O	10:J:14:VAL:HG23	1.71	0.89
1:A:107:CYS:SG	1:A:148:CYS:HB2	2.12	0.89
2:B:732:SER:HB2	2:B:734:HIS:CE1	2.07	0.89
3:C:43:THR:CG2	3:C:44:LEU:H	1.85	0.89
8:H:130:ARG:HB2	8:H:130:ARG:NH1	1.88	0.89
1:A:1006:ILE:HD11	5:E:163:GLU:HG3	1.51	0.89
2:B:653:VAL:HG23	2:B:689:LEU:HB3	1.55	0.89
6:F:103:MET:HE2	7:G:66:GLY:H	1.36	0.89
7:G:62:LEU:HD13	7:G:63:PRO:CD	2.02	0.89
8:H:59:ILE:HG22	8:H:60:ALA:H	1.37	0.89
1:A:830:LYS:HE2	1:A:1081:LEU:HD12	1.55	0.88
2:B:542:MET:HE2	2:B:747:MET:HG3	1.55	0.88
8:H:82:PRO:C	8:H:84:ALA:H	1.76	0.88
5:E:22:MET:HE3	5:E:26:ARG:NE	1.89	0.88
1:A:666:ILE:HD12	1:A:667:GLY:H	1.38	0.88
3:C:186:LEU:HD21	3:C:224:GLN:O	1.73	0.88
3:C:238:ILE:HD11	3:C:246:ARG:CZ	2.03	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:33:LEU:HG	3:C:37:MET:HE2	1.52	0.88
11:K:58:PHE:HB3	11:K:76:GLN:HB3	1.54	0.88
1:A:316:GLN:HG2	1:A:317:LYS:HD2	1.56	0.88
1:A:902:LEU:HG	1:A:926:GLN:HG3	1.55	0.88
1:A:1418:LEU:HD23	2:B:1222:ARG:HD3	1.56	0.88
2:B:102:VAL:HG23	2:B:112:LEU:HB2	1.54	0.88
2:B:172:ILE:HD13	2:B:178:ASN:HD22	1.38	0.88
5:E:2:ASP:O	5:E:3:GLN:HG2	1.74	0.88
1:A:351:THR:HG22	2:B:1103:ILE:HA	1.53	0.87
2:B:707:PRO:HG2	2:B:708:GLU:H	1.37	0.87
1:A:11:LEU:O	1:A:11:LEU:HD23	1.74	0.87
1:A:741:ASN:ND2	1:A:744:LYS:H	1.72	0.87
1:A:14:VAL:H	1:A:1432:GLN:NE2	1.72	0.87
1:A:563:PRO:HG3	1:A:572:TRP:CZ2	2.10	0.87
9:I:8:ARG:HG3	9:I:34:TYR:CE1	2.09	0.87
3:C:175:ALA:CB	10:J:43:ARG:HH22	1.87	0.87
1:A:49:LYS:HZ3	1:A:61:ILE:HG13	1.38	0.87
1:A:961:ARG:HG2	1:A:965:GLN:NE2	1.90	0.87
1:A:1095:THR:HG21	1:A:1112:LYS:HB2	1.57	0.87
1:A:225:ASN:ND2	1:A:228:PHE:H	1.72	0.87
2:B:37:PHE:HE1	2:B:41:LYS:HG3	1.40	0.87
6:F:109:VAL:HG11	6:F:123:LYS:HE3	1.56	0.86
2:B:59:LEU:HD12	2:B:417:PHE:CE2	2.10	0.86
3:C:101:LEU:HD13	3:C:118:LEU:HD23	1.57	0.86
7:G:34:VAL:HG11	7:G:74:TYR:HE1	1.39	0.86
1:A:903:ASN:HD22	1:A:904:THR:N	1.73	0.86
1:A:1161:THR:HG21	1:A:1163:ILE:HD12	1.56	0.86
2:B:64:CYS:HA	2:B:67:SER:OG	1.74	0.86
1:A:684:ALA:O	1:A:687:LYS:HB2	1.75	0.86
11:K:55:LYS:HB3	11:K:81:TYR:HD1	1.40	0.86
1:A:1169:ILE:H	1:A:1169:ILE:HD12	1.41	0.86
6:F:69:LEU:HB3	6:F:71:GLU:OE1	1.76	0.86
2:B:559:SER:CA	2:B:563:MET:HB3	2.04	0.86
1:A:62:ASP:O	1:A:64:ASN:HB2	1.76	0.86
1:A:1224:LEU:HD11	1:A:1240:CYS:HB3	1.56	0.86
1:A:55:ASP:N	1:A:56:PRO:HD3	1.89	0.85
2:B:824:ILE:HG12	10:J:48:ARG:HH12	1.38	0.85
2:B:999:MET:HG3	2:B:1000:PRO:HD2	1.58	0.85
2:B:579:ARG:HB2	2:B:586:TRP:NE1	1.91	0.85
8:H:59:ILE:HG22	8:H:60:ALA:N	1.88	0.85
14:T:10:DA:H2"	14:T:11:DA:C8	2.12	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:128:ASN:O	3:C:129:ILE:HG13	1.77	0.85
1:A:66:LYS:HZ3	1:A:68:GLN:H	1.21	0.85
9:I:8:ARG:HG3	9:I:34:TYR:HE1	1.41	0.85
1:A:567:LYS:HD2	1:A:568:PRO:HD2	1.58	0.85
4:D:220:LEU:HG	4:D:221:TYR:H	1.42	0.85
1:A:567:LYS:CB	1:A:568:PRO:HD2	2.06	0.85
7:G:88:ASP:HB3	7:G:144:ARG:HA	1.58	0.85
2:B:613:VAL:HG13	2:B:627:PHE:O	1.77	0.85
1:A:55:ASP:C	1:A:57:ARG:H	1.78	0.84
1:A:310:GLY:O	1:A:312:PRO:HD2	1.76	0.84
2:B:193:LYS:NZ	12:L:32:ALA:HB1	1.92	0.84
3:C:17:ASN:N	3:C:240:VAL:HG11	1.91	0.84
8:H:81:PRO:HB2	8:H:82:PRO:HD2	1.59	0.84
2:B:277:LYS:HD3	2:B:336:ARG:C	2.01	0.84
6:F:119:ARG:HH11	6:F:119:ARG:HG3	1.39	0.84
1:A:710:LEU:H	1:A:710:LEU:HD12	1.41	0.84
1:A:1323:ASP:OD1	1:A:1325:THR:HG22	1.77	0.84
1:A:858:ASN:C	1:A:858:ASN:HD22	1.82	0.84
1:A:900:ASP:HA	1:A:926:GLN:NE2	1.93	0.84
1:A:317:LYS:HA	2:B:471:LYS:HZ3	1.42	0.84
1:A:665:GLY:HA2	2:B:1026:LEU:HD22	1.60	0.84
2:B:731:VAL:HG12	2:B:732:SER:H	1.41	0.84
2:B:914:LYS:HE2	2:B:937:ALA:HB1	1.59	0.84
5:E:16:PHE:CZ	5:E:20:LYS:HE2	2.12	0.84
5:E:31:THR:HG23	5:E:34:GLU:HB2	1.60	0.84
10:J:57:ILE:HA	10:J:60:PHE:HD2	1.43	0.84
2:B:277:LYS:H	2:B:277:LYS:HD2	1.42	0.84
7:G:14:HIS:CD2	7:G:16:SER:H	1.96	0.84
9:I:85:PHE:H	9:I:85:PHE:HD2	1.25	0.83
1:A:288:ALA:HA	1:A:291:GLU:CD	2.02	0.83
1:A:567:LYS:CG	1:A:568:PRO:HD2	2.07	0.83
2:B:165:VAL:HG11	2:B:448:ILE:HD13	1.61	0.83
2:B:805:THR:HG23	2:B:809:MET:HE3	1.59	0.83
2:B:863:GLU:OE2	2:B:873:THR:HA	1.78	0.83
8:H:89:LEU:C	8:H:91:ASP:H	1.86	0.83
3:C:36:VAL:HG21	3:C:251:LEU:HB2	1.58	0.83
6:F:79:ARG:HG2	6:F:144:GLU:HB3	1.61	0.83
1:A:1121:GLU:HG2	1:A:1122:PRO:HD2	1.60	0.83
5:E:180:ARG:HH21	5:E:192:ARG:HB2	1.43	0.83
8:H:130:ARG:HH11	8:H:130:ARG:CB	1.91	0.83
1:A:14:VAL:N	1:A:1432:GLN:HE22	1.76	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:34:LYS:NZ	1:A:57:ARG:NH2	2.26	0.83
2:B:778:MET:CE	2:B:1094:ARG:HD3	2.08	0.83
1:A:438:ASP:O	1:A:439:ASN:HB2	1.76	0.83
2:B:549:THR:HG22	2:B:550:ASP:H	1.41	0.83
1:A:1161:THR:HG22	1:A:1163:ILE:H	1.43	0.83
1:A:1308:THR:HG23	1:A:1309:ASP:N	1.92	0.83
1:A:446:ARG:HB3	1:A:478:TYR:HB3	1.60	0.83
1:A:899:VAL:HB	1:A:929:LEU:CD1	2.04	0.83
1:A:913:LEU:HD12	1:A:914:GLU:N	1.92	0.83
1:A:1006:ILE:HD12	5:E:167:ARG:HB2	1.61	0.83
2:B:839:MET:HE1	2:B:980:PHE:HB2	1.61	0.83
10:J:1:MET:H1	10:J:56:LEU:N	1.75	0.83
11:K:55:LYS:HB3	11:K:81:TYR:CD1	2.14	0.83
1:A:600:PRO:HG2	1:A:601:LYS:H	1.42	0.82
1:A:381:THR:HG23	1:A:382:PRO:HD2	1.60	0.82
1:A:381:THR:HG22	1:A:383:TYR:H	1.42	0.82
2:B:806:THR:HG22	2:B:809:MET:H	1.44	0.82
3:C:177:GLU:HG3	3:C:231:ASN:HB3	1.61	0.82
6:F:103:MET:CE	7:G:66:GLY:H	1.91	0.82
1:A:567:LYS:CB	8:H:95:TYR:HA	2.08	0.82
2:B:842:ASN:ND2	2:B:845:SER:H	1.77	0.82
4:D:66:ARG:HD2	4:D:133:THR:HB	1.59	0.82
2:B:737:THR:HG21	9:I:66:PRO:HA	1.60	0.82
7:G:26:LEU:HD12	7:G:56:ILE:CD1	2.09	0.82
2:B:351:TYR:O	2:B:355:ILE:HG13	1.80	0.82
2:B:705:MET:HA	2:B:705:MET:HE3	1.62	0.82
7:G:15:PRO:HA	7:G:18:PHE:CE1	2.14	0.82
12:L:38:LEU:HG	12:L:39:SER:H	1.42	0.82
1:A:567:LYS:HB2	1:A:568:PRO:CD	2.09	0.82
2:B:278:GLN:HG2	2:B:279:ASP:N	1.95	0.82
2:B:345:LYS:HA	2:B:348:ARG:HE	1.45	0.82
2:B:345:LYS:HG2	2:B:346:GLU:H	1.44	0.82
2:B:428:ILE:HG22	2:B:432:MET:HE2	1.60	0.82
2:B:616:ILE:HD12	2:B:616:ILE:N	1.94	0.82
1:A:1202:MET:HE1	1:A:1212:VAL:HG21	1.62	0.82
13:N:4:DA:H2"	13:N:5:DC:C6	2.15	0.82
1:A:341:MET:HE1	2:B:1135:ARG:NH1	1.95	0.81
6:F:109:VAL:CG1	6:F:123:LYS:HE3	2.10	0.81
2:B:120:ARG:NH1	12:L:54:ARG:HD3	1.95	0.81
3:C:244:VAL:O	3:C:248:ILE:HG13	1.80	0.81
5:E:19:VAL:O	5:E:23:VAL:HG23	1.79	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1099:VAL:HG13	2:B:1100:ASP:N	1.96	0.81
2:B:1180:PHE:HB3	2:B:1191:ILE:HD12	1.63	0.81
12:L:32:ALA:CB	12:L:55:ILE:HG13	2.11	0.81
5:E:117:THR:HB	5:E:120:ALA:CB	2.10	0.81
1:A:34:LYS:HZ2	1:A:57:ARG:NH2	1.78	0.81
2:B:345:LYS:O	2:B:347:LYS:HG2	1.79	0.81
2:B:526:GLU:HG3	2:B:771:SER:HB3	1.59	0.81
3:C:7:GLN:N	3:C:7:GLN:HE21	1.78	0.81
1:A:665:GLY:O	1:A:667:GLY:N	2.13	0.81
1:A:534:LEU:O	1:A:574:GLY:HA3	1.81	0.81
2:B:23:ALA:HB1	2:B:24:PRO:HD2	1.61	0.81
7:G:111:THR:CG2	7:G:114:LEU:HD13	2.10	0.81
3:C:35:ARG:HH12	11:K:41:THR:H	1.25	0.81
3:C:102:GLN:HG2	3:C:154:LYS:HG3	1.61	0.81
1:A:567:LYS:HB2	8:H:95:TYR:HA	1.61	0.81
2:B:582:VAL:HG22	2:B:626:ILE:HB	1.61	0.81
14:T:10:DA:H2''	14:T:11:DA:N7	1.95	0.81
1:A:591:PHE:HD2	1:A:595:THR:HB	1.45	0.80
1:A:1101:LEU:O	1:A:1105:LEU:HD12	1.81	0.80
1:A:1259:MET:HA	1:A:1262:LYS:CD	2.11	0.80
8:H:42:ILE:HG23	8:H:95:TYR:HE1	1.44	0.80
8:H:82:PRO:HG2	8:H:83:GLN:H	1.44	0.80
2:B:770:GLN:OE1	2:B:983:ARG:HA	1.80	0.80
4:D:69:ALA:HB2	4:D:72:ARG:NH1	1.96	0.80
7:G:139:ILE:HG23	7:G:140:LYS:H	1.45	0.80
1:A:98:LYS:O	1:A:102:VAL:HG23	1.81	0.80
1:A:744:LYS:HG2	1:A:748:MET:HE2	1.63	0.80
1:A:946:VAL:HG22	5:E:201:LYS:HD2	1.63	0.80
2:B:1169:MET:HE1	2:B:1201:LYS:HA	1.63	0.80
1:A:110:CYS:HB3	1:A:167:CYS:SG	2.22	0.80
1:A:1259:MET:HE3	1:A:1263:ILE:HD11	1.63	0.80
2:B:906:SER:O	2:B:941:LEU:HD23	1.81	0.80
1:A:244:PRO:HB2	1:A:245:PRO:CD	2.12	0.80
1:A:315:LEU:HD12	2:B:471:LYS:HB3	1.64	0.80
1:A:709:THR:HG22	1:A:710:LEU:H	1.46	0.80
2:B:221:ASN:OD1	2:B:242:SER:HA	1.81	0.80
3:C:32:SER:O	3:C:36:VAL:HG23	1.82	0.80
1:A:839:ARG:HG2	1:A:839:ARG:HH11	1.45	0.80
2:B:289:LEU:HD13	2:B:375:ALA:HB2	1.62	0.80
3:C:167:HIS:CD2	12:L:70:ARG:HB3	2.17	0.80
1:A:1167:GLU:O	1:A:1170:ILE:HD12	1.81	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1341:ILE:HG23	1:A:1342:GLU:N	1.96	0.79
2:B:39:ARG:HH21	2:B:665:GLU:HG2	1.46	0.79
8:H:95:TYR:HE2	8:H:97:MET:HG3	1.46	0.79
1:A:66:LYS:NZ	1:A:68:GLN:H	1.79	0.79
1:A:701:LEU:HD21	9:I:114:GLN:HB2	1.65	0.79
1:A:925:LEU:HD13	1:A:983:ILE:HG21	1.62	0.79
5:E:127:ILE:O	5:E:127:ILE:HG13	1.81	0.79
1:A:87:ALA:HB3	1:A:276:LEU:HD23	1.64	0.79
1:A:754:SER:N	1:A:757:ASN:HD22	1.76	0.79
2:B:360:PHE:CE2	2:B:361:LEU:HD13	2.16	0.79
2:B:498:THR:HG22	2:B:537:LYS:O	1.83	0.79
1:A:629:LEU:O	1:A:633:VAL:HG23	1.82	0.79
2:B:846:ILE:HG23	2:B:974:PRO:HG2	1.63	0.79
8:H:58:THR:HB	8:H:143:LEU:HD13	1.63	0.79
1:A:34:LYS:HG2	1:A:36:ARG:HH21	1.48	0.79
6:F:90:ARG:HG3	6:F:91:ALA:N	1.96	0.79
10:J:7:CYS:HA	10:J:49:MET:HE3	1.65	0.79
12:L:55:ILE:CG1	12:L:56:LEU:N	2.35	0.79
1:A:35:ILE:HA	1:A:52:GLY:O	1.83	0.79
1:A:866:PHE:C	1:A:867:ILE:HD12	2.08	0.79
2:B:957:ASN:HD22	2:B:961:LEU:HB2	1.45	0.79
3:C:189:THR:HG22	3:C:190:ASP:N	1.98	0.79
1:A:1205:LYS:O	1:A:1207:LEU:HG	1.83	0.79
2:B:805:THR:HG22	2:B:806:THR:H	1.48	0.79
2:B:1138:MET:HE2	2:B:1146:PHE:CD2	2.18	0.79
3:C:208:GLU:O	3:C:210:GLU:N	2.15	0.79
8:H:40:LEU:HD13	8:H:123:MET:HE3	1.65	0.79
1:A:150:THR:HG23	1:A:166:GLY:HA2	1.63	0.79
1:A:205:GLU:H	1:A:205:GLU:CD	1.88	0.79
1:A:982:THR:HB	1:A:985:ASP:H	1.48	0.79
1:A:317:LYS:HA	2:B:471:LYS:NZ	1.97	0.78
1:A:388:LEU:O	1:A:392:VAL:HG23	1.82	0.78
1:A:1420:ASP:HB3	1:A:1422:ARG:HG3	1.65	0.78
2:B:583:ASN:HD21	2:B:628:THR:HG22	1.48	0.78
2:B:758:PHE:CE2	2:B:1044:ALA:HA	2.19	0.78
15:P:1:C:H4'	15:P:2:A:C5'	2.13	0.78
1:A:1107:VAL:HG12	1:A:1107:VAL:O	1.81	0.78
1:A:2:VAL:HG11	2:B:1157:ALA:O	1.82	0.78
1:A:834:THR:HG21	1:A:1077:THR:HG23	1.66	0.78
2:B:293:PRO:HD2	2:B:296:GLU:OE1	1.83	0.78
1:A:288:ALA:HA	1:A:291:GLU:OE1	1.82	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1081:LEU:HD11	1:A:1098:VAL:H	1.48	0.78
3:C:124:LEU:O	3:C:127:ARG:HG2	1.82	0.78
5:E:14:ARG:HH21	5:E:141:VAL:HG12	1.47	0.78
8:H:12:VAL:HA	8:H:28:ALA:HB2	1.64	0.78
1:A:323:LYS:H	1:A:323:LYS:HD2	1.49	0.78
2:B:429:PHE:HA	2:B:432:MET:HE3	1.65	0.78
2:B:1113:VAL:H	15:P:1:C:C5'	1.95	0.78
4:D:56:ARG:HD3	4:D:149:THR:HA	1.66	0.78
5:E:120:ALA:O	5:E:123:LEU:HG	1.84	0.78
1:A:591:PHE:HA	1:A:595:THR:HG21	1.66	0.78
1:A:683:ILE:HG21	1:A:801:GLU:HG3	1.64	0.78
1:A:1279:ILE:HD11	1:A:1316:VAL:HG21	1.66	0.78
8:H:24:CYS:HB2	8:H:44:VAL:HG21	1.65	0.78
2:B:637:LEU:HD22	2:B:741:CYS:O	1.83	0.78
2:B:1187:ASN:O	2:B:1188:LYS:HB2	1.83	0.78
4:D:155:ARG:HD3	4:D:221:TYR:CE1	2.19	0.78
8:H:15:VAL:HG13	8:H:26:ILE:HB	1.66	0.78
8:H:104:PHE:CZ	8:H:136:LYS:HA	2.19	0.78
1:A:372:LYS:HA	1:A:435:HIS:ND1	1.99	0.78
2:B:284:ILE:HD13	2:B:333:PHE:CE2	2.18	0.78
3:C:11:ARG:HH12	3:C:205:LYS:NZ	1.81	0.78
3:C:57:VAL:HG23	3:C:58:LEU:HD23	1.64	0.78
1:A:567:LYS:CD	1:A:568:PRO:HD2	2.14	0.78
2:B:1072:MET:CE	2:B:1085:ILE:HB	2.10	0.78
3:C:73:GLN:NE2	3:C:75:MET:HB2	1.98	0.78
1:A:567:LYS:HB3	8:H:96:VAL:H	1.46	0.77
4:D:68:ARG:HG2	4:D:72:ARG:NH2	1.99	0.77
10:J:1:MET:H2	10:J:57:ILE:H	0.80	0.77
2:B:90:ILE:HD12	2:B:432:MET:SD	2.24	0.77
5:E:98:ILE:HA	5:E:101:GLN:HB3	1.64	0.77
5:E:169:ARG:HD3	6:F:140:ASP:OD2	1.84	0.77
6:F:99:LEU:O	6:F:103:MET:HG2	1.84	0.77
1:A:1409:LEU:HD13	2:B:1207:LEU:HD11	1.65	0.77
2:B:1112:GLN:CA	15:P:1:C:H5'	2.14	0.77
2:B:654:ARG:H	2:B:657:HIS:HD2	1.28	0.77
1:A:425:GLN:N	1:A:425:GLN:CD	2.42	0.77
2:B:654:ARG:HH11	2:B:654:ARG:HG3	1.48	0.77
2:B:1112:GLN:HG3	15:P:1:C:C5'	2.15	0.77
5:E:198:ILE:HD11	5:E:212:ARG:HG3	1.67	0.77
1:A:224:PHE:CE2	1:A:234:MET:HE2	2.19	0.77
2:B:597:MET:HA	2:B:597:MET:CE	2.15	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1444:MET:HG2	7:G:60:ARG:CA	2.15	0.77
2:B:542:MET:HG2	2:B:747:MET:HE3	1.66	0.77
8:H:84:ALA:HB2	8:H:87:ARG:HD2	1.65	0.77
9:I:93:LYS:H	9:I:93:LYS:CD	1.95	0.77
11:K:49:GLU:HG3	11:K:94:ILE:HG13	1.64	0.77
1:A:390:GLN:HE21	1:A:394:ASN:HD22	1.30	0.77
1:A:715:GLU:OE1	1:A:774:ARG:HD3	1.85	0.77
2:B:193:LYS:HZ2	12:L:32:ALA:HB1	1.49	0.77
3:C:137:LYS:HB3	3:C:138:GLU:OE1	1.85	0.77
1:A:783:THR:HG21	1:A:815:PHE:CZ	2.20	0.77
2:B:865:LYS:NZ	2:B:869:SER:HA	2.00	0.77
8:H:38:LEU:HD12	8:H:124:ARG:O	1.85	0.77
11:K:57:LEU:HB2	11:K:76:GLN:HG2	1.67	0.77
2:B:309:GLN:HE21	2:B:309:GLN:HA	1.49	0.76
2:B:39:ARG:HH21	2:B:665:GLU:CG	1.96	0.76
7:G:1:MET:SD	7:G:2:PHE:N	2.58	0.76
1:A:122:MET:HA	1:A:141:LEU:HD11	1.66	0.76
1:A:763:ALA:O	1:A:803:SER:HB3	1.86	0.76
1:A:883:LEU:HD11	1:A:1017:LEU:HD11	1.65	0.76
1:A:903:ASN:HD22	1:A:904:THR:H	1.29	0.76
2:B:505:ASP:HA	13:N:1:DA:C8	2.21	0.76
9:I:50:THR:HG23	9:I:52:ILE:H	1.49	0.76
1:A:843:LYS:HD3	1:A:846:GLU:OE2	1.84	0.76
2:B:101:MET:HE2	2:B:126:SER:HA	1.65	0.76
2:B:914:LYS:HE2	2:B:937:ALA:CB	2.15	0.76
4:D:159:THR:O	4:D:163:VAL:HG23	1.83	0.76
2:B:882:THR:HG23	2:B:884:ARG:HB2	1.67	0.76
4:D:195:ILE:HG22	4:D:198:LEU:HG	1.66	0.76
1:A:93:VAL:HG22	1:A:301:ALA:HA	1.67	0.76
2:B:708:GLU:O	2:B:710:LEU:N	2.19	0.76
5:E:23:VAL:O	5:E:28:TYR:HB2	1.86	0.76
8:H:62:SER:O	8:H:63:LEU:HG	1.86	0.76
1:A:90:VAL:HG12	1:A:297:GLN:NE2	2.01	0.76
2:B:114:PRO:HG2	2:B:115:GLN:H	1.51	0.76
2:B:216:GLU:OE1	2:B:537:LYS:HE2	1.86	0.76
2:B:558:LEU:HD21	2:B:600:LEU:HD11	1.68	0.76
1:A:698:GLN:HA	9:I:97:MET:O	1.86	0.75
3:C:123:ASN:ND2	3:C:125:MET:HG2	2.01	0.75
1:A:69:THR:O	1:A:71:GLN:HG2	1.85	0.75
1:A:694:THR:O	1:A:698:GLN:HG3	1.86	0.75
1:A:960:ILE:HA	1:A:963:ILE:HG22	1.66	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1027:ALA:O	1:A:1031:VAL:HG23	1.84	0.75
1:A:1437:GLY:O	1:A:1439:GLY:N	2.20	0.75
2:B:744:HIS:HD2	2:B:745:PRO:CD	1.98	0.75
10:J:35:ALA:O	10:J:38:ARG:HB3	1.86	0.75
1:A:66:LYS:HZ3	1:A:68:GLN:N	1.84	0.75
2:B:172:ILE:HD13	2:B:178:ASN:ND2	2.01	0.75
3:C:175:ALA:O	3:C:176:ILE:HG13	1.85	0.75
1:A:1141:THR:CG2	1:A:1205:LYS:HD3	2.15	0.75
2:B:766:ARG:HA	2:B:766:ARG:HH11	1.52	0.75
10:J:44:TYR:H	10:J:44:TYR:HD2	1.35	0.75
1:A:41:MET:HB2	1:A:49:LYS:HA	1.69	0.75
2:B:613:VAL:HG22	2:B:628:THR:HA	1.68	0.75
2:B:744:HIS:CD2	2:B:745:PRO:HD2	2.18	0.75
3:C:50:GLU:HG2	12:L:64:LEU:HD22	1.68	0.75
9:I:74:GLU:HB3	9:I:81:ARG:NE	2.02	0.75
1:A:66:LYS:HD3	1:A:67:CYS:N	2.00	0.75
2:B:1065:GLN:HE21	2:B:1067:ARG:N	1.81	0.75
5:E:117:THR:HB	5:E:120:ALA:HB2	1.68	0.75
1:A:1015:VAL:HG12	1:A:1019:CYS:SG	2.26	0.75
1:A:1208:THR:HB	1:A:1211:GLN:CG	2.15	0.75
5:E:94:LYS:CE	5:E:98:ILE:HD11	2.12	0.75
7:G:91:VAL:HG23	7:G:141:SER:O	1.87	0.75
8:H:30:SER:HB2	8:H:36:CYS:HB3	1.67	0.75
1:A:1118:VAL:HG23	1:A:1306:LEU:HB2	1.69	0.75
1:A:1418:LEU:HB3	2:B:1222:ARG:NH1	2.00	0.75
2:B:101:MET:HA	2:B:112:LEU:H	1.52	0.75
2:B:852:ARG:HH22	12:L:70:ARG:C	1.94	0.75
1:A:146:MET:HA	1:A:171:GLN:HB2	1.68	0.75
1:A:831:THR:HG23	1:A:832:ALA:N	2.01	0.75
1:A:963:ILE:HD11	1:A:1048:ASN:HB2	1.68	0.75
3:C:11:ARG:HH12	3:C:205:LYS:HZ3	1.35	0.75
3:C:69:LEU:HD12	3:C:69:LEU:N	2.02	0.75
1:A:2:VAL:HG11	2:B:1157:ALA:C	2.11	0.74
1:A:886:ILE:HG23	1:A:887:GLY:N	2.02	0.74
1:A:1243:VAL:O	1:A:1245:PRO:HD3	1.87	0.74
1:A:1325:THR:O	5:E:148:GLU:HB2	1.85	0.74
9:I:80:SER:OG	9:I:105:SER:HB2	1.87	0.74
1:A:806:ARG:HH12	2:B:729:ILE:HD12	1.52	0.74
5:E:138:ALA:HA	5:E:141:VAL:HG23	1.70	0.74
1:A:34:LYS:HZ2	1:A:57:ARG:HH22	1.32	0.74
1:A:70:CYS:O	1:A:72:GLU:HG2	1.86	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1030:ARG:HG3	1:A:1034:GLU:OE2	1.85	0.74
1:A:524:VAL:HG12	1:A:525:GLN:H	1.52	0.74
1:A:1424:VAL:HG11	2:B:1139:ILE:HD13	1.70	0.74
7:G:131:GLN:HG2	7:G:136:VAL:HG13	1.68	0.74
1:A:353:ILE:HG21	1:A:487:MET:HG3	1.68	0.74
1:A:1313:LEU:HB3	1:A:1338:VAL:HG21	1.68	0.74
1:A:1317:MET:HE2	5:E:142:VAL:HG11	1.67	0.74
2:B:37:PHE:HE2	2:B:542:MET:HA	1.52	0.74
1:A:172:PRO:HB3	1:A:185:TRP:CD2	2.23	0.74
1:A:1148:ILE:HG12	1:A:1198:ASP:HB2	1.70	0.74
3:C:196:ASP:HB3	3:C:199:LYS:HB2	1.68	0.74
1:A:154:SER:HB3	1:A:162:VAL:HG21	1.70	0.74
1:A:341:MET:HE2	1:A:843:LYS:HZ1	1.48	0.74
1:A:898:ARG:HD2	1:A:899:VAL:H	1.52	0.74
2:B:593:PRO:HG2	2:B:617:ARG:NH2	2.03	0.74
7:G:142:ARG:HB3	7:G:171:ILE:HD12	1.68	0.74
9:I:111:THR:HG22	9:I:112:SER:H	1.51	0.74
1:A:960:ILE:HA	1:A:963:ILE:CG2	2.18	0.74
1:A:1227:ILE:HG22	1:A:1228:TRP:H	1.49	0.74
3:C:189:THR:HG22	3:C:190:ASP:H	1.52	0.74
2:B:549:THR:HB	2:B:628:THR:OG1	1.88	0.74
12:L:40:LEU:HD13	12:L:44:ASP:HB3	1.70	0.74
2:B:1183:LYS:N	2:B:1183:LYS:HE3	2.02	0.73
1:A:821:ARG:HB2	1:A:821:ARG:NH1	2.03	0.73
2:B:637:LEU:HB2	2:B:693:ILE:HD11	1.68	0.73
4:D:13:ARG:C	4:D:15:LEU:H	1.94	0.73
1:A:335:ARG:O	1:A:339:ASN:HB2	1.89	0.73
1:A:568:PRO:HG2	8:H:46:LEU:HD22	1.69	0.73
1:A:718:VAL:HG12	1:A:722:LEU:HD11	1.70	0.73
1:A:1187:GLN:O	1:A:1244:ARG:HB2	1.87	0.73
2:B:36:ALA:HA	2:B:39:ARG:HD2	1.70	0.73
5:E:134:THR:C	5:E:135:PHE:HD1	1.97	0.73
8:H:77:ARG:HB2	8:H:77:ARG:CZ	2.17	0.73
1:A:62:ASP:O	1:A:63:ARG:C	2.31	0.73
1:A:89:PRO:HG2	1:A:204:THR:HB	1.70	0.73
2:B:806:THR:HG23	2:B:808:ALA:N	2.03	0.73
12:L:34:CYS:HB3	12:L:51:CYS:SG	2.29	0.73
1:A:1254:ALA:O	1:A:1255:GLU:HB2	1.88	0.73
2:B:273:LEU:HB2	2:B:276:ILE:HD12	1.70	0.73
2:B:805:THR:HG22	2:B:809:MET:HG3	1.68	0.73
5:E:69:ILE:N	5:E:69:ILE:HD12	2.04	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:157:SER:C	5:E:159:ASP:H	1.95	0.73
6:F:103:MET:O	6:F:104:ASN:HB2	1.87	0.73
8:H:139:ASN:O	8:H:140:ALA:HB2	1.88	0.73
9:I:93:LYS:HD3	9:I:93:LYS:N	2.02	0.73
1:A:19:PHE:O	1:A:1416:ALA:HA	1.89	0.73
2:B:359:GLU:O	2:B:362:PRO:HD3	1.88	0.73
2:B:435:THR:C	2:B:437:GLU:H	1.93	0.73
5:E:84:ASP:O	5:E:86:PRO:HD3	1.88	0.73
11:K:67:PHE:C	11:K:68:PHE:HD2	1.97	0.73
1:A:39:GLU:N	1:A:39:GLU:OE2	2.22	0.73
1:A:565:ILE:HD13	1:A:567:LYS:HE2	1.68	0.73
4:D:14:ARG:HB3	4:D:14:ARG:HH11	1.53	0.73
2:B:261:ARG:HB3	2:B:261:ARG:NH1	2.02	0.73
2:B:282:ILE:CD1	2:B:382:ILE:HD13	2.19	0.73
2:B:347:LYS:HG3	2:B:348:ARG:H	1.53	0.73
2:B:811:TYR:N	2:B:811:TYR:CD1	2.53	0.73
7:G:49:LEU:HG	7:G:76:ALA:HA	1.71	0.73
1:A:896:ARG:HD3	1:A:897:TYR:CE1	2.24	0.73
3:C:125:MET:HE2	3:C:127:ARG:NH2	2.04	0.73
9:I:7:CYS:SG	9:I:8:ARG:O	2.46	0.73
1:A:7:SER:HB3	2:B:1193:GLN:HE22	1.54	0.73
1:A:285:PRO:HG2	1:A:288:ALA:HB3	1.69	0.73
2:B:222:ILE:H	2:B:240:ILE:HD12	1.53	0.73
1:A:51:GLY:O	1:A:56:PRO:HB3	1.89	0.72
9:I:65:ASP:HB3	9:I:68:LEU:HD13	1.70	0.72
10:J:14:VAL:CG1	10:J:50:ILE:HD11	2.19	0.72
1:A:666:ILE:CD1	1:A:667:GLY:H	2.01	0.72
10:J:23:ASN:C	10:J:25:LEU:H	1.96	0.72
1:A:1118:VAL:CG2	1:A:1306:LEU:HB2	2.19	0.72
2:B:39:ARG:NH2	2:B:665:GLU:HG2	2.03	0.72
2:B:254:LEU:HD23	2:B:381:MET:HE1	1.70	0.72
2:B:890:TYR:O	2:B:893:LEU:HB2	1.90	0.72
1:A:416:ARG:NH1	1:A:417:TYR:HE2	1.88	0.72
1:A:590:ARG:O	1:A:591:PHE:HB2	1.89	0.72
1:A:828:ALA:CB	2:B:530:GLY:HA2	2.20	0.72
2:B:259:TYR:HB2	2:B:268:THR:HG23	1.71	0.72
2:B:996:ARG:HH12	3:C:174:ALA:HA	1.54	0.72
2:B:376:PHE:CZ	2:B:569:TYR:HB3	2.25	0.72
3:C:6:PRO:HG2	11:K:101:LEU:HB2	1.70	0.72
1:A:341:MET:HE2	1:A:843:LYS:HZ3	1.50	0.72
1:A:898:ARG:HD2	1:A:899:VAL:N	2.04	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:418:LYS:HD3	2:B:422:LYS:NZ	2.04	0.72
6:F:82:THR:HG22	6:F:84:TYR:H	1.54	0.72
10:J:9:SER:HB2	10:J:45:CYS:HB2	1.72	0.72
2:B:880:THR:HB	2:B:934:LYS:HG3	1.71	0.72
5:E:207:ARG:HH11	5:E:207:ARG:CB	2.03	0.72
10:J:36:LEU:CB	10:J:47:ARG:HH12	2.01	0.72
11:K:23:PRO:HA	11:K:31:VAL:HG13	1.72	0.72
1:A:547:LEU:HD13	11:K:58:PHE:CD1	2.24	0.72
1:A:1004:ASN:ND2	5:E:167:ARG:HD2	2.04	0.72
2:B:710:LEU:HA	2:B:733:HIS:HB3	1.69	0.72
2:B:873:THR:O	2:B:914:LYS:HA	1.89	0.72
3:C:56:THR:HG21	3:C:145:CYS:SG	2.30	0.72
7:G:7:LEU:HB2	7:G:74:TYR:CE2	2.24	0.72
8:H:81:PRO:CB	8:H:82:PRO:HD2	2.18	0.72
1:A:145:LYS:HA	1:A:145:LYS:CE	2.19	0.72
3:C:108:GLU:OE1	3:C:108:GLU:HA	1.87	0.72
1:A:69:THR:O	1:A:71:GLN:N	2.23	0.72
1:A:903:ASN:ND2	1:A:904:THR:N	2.36	0.72
1:A:1094:VAL:HA	1:A:1113:THR:HG21	1.71	0.72
1:A:1438:THR:HG23	6:F:92:ARG:HB2	1.70	0.72
7:G:111:THR:HG21	7:G:114:LEU:HD13	1.70	0.72
2:B:461:LEU:HD12	2:B:461:LEU:H	1.54	0.71
2:B:758:PHE:CE1	2:B:1027:ILE:HG22	2.25	0.71
3:C:167:HIS:HA	11:K:6:ARG:HH12	1.55	0.71
4:D:4:SER:O	4:D:5:THR:HB	1.89	0.71
7:G:21:ARG:HD2	7:G:24:GLN:CB	2.20	0.71
1:A:67:CYS:C	1:A:68:GLN:HG3	2.14	0.71
1:A:399:HIS:HB3	1:A:400:PRO:CD	2.16	0.71
1:A:803:SER:OG	1:A:806:ARG:HG3	1.90	0.71
1:A:1211:GLN:O	1:A:1214:GLU:HB2	1.90	0.71
1:A:1267:MET:HA	1:A:1271:ILE:HD12	1.73	0.71
2:B:254:LEU:HD11	2:B:273:LEU:HD23	1.72	0.71
2:B:291:ILE:HG12	2:B:300:HIS:NE2	2.05	0.71
2:B:294:ASP:O	2:B:296:GLU:N	2.22	0.71
2:B:357:GLN:O	2:B:366:GLN:HA	1.90	0.71
7:G:111:THR:HG23	7:G:114:LEU:HB2	1.72	0.71
7:G:139:ILE:HG23	7:G:140:LYS:N	2.04	0.71
1:A:265:LYS:CE	1:A:302:THR:HG23	2.20	0.71
7:G:1:MET:HE2	7:G:1:MET:HA	1.73	0.71
7:G:115:MET:HB3	7:G:116:PRO:HD2	1.72	0.71
9:I:55:THR:HG23	9:I:86:PHE:HZ	1.56	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:407:ARG:HG2	1:A:430:TRP:CZ2	2.26	0.71
1:A:946:VAL:HG12	1:A:947:PHE:CD2	2.26	0.71
1:A:1189:SER:O	1:A:1241:ARG:HD3	1.91	0.71
5:E:99:HIS:CE1	5:E:103:LYS:HD2	2.25	0.71
9:I:34:TYR:CD2	9:I:35:VAL:N	2.58	0.71
1:A:1095:THR:HG21	1:A:1112:LYS:CB	2.20	0.71
1:A:1444:MET:CG	7:G:60:ARG:HA	2.18	0.71
2:B:553:PRO:O	2:B:557:PHE:HB2	1.91	0.71
12:L:34:CYS:O	12:L:34:CYS:SG	2.49	0.71
12:L:42:ARG:HH11	12:L:42:ARG:HG3	1.53	0.71
1:A:821:ARG:HB2	1:A:821:ARG:HH11	1.53	0.71
1:A:203:SER:OG	1:A:206:GLU:HB2	1.89	0.71
1:A:1420:ASP:O	1:A:1421:CYS:HB2	1.90	0.71
2:B:120:ARG:HG2	2:B:955:THR:HG21	1.73	0.71
2:B:333:PHE:HE1	2:B:336:ARG:NH1	1.88	0.71
3:C:251:LEU:O	3:C:255:VAL:HG23	1.90	0.71
12:L:49:LYS:O	12:L:50:ASP:HB2	1.91	0.71
1:A:565:ILE:HG23	1:A:567:LYS:HG2	1.73	0.71
1:A:722:LEU:H	1:A:722:LEU:HD12	1.56	0.71
2:B:859:TYR:CZ	2:B:941:LEU:HD12	2.25	0.71
4:D:8:PHE:CD2	7:G:6:ASP:HB2	2.25	0.71
4:D:119:ARG:HB3	4:D:119:ARG:NH1	2.06	0.71
11:K:63:VAL:HG23	11:K:63:VAL:O	1.90	0.71
1:A:416:ARG:HH11	1:A:417:TYR:HE2	1.39	0.70
2:B:53:GLN:HG2	2:B:547:VAL:HG22	1.72	0.70
2:B:390:LEU:O	2:B:392:ARG:N	2.24	0.70
1:A:399:HIS:CB	1:A:400:PRO:HD3	2.20	0.70
1:A:478:TYR:O	1:A:479:ASN:HB2	1.91	0.70
2:B:603:LEU:HD13	2:B:608:ASP:HB2	1.71	0.70
3:C:236:GLY:O	3:C:238:ILE:N	2.25	0.70
3:C:253:LYS:O	3:C:256:ALA:HB3	1.91	0.70
4:D:154:PHE:HE1	4:D:163:VAL:HG11	1.55	0.70
12:L:30:ILE:O	12:L:56:LEU:HA	1.91	0.70
1:A:224:PHE:HE2	1:A:234:MET:HE2	1.53	0.70
1:A:302:THR:HA	1:A:305:ASP:O	1.91	0.70
1:A:921:GLY:O	1:A:923:LEU:HD12	1.91	0.70
2:B:333:PHE:CE1	2:B:336:ARG:NH1	2.59	0.70
7:G:59:GLY:HA3	7:G:70:PHE:CD2	2.26	0.70
1:A:91:PHE:H	1:A:297:GLN:HE22	1.37	0.70
1:A:886:ILE:HG23	1:A:887:GLY:H	1.56	0.70
1:A:1445:ILE:HD12	1:A:1445:ILE:N	2.04	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:857:ARG:HH21	2:B:942:ARG:CZ	2.03	0.70
2:B:865:LYS:HZ2	2:B:869:SER:HA	1.57	0.70
3:C:242:GLN:HA	3:C:245:VAL:CG2	2.21	0.70
4:D:18:VAL:O	4:D:19:GLU:HB2	1.89	0.70
1:A:866:PHE:O	1:A:867:ILE:HD12	1.90	0.70
2:B:582:VAL:HB	2:B:587:HIS:CD2	2.27	0.70
4:D:51:ASN:O	4:D:52:LEU:O	2.10	0.70
1:A:535:THR:CG2	1:A:616:VAL:HA	2.20	0.70
1:A:1116:LEU:HB3	1:A:1308:THR:HG21	1.72	0.70
2:B:465:ASN:HD22	2:B:465:ASN:N	1.89	0.70
2:B:872:GLU:CD	2:B:914:LYS:HE3	2.17	0.70
4:D:118:THR:HB	4:D:121:LYS:HB2	1.73	0.70
7:G:34:VAL:HG11	7:G:74:TYR:CE1	2.24	0.70
8:H:123:MET:HE1	8:H:142:LEU:HD21	1.73	0.70
15:P:3:A:H2'	15:P:4:C:C6	2.26	0.70
1:A:961:ARG:HG2	1:A:965:GLN:HE21	1.54	0.70
1:A:1438:THR:HG22	6:F:92:ARG:HD3	1.73	0.70
2:B:31:TRP:CE3	2:B:34:ILE:HD12	2.27	0.70
2:B:189:LEU:O	2:B:192:LEU:N	2.25	0.70
2:B:241:ARG:HG2	2:B:253:THR:CG2	2.22	0.70
2:B:583:ASN:HD21	2:B:628:THR:CG2	2.05	0.70
10:J:63:TYR:O	10:J:64:ASN:HB2	1.92	0.70
12:L:55:ILE:CD1	12:L:56:LEU:H	2.04	0.70
2:B:745:PRO:O	2:B:748:ILE:HG12	1.91	0.70
2:B:897:GLY:O	2:B:898:LEU:HD23	1.91	0.70
2:B:955:THR:CG2	2:B:956:THR:N	2.55	0.70
2:B:995:ARG:HH11	3:C:165:LYS:HA	1.57	0.70
4:D:139:LYS:HD3	4:D:143:ASN:HD22	1.55	0.70
5:E:90:VAL:HG23	5:E:123:LEU:HD11	1.73	0.70
1:A:353:ILE:HD12	1:A:487:MET:HE2	1.74	0.70
2:B:300:HIS:O	2:B:303:TYR:HE2	1.75	0.70
5:E:93:MET:CG	5:E:123:LEU:HD12	2.21	0.70
10:J:64:ASN:HB3	10:J:65:PRO:HD2	1.73	0.70
11:K:48:ALA:O	11:K:51:LEU:HB2	1.92	0.70
1:A:533:LYS:NZ	1:A:745:GLN:HE22	1.89	0.70
1:A:828:ALA:HB2	2:B:530:GLY:HA2	1.73	0.70
2:B:294:ASP:H	9:I:12:ASN:ND2	1.89	0.70
3:C:46:ILE:HD12	3:C:67:LEU:HB3	1.74	0.70
6:F:90:ARG:HD2	6:F:155:LEU:HD13	1.73	0.70
1:A:42:ASP:O	1:A:44:THR:N	2.25	0.69
1:A:87:ALA:CB	1:A:276:LEU:HD23	2.22	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:381:THR:CG2	1:A:382:PRO:HD2	2.22	0.69
1:A:714:PHE:HB2	9:I:97:MET:HE1	1.74	0.69
1:A:335:ARG:HA	1:A:339:ASN:HD22	1.57	0.69
2:B:291:ILE:H	2:B:291:ILE:HD12	1.57	0.69
2:B:728:ARG:O	2:B:729:ILE:HG13	1.92	0.69
8:H:8:ASP:CG	8:H:9:ILE:H	2.00	0.69
1:A:106:VAL:HG21	1:A:214:ILE:HD13	1.75	0.69
2:B:824:ILE:HG12	10:J:48:ARG:NH1	2.07	0.69
9:I:116:ASN:C	9:I:117:LYS:HD2	2.16	0.69
10:J:3:VAL:HG21	10:J:18:TRP:CB	2.20	0.69
15:P:1:C:C4'	15:P:2:A:H5''	2.22	0.69
1:A:337:ARG:NE	1:A:839:ARG:NH2	2.39	0.69
1:A:350:ARG:HB3	2:B:1128:LEU:HD11	1.74	0.69
1:A:959:ASN:HD22	1:A:962:ARG:NH2	1.89	0.69
1:A:964:ILE:O	1:A:967:ALA:HB3	1.92	0.69
1:A:1110:ASN:HD22	1:A:1110:ASN:N	1.90	0.69
2:B:291:ILE:HD12	2:B:291:ILE:N	2.07	0.69
3:C:35:ARG:NH1	11:K:41:THR:H	1.91	0.69
1:A:122:MET:HA	1:A:141:LEU:CD1	2.22	0.69
1:A:696:GLU:OE2	1:A:702:LEU:HD21	1.93	0.69
1:A:836:TYR:CE2	1:A:840:ARG:HD2	2.26	0.69
2:B:34:ILE:HG12	2:B:542:MET:HE1	1.74	0.69
2:B:618:ASP:OD1	2:B:621:GLU:HB3	1.93	0.69
12:L:30:ILE:HG22	12:L:31:CYS:H	1.57	0.69
1:A:347:PHE:HE2	1:A:375:THR:HG23	1.57	0.69
1:A:567:LYS:CB	1:A:568:PRO:CD	2.69	0.69
1:A:1202:MET:HE1	1:A:1212:VAL:CG2	2.23	0.69
1:A:1418:LEU:HB3	2:B:1222:ARG:HH11	1.56	0.69
2:B:497:ARG:NH2	2:B:775:LYS:NZ	2.40	0.69
3:C:18:VAL:HG12	3:C:18:VAL:O	1.90	0.69
7:G:85:GLU:HB3	7:G:147:ILE:HD12	1.73	0.69
10:J:64:ASN:HB3	10:J:65:PRO:HD3	1.72	0.69
1:A:353:ILE:CD1	1:A:487:MET:HE2	2.23	0.69
1:A:639:PRO:HG2	1:A:640:GLN:HE21	1.55	0.69
1:A:853:ASP:OD1	1:A:855:THR:HG22	1.92	0.69
2:B:773:MET:SD	2:B:987:LYS:HD2	2.32	0.69
1:A:683:ILE:HD13	1:A:801:GLU:HG3	1.74	0.69
2:B:26:THR:HB	2:B:708:GLU:OE1	1.92	0.69
2:B:288:ALA:O	2:B:331:LEU:HD11	1.91	0.69
2:B:483:LEU:HD11	2:B:491:THR:CG2	2.16	0.69
2:B:577:ALA:CB	2:B:589:VAL:HG11	2.20	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:109:VAL:HG12	6:F:110:ASP:N	2.08	0.69
8:H:58:THR:HG22	8:H:59:ILE:H	1.58	0.69
12:L:61:THR:CG2	12:L:63:ARG:HG3	2.22	0.69
1:A:858:ASN:ND2	1:A:858:ASN:C	2.51	0.69
1:A:1148:ILE:HD11	1:A:1198:ASP:HA	1.75	0.69
7:G:21:ARG:HD2	7:G:24:GLN:HB2	1.74	0.69
1:A:963:ILE:HD11	1:A:1048:ASN:CB	2.22	0.69
2:B:731:VAL:HG12	2:B:732:SER:N	2.08	0.69
2:B:810:GLU:HB3	2:B:811:TYR:CE1	2.28	0.69
8:H:12:VAL:CG1	8:H:26:ILE:HD11	2.23	0.69
8:H:95:TYR:HE2	8:H:97:MET:CG	2.06	0.69
8:H:130:ARG:HD3	8:H:130:ARG:H	1.56	0.69
12:L:32:ALA:HB2	12:L:55:ILE:HG13	1.74	0.69
1:A:390:GLN:O	1:A:394:ASN:HB2	1.92	0.68
2:B:751:VAL:HG13	2:B:812:LEU:HD22	1.75	0.68
1:A:55:ASP:C	1:A:57:ARG:N	2.50	0.68
4:D:208:GLU:HA	4:D:211:LEU:HD12	1.75	0.68
5:E:78:LEU:HD11	5:E:109:ILE:HD12	1.75	0.68
5:E:114:ASN:O	5:E:115:ASN:HB3	1.92	0.68
1:A:1223:ASP:HA	1:A:1243:VAL:CG2	2.21	0.68
2:B:244:LEU:O	2:B:249:ARG:HG3	1.93	0.68
2:B:642:ASP:CA	2:B:649:LYS:HA	2.19	0.68
4:D:17:LYS:HD2	4:D:18:VAL:HG13	1.75	0.68
5:E:92:THR:O	5:E:95:THR:HB	1.94	0.68
8:H:12:VAL:HG13	8:H:26:ILE:HD11	1.74	0.68
9:I:85:PHE:CD1	9:I:99:LEU:HD13	2.28	0.68
1:A:172:PRO:HB3	1:A:185:TRP:CE2	2.28	0.68
1:A:340:LEU:HD13	1:A:1429:ILE:HG23	1.75	0.68
9:I:74:GLU:HB3	9:I:81:ARG:HE	1.56	0.68
1:A:427:GLN:HB2	1:A:430:TRP:CD1	2.29	0.68
1:A:1223:ASP:CA	1:A:1243:VAL:HG22	2.23	0.68
1:A:284:ALA:O	1:A:286:HIS:N	2.25	0.68
1:A:899:VAL:CB	1:A:929:LEU:HD11	2.08	0.68
1:A:1149:ALA:HB2	9:I:47:GLU:HA	1.74	0.68
2:B:819:ALA:O	2:B:1093:GLN:HG2	1.94	0.68
2:B:975:GLN:O	2:B:990:ILE:HD12	1.94	0.68
9:I:44:TYR:HD1	9:I:45:ARG:N	1.91	0.68
9:I:99:LEU:C	9:I:100:PHE:HD1	2.02	0.68
1:A:1385:THR:HG22	1:A:1386:ARG:H	1.59	0.68
2:B:101:MET:HB2	2:B:109:THR:HG22	1.75	0.68
1:A:567:LYS:HZ1	8:H:43:ASN:HB3	1.59	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:718:VAL:O	1:A:722:LEU:HD12	1.94	0.68
1:A:1076:ALA:HA	1:A:1079:MET:HE2	1.76	0.68
2:B:705:MET:H	2:B:710:LEU:HD12	1.59	0.68
2:B:911:ILE:HD11	2:B:941:LEU:HD13	1.76	0.68
3:C:69:LEU:HB3	10:J:6:ARG:CD	2.24	0.68
8:H:127:GLY:O	8:H:128:ASN:HB2	1.91	0.68
1:A:134:ARG:HD2	1:A:221:SER:O	1.94	0.68
1:A:709:THR:HG23	9:I:94:ASP:HA	1.75	0.68
2:B:169:ARG:HB2	2:B:454:THR:HG23	1.75	0.68
2:B:789:MET:HE2	2:B:953:LEU:HD22	1.75	0.68
3:C:183:TRP:CZ2	3:C:207:CYS:HB3	2.29	0.68
6:F:119:ARG:HH11	6:F:119:ARG:CG	2.07	0.68
11:K:60:ALA:O	11:K:73:LEU:HD12	1.92	0.68
12:L:31:CYS:HA	12:L:55:ILE:HD11	1.76	0.68
1:A:57:ARG:O	1:A:68:GLN:HG2	1.94	0.68
1:A:445:ASN:HB2	1:A:455:MET:HG2	1.76	0.68
1:A:447:GLN:NE2	14:T:20:DG:H4'	2.09	0.68
1:A:709:THR:HB	1:A:712:GLU:H	1.59	0.68
2:B:307:ASP:OD2	2:B:310:MET:HB2	1.92	0.68
5:E:98:ILE:HG22	5:E:102:GLU:HG3	1.76	0.68
1:A:407:ARG:HG2	1:A:430:TRP:CH2	2.29	0.67
1:A:857:ARG:HD3	1:A:861:GLY:O	1.95	0.67
1:A:1120:LEU:HD13	1:A:1124:HIS:O	1.94	0.67
1:A:1237:ILE:HG22	1:A:1238:ILE:N	2.09	0.67
2:B:737:THR:CG2	9:I:66:PRO:HA	2.22	0.67
2:B:830:TYR:CE2	2:B:1000:PRO:HD3	2.28	0.67
2:B:868:MET:O	2:B:870:ILE:HG13	1.93	0.67
3:C:138:GLU:OE1	3:C:138:GLU:N	2.26	0.67
8:H:95:TYR:CE2	8:H:97:MET:HG3	2.27	0.67
1:A:745:GLN:HA	1:A:748:MET:HE3	1.76	0.67
1:A:923:LEU:O	1:A:927:VAL:HG23	1.94	0.67
2:B:918:ILE:HD12	2:B:935:ARG:NH1	2.08	0.67
2:B:1180:PHE:HB3	2:B:1191:ILE:CD1	2.23	0.67
5:E:117:THR:HG22	5:E:119:SER:N	2.08	0.67
8:H:42:ILE:HG23	8:H:95:TYR:CE1	2.26	0.67
1:A:1037:LEU:HD13	1:A:1041:ALA:HB1	1.76	0.67
1:A:1147:THR:HB	9:I:48:LEU:HD12	1.75	0.67
2:B:653:VAL:CG2	2:B:689:LEU:HB3	2.24	0.67
2:B:811:TYR:H	2:B:811:TYR:HD1	1.43	0.67
6:F:76:LYS:HA	6:F:79:ARG:HD2	1.75	0.67
11:K:107:THR:HG22	11:K:108:GLU:N	2.09	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:596:THR:C	1:A:598:LEU:H	2.02	0.67
1:A:1076:ALA:HA	1:A:1079:MET:CE	2.24	0.67
1:A:1258:HIS:O	1:A:1262:LYS:HG3	1.95	0.67
2:B:131:ASP:HA	2:B:164:LYS:HB3	1.76	0.67
1:A:829:VAL:C	1:A:831:THR:H	2.01	0.67
2:B:273:LEU:O	2:B:276:ILE:HG13	1.95	0.67
2:B:705:MET:N	2:B:710:LEU:HD12	2.08	0.67
1:A:153:PRO:HD3	1:A:161:LEU:HD13	1.74	0.67
1:A:407:ARG:HD2	1:A:413:ILE:HD11	1.76	0.67
1:A:442:VAL:HG12	1:A:491:VAL:HA	1.77	0.67
1:A:1329:THR:HG22	1:A:1331:SER:N	2.08	0.67
3:C:76:ASP:C	3:C:129:ILE:HD11	2.20	0.67
1:A:196:GLU:HG2	1:A:197:PRO:HD2	1.77	0.67
1:A:1227:ILE:HG22	1:A:1228:TRP:N	2.10	0.67
1:A:1436:ILE:O	1:A:1437:GLY:C	2.36	0.67
2:B:308:TRP:CH2	9:I:45:ARG:HG2	2.30	0.67
5:E:78:LEU:HD23	5:E:78:LEU:C	2.19	0.67
2:B:305:VAL:O	2:B:305:VAL:HG12	1.95	0.67
2:B:383:ASN:ND2	2:B:387:LEU:HD12	2.09	0.67
2:B:732:SER:HB2	2:B:734:HIS:NE2	2.10	0.67
2:B:992:ILE:HD11	11:K:66:PRO:HB2	1.76	0.67
2:B:1099:VAL:HG13	2:B:1100:ASP:H	1.59	0.67
2:B:1159:ARG:HB3	2:B:1159:ARG:HH11	1.59	0.67
2:B:193:LYS:HD3	2:B:787:VAL:HG11	1.77	0.67
2:B:515:HIS:CD2	2:B:516:ASN:N	2.61	0.67
2:B:953:LEU:O	2:B:964:VAL:HG23	1.95	0.67
1:A:12:ARG:HG2	1:A:13:THR:H	1.60	0.67
2:B:1002:THR:OG1	2:B:1006:ILE:HG13	1.94	0.67
3:C:35:ARG:NH1	11:K:41:THR:N	2.43	0.67
11:K:45:LEU:HG	11:K:94:ILE:CD1	2.25	0.67
1:A:134:ARG:HH11	1:A:221:SER:HA	1.59	0.66
2:B:769:TYR:HB3	2:B:773:MET:HE3	1.77	0.66
3:C:18:VAL:O	3:C:20:PHE:HD2	1.78	0.66
3:C:50:GLU:OE1	12:L:64:LEU:HD13	1.95	0.66
3:C:238:ILE:HD11	3:C:246:ARG:NE	2.09	0.66
4:D:24:ALA:HB3	4:D:26:THR:HG23	1.76	0.66
5:E:103:LYS:HD3	5:E:105:PHE:CZ	2.30	0.66
1:A:62:ASP:O	1:A:64:ASN:N	2.27	0.66
1:A:524:VAL:HG12	1:A:525:GLN:N	2.10	0.66
1:A:870:GLU:HG2	5:E:208:TYR:CG	2.30	0.66
2:B:281:PRO:O	2:B:283:VAL:N	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:289:LEU:HD13	2:B:375:ALA:CB	2.25	0.66
2:B:434:ARG:O	2:B:436:VAL:HG23	1.94	0.66
2:B:883:LEU:O	2:B:885:MET:N	2.28	0.66
9:I:26:LEU:HD22	9:I:35:VAL:HG12	1.76	0.66
1:A:7:SER:OG	2:B:1161:HIS:HE1	1.76	0.66
1:A:1029:ARG:HH11	1:A:1029:ARG:HG3	1.58	0.66
2:B:803:LEU:HD12	2:B:1032:SER:HB3	1.77	0.66
2:B:1102:LYS:O	2:B:1103:ILE:C	2.38	0.66
6:F:89:GLU:OE2	6:F:134:ILE:HG21	1.96	0.66
2:B:575:PRO:HG2	2:B:576:ASP:H	1.60	0.66
2:B:978:ASP:OD2	2:B:1098:MET:HG2	1.96	0.66
3:C:101:LEU:C	3:C:102:GLN:HG3	2.21	0.66
3:C:184:ASN:OD1	3:C:187:LYS:HA	1.95	0.66
6:F:105:ALA:HB1	6:F:106:PRO:HD2	1.77	0.66
2:B:203:PHE:HB3	2:B:205:ILE:CD1	2.25	0.66
2:B:505:ASP:OD2	13:N:1:DA:H5"	1.96	0.66
2:B:995:ARG:NH1	3:C:165:LYS:HG2	2.10	0.66
2:B:1017:ILE:H	2:B:1018:PRO:CD	2.08	0.66
12:L:58:LYS:O	12:L:59:ALA:O	2.14	0.66
1:A:265:LYS:HE3	1:A:302:THR:HG23	1.76	0.66
1:A:320:ARG:HB3	1:A:320:ARG:HH11	1.60	0.66
1:A:567:LYS:NZ	8:H:43:ASN:HB3	2.09	0.66
1:A:1155:ASP:OD2	1:A:1161:THR:HG23	1.96	0.66
2:B:600:LEU:O	2:B:609:ILE:HD11	1.96	0.66
4:D:124:GLU:O	4:D:128:VAL:HG23	1.94	0.66
7:G:52:ASP:C	7:G:53:ASN:HD22	2.03	0.66
8:H:26:ILE:HD12	8:H:49:VAL:HG11	1.76	0.66
1:A:146:MET:CA	1:A:171:GLN:HB2	2.26	0.66
1:A:316:GLN:HE21	1:A:317:LYS:HZ2	1.44	0.66
3:C:101:LEU:HD13	3:C:118:LEU:CD2	2.26	0.66
3:C:133:ILE:HD12	3:C:237:SER:N	2.10	0.66
4:D:71:LYS:HA	4:D:74:GLN:CB	2.24	0.66
9:I:61:ASP:C	9:I:63:GLY:H	2.03	0.66
12:L:30:ILE:HG22	12:L:31:CYS:N	2.09	0.66
1:A:12:ARG:NH2	2:B:1192:TYR:HE2	1.94	0.66
1:A:332:LYS:C	1:A:334:GLY:H	2.02	0.66
1:A:447:GLN:HE22	14:T:20:DG:H4'	1.60	0.66
2:B:31:TRP:CZ3	2:B:34:ILE:HD12	2.31	0.66
2:B:589:VAL:HG12	2:B:590:HIS:N	2.11	0.66
2:B:611:PRO:HG2	2:B:685:LEU:HD21	1.76	0.66
5:E:14:ARG:HH21	5:E:141:VAL:CG1	2.08	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:82:PRO:O	8:H:84:ALA:N	2.25	0.66
1:A:900:ASP:HA	1:A:926:GLN:HE22	1.61	0.66
3:C:177:GLU:CG	3:C:231:ASN:HD22	2.09	0.66
1:A:1116:LEU:H	1:A:1308:THR:HG22	1.59	0.66
2:B:307:ASP:OD2	2:B:310:MET:HE3	1.96	0.66
2:B:417:PHE:HE1	2:B:453:ILE:HD13	1.62	0.66
2:B:597:MET:SD	2:B:624:LEU:HD11	2.36	0.66
2:B:654:ARG:H	2:B:657:HIS:CD2	2.12	0.66
5:E:48:ASP:HB3	5:E:54:GLN:NE2	2.11	0.66
5:E:112:TYR:OH	5:E:136:ASN:HB2	1.95	0.66
1:A:299:HIS:HA	1:A:302:THR:CG2	2.26	0.65
1:A:682:THR:HG23	1:A:728:LYS:CE	2.25	0.65
1:A:1105:LEU:HD23	1:A:1384:VAL:HG21	1.77	0.65
4:D:155:ARG:HB2	4:D:155:ARG:CZ	2.26	0.65
8:H:17:PRO:HB3	8:H:24:CYS:HG	1.58	0.65
1:A:49:LYS:HE2	1:A:61:ILE:HD12	1.77	0.65
1:A:471:ASN:OD1	1:A:472:LEU:N	2.28	0.65
1:A:493:GLN:H	1:A:497:THR:HG21	1.62	0.65
1:A:567:LYS:HB3	8:H:96:VAL:N	2.10	0.65
1:A:682:THR:CG2	1:A:728:LYS:HE3	2.22	0.65
2:B:244:LEU:HD12	2:B:247:GLY:O	1.95	0.65
2:B:259:TYR:HD1	2:B:259:TYR:H	1.44	0.65
2:B:291:ILE:H	2:B:291:ILE:CD1	2.09	0.65
2:B:956:THR:HG22	2:B:960:GLY:HA2	1.77	0.65
3:C:184:ASN:HD21	3:C:189:THR:H	1.44	0.65
4:D:12:ARG:HH12	4:D:14:ARG:HA	1.62	0.65
4:D:156:ASP:O	4:D:158:GLU:N	2.30	0.65
4:D:210:ILE:O	4:D:214:LEU:HD23	1.96	0.65
5:E:98:ILE:HA	5:E:101:GLN:CB	2.25	0.65
5:E:128:PRO:HA	5:E:129:PRO:C	2.20	0.65
12:L:48:CYS:HB3	12:L:51:CYS:O	1.95	0.65
1:A:464:PRO:HG2	1:A:465:TYR:CD1	2.31	0.65
8:H:76:THR:HG21	8:H:141:TYR:OH	1.95	0.65
8:H:139:ASN:O	8:H:140:ALA:CB	2.44	0.65
2:B:839:MET:HE3	2:B:1010:LEU:HD21	1.77	0.65
9:I:67:THR:OG1	9:I:68:LEU:HD12	1.96	0.65
11:K:17:SER:O	11:K:18:LYS:C	2.38	0.65
1:A:320:ARG:HB3	1:A:320:ARG:NH1	2.11	0.65
2:B:810:GLU:HB3	2:B:811:TYR:CD1	2.30	0.65
2:B:824:ILE:HG22	2:B:1087:PHE:CE2	2.31	0.65
4:D:185:CYS:O	4:D:211:LEU:HD22	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:82:GLU:O	9:I:104:LEU:HG	1.96	0.65
1:A:687:LYS:O	1:A:690:VAL:HB	1.97	0.65
2:B:205:ILE:N	2:B:205:ILE:HD12	2.11	0.65
2:B:589:VAL:HG12	2:B:590:HIS:H	1.62	0.65
4:D:12:ARG:HG2	4:D:12:ARG:HH11	1.61	0.65
4:D:69:ALA:HB2	4:D:72:ARG:HH12	1.59	0.65
8:H:30:SER:CB	8:H:36:CYS:HB3	2.26	0.65
9:I:44:TYR:CD1	9:I:45:ARG:N	2.65	0.65
9:I:111:THR:HG21	9:I:113:ASP:HB2	1.77	0.65
1:A:12:ARG:NH2	2:B:1192:TYR:CE2	2.64	0.65
1:A:105:CYS:SG	1:A:139:TRP:HA	2.37	0.65
1:A:688:LYS:HG3	1:A:691:LEU:HD23	1.77	0.65
1:A:1121:GLU:CG	1:A:1122:PRO:HD2	2.27	0.65
2:B:866:TYR:CB	2:B:870:ILE:HB	2.25	0.65
2:B:1202:LEU:O	2:B:1206:GLU:HG3	1.96	0.65
4:D:118:THR:HG22	4:D:118:THR:O	1.97	0.65
7:G:119:LEU:HD13	7:G:132:SER:HB2	1.77	0.65
1:A:125:ALA:C	1:A:127:ALA:H	2.03	0.65
1:A:332:LYS:O	1:A:333:GLU:HB2	1.96	0.65
1:A:537:ARG:HD2	8:H:20:TYR:CE1	2.30	0.65
1:A:1041:ALA:O	1:A:1045:VAL:HG23	1.97	0.65
2:B:284:ILE:HG21	2:B:333:PHE:HD2	1.61	0.65
2:B:846:ILE:CG2	2:B:974:PRO:HG2	2.27	0.65
8:H:93:TYR:HB3	8:H:144:ILE:O	1.97	0.65
1:A:298:PHE:O	1:A:302:THR:HG22	1.97	0.65
2:B:254:LEU:HD23	2:B:381:MET:CE	2.26	0.65
2:B:277:LYS:H	2:B:277:LYS:CD	2.10	0.65
2:B:520:GLY:H	2:B:748:ILE:HG22	1.62	0.65
3:C:147:LEU:HB2	3:C:151:GLN:HB2	1.79	0.65
5:E:40:GLU:H	5:E:40:GLU:CD	2.05	0.65
5:E:124:VAL:HA	5:E:132:ILE:HD12	1.77	0.65
8:H:38:LEU:HD13	8:H:125:LEU:HD12	1.77	0.65
9:I:68:LEU:HD12	9:I:68:LEU:N	2.12	0.65
12:L:38:LEU:CG	12:L:39:SER:H	2.05	0.65
1:A:288:ALA:HA	1:A:291:GLU:CG	2.27	0.65
1:A:567:LYS:HB3	8:H:95:TYR:HA	1.77	0.65
1:A:1094:VAL:HG13	1:A:1113:THR:HB	1.79	0.65
1:A:1341:ILE:CG2	1:A:1342:GLU:N	2.58	0.65
2:B:165:VAL:CG1	2:B:448:ILE:HD13	2.27	0.65
2:B:785:TYR:CD1	2:B:786:ASN:N	2.65	0.65
1:A:568:PRO:CG	8:H:46:LEU:HD22	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1011:GLN:NE2	1:A:1015:VAL:HG21	2.13	0.64
2:B:855:PHE:CD2	2:B:972:LYS:HE3	2.32	0.64
2:B:878:GLN:HB3	2:B:879:ARG:NH1	2.11	0.64
2:B:1034:VAL:O	2:B:1037:LEU:N	2.30	0.64
2:B:1163:CYS:SG	2:B:1165:ILE:HB	2.36	0.64
3:C:196:ASP:CB	3:C:199:LYS:HD3	2.27	0.64
4:D:29:LEU:HD22	4:D:29:LEU:N	2.12	0.64
7:G:125:SER:OG	7:G:128:PRO:HA	1.98	0.64
9:I:82:GLU:C	9:I:104:LEU:HG	2.22	0.64
10:J:14:VAL:O	10:J:14:VAL:HG12	1.97	0.64
11:K:47:ARG:HH11	11:K:47:ARG:CB	2.08	0.64
2:B:1182:CYS:O	2:B:1182:CYS:SG	2.54	0.64
3:C:50:GLU:CG	12:L:64:LEU:HD22	2.27	0.64
5:E:15:ALA:O	5:E:19:VAL:HG23	1.97	0.64
2:B:20:ASP:O	2:B:22:SER:N	2.28	0.64
2:B:20:ASP:C	2:B:22:SER:H	2.05	0.64
2:B:622:LYS:NZ	9:I:59:VAL:HG13	2.13	0.64
3:C:69:LEU:HB3	10:J:6:ARG:HD3	1.79	0.64
4:D:69:ALA:C	4:D:71:LYS:H	2.05	0.64
11:K:47:ARG:O	11:K:47:ARG:HD2	1.97	0.64
14:T:22:DC:H2"	14:T:23:BRU:OP2	1.97	0.64
1:A:107:CYS:HA	1:A:171:GLN:HE22	1.63	0.64
1:A:697:ALA:HB2	1:A:702:LEU:HD12	1.79	0.64
2:B:653:VAL:HA	2:B:657:HIS:CD2	2.32	0.64
10:J:24:LEU:CD1	10:J:38:ARG:HG2	2.28	0.64
12:L:28:LYS:HB3	12:L:39:SER:HB2	1.80	0.64
1:A:839:ARG:HG2	1:A:839:ARG:NH1	2.10	0.64
1:A:898:ARG:HD3	1:A:933:TYR:CD1	2.33	0.64
1:A:1173:HIS:CD2	1:A:1227:ILE:HG23	2.33	0.64
2:B:464:GLY:O	2:B:477:ALA:HA	1.98	0.64
2:B:999:MET:HA	2:B:999:MET:CE	2.23	0.64
3:C:242:GLN:HA	3:C:245:VAL:HG23	1.79	0.64
4:D:50:LEU:HD21	7:G:4:ILE:HD11	1.78	0.64
1:A:228:PHE:HE2	4:D:15:LEU:HD23	1.63	0.64
1:A:901:LEU:HB2	1:A:926:GLN:HG2	1.78	0.64
1:A:1168:GLU:OE2	1:A:1172:LEU:HD11	1.98	0.64
2:B:126:SER:OG	2:B:172:ILE:HD11	1.98	0.64
4:D:195:ILE:CG2	4:D:198:LEU:HG	2.27	0.64
5:E:124:VAL:HG13	5:E:132:ILE:HB	1.80	0.64
1:A:73:GLY:O	1:A:75:ASN:N	2.31	0.64
1:A:344:ARG:HB3	1:A:344:ARG:HH11	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:114:PRO:HG3	2:B:181:LEU:HD11	1.80	0.64
4:D:12:ARG:HG2	4:D:12:ARG:NH1	2.13	0.64
4:D:15:LEU:O	4:D:15:LEU:HD12	1.97	0.64
5:E:120:ALA:C	5:E:123:LEU:HG	2.23	0.64
5:E:212:ARG:HG3	5:E:212:ARG:HH11	1.63	0.64
6:F:88:TYR:O	6:F:89:GLU:C	2.41	0.64
1:A:35:ILE:HG22	1:A:35:ILE:O	1.96	0.64
1:A:875:ALA:HB2	1:A:1366:ARG:HD2	1.80	0.64
2:B:365:THR:HG23	2:B:367:LEU:H	1.62	0.64
3:C:172:PRO:O	3:C:235:VAL:HG23	1.96	0.64
3:C:252:GLN:HG3	11:K:95:ILE:HG23	1.80	0.64
5:E:32:GLN:HG3	5:E:36:GLU:OE2	1.98	0.64
11:K:47:ARG:HB3	11:K:47:ARG:NH1	2.09	0.64
1:A:144:THR:O	1:A:146:MET:HE2	1.98	0.64
1:A:896:ARG:NH2	1:A:1030:ARG:NH2	2.46	0.64
2:B:92:PHE:HB3	2:B:130:VAL:HG11	1.79	0.64
2:B:1071:VAL:HG22	2:B:1084:GLN:HG3	1.79	0.64
3:C:82:TYR:O	3:C:83:SER:C	2.42	0.64
3:C:112:ASN:HB3	3:C:114:TYR:CE1	2.33	0.64
5:E:135:PHE:HB3	5:E:140:LEU:HD21	1.78	0.64
6:F:109:VAL:HG12	6:F:110:ASP:H	1.63	0.64
7:G:81:PRO:HB3	7:G:106:MET:HE1	1.80	0.64
11:K:21:ILE:HG23	11:K:33:ILE:HG12	1.80	0.64
14:T:16:DT:H1'	14:T:17:DT:H5'	1.78	0.64
1:A:414:ASP:OD1	1:A:416:ARG:HG2	1.97	0.63
2:B:800:GLN:HB3	10:J:52:THR:CG2	2.28	0.63
4:D:69:ALA:HA	4:D:72:ARG:HG3	1.80	0.63
4:D:146:GLN:O	4:D:149:THR:HG22	1.98	0.63
8:H:4:THR:HA	8:H:60:ALA:CB	2.16	0.63
8:H:32:THR:HG22	8:H:33:GLN:OE1	1.98	0.63
10:J:43:ARG:CD	10:J:43:ARG:H	2.11	0.63
11:K:32:VAL:HG22	11:K:74:ARG:HG3	1.80	0.63
1:A:280:GLU:HG2	1:A:289:ILE:HD11	1.79	0.63
1:A:677:ARG:HD2	1:A:678:GLU:N	2.12	0.63
2:B:29:ASP:CG	2:B:658:ILE:HD13	2.22	0.63
2:B:221:ASN:O	2:B:222:ILE:HG13	1.98	0.63
2:B:882:THR:HG22	2:B:883:LEU:N	2.12	0.63
2:B:1001:PHE:CE1	2:B:1073:TYR:HB2	2.33	0.63
4:D:134:THR:HG22	4:D:136:GLY:H	1.62	0.63
5:E:153:HIS:O	5:E:154:ILE:HG13	1.98	0.63
1:A:825:ILE:HD11	2:B:512:ARG:O	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1037:LEU:HD13	1:A:1041:ALA:CB	2.29	0.63
2:B:880:THR:CG2	2:B:934:LYS:HG3	2.29	0.63
4:D:24:ALA:CB	4:D:26:THR:HG23	2.28	0.63
7:G:155:SER:O	7:G:156:SER:HB3	1.97	0.63
8:H:56:THR:HB	8:H:145:ARG:HG2	1.80	0.63
11:K:12:LEU:HD21	11:K:18:LYS:N	2.12	0.63
1:A:61:ILE:HG22	1:A:62:ASP:H	1.64	0.63
1:A:380:VAL:HG12	1:A:428:TYR:HA	1.80	0.63
1:A:973:ILE:HD11	1:A:1038:THR:HG23	1.80	0.63
2:B:57:TYR:CD1	2:B:57:TYR:N	2.67	0.63
3:C:80:LEU:HD12	3:C:81:GLU:H	1.63	0.63
3:C:88:CYS:SG	3:C:91:HIS:C	2.82	0.63
3:C:89:GLU:O	3:C:90:ASP:HB3	1.98	0.63
3:C:208:GLU:C	3:C:210:GLU:H	2.06	0.63
4:D:213:GLU:OE1	4:D:213:GLU:HA	1.97	0.63
8:H:81:PRO:CB	8:H:82:PRO:CD	2.77	0.63
1:A:305:ASP:OD2	1:A:326:ARG:HD3	1.98	0.63
1:A:774:ARG:NH1	1:A:797:LYS:HG3	2.13	0.63
1:A:934:LYS:O	1:A:937:VAL:HG12	1.98	0.63
2:B:834:ASN:HB3	2:B:840:ILE:HG13	1.81	0.63
2:B:1103:ILE:HG23	2:B:1103:ILE:O	1.98	0.63
4:D:54:GLU:O	4:D:58:VAL:HG23	1.99	0.63
4:D:175:PHE:HZ	7:G:85:GLU:HG3	1.63	0.63
1:A:38:PRO:HA	1:A:270:LEU:HD23	1.81	0.63
1:A:172:PRO:HD3	1:A:185:TRP:NE1	2.14	0.63
2:B:507:LYS:C	2:B:508:LEU:HD23	2.24	0.63
3:C:175:ALA:HB2	10:J:43:ARG:HH22	1.62	0.63
3:C:232:VAL:HG21	3:C:244:VAL:HG22	1.79	0.63
6:F:69:LEU:HB3	6:F:71:GLU:CD	2.24	0.63
1:A:57:ARG:O	1:A:58:LEU:O	2.15	0.63
1:A:63:ARG:HA	1:A:74:MET:HE2	1.81	0.63
1:A:100:LYS:HE2	1:A:104:GLU:OE2	1.99	0.63
1:A:207:ILE:HG22	1:A:211:PHE:CE2	2.33	0.63
1:A:567:LYS:HZ1	8:H:43:ASN:HD22	1.45	0.63
1:A:1141:THR:HG23	1:A:1205:LYS:HD3	1.80	0.63
1:A:1436:ILE:HD13	2:B:1139:ILE:HG23	1.79	0.63
4:D:32:GLU:HG3	7:G:5:LYS:HE2	1.81	0.63
5:E:23:VAL:HG13	5:E:78:LEU:HD13	1.79	0.63
5:E:77:SER:O	5:E:105:PHE:HB3	1.99	0.63
7:G:18:PHE:HA	7:G:22:MET:HE3	1.81	0.63
1:A:709:THR:HG22	1:A:710:LEU:N	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1115:SER:H	1:A:1330:ASN:HD21	1.47	0.63
2:B:579:ARG:HG2	2:B:579:ARG:HH11	1.63	0.63
2:B:831:SER:HB3	2:B:994:TYR:OH	1.99	0.63
5:E:22:MET:CE	5:E:26:ARG:HH21	2.12	0.63
6:F:90:ARG:CD	6:F:155:LEU:HD13	2.29	0.63
8:H:11:GLN:C	8:H:28:ALA:HB1	2.24	0.63
8:H:130:ARG:HB3	8:H:134:ASN:H	1.62	0.63
1:A:56:PRO:O	1:A:57:ARG:HG3	1.98	0.63
1:A:251:SER:HA	1:A:257:ARG:O	1.98	0.63
1:A:605:MET:HE2	1:A:607:ILE:CG1	2.27	0.63
1:A:869:GLY:O	5:E:204:THR:HG21	1.99	0.63
1:A:1353:TYR:C	1:A:1353:TYR:CD2	2.77	0.63
2:B:622:LYS:HZ3	9:I:59:VAL:HG13	1.62	0.63
2:B:850:LEU:HD12	2:B:851:PHE:N	2.14	0.63
3:C:114:TYR:CD2	3:C:140:ASN:HB3	2.33	0.63
6:F:94:LEU:HD22	6:F:122:MET:HG2	1.80	0.63
1:A:1079:MET:HG2	1:A:1359:ASP:OD1	1.98	0.62
2:B:393:LYS:HA	2:B:393:LYS:HE3	1.79	0.62
6:F:111:LEU:HD12	6:F:111:LEU:H	1.64	0.62
12:L:38:LEU:CD2	12:L:48:CYS:HA	2.29	0.62
14:T:14:DA:H2"	14:T:15:DG:C8	2.33	0.62
1:A:50:ILE:C	1:A:52:GLY:H	2.06	0.62
2:B:582:VAL:HB	2:B:587:HIS:HD2	1.62	0.62
7:G:44:TYR:CD2	7:G:105:PRO:HB2	2.35	0.62
9:I:58:VAL:O	9:I:58:VAL:HG12	1.98	0.62
1:A:794:PRO:C	1:A:796:SER:H	2.06	0.62
1:A:809:THR:OG1	1:A:812:GLU:HG3	1.97	0.62
1:A:1147:THR:HB	9:I:48:LEU:CD1	2.29	0.62
1:A:1329:THR:HG22	1:A:1331:SER:H	1.64	0.62
1:A:1385:THR:HG21	1:A:1387:HIS:CD2	2.33	0.62
6:F:111:LEU:O	6:F:113:GLY:N	2.29	0.62
1:A:145:LYS:HD2	1:A:149:GLU:OE1	1.98	0.62
2:B:333:PHE:HE1	2:B:336:ARG:HH11	1.46	0.62
2:B:806:THR:H	2:B:809:MET:HG3	1.63	0.62
2:B:848:ARG:HH22	2:B:996:ARG:HD3	1.64	0.62
4:D:5:THR:O	4:D:5:THR:HG23	2.00	0.62
6:F:76:LYS:HE3	6:F:150:GLU:OE2	2.00	0.62
6:F:76:LYS:O	6:F:79:ARG:HD3	1.99	0.62
7:G:14:HIS:HD2	7:G:16:SER:H	1.43	0.62
2:B:69:LEU:HD13	2:B:432:MET:HE1	1.81	0.62
2:B:211:VAL:HG23	2:B:483:LEU:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:284:ILE:HD13	2:B:333:PHE:CD2	2.33	0.62
2:B:990:ILE:HG22	2:B:991:GLY:N	2.14	0.62
2:B:1007:VAL:CG2	2:B:1008:PRO:HD2	2.29	0.62
2:B:1007:VAL:HG23	2:B:1008:PRO:HD2	1.82	0.62
2:B:1069:PHE:H	2:B:1069:PHE:HD1	1.47	0.62
8:H:89:LEU:HD12	8:H:91:ASP:OD1	2.00	0.62
8:H:94:ASP:O	8:H:95:TYR:HB2	1.99	0.62
1:A:504:LEU:HD11	6:F:91:ALA:CB	2.30	0.62
1:A:873:MET:C	1:A:1058:VAL:HG23	2.24	0.62
1:A:916:GLY:O	1:A:919:ILE:HG22	1.99	0.62
1:A:1135:ARG:HG2	1:A:1136:SER:N	2.13	0.62
2:B:425:THR:HA	2:B:428:ILE:HD12	1.82	0.62
2:B:1058:LEU:O	2:B:1061:GLU:HB2	1.99	0.62
3:C:165:LYS:O	11:K:6:ARG:NH1	2.33	0.62
6:F:69:LEU:O	6:F:71:GLU:HG3	1.99	0.62
8:H:11:GLN:HA	8:H:53:ASP:O	2.00	0.62
1:A:216:VAL:O	1:A:219:PHE:HB2	1.99	0.62
1:A:230:ARG:H	1:A:233:TRP:HE3	1.47	0.62
1:A:809:THR:H	1:A:812:GLU:HB2	1.63	0.62
1:A:1006:ILE:HD12	5:E:167:ARG:CB	2.30	0.62
2:B:955:THR:HG23	2:B:956:THR:H	1.64	0.62
3:C:189:THR:CG2	3:C:190:ASP:H	2.12	0.62
6:F:111:LEU:HD12	6:F:111:LEU:N	2.15	0.62
1:A:51:GLY:HA2	1:A:56:PRO:HA	1.82	0.62
1:A:66:LYS:NZ	1:A:68:GLN:N	2.46	0.62
2:B:365:THR:HG23	2:B:367:LEU:N	2.14	0.62
2:B:859:TYR:OH	2:B:941:LEU:HD12	1.99	0.62
3:C:177:GLU:HG3	3:C:231:ASN:ND2	2.09	0.62
3:C:183:TRP:O	3:C:185:LYS:N	2.33	0.62
6:F:103:MET:HE2	7:G:66:GLY:N	2.11	0.62
7:G:13:LEU:HD21	7:G:17:PHE:HB2	1.81	0.62
8:H:26:ILE:HG22	8:H:40:LEU:O	2.00	0.62
9:I:61:ASP:O	9:I:64:SER:N	2.32	0.62
1:A:1149:ALA:CB	9:I:47:GLU:HA	2.30	0.62
1:A:1317:MET:HE2	5:E:142:VAL:CG1	2.30	0.62
2:B:125:SER:HA	2:B:171:PRO:HA	1.81	0.62
2:B:505:ASP:CG	13:N:1:DA:H8	2.08	0.62
2:B:604:ARG:NH1	2:B:691:GLU:OE2	2.32	0.62
2:B:996:ARG:NH2	3:C:38:ILE:HG23	2.15	0.62
3:C:124:LEU:O	3:C:125:MET:C	2.42	0.62
7:G:87:VAL:CG2	7:G:103:VAL:HG21	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:103:LYS:HB3	8:H:115:TYR:CD1	2.35	0.62
9:I:10:CYS:SG	9:I:32:CYS:HB3	2.38	0.62
1:A:946:VAL:CG2	5:E:201:LYS:HD2	2.30	0.62
2:B:948:ILE:HG22	2:B:949:VAL:O	2.00	0.62
2:B:1096:ARG:O	2:B:1097:HIS:HB2	2.00	0.62
4:D:130:LEU:HD13	4:D:142:LYS:HG2	1.81	0.62
5:E:195:VAL:HG22	5:E:213:ILE:HG13	1.82	0.62
5:E:204:THR:HG23	5:E:205:SER:H	1.64	0.62
10:J:30:LEU:HD23	10:J:31:ASP:H	1.65	0.62
1:A:157:ASP:OD2	1:A:160:GLN:HG3	2.00	0.61
1:A:399:HIS:O	1:A:401:GLY:N	2.33	0.61
2:B:100:PRO:O	2:B:180:TYR:OH	2.17	0.61
2:B:473:MET:HE3	2:B:474:SER:HA	1.82	0.61
3:C:179:GLU:HG2	3:C:180:TYR:N	2.15	0.61
4:D:50:LEU:HD13	4:D:55:ALA:HA	1.81	0.61
12:L:32:ALA:HB3	12:L:33:GLU:OE2	1.99	0.61
2:B:57:TYR:N	2:B:57:TYR:HD1	1.98	0.61
2:B:241:ARG:HG2	2:B:253:THR:HG22	1.81	0.61
2:B:619:ILE:HG22	2:B:620:ARG:N	2.15	0.61
2:B:815:ARG:HD3	2:B:1041:GLU:OE2	1.99	0.61
2:B:885:MET:HA	2:B:936:ASP:CB	2.26	0.61
5:E:93:MET:HG2	5:E:123:LEU:HD12	1.80	0.61
7:G:9:LEU:HD12	7:G:10:ASN:H	1.64	0.61
10:J:1:MET:N	10:J:56:LEU:N	2.48	0.61
12:L:38:LEU:O	12:L:39:SER:HB3	2.00	0.61
1:A:1171:GLN:OE1	1:A:1172:LEU:HG	2.01	0.61
3:C:186:LEU:N	3:C:186:LEU:HD12	2.15	0.61
4:D:122:GLU:HA	4:D:125:SER:HB3	1.81	0.61
6:F:90:ARG:HH21	6:F:94:LEU:HD11	1.64	0.61
8:H:25:ARG:HA	8:H:41:ASP:HA	1.81	0.61
1:A:322:VAL:HG13	1:A:322:VAL:O	1.99	0.61
1:A:718:VAL:O	1:A:721:PHE:HB2	2.00	0.61
1:A:782:ARG:NH2	2:B:699:GLU:O	2.32	0.61
1:A:855:THR:HA	1:A:866:PHE:O	2.00	0.61
1:A:1127:ASP:CG	1:A:1130:GLN:HB2	2.25	0.61
10:J:64:ASN:CB	10:J:65:PRO:CD	2.76	0.61
1:A:743:VAL:O	1:A:747:VAL:HG23	2.01	0.61
1:A:1438:THR:HB	2:B:1144:ALA:HB3	1.82	0.61
2:B:345:LYS:HG2	2:B:349:ILE:HD11	1.82	0.61
2:B:839:MET:CE	2:B:980:PHE:HB2	2.29	0.61
3:C:235:VAL:HG11	10:J:6:ARG:NH2	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:108:GLY:HA3	5:E:132:ILE:HG23	1.81	0.61
7:G:45:ILE:HA	7:G:78:VAL:HG12	1.83	0.61
1:A:21:LEU:HD11	1:A:1414:ALA:HA	1.82	0.61
1:A:297:GLN:HG3	1:A:297:GLN:O	1.99	0.61
1:A:311:GLN:O	1:A:313:GLN:N	2.33	0.61
1:A:445:ASN:ND2	1:A:455:MET:HE3	2.14	0.61
1:A:665:GLY:C	1:A:666:ILE:HD12	2.25	0.61
1:A:1048:ASN:O	1:A:1049:ILE:C	2.43	0.61
2:B:570:VAL:HG21	2:B:573:GLN:CD	2.25	0.61
3:C:25:VAL:HG12	3:C:26:ASP:H	1.66	0.61
3:C:52:GLU:OE2	3:C:154:LYS:HD2	2.01	0.61
3:C:88:CYS:SG	3:C:91:HIS:CA	2.88	0.61
6:F:152:ILE:HG22	6:F:153:VAL:N	2.15	0.61
8:H:43:ASN:ND2	8:H:46:LEU:HB2	2.15	0.61
8:H:84:ALA:HB1	8:H:87:ARG:HB2	1.82	0.61
14:T:14:DA:H2"	14:T:15:DG:H8	1.66	0.61
1:A:1141:THR:HG23	1:A:1205:LYS:HZ2	1.66	0.61
2:B:326:ASP:OD2	2:B:328:GLU:HB3	2.01	0.61
2:B:806:THR:CG2	2:B:808:ALA:HB3	2.30	0.61
3:C:189:THR:CG2	3:C:190:ASP:N	2.64	0.61
7:G:1:MET:SD	7:G:79:PHE:CD1	2.94	0.61
12:L:52:GLY:O	12:L:53:HIS:C	2.43	0.61
1:A:34:LYS:CG	1:A:36:ARG:HH21	2.14	0.61
1:A:868:TYR:CD2	1:A:1058:VAL:HG21	2.36	0.61
2:B:186:GLU:HG2	10:J:62:ARG:NH2	2.16	0.61
2:B:542:MET:SD	2:B:747:MET:HE2	2.40	0.61
9:I:53:GLY:O	9:I:89:GLN:HB2	2.00	0.61
12:L:61:THR:HG22	12:L:63:ARG:HG3	1.82	0.61
1:A:1438:THR:O	6:F:92:ARG:NH1	2.34	0.61
2:B:129:PHE:CE2	2:B:166:PHE:HB2	2.36	0.61
2:B:466:TRP:O	2:B:468:GLU:N	2.34	0.61
2:B:611:PRO:HB3	2:B:685:LEU:HD11	1.82	0.61
4:D:7:THR:O	4:D:9:GLN:N	2.32	0.61
4:D:220:LEU:HG	4:D:221:TYR:N	2.15	0.61
6:F:128:LYS:HD3	6:F:149:GLU:O	2.00	0.61
7:G:114:LEU:HD23	7:G:162:SER:HB3	1.82	0.61
1:A:1353:TYR:C	1:A:1353:TYR:HD2	2.09	0.61
2:B:41:LYS:HE2	2:B:41:LYS:HA	1.83	0.61
2:B:230:ALA:HB3	2:B:231:PRO:HD3	1.83	0.61
2:B:378:LEU:HD12	2:B:378:LEU:O	1.99	0.61
2:B:734:HIS:O	2:B:735:ALA:HB2	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:112:ASN:CB	3:C:114:TYR:HE1	2.13	0.61
3:C:124:LEU:H	3:C:124:LEU:HD12	1.66	0.61
7:G:1:MET:SD	7:G:1:MET:C	2.82	0.61
8:H:11:GLN:O	8:H:28:ALA:HB1	2.01	0.61
10:J:1:MET:N	10:J:57:ILE:N	2.34	0.61
12:L:38:LEU:HD11	12:L:49:LYS:HE2	1.82	0.61
1:A:23:SER:HA	1:A:233:TRP:CD1	2.36	0.60
1:A:93:VAL:HG23	1:A:304:MET:HE3	1.83	0.60
1:A:157:ASP:OD2	1:A:159:THR:HB	2.01	0.60
1:A:567:LYS:HZ2	8:H:46:LEU:HB2	1.64	0.60
1:A:590:ARG:HG2	1:A:604:GLY:HA2	1.82	0.60
1:A:741:ASN:HD21	1:A:743:VAL:HB	1.66	0.60
1:A:1215:ARG:NH1	1:A:1272:THR:O	2.34	0.60
2:B:29:ASP:OD1	2:B:658:ILE:HD13	2.01	0.60
2:B:101:MET:CE	2:B:126:SER:HA	2.31	0.60
2:B:582:VAL:HG22	2:B:626:ILE:CB	2.29	0.60
2:B:1031:LEU:HB2	2:B:1055:ILE:HD13	1.82	0.60
2:B:1084:GLN:N	2:B:1084:GLN:NE2	2.49	0.60
4:D:192:LYS:HD2	4:D:199:ASN:HA	1.82	0.60
4:D:219:THR:HG22	4:D:220:LEU:O	2.01	0.60
8:H:89:LEU:O	8:H:91:ASP:N	2.34	0.60
1:A:332:LYS:HB2	1:A:337:ARG:HH12	1.64	0.60
1:A:482:PHE:C	1:A:484:GLY:H	2.09	0.60
1:A:786:HIS:N	1:A:786:HIS:CD2	2.69	0.60
2:B:39:ARG:HE	2:B:665:GLU:HG2	1.65	0.60
2:B:424:LEU:O	2:B:427:ASP:HB3	2.01	0.60
2:B:1099:VAL:CG1	2:B:1100:ASP:N	2.64	0.60
3:C:31:ASN:O	3:C:34:ARG:HB3	2.01	0.60
5:E:69:ILE:HD12	5:E:69:ILE:H	1.66	0.60
1:A:90:VAL:CG1	1:A:297:GLN:HA	2.31	0.60
1:A:167:CYS:HB2	1:A:169:ASN:HD21	1.67	0.60
1:A:818:MET:HE3	2:B:514:LEU:O	2.01	0.60
1:A:1208:THR:HG22	1:A:1210:GLY:H	1.66	0.60
2:B:56:ASP:HB3	2:B:57:TYR:CD1	2.36	0.60
2:B:957:ASN:O	2:B:960:GLY:N	2.34	0.60
4:D:207:LEU:O	4:D:211:LEU:HD12	2.01	0.60
11:K:88:LYS:O	11:K:91:CYS:HB2	2.01	0.60
1:A:63:ARG:HA	1:A:74:MET:CE	2.31	0.60
1:A:321:PRO:O	1:A:322:VAL:HB	2.01	0.60
1:A:929:LEU:O	1:A:929:LEU:HD13	2.02	0.60
1:A:1168:GLU:O	1:A:1171:GLN:OE1	2.19	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1206:ASP:O	1:A:1207:LEU:HD23	2.00	0.60
2:B:199:MET:HE2	2:B:492:LEU:CD2	2.31	0.60
2:B:770:GLN:OE1	2:B:983:ARG:CA	2.47	0.60
2:B:849:GLY:O	2:B:850:LEU:C	2.44	0.60
3:C:196:ASP:CG	3:C:199:LYS:HD3	2.26	0.60
5:E:80:VAL:HG12	5:E:82:PHE:HE1	1.66	0.60
7:G:26:LEU:HD11	7:G:70:PHE:CD1	2.36	0.60
12:L:33:GLU:H	12:L:33:GLU:CD	2.09	0.60
1:A:67:CYS:O	1:A:68:GLN:HG3	2.02	0.60
1:A:616:VAL:HG12	1:A:617:VAL:N	2.16	0.60
1:A:719:VAL:HA	1:A:722:LEU:HD13	1.83	0.60
1:A:982:THR:C	1:A:984:LYS:N	2.58	0.60
1:A:1153:TYR:CD2	1:A:1163:ILE:HD11	2.37	0.60
2:B:102:VAL:CG2	2:B:112:LEU:HD22	2.32	0.60
2:B:217:ARG:NE	2:B:405:ARG:HB2	2.13	0.60
2:B:361:LEU:O	2:B:363:HIS:O	2.19	0.60
2:B:644:GLU:HB2	2:B:648:HIS:O	2.02	0.60
5:E:204:THR:HG23	5:E:205:SER:N	2.17	0.60
6:F:90:ARG:HH21	6:F:94:LEU:CD1	2.14	0.60
1:A:596:THR:O	1:A:598:LEU:N	2.34	0.60
1:A:1102:LYS:O	1:A:1106:ASN:ND2	2.34	0.60
2:B:639:ILE:HG22	2:B:641:GLU:HG2	1.84	0.60
2:B:831:SER:CB	2:B:994:TYR:OH	2.48	0.60
3:C:146:LYS:C	3:C:147:LEU:HD23	2.26	0.60
3:C:175:ALA:HB2	10:J:43:ARG:NH2	2.17	0.60
5:E:161:LYS:HD2	5:E:195:VAL:HG23	1.84	0.60
8:H:15:VAL:HG13	8:H:26:ILE:CB	2.31	0.60
1:A:1035:TYR:HB3	1:A:1037:LEU:HD23	1.83	0.60
1:A:1341:ILE:CG2	1:A:1342:GLU:H	2.14	0.60
2:B:105:SER:O	2:B:106:ASP:HB2	2.00	0.60
4:D:56:ARG:NH2	4:D:155:ARG:HB3	2.16	0.60
4:D:220:LEU:CG	4:D:221:TYR:H	2.14	0.60
14:T:18:DA:H3'	14:T:18:DA:OP1	2.00	0.60
1:A:148:CYS:HB3	1:A:167:CYS:O	2.02	0.60
1:A:688:LYS:C	1:A:690:VAL:N	2.57	0.60
3:C:79:GLN:HE21	3:C:127:ARG:HD3	1.67	0.60
3:C:242:GLN:C	3:C:244:VAL:H	2.10	0.60
5:E:157:SER:C	5:E:159:ASP:N	2.58	0.60
5:E:186:LEU:O	5:E:189:GLY:N	2.27	0.60
7:G:115:MET:HG2	7:G:163:ILE:HD11	1.84	0.60
1:A:129:LYS:O	1:A:130:ASP:HB2	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1293:SER:OG	1:A:1295:THR:HG23	2.02	0.60
2:B:210:LYS:HD3	2:B:482:VAL:HG22	1.84	0.60
2:B:233:PRO:HG2	2:B:234:ILE:HD13	1.83	0.60
2:B:430:ARG:HB3	2:B:434:ARG:NH2	2.16	0.60
2:B:810:GLU:HA	2:B:815:ARG:HH22	1.67	0.60
2:B:880:THR:CB	2:B:934:LYS:HG3	2.31	0.60
2:B:999:MET:HB3	2:B:1007:VAL:HG21	1.84	0.60
4:D:47:LEU:HD11	7:G:3:PHE:CD2	2.37	0.60
7:G:55:ASP:OD1	7:G:57:GLN:HG3	2.02	0.60
7:G:106:MET:HG2	7:G:107:LYS:N	2.16	0.60
1:A:310:GLY:C	1:A:312:PRO:HD2	2.27	0.60
1:A:332:LYS:HA	1:A:337:ARG:NH1	2.17	0.60
1:A:335:ARG:NH1	2:B:1206:GLU:CD	2.59	0.60
1:A:347:PHE:CE2	1:A:375:THR:HG23	2.37	0.60
1:A:427:GLN:HG3	1:A:430:TRP:CZ2	2.37	0.60
1:A:728:LYS:HA	1:A:731:ARG:NH1	2.17	0.60
2:B:176:SER:O	2:B:182:SER:HB3	2.01	0.60
2:B:426:LYS:HG3	2:B:426:LYS:O	2.02	0.60
2:B:654:ARG:N	2:B:657:HIS:HD2	1.98	0.60
2:B:758:PHE:HE1	2:B:1027:ILE:HG22	1.66	0.60
2:B:807:ARG:HG2	2:B:1045:SER:OG	2.02	0.60
2:B:1023:VAL:HA	2:B:1026:LEU:HD12	1.84	0.60
3:C:76:ASP:OD2	3:C:128:ASN:N	2.35	0.60
5:E:14:ARG:NH2	5:E:141:VAL:HG12	2.17	0.60
1:A:332:LYS:H	1:A:337:ARG:CB	2.15	0.59
1:A:897:TYR:HB3	1:A:936:LEU:CD1	2.32	0.59
1:A:1109:LYS:HG3	1:A:1110:ASN:HD22	1.66	0.59
2:B:604:ARG:HB2	2:B:609:ILE:HG13	1.83	0.59
2:B:906:SER:HA	2:B:946:ASN:HB2	1.83	0.59
2:B:912:ILE:O	2:B:938:SER:HB3	2.02	0.59
2:B:984:HIS:HD2	2:B:1025:HIS:CD2	2.20	0.59
2:B:995:ARG:NH1	3:C:165:LYS:HA	2.16	0.59
3:C:88:CYS:SG	3:C:91:HIS:HA	2.42	0.59
7:G:87:VAL:HG23	7:G:103:VAL:HG21	1.82	0.59
8:H:82:PRO:C	8:H:84:ALA:N	2.50	0.59
1:A:90:VAL:HG11	1:A:297:GLN:HA	1.83	0.59
1:A:269:ILE:HG12	1:A:299:HIS:HB3	1.84	0.59
1:A:524:VAL:HG12	1:A:525:GLN:HG2	1.84	0.59
1:A:720:ARG:O	1:A:724:GLU:HB2	2.01	0.59
1:A:1158:PRO:C	1:A:1159:ARG:HD2	2.27	0.59
1:A:1341:ILE:HG23	1:A:1342:GLU:H	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:12:ARG:NH1	4:D:14:ARG:HA	2.18	0.59
4:D:13:ARG:C	4:D:15:LEU:N	2.57	0.59
5:E:13:TRP:O	5:E:16:PHE:HB3	2.02	0.59
6:F:103:MET:HE1	7:G:65:ASP:HB2	1.83	0.59
7:G:129:SER:HB3	7:G:138:THR:HB	1.84	0.59
8:H:102:TYR:OH	8:H:122:LEU:HD22	2.02	0.59
8:H:135:LEU:HB2	8:H:137:GLN:HG2	1.83	0.59
9:I:26:LEU:HD22	9:I:35:VAL:CG1	2.31	0.59
12:L:38:LEU:CG	12:L:39:SER:N	2.65	0.59
15:P:5:C:H2'	15:P:6:A:O4'	2.01	0.59
1:A:211:PHE:HA	1:A:214:ILE:HG13	1.84	0.59
1:A:289:ILE:CG2	1:A:290:GLU:N	2.65	0.59
1:A:770:VAL:HG12	1:A:771:GLU:HG3	1.84	0.59
1:A:852:TYR:CD2	1:A:1060:PRO:HB2	2.36	0.59
1:A:868:TYR:HE1	1:A:1064:VAL:CG1	2.16	0.59
2:B:637:LEU:CD2	2:B:742:GLU:HA	2.32	0.59
2:B:874:PHE:HA	2:B:913:GLY:O	2.01	0.59
4:D:118:THR:O	4:D:120:GLU:N	2.35	0.59
7:G:146:LYS:HB2	7:G:168:LEU:HD11	1.83	0.59
9:I:101:PHE:N	9:I:101:PHE:CD1	2.70	0.59
12:L:32:ALA:H	12:L:55:ILE:HD11	1.67	0.59
1:A:850:VAL:HG21	1:A:1058:VAL:HG11	1.84	0.59
1:A:853:ASP:O	1:A:854:ASN:HB2	2.01	0.59
2:B:401:PHE:HB2	2:B:517:THR:OG1	2.02	0.59
2:B:710:LEU:CA	2:B:733:HIS:HB3	2.31	0.59
2:B:973:ILE:HG23	2:B:974:PRO:HD2	1.83	0.59
5:E:17:ARG:O	5:E:20:LYS:HB2	2.01	0.59
5:E:35:VAL:O	5:E:37:LEU:N	2.36	0.59
5:E:99:HIS:O	5:E:103:LYS:HB2	2.02	0.59
5:E:120:ALA:HA	5:E:123:LEU:HD11	1.85	0.59
12:L:27:LEU:HD23	12:L:27:LEU:N	2.18	0.59
1:A:23:SER:HA	1:A:233:TRP:NE1	2.18	0.59
1:A:228:PHE:CE2	4:D:15:LEU:HD23	2.37	0.59
1:A:326:ARG:HG2	1:A:326:ARG:HH11	1.67	0.59
1:A:590:ARG:NH1	1:A:592:ASP:OD2	2.35	0.59
1:A:675:THR:OG1	1:A:736:ASN:ND2	2.36	0.59
1:A:1208:THR:HG22	1:A:1210:GLY:N	2.17	0.59
3:C:31:ASN:OD1	3:C:34:ARG:HD3	2.03	0.59
3:C:212:PRO:HB3	3:C:213:PRO:HD2	1.85	0.59
4:D:39:ASN:HD22	4:D:41:GLN:HB2	1.67	0.59
4:D:124:GLU:HA	4:D:127:ASP:HB2	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:153:ARG:HB3	4:D:154:PHE:CE2	2.37	0.59
5:E:94:LYS:HE2	5:E:98:ILE:CD1	2.21	0.59
5:E:121:MET:C	5:E:123:LEU:H	2.09	0.59
7:G:13:LEU:CD2	7:G:17:PHE:HB2	2.32	0.59
9:I:78:CYS:SG	9:I:106:CYS:HB3	2.42	0.59
2:B:225:VAL:HG21	2:B:384:ARG:HH21	1.67	0.59
2:B:622:LYS:HE2	9:I:59:VAL:CG2	2.33	0.59
2:B:882:THR:HG22	2:B:884:ARG:N	2.16	0.59
2:B:1050:ILE:HG22	2:B:1051:THR:N	2.17	0.59
2:B:1065:GLN:NE2	2:B:1066:SER:N	2.50	0.59
3:C:147:LEU:HD23	3:C:147:LEU:N	2.16	0.59
3:C:193:TYR:C	3:C:193:TYR:CD1	2.80	0.59
3:C:213:PRO:O	3:C:214:ASN:HB3	2.02	0.59
5:E:144:ILE:HG13	5:E:145:THR:N	2.18	0.59
6:F:82:THR:HG22	6:F:84:TYR:N	2.17	0.59
7:G:112:LYS:HA	7:G:115:MET:CE	2.29	0.59
8:H:40:LEU:HB2	8:H:123:MET:HE3	1.85	0.59
10:J:43:ARG:H	10:J:43:ARG:HD2	1.67	0.59
1:A:335:ARG:NH1	2:B:1206:GLU:OE1	2.35	0.59
1:A:356:ASP:HB2	1:A:469:ARG:NH1	2.18	0.59
2:B:785:TYR:CD2	2:B:795:ILE:HG12	2.37	0.59
2:B:798:TYR:HE2	3:C:62:PHE:CZ	2.20	0.59
2:B:1204:PHE:CE1	2:B:1216:LEU:HD11	2.37	0.59
3:C:249:ASP:O	3:C:252:GLN:N	2.31	0.59
4:D:51:ASN:C	4:D:52:LEU:O	2.45	0.59
6:F:84:TYR:N	6:F:84:TYR:CD1	2.69	0.59
7:G:37:SER:OG	7:G:45:ILE:HG13	2.03	0.59
1:A:108:MET:O	1:A:109:HIS:HB3	2.03	0.59
1:A:665:GLY:HA2	2:B:1026:LEU:CD2	2.31	0.59
1:A:1200:ALA:HA	1:A:1203:ASN:ND2	2.17	0.59
1:A:1353:TYR:CE2	1:A:1357:ALA:HB2	2.38	0.59
2:B:64:CYS:HA	2:B:67:SER:HG	1.66	0.59
2:B:100:PRO:HD2	2:B:180:TYR:CE1	2.38	0.59
2:B:332:ASP:C	2:B:334:ILE:H	2.10	0.59
2:B:505:ASP:O	2:B:508:LEU:HD22	2.03	0.59
9:I:84:VAL:HG13	9:I:84:VAL:O	2.02	0.59
1:A:399:HIS:CB	1:A:400:PRO:CD	2.80	0.59
1:A:1148:ILE:CG1	1:A:1198:ASP:HB2	2.33	0.59
2:B:108:VAL:HG12	2:B:109:THR:N	2.18	0.59
2:B:291:ILE:HG22	2:B:297:ILE:HG12	1.85	0.59
2:B:294:ASP:HB2	9:I:12:ASN:HA	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:621:GLU:HG3	2:B:621:GLU:O	2.01	0.59
2:B:654:ARG:HG3	2:B:654:ARG:NH1	2.17	0.59
2:B:773:MET:CE	2:B:987:LYS:HD2	2.32	0.59
5:E:48:ASP:CG	5:E:49:SER:H	2.09	0.59
6:F:118:LEU:O	6:F:122:MET:HG3	2.03	0.59
1:A:518:LYS:HE2	1:A:624:SER:O	2.03	0.59
1:A:897:TYR:CD2	1:A:936:LEU:HD13	2.38	0.59
1:A:982:THR:C	1:A:984:LYS:H	2.10	0.59
2:B:25:ILE:HD11	2:B:653:VAL:C	2.27	0.59
2:B:582:VAL:CG2	2:B:626:ILE:HB	2.33	0.59
2:B:798:TYR:HE2	3:C:62:PHE:CE2	2.21	0.59
3:C:183:TRP:CZ2	3:C:212:PRO:HG3	2.38	0.59
5:E:40:GLU:HA	5:E:43:LYS:CE	2.27	0.59
5:E:78:LEU:HA	5:E:107:THR:HB	1.83	0.59
7:G:1:MET:HG2	7:G:85:GLU:OE2	2.03	0.59
9:I:55:THR:HG22	9:I:58:VAL:HG21	1.84	0.59
11:K:12:LEU:HD21	11:K:17:SER:HA	1.85	0.59
11:K:108:GLU:O	11:K:112:GLN:HG2	2.03	0.59
1:A:2:VAL:HG22	1:A:3:GLY:H	1.68	0.58
1:A:178:GLY:C	1:A:179:LEU:HD23	2.27	0.58
1:A:1015:VAL:CG1	1:A:1019:CYS:SG	2.91	0.58
2:B:245:GLU:O	2:B:246:LYS:HG3	2.03	0.58
2:B:992:ILE:HD11	11:K:66:PRO:CB	2.32	0.58
2:B:1034:VAL:HG12	2:B:1035:ALA:N	2.17	0.58
8:H:143:LEU:HD12	8:H:143:LEU:N	2.17	0.58
1:A:443:LEU:HD12	2:B:1146:PHE:CE2	2.39	0.58
1:A:598:LEU:HD23	8:H:25:ARG:NH1	2.18	0.58
1:A:754:SER:N	1:A:757:ASN:ND2	2.45	0.58
1:A:883:LEU:O	1:A:886:ILE:HG22	2.03	0.58
1:A:1111:MET:HG3	1:A:1114:PRO:HB3	1.85	0.58
2:B:58:THR:O	2:B:62:ILE:HG13	2.04	0.58
2:B:351:TYR:CE1	2:B:355:ILE:HD11	2.38	0.58
2:B:952:VAL:HG12	2:B:953:LEU:N	2.18	0.58
2:B:1112:GLN:HG3	15:P:1:C:O5'	2.03	0.58
5:E:136:ASN:OD1	5:E:138:ALA:N	2.36	0.58
8:H:101:ALA:HB2	8:H:116:TYR:CE2	2.38	0.58
10:J:24:LEU:HD13	10:J:38:ARG:HG2	1.84	0.58
10:J:44:TYR:HA	10:J:47:ARG:HB2	1.84	0.58
12:L:42:ARG:HG3	12:L:42:ARG:NH1	2.18	0.58
1:A:43:GLU:CG	1:A:46:THR:HB	2.27	0.58
1:A:90:VAL:HG12	1:A:297:GLN:HE21	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:925:LEU:HD13	1:A:983:ILE:CG2	2.31	0.58
1:A:1312:ASN:O	1:A:1316:VAL:HG23	2.02	0.58
2:B:37:PHE:CD1	2:B:41:LYS:HG3	2.38	0.58
2:B:294:ASP:H	9:I:12:ASN:HD22	1.48	0.58
2:B:365:THR:HG21	2:B:370:PHE:CD1	2.38	0.58
2:B:603:LEU:HD12	2:B:609:ILE:HG12	1.85	0.58
3:C:99:LEU:N	3:C:99:LEU:CD2	2.66	0.58
5:E:213:ILE:HG12	5:E:214:CYS:H	1.67	0.58
8:H:4:THR:O	8:H:5:LEU:HD23	2.04	0.58
1:A:108:MET:CA	1:A:210:ILE:HD13	2.30	0.58
1:A:321:PRO:O	1:A:322:VAL:CB	2.51	0.58
1:A:322:VAL:O	1:A:322:VAL:CG1	2.50	0.58
1:A:675:THR:O	1:A:679:ILE:HG13	2.02	0.58
1:A:1161:THR:CG2	1:A:1163:ILE:HD12	2.31	0.58
2:B:601:ARG:O	2:B:605:ARG:HG3	2.04	0.58
2:B:955:THR:HG23	2:B:956:THR:N	2.17	0.58
3:C:33:LEU:O	3:C:33:LEU:HD12	2.04	0.58
3:C:161:LYS:O	3:C:170:TRP:NE1	2.37	0.58
4:D:4:SER:O	4:D:5:THR:CB	2.52	0.58
5:E:56:LYS:CE	5:E:84:ASP:H	2.16	0.58
8:H:136:LYS:N	8:H:136:LYS:HD2	2.17	0.58
11:K:40:HIS:ND1	11:K:61:TYR:OH	2.22	0.58
1:A:451:HIS:CD2	1:A:1074:GLU:HG3	2.39	0.58
1:A:831:THR:CG2	1:A:832:ALA:H	2.12	0.58
1:A:1279:ILE:CD1	1:A:1316:VAL:HG21	2.32	0.58
1:A:1313:LEU:HD23	1:A:1338:VAL:HG21	1.86	0.58
1:A:1352:VAL:O	1:A:1355:VAL:HG12	2.04	0.58
2:B:90:ILE:CD1	2:B:432:MET:SD	2.91	0.58
2:B:308:TRP:HA	2:B:311:LEU:HD12	1.86	0.58
2:B:506:GLY:O	2:B:507:LYS:HB2	2.02	0.58
2:B:705:MET:H	2:B:710:LEU:CD1	2.15	0.58
9:I:34:TYR:CE2	9:I:36:GLU:HB3	2.39	0.58
1:A:61:ILE:HG22	1:A:62:ASP:N	2.19	0.58
1:A:95:PHE:O	1:A:96:ILE:C	2.46	0.58
1:A:517:ASN:HD22	1:A:1364:ASN:HD22	1.50	0.58
1:A:1066:VAL:O	1:A:1070:GLN:HG3	2.03	0.58
1:A:1209:MET:CE	1:A:1236:LEU:HB3	2.32	0.58
2:B:309:GLN:OE1	9:I:52:ILE:HD11	2.04	0.58
2:B:315:LYS:N	2:B:316:PRO:HD2	2.17	0.58
2:B:865:LYS:C	2:B:866:TYR:HD1	2.12	0.58
7:G:53:ASN:HD22	7:G:53:ASN:N	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:26:ILE:CD1	8:H:49:VAL:HG11	2.34	0.58
8:H:84:ALA:CB	8:H:87:ARG:HB2	2.33	0.58
1:A:91:PHE:N	1:A:297:GLN:HE22	2.01	0.58
1:A:167:CYS:HB2	1:A:169:ASN:ND2	2.18	0.58
1:A:369:SER:HB3	11:K:2:ASN:OD1	2.03	0.58
2:B:1187:ASN:O	2:B:1188:LYS:CB	2.49	0.58
3:C:67:LEU:HD11	3:C:155:LEU:CD1	2.33	0.58
4:D:59:ILE:HG21	4:D:145:MET:SD	2.43	0.58
4:D:183:LEU:HD22	7:G:144:ARG:NH2	2.18	0.58
7:G:106:MET:CG	7:G:107:LYS:N	2.66	0.58
8:H:36:CYS:HA	8:H:126:GLU:HB3	1.86	0.58
10:J:43:ARG:CD	10:J:43:ARG:N	2.67	0.58
11:K:85:ASP:O	11:K:88:LYS:HB2	2.03	0.58
12:L:70:ARG:HG2	12:L:70:ARG:HH11	1.69	0.58
1:A:260:ASP:OD1	1:A:261:ASP:N	2.36	0.58
1:A:299:HIS:HA	1:A:302:THR:HG22	1.84	0.58
1:A:595:THR:C	1:A:596:THR:HG23	2.29	0.58
1:A:1428:VAL:HG13	2:B:1151:LEU:HD21	1.86	0.58
2:B:217:ARG:HD2	2:B:217:ARG:C	2.29	0.58
2:B:402:GLY:HA2	2:B:695:ALA:HB3	1.85	0.58
2:B:769:TYR:HB3	2:B:773:MET:CE	2.33	0.58
2:B:898:LEU:HD13	2:B:952:VAL:HG11	1.85	0.58
2:B:1073:TYR:CE2	2:B:1080:LYS:HG2	2.38	0.58
3:C:258:ILE:HD12	3:C:258:ILE:N	2.19	0.58
8:H:81:PRO:HB2	8:H:82:PRO:CD	2.32	0.58
10:J:44:TYR:CD2	10:J:44:TYR:N	2.71	0.58
15:P:1:C:O2'	15:P:2:A:H5'	2.04	0.58
1:A:7:SER:HB3	2:B:1193:GLN:NE2	2.18	0.58
1:A:1130:GLN:O	1:A:1134:ILE:HG13	2.03	0.58
2:B:242:SER:O	2:B:251:ILE:HA	2.04	0.58
2:B:882:THR:CG2	2:B:884:ARG:H	2.17	0.58
2:B:916:THR:CG2	2:B:935:ARG:HD2	2.33	0.58
3:C:6:PRO:HB2	3:C:25:VAL:HG22	1.86	0.58
3:C:114:TYR:OH	10:J:19:GLU:OE1	2.18	0.58
5:E:156:LEU:HA	5:E:160:GLU:OE1	2.03	0.58
1:A:767:GLN:HA	1:A:799:PHE:HA	1.86	0.58
1:A:1315:GLU:C	1:A:1317:MET:H	2.11	0.58
1:A:1376:THR:O	1:A:1377:THR:C	2.47	0.58
1:A:1437:GLY:C	1:A:1439:GLY:H	2.12	0.58
2:B:211:VAL:CG2	2:B:483:LEU:HB2	2.34	0.58
2:B:516:ASN:N	2:B:516:ASN:ND2	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:880:THR:O	2:B:881:ASN:HB2	2.04	0.58
2:B:1113:VAL:HG23	15:P:1:C:O4'	2.04	0.58
2:B:1119:VAL:O	2:B:1126:GLY:HA3	2.04	0.58
3:C:239:PRO:HB2	3:C:241:ASP:OD1	2.04	0.58
5:E:56:LYS:HE2	5:E:84:ASP:CB	2.22	0.58
6:F:119:ARG:CG	6:F:119:ARG:NH1	2.67	0.58
9:I:50:THR:HG23	9:I:51:ASN:N	2.19	0.58
1:A:427:GLN:HB2	1:A:430:TRP:CE2	2.39	0.57
1:A:523:ILE:CG1	1:A:622:VAL:HG22	2.34	0.57
1:A:853:ASP:OD1	1:A:853:ASP:C	2.47	0.57
1:A:962:ARG:O	1:A:964:ILE:N	2.37	0.57
1:A:1100:ARG:O	1:A:1103:GLU:HB3	2.03	0.57
1:A:1152:ILE:HG12	1:A:1260:LEU:HD23	1.87	0.57
1:A:1241:ARG:O	1:A:1242:VAL:CB	2.52	0.57
1:A:1444:MET:HE1	6:F:135:ARG:HB2	1.84	0.57
2:B:29:ASP:HB3	2:B:658:ILE:CD1	2.33	0.57
2:B:168:GLY:HA2	2:B:454:THR:OG1	2.04	0.57
2:B:364:ILE:HG13	2:B:585:VAL:HG13	1.85	0.57
2:B:637:LEU:HD21	2:B:742:GLU:HA	1.86	0.57
2:B:641:GLU:C	2:B:643:ASP:H	2.12	0.57
2:B:881:ASN:HB2	2:B:933:SER:N	2.19	0.57
3:C:242:GLN:OE1	3:C:245:VAL:HG21	2.04	0.57
4:D:47:LEU:HD11	7:G:3:PHE:HD2	1.68	0.57
4:D:147:TYR:OH	7:G:103:VAL:HG13	2.03	0.57
1:A:335:ARG:HH12	2:B:1206:GLU:CD	2.11	0.57
1:A:1200:ALA:HA	1:A:1203:ASN:HD22	1.69	0.57
1:A:1264:GLU:HG3	1:A:1265:ASN:N	2.19	0.57
1:A:1385:THR:HG22	1:A:1386:ARG:N	2.19	0.57
2:B:172:ILE:CD1	2:B:178:ASN:HD22	2.13	0.57
3:C:111:THR:C	3:C:112:ASN:HD22	2.12	0.57
6:F:69:LEU:HB2	6:F:72:LYS:HD2	1.86	0.57
7:G:50:ASP:O	7:G:51:TYR:C	2.47	0.57
9:I:8:ARG:CG	9:I:34:TYR:HE1	2.14	0.57
9:I:16:PRO:HD3	9:I:27:PHE:CD2	2.39	0.57
1:A:598:LEU:HD23	1:A:598:LEU:O	2.04	0.57
1:A:1313:LEU:O	1:A:1315:GLU:N	2.38	0.57
2:B:405:ARG:NE	2:B:629:ASP:OD2	2.29	0.57
2:B:642:ASP:HB3	2:B:649:LYS:CD	2.30	0.57
2:B:975:GLN:HG2	2:B:976:ILE:H	1.68	0.57
3:C:29:MET:HE2	11:K:98:LEU:CD2	2.34	0.57
5:E:145:THR:HG21	5:E:187:TYR:CE2	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:84:ALA:CB	8:H:87:ARG:HD2	2.35	0.57
1:A:93:VAL:HG21	1:A:301:ALA:O	2.03	0.57
1:A:443:LEU:HD12	2:B:1146:PHE:CZ	2.40	0.57
1:A:683:ILE:HG21	1:A:801:GLU:CG	2.34	0.57
1:A:1236:LEU:O	1:A:1237:ILE:HG13	2.05	0.57
1:A:1253:GLU:O	1:A:1254:ALA:HB3	2.04	0.57
1:A:1336:MET:HE3	1:A:1381:LEU:HD12	1.86	0.57
1:A:1340:GLY:HA2	5:E:183:PRO:HD2	1.85	0.57
2:B:241:ARG:HH11	2:B:241:ARG:HG3	1.70	0.57
7:G:64:THR:CG2	7:G:65:ASP:N	2.67	0.57
14:T:15:DG:N9	14:T:16:DT:H72	2.19	0.57
1:A:512:VAL:HA	1:A:519:PRO:HA	1.85	0.57
1:A:774:ARG:HG3	1:A:797:LYS:HE3	1.87	0.57
2:B:108:VAL:HG12	2:B:109:THR:H	1.67	0.57
2:B:644:GLU:C	2:B:646:LEU:H	2.12	0.57
4:D:215:SER:HA	4:D:218:GLU:OE2	2.04	0.57
5:E:176:PRO:O	5:E:212:ARG:HA	2.05	0.57
7:G:27:LYS:O	7:G:31:LEU:HG	2.05	0.57
9:I:61:ASP:C	9:I:63:GLY:N	2.61	0.57
1:A:70:CYS:HA	2:B:1174:LYS:HG2	1.87	0.57
1:A:915:SER:O	1:A:919:ILE:HB	2.04	0.57
1:A:1124:HIS:HB2	1:A:1130:GLN:HG2	1.86	0.57
1:A:1315:GLU:O	1:A:1317:MET:N	2.37	0.57
2:B:209:GLU:OE2	2:B:485:ARG:NE	2.37	0.57
2:B:604:ARG:C	2:B:606:LYS:H	2.11	0.57
2:B:1192:TYR:CD2	2:B:1218:THR:HG21	2.39	0.57
3:C:11:ARG:NH2	3:C:206:ASN:OD1	2.38	0.57
4:D:29:LEU:HD12	7:G:82:PHE:CZ	2.39	0.57
5:E:198:ILE:CD1	5:E:212:ARG:HG3	2.33	0.57
1:A:265:LYS:HG2	1:A:303:TYR:HB2	1.85	0.57
1:A:925:LEU:O	1:A:927:VAL:N	2.38	0.57
1:A:1329:THR:H	1:A:1335:ILE:HD11	1.69	0.57
2:B:345:LYS:HA	2:B:348:ARG:NE	2.16	0.57
2:B:542:MET:HG2	2:B:747:MET:CE	2.32	0.57
5:E:4:GLU:HB3	5:E:7:ARG:HE	1.70	0.57
7:G:17:PHE:C	7:G:19:GLY:H	2.13	0.57
7:G:21:ARG:HD2	7:G:24:GLN:HB3	1.85	0.57
1:A:351:THR:HG21	2:B:1103:ILE:HG13	1.85	0.57
1:A:452:LYS:HB3	2:B:1141:HIS:CE1	2.39	0.57
2:B:203:PHE:HB3	2:B:205:ILE:HD11	1.87	0.57
2:B:254:LEU:HD22	2:B:361:LEU:CD1	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:916:THR:O	2:B:935:ARG:HG2	2.04	0.57
5:E:22:MET:HE1	5:E:26:ARG:HH21	1.69	0.57
5:E:157:SER:O	5:E:159:ASP:N	2.38	0.57
9:I:14:LEU:HD22	9:I:28:GLU:C	2.30	0.57
9:I:65:ASP:HB3	9:I:68:LEU:CD1	2.33	0.57
1:A:325:ILE:HG22	2:B:1210:MET:HE2	1.87	0.57
1:A:845:LEU:O	1:A:846:GLU:C	2.48	0.57
1:A:901:LEU:H	1:A:926:GLN:HE21	0.73	0.57
2:B:39:ARG:NE	2:B:665:GLU:HG2	2.19	0.57
2:B:461:LEU:HD12	2:B:461:LEU:N	2.20	0.57
2:B:510:LYS:HB3	2:B:511:PRO:HD3	1.86	0.57
2:B:695:ALA:O	2:B:698:GLU:HB3	2.05	0.57
2:B:777:ALA:HA	2:B:1095:LEU:HA	1.87	0.57
2:B:953:LEU:CD2	2:B:965:LYS:HB2	2.30	0.57
9:I:50:THR:CG2	9:I:51:ASN:N	2.66	0.57
9:I:55:THR:HG22	9:I:55:THR:O	2.05	0.57
1:A:256:GLN:O	1:A:257:ARG:HB2	2.04	0.57
1:A:852:TYR:CE2	1:A:1060:PRO:HB2	2.40	0.57
1:A:898:ARG:O	1:A:1029:ARG:NH1	2.38	0.57
2:B:222:ILE:N	2:B:240:ILE:HD12	2.19	0.57
2:B:755:ILE:O	2:B:755:ILE:HG22	2.05	0.57
3:C:71:PRO:O	3:C:72:LEU:HD23	2.05	0.57
3:C:92:CYS:SG	3:C:94:LYS:HB3	2.45	0.57
4:D:16:LYS:O	4:D:18:VAL:N	2.37	0.57
4:D:35:LEU:HD11	4:D:173:HIS:CD2	2.39	0.57
11:K:82:ASP:OD1	11:K:84:LYS:HB2	2.04	0.57
12:L:40:LEU:HD11	12:L:49:LYS:NZ	2.20	0.57
1:A:113:LEU:HD12	1:A:218:ASP:OD1	2.05	0.56
1:A:779:PHE:O	1:A:780:VAL:C	2.47	0.56
1:A:962:ARG:C	1:A:964:ILE:H	2.13	0.56
1:A:993:LEU:HD11	1:A:997:LEU:HD21	1.86	0.56
1:A:1159:ARG:HD2	1:A:1159:ARG:N	2.20	0.56
1:A:1258:HIS:O	1:A:1262:LYS:HE3	2.04	0.56
1:A:1285:MET:O	1:A:1304:TRP:HA	2.05	0.56
1:A:1287:TYR:CD1	1:A:1305:VAL:HG21	2.40	0.56
2:B:225:VAL:HA	2:B:237:VAL:O	2.05	0.56
2:B:435:THR:C	2:B:437:GLU:N	2.63	0.56
2:B:770:GLN:OE1	2:B:983:ARG:C	2.48	0.56
3:C:106:GLU:HA	3:C:106:GLU:OE2	2.03	0.56
5:E:147:HIS:HB3	5:E:150:VAL:HG23	1.87	0.56
7:G:37:SER:OG	7:G:45:ILE:HB	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:47:ARG:HD2	11:K:47:ARG:C	2.30	0.56
1:A:527:THR:CG2	1:A:650:GLN:HA	2.35	0.56
1:A:838:GLN:HG2	1:A:1073:GLY:HA3	1.86	0.56
1:A:1312:ASN:HD21	1:A:1315:GLU:HG3	1.69	0.56
2:B:59:LEU:HD12	2:B:417:PHE:HE2	1.66	0.56
2:B:169:ARG:HD2	2:B:454:THR:HG21	1.87	0.56
2:B:416:LEU:HD23	2:B:420:LEU:HG	1.86	0.56
3:C:148:ARG:CG	3:C:149:LYS:H	2.18	0.56
8:H:8:ASP:CG	8:H:9:ILE:N	2.62	0.56
1:A:295:LEU:O	1:A:298:PHE:HB3	2.05	0.56
1:A:595:THR:O	1:A:596:THR:HG23	2.05	0.56
1:A:598:LEU:HA	8:H:122:LEU:HD13	1.87	0.56
1:A:701:LEU:HA	9:I:115:LYS:HE3	1.87	0.56
2:B:25:ILE:HD11	2:B:653:VAL:HG12	1.85	0.56
2:B:118:ARG:HH22	2:B:194:GLU:CD	2.13	0.56
2:B:118:ARG:HG3	2:B:204:ILE:HD13	1.87	0.56
2:B:327:ARG:O	2:B:331:LEU:HD13	2.05	0.56
2:B:891:ASP:C	2:B:893:LEU:H	2.13	0.56
2:B:1172:ILE:HG22	2:B:1172:ILE:O	2.04	0.56
3:C:124:LEU:HD12	3:C:124:LEU:N	2.20	0.56
3:C:242:GLN:C	3:C:244:VAL:N	2.62	0.56
5:E:9:ILE:HD11	5:E:53:PRO:HD3	1.86	0.56
5:E:90:VAL:HA	5:E:120:ALA:HB2	1.87	0.56
11:K:12:LEU:HD21	11:K:18:LYS:H	1.67	0.56
11:K:82:ASP:OD1	11:K:84:LYS:N	2.38	0.56
1:A:55:ASP:N	1:A:56:PRO:CD	2.65	0.56
1:A:56:PRO:HD2	1:A:58:LEU:HG	1.88	0.56
1:A:547:LEU:HD21	1:A:560:ILE:HD13	1.87	0.56
1:A:670:ILE:HD12	2:B:1067:ARG:NH2	2.20	0.56
1:A:730:GLY:O	1:A:731:ARG:C	2.48	0.56
1:A:1242:VAL:HG12	1:A:1243:VAL:N	2.21	0.56
2:B:756:ILE:O	2:B:759:PRO:HD3	2.05	0.56
2:B:1122:ARG:HB3	14:T:22:DC:OP1	2.06	0.56
9:I:29:CYS:SG	9:I:32:CYS:N	2.72	0.56
11:K:45:LEU:HG	11:K:94:ILE:HD11	1.88	0.56
2:B:345:LYS:CA	2:B:348:ARG:HE	2.16	0.56
2:B:642:ASP:C	2:B:644:GLU:H	2.14	0.56
3:C:66:ARG:NH2	10:J:3:VAL:O	2.38	0.56
3:C:115:SER:HB3	3:C:141:GLY:O	2.05	0.56
3:C:166:GLU:C	11:K:6:ARG:NH1	2.63	0.56
4:D:130:LEU:HD13	4:D:142:LYS:CG	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:154:PHE:HD1	4:D:163:VAL:HG21	1.64	0.56
1:A:225:ASN:HD22	1:A:228:PHE:N	1.86	0.56
1:A:464:PRO:HG2	1:A:465:TYR:HD1	1.69	0.56
1:A:483:ASP:HB2	2:B:987:LYS:HG2	1.88	0.56
1:A:483:ASP:O	2:B:979:LYS:HE3	2.05	0.56
1:A:535:THR:O	1:A:575:LYS:HE2	2.06	0.56
1:A:1241:ARG:O	1:A:1242:VAL:HB	2.06	0.56
2:B:882:THR:HG21	2:B:934:LYS:O	2.05	0.56
3:C:34:ARG:NH1	3:C:35:ARG:HG2	2.20	0.56
4:D:14:ARG:C	4:D:16:LYS:H	2.14	0.56
5:E:35:VAL:C	5:E:37:LEU:H	2.13	0.56
7:G:79:PHE:CE2	7:G:106:MET:HE2	2.41	0.56
8:H:59:ILE:CG2	8:H:60:ALA:N	2.61	0.56
1:A:34:LYS:HD3	1:A:34:LYS:N	2.21	0.56
1:A:34:LYS:HZ1	1:A:57:ARG:NH2	2.02	0.56
1:A:55:ASP:CG	1:A:55:ASP:O	2.46	0.56
1:A:153:PRO:HB2	1:A:158:PRO:HA	1.88	0.56
1:A:341:MET:CE	1:A:843:LYS:HZ3	2.17	0.56
1:A:626:ASN:O	1:A:631:HIS:CD2	2.59	0.56
1:A:1063:MET:SD	1:A:1436:ILE:CG1	2.89	0.56
1:A:1100:ARG:NH2	1:A:1351:GLU:CG	2.69	0.56
1:A:1210:GLY:O	1:A:1214:GLU:HG2	2.05	0.56
2:B:376:PHE:CE2	2:B:569:TYR:HD2	2.24	0.56
3:C:80:LEU:HD11	3:C:95:CYS:C	2.31	0.56
4:D:50:LEU:HD21	7:G:4:ILE:CD1	2.34	0.56
5:E:161:LYS:HD2	5:E:195:VAL:CG2	2.35	0.56
7:G:51:TYR:O	7:G:54:ILE:HG13	2.05	0.56
9:I:68:LEU:HD12	9:I:68:LEU:H	1.70	0.56
1:A:182:VAL:HG22	1:A:201:VAL:HA	1.88	0.56
1:A:286:HIS:O	1:A:289:ILE:HG22	2.06	0.56
1:A:332:LYS:C	1:A:334:GLY:N	2.63	0.56
1:A:710:LEU:HD12	1:A:710:LEU:N	2.17	0.56
1:A:1107:VAL:O	1:A:1107:VAL:CG1	2.54	0.56
1:A:1385:THR:HB	1:A:1388:GLY:H	1.70	0.56
2:B:448:ILE:O	2:B:450:ALA:N	2.39	0.56
2:B:1159:ARG:HB3	2:B:1159:ARG:NH1	2.21	0.56
2:B:1217:TYR:CD2	4:D:13:ARG:CZ	2.89	0.56
3:C:175:ALA:HB1	10:J:43:ARG:HH22	1.70	0.56
4:D:24:ALA:HB3	4:D:26:THR:CG2	2.35	0.56
4:D:138:ASN:HB3	4:D:141:LEU:HB3	1.87	0.56
7:G:80:LYS:O	7:G:82:PHE:CE1	2.59	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:50:THR:HG23	9:I:52:ILE:N	2.21	0.56
11:K:45:LEU:HG	11:K:94:ILE:HD13	1.88	0.56
1:A:203:SER:O	1:A:207:ILE:HG12	2.05	0.56
1:A:683:ILE:HD13	1:A:801:GLU:CG	2.35	0.56
1:A:767:GLN:NE2	1:A:774:ARG:CB	2.69	0.56
1:A:886:ILE:CG2	1:A:887:GLY:N	2.69	0.56
1:A:949:ASP:OD1	1:A:951:GLU:HB2	2.06	0.56
1:A:1214:GLU:O	1:A:1218:GLN:HG2	2.06	0.56
1:A:1445:ILE:H	1:A:1445:ILE:CD1	2.00	0.56
2:B:205:ILE:CD1	2:B:205:ILE:N	2.68	0.56
2:B:508:LEU:O	2:B:509:ALA:CB	2.54	0.56
2:B:603:LEU:CD1	2:B:609:ILE:HG12	2.36	0.56
2:B:794:ASN:C	2:B:795:ILE:HD12	2.31	0.56
2:B:797:TYR:HE1	2:B:854:LEU:HD23	1.71	0.56
3:C:47:ASP:HA	12:L:69:ALA:HB3	1.87	0.56
5:E:103:LYS:HD3	5:E:105:PHE:HZ	1.70	0.56
5:E:108:GLY:O	5:E:132:ILE:HG22	2.06	0.56
5:E:182:ASP:OD1	5:E:183:PRO:HD2	2.06	0.56
6:F:86:THR:HG23	6:F:89:GLU:OE1	2.06	0.56
8:H:12:VAL:CG1	8:H:51:ALA:HA	2.36	0.56
8:H:101:ALA:HB2	8:H:116:TYR:CZ	2.41	0.56
12:L:55:ILE:CD1	12:L:56:LEU:N	2.68	0.56
12:L:61:THR:HG21	12:L:63:ARG:HG3	1.86	0.56
1:A:218:ASP:O	1:A:219:PHE:C	2.48	0.56
1:A:483:ASP:OD1	2:B:987:LYS:HG3	2.05	0.56
1:A:555:ASP:O	1:A:556:TRP:C	2.49	0.56
1:A:754:SER:O	1:A:757:ASN:HB2	2.06	0.56
1:A:1278:ASN:O	1:A:1310:GLY:HA3	2.06	0.56
1:A:1369:ALA:O	1:A:1370:LEU:C	2.49	0.56
1:A:1451:VAL:O	1:A:1454:MET:HG2	2.06	0.56
2:B:235:SER:C	2:B:236:HIS:HD2	2.14	0.56
2:B:557:PHE:CZ	2:B:603:LEU:HD11	2.41	0.56
2:B:681:TRP:HA	2:B:684:LEU:HD12	1.88	0.56
2:B:825:VAL:HG22	2:B:1010:LEU:HB2	1.88	0.56
3:C:226:ASP:O	3:C:227:THR:HB	2.06	0.56
4:D:155:ARG:CD	4:D:221:TYR:HE1	2.19	0.56
5:E:78:LEU:HD23	5:E:79:TRP:N	2.21	0.56
9:I:54:GLU:OE1	9:I:118:ARG:NH2	2.39	0.56
1:A:38:PRO:CA	1:A:270:LEU:HD23	2.36	0.55
1:A:317:LYS:O	1:A:318:SER:CB	2.54	0.55
1:A:463:ILE:CD1	1:A:469:ARG:HG3	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:979:SER:OG	1:A:980:ASP:N	2.38	0.55
1:A:1112:LYS:O	1:A:1114:PRO:HD3	2.06	0.55
1:A:1166:ASP:OD2	1:A:1239:ARG:HD2	2.06	0.55
2:B:101:MET:HE1	2:B:169:ARG:NH1	2.21	0.55
2:B:508:LEU:O	2:B:509:ALA:HB2	2.06	0.55
2:B:527:THR:OG1	2:B:528:PRO:HD2	2.06	0.55
3:C:254:LYS:O	3:C:258:ILE:HD13	2.07	0.55
7:G:139:ILE:CG2	7:G:140:LYS:H	2.18	0.55
8:H:104:PHE:CE2	8:H:136:LYS:HG3	2.41	0.55
11:K:68:PHE:N	11:K:68:PHE:CD2	2.72	0.55
1:A:953:ASN:C	1:A:954:TRP:CD1	2.84	0.55
1:A:1312:ASN:ND2	1:A:1315:GLU:HG3	2.21	0.55
2:B:170:LEU:O	2:B:172:ILE:HG13	2.05	0.55
2:B:794:ASN:O	2:B:795:ILE:HD12	2.06	0.55
5:E:56:LYS:NZ	5:E:84:ASP:H	2.04	0.55
12:L:32:ALA:HB3	12:L:55:ILE:HG13	1.85	0.55
1:A:72:GLU:HB3	1:A:76:GLU:HG2	1.88	0.55
1:A:1163:ILE:HG22	1:A:1165:GLU:HG2	1.88	0.55
1:A:1438:THR:CG2	6:F:92:ARG:HB2	2.37	0.55
2:B:120:ARG:NH1	12:L:54:ARG:HH11	2.05	0.55
2:B:640:VAL:O	2:B:641:GLU:C	2.50	0.55
2:B:805:THR:HA	2:B:809:MET:HE2	1.86	0.55
2:B:917:PRO:O	2:B:918:ILE:HG13	2.05	0.55
4:D:153:ARG:C	4:D:154:PHE:CD2	2.84	0.55
8:H:84:ALA:C	8:H:86:ASP:N	2.58	0.55
9:I:26:LEU:HD23	9:I:37:GLU:HA	1.87	0.55
10:J:7:CYS:CA	10:J:49:MET:HE3	2.35	0.55
1:A:280:GLU:CG	1:A:289:ILE:HD11	2.36	0.55
1:A:388:LEU:HD22	1:A:432:VAL:HB	1.88	0.55
1:A:1261:LYS:HE2	9:I:44:TYR:HD2	1.71	0.55
2:B:649:LYS:HD3	2:B:736:THR:O	2.07	0.55
2:B:1072:MET:O	2:B:1081:LEU:HB2	2.07	0.55
4:D:7:THR:O	4:D:7:THR:HG23	2.07	0.55
4:D:12:ARG:HH12	4:D:13:ARG:C	2.14	0.55
5:E:190:LEU:C	5:E:191:LYS:HG2	2.32	0.55
1:A:26:GLU:O	1:A:29:ALA:HB3	2.07	0.55
1:A:54:ASN:HA	1:A:58:LEU:HD12	1.88	0.55
1:A:80:HIS:H	1:A:243:PRO:CB	2.19	0.55
1:A:93:VAL:HG13	1:A:301:ALA:HB1	1.87	0.55
1:A:256:GLN:O	1:A:257:ARG:CB	2.53	0.55
1:A:691:LEU:HD11	1:A:695:LYS:HE3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:959:ASN:HD22	1:A:962:ARG:HH21	1.54	0.55
2:B:497:ARG:HH21	2:B:775:LYS:HZ1	1.54	0.55
2:B:605:ARG:CZ	2:B:639:ILE:HD13	2.37	0.55
3:C:112:ASN:HD22	3:C:112:ASN:N	2.04	0.55
4:D:39:ASN:ND2	4:D:41:GLN:HB2	2.22	0.55
4:D:130:LEU:C	4:D:132:GLN:H	2.15	0.55
8:H:98:TYR:C	8:H:118:PHE:HD2	2.14	0.55
1:A:168:GLY:O	1:A:169:ASN:C	2.49	0.55
1:A:317:LYS:O	1:A:318:SER:HB3	2.07	0.55
1:A:549:MET:SD	1:A:577:ILE:CD1	2.94	0.55
1:A:871:ASP:OD1	1:A:1366:ARG:NH2	2.40	0.55
1:A:1116:LEU:HB2	1:A:1329:THR:OG1	2.06	0.55
2:B:487:THR:CG2	2:B:488:TYR:N	2.69	0.55
2:B:554:ILE:HD12	2:B:554:ILE:H	1.72	0.55
5:E:117:THR:HB	5:E:120:ALA:HB3	1.87	0.55
8:H:91:ASP:C	8:H:93:TYR:H	2.15	0.55
9:I:76:PRO:HD3	9:I:110:PHE:CD2	2.41	0.55
1:A:470:LEU:HD13	1:A:487:MET:HE1	1.89	0.55
1:A:526:ASP:O	1:A:527:THR:C	2.49	0.55
1:A:756:ILE:O	1:A:760:GLN:HG3	2.06	0.55
1:A:870:GLU:HG2	5:E:208:TYR:CD2	2.41	0.55
1:A:981:LEU:HD21	1:A:1039:LYS:HA	1.88	0.55
1:A:1277:GLU:C	1:A:1279:ILE:H	2.14	0.55
2:B:39:ARG:HG2	2:B:39:ARG:HH11	1.72	0.55
2:B:101:MET:HB2	2:B:109:THR:CG2	2.36	0.55
2:B:134:LYS:HD3	2:B:134:LYS:H	1.69	0.55
2:B:226:PHE:HA	2:B:395:GLN:HG3	1.87	0.55
2:B:360:PHE:O	2:B:361:LEU:C	2.49	0.55
2:B:604:ARG:HG3	2:B:611:PRO:HA	1.88	0.55
3:C:174:ALA:O	3:C:175:ALA:HB3	2.07	0.55
5:E:22:MET:HG3	5:E:187:TYR:CD1	2.42	0.55
5:E:113:GLN:HG2	5:E:137:GLU:OE1	2.07	0.55
8:H:4:THR:HG23	8:H:58:THR:HG22	1.89	0.55
9:I:44:TYR:CD1	9:I:44:TYR:C	2.85	0.55
1:A:573:SER:O	1:A:576:GLN:HB2	2.07	0.55
1:A:765:VAL:HB	1:A:800:VAL:CG1	2.36	0.55
1:A:920:LEU:HD23	1:A:921:GLY:N	2.22	0.55
1:A:954:TRP:HB3	1:A:955:PRO:HD2	1.89	0.55
2:B:249:ARG:O	2:B:251:ILE:HG13	2.06	0.55
2:B:345:LYS:O	2:B:346:GLU:HB2	2.05	0.55
2:B:464:GLY:C	2:B:465:ASN:HD22	2.14	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:579:ARG:CB	2:B:586:TRP:HE1	2.13	0.55
2:B:635:ARG:NH1	2:B:742:GLU:OE2	2.40	0.55
2:B:696:GLU:O	2:B:699:GLU:HB2	2.07	0.55
3:C:58:LEU:HD23	3:C:58:LEU:N	2.21	0.55
3:C:148:ARG:HD3	3:C:149:LYS:HG3	1.89	0.55
4:D:14:ARG:HH12	4:D:16:LYS:NZ	2.05	0.55
4:D:216:ASN:C	4:D:218:GLU:N	2.61	0.55
5:E:155:ARG:O	5:E:156:LEU:HD23	2.06	0.55
14:T:15:DG:H2'	14:T:16:DT:H72	1.88	0.55
1:A:767:GLN:HE21	1:A:774:ARG:HB3	1.71	0.55
1:A:828:ALA:C	1:A:831:THR:HG22	2.31	0.55
1:A:832:ALA:O	14:T:18:DA:H5'	2.07	0.55
1:A:963:ILE:HD13	1:A:1049:ILE:HG12	1.89	0.55
1:A:993:LEU:HD22	1:A:1046:LEU:HD22	1.89	0.55
1:A:1193:LEU:HD12	1:A:1194:ARG:N	2.22	0.55
1:A:1235:LYS:O	1:A:1237:ILE:HD12	2.07	0.55
2:B:446:LEU:O	2:B:448:ILE:HG13	2.07	0.55
4:D:173:HIS:O	4:D:177:VAL:HG23	2.05	0.55
8:H:12:VAL:HG11	8:H:15:VAL:HG22	1.89	0.55
9:I:58:VAL:O	9:I:59:VAL:C	2.50	0.55
10:J:47:ARG:HG2	10:J:47:ARG:NH1	2.21	0.55
1:A:135:PHE:CD1	1:A:222:LEU:HD22	2.42	0.55
1:A:205:GLU:CD	1:A:205:GLU:N	2.63	0.55
1:A:331:GLY:O	1:A:332:LYS:O	2.25	0.55
1:A:722:LEU:HD23	1:A:799:PHE:CD1	2.41	0.55
1:A:886:ILE:CG2	1:A:952:ALA:HB2	2.36	0.55
1:A:1120:LEU:O	1:A:1323:ASP:HB2	2.07	0.55
1:A:1241:ARG:O	1:A:1242:VAL:HG23	2.07	0.55
2:B:100:PRO:HB2	2:B:180:TYR:HE1	1.72	0.55
2:B:189:LEU:HD13	2:B:196:PRO:HA	1.89	0.55
2:B:508:LEU:HG	2:B:509:ALA:H	1.72	0.55
2:B:542:MET:CE	2:B:747:MET:HG3	2.33	0.55
2:B:758:PHE:HB3	2:B:761:HIS:HD2	1.72	0.55
2:B:899:ILE:HG22	2:B:900:ALA:N	2.21	0.55
3:C:6:PRO:CB	3:C:25:VAL:HG22	2.37	0.55
3:C:215:GLU:O	3:C:217:ASP:N	2.40	0.55
4:D:8:PHE:HD2	7:G:6:ASP:HB2	1.70	0.55
4:D:14:ARG:NH1	4:D:16:LYS:HD2	2.22	0.55
4:D:155:ARG:CD	4:D:221:TYR:CE1	2.90	0.55
5:E:112:TYR:CZ	5:E:136:ASN:HB2	2.42	0.55
9:I:55:THR:HG23	9:I:86:PHE:CZ	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:49:GLU:HB3	11:K:90:ALA:HB1	1.88	0.55
1:A:446:ARG:HB2	1:A:487:MET:SD	2.46	0.54
1:A:527:THR:O	1:A:653:VAL:HG11	2.07	0.54
1:A:820:GLY:O	1:A:822:GLU:N	2.40	0.54
1:A:853:ASP:CG	1:A:855:THR:HG22	2.32	0.54
1:A:1308:THR:HG23	1:A:1309:ASP:H	1.71	0.54
1:A:1443:VAL:C	1:A:1444:MET:HG3	2.33	0.54
2:B:470:LYS:C	2:B:472:ALA:H	2.15	0.54
2:B:637:LEU:HD12	2:B:693:ILE:HD11	1.87	0.54
3:C:235:VAL:CG1	10:J:13:VAL:HG13	2.37	0.54
4:D:136:GLY:HA2	4:D:142:LYS:NZ	2.22	0.54
5:E:129:PRO:O	5:E:130:ALA:C	2.50	0.54
1:A:583:PRO:HG2	1:A:586:ILE:HG13	1.89	0.54
1:A:595:THR:O	1:A:596:THR:CG2	2.54	0.54
1:A:886:ILE:CG2	1:A:887:GLY:H	2.19	0.54
1:A:890:ASP:H	1:A:1296:GLY:HA3	1.71	0.54
2:B:48:LEU:O	2:B:51:PHE:N	2.31	0.54
2:B:244:LEU:HD11	2:B:250:PHE:HB2	1.89	0.54
2:B:309:GLN:HE21	2:B:309:GLN:CA	2.11	0.54
2:B:364:ILE:CG1	2:B:585:VAL:HG13	2.37	0.54
2:B:805:THR:HG22	2:B:806:THR:N	2.19	0.54
2:B:1069:PHE:HA	2:B:1085:ILE:O	2.08	0.54
3:C:34:ARG:O	3:C:38:ILE:HG13	2.07	0.54
10:J:42:LYS:HG2	10:J:43:ARG:N	2.22	0.54
12:L:32:ALA:H	12:L:55:ILE:CG1	2.21	0.54
1:A:12:ARG:HB3	2:B:1218:THR:CG2	2.38	0.54
1:A:133:LYS:O	1:A:136:ALA:HB3	2.08	0.54
1:A:153:PRO:CD	1:A:161:LEU:HD13	2.37	0.54
1:A:491:VAL:HG12	1:A:492:PRO:O	2.06	0.54
1:A:600:PRO:HG2	1:A:601:LYS:N	2.18	0.54
1:A:670:ILE:HG22	1:A:676:MET:HE2	1.89	0.54
1:A:829:VAL:C	1:A:831:THR:N	2.66	0.54
1:A:999:VAL:HG12	1:A:1000:LEU:N	2.23	0.54
1:A:1161:THR:HG22	1:A:1163:ILE:N	2.17	0.54
2:B:412:LEU:HB3	2:B:466:TRP:NE1	2.21	0.54
2:B:622:LYS:HE2	9:I:59:VAL:HG22	1.88	0.54
2:B:879:ARG:HH22	2:B:885:MET:HE1	1.73	0.54
2:B:1037:LEU:HD21	2:B:1064:TYR:HE1	1.72	0.54
3:C:7:GLN:HE21	3:C:7:GLN:CA	2.20	0.54
3:C:233:GLU:CG	3:C:234:SER:H	2.20	0.54
3:C:249:ASP:O	3:C:252:GLN:HB3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:220:LEU:CG	4:D:221:TYR:N	2.68	0.54
5:E:28:TYR:C	5:E:65:THR:HG22	2.32	0.54
1:A:125:ALA:C	1:A:127:ALA:N	2.65	0.54
1:A:853:ASP:OD1	1:A:855:THR:N	2.39	0.54
1:A:897:TYR:N	1:A:897:TYR:CD1	2.75	0.54
1:A:1402:PHE:CD1	1:A:1403:GLU:HG2	2.42	0.54
2:B:295:GLY:H	2:B:298:LEU:HD23	1.71	0.54
2:B:707:PRO:HG2	2:B:708:GLU:N	2.16	0.54
2:B:758:PHE:CE1	2:B:1027:ILE:CG2	2.90	0.54
2:B:763:GLN:HG2	2:B:765:PRO:HD2	1.90	0.54
3:C:260:LEU:O	3:C:263:THR:HB	2.07	0.54
4:D:129:LEU:HD12	4:D:129:LEU:O	2.07	0.54
4:D:155:ARG:HB2	4:D:155:ARG:NH1	2.21	0.54
1:A:306:ASN:ND2	1:A:322:VAL:HG12	2.22	0.54
1:A:761:MET:HA	1:A:804:TYR:HB2	1.89	0.54
1:A:1339:LEU:HD13	5:E:147:HIS:CD2	2.43	0.54
1:A:1412:ALA:HA	1:A:1417:GLU:OE2	2.08	0.54
2:B:363:HIS:O	2:B:364:ILE:HB	2.06	0.54
2:B:578:THR:C	2:B:589:VAL:HG13	2.33	0.54
2:B:882:THR:CG2	2:B:934:LYS:O	2.55	0.54
2:B:891:ASP:C	2:B:893:LEU:N	2.65	0.54
2:B:1001:PHE:CE2	3:C:34:ARG:NE	2.76	0.54
4:D:32:GLU:OE1	7:G:41:LYS:HE2	2.08	0.54
4:D:156:ASP:HB2	4:D:159:THR:OG1	2.06	0.54
5:E:138:ALA:HA	5:E:141:VAL:CG2	2.36	0.54
5:E:157:SER:OG	5:E:160:GLU:HG3	2.07	0.54
8:H:15:VAL:HG13	8:H:26:ILE:CG1	2.38	0.54
12:L:66:GLN:HG2	12:L:67:PHE:N	2.22	0.54
1:A:91:PHE:H	1:A:297:GLN:NE2	2.04	0.54
1:A:115:LEU:HD12	1:A:142:CYS:HB3	1.90	0.54
1:A:897:TYR:HD2	1:A:936:LEU:HD13	1.72	0.54
1:A:1283:VAL:O	1:A:1306:LEU:HA	2.08	0.54
2:B:277:LYS:HD2	2:B:277:LYS:N	2.15	0.54
2:B:707:PRO:CG	2:B:708:GLU:H	2.12	0.54
2:B:768:THR:O	2:B:771:SER:HB2	2.07	0.54
2:B:986:GLN:HE22	2:B:1022:THR:HG21	1.72	0.54
2:B:1003:ALA:HB1	3:C:179:GLU:HB2	1.90	0.54
3:C:137:LYS:HE2	3:C:138:GLU:OE1	2.08	0.54
4:D:12:ARG:HH12	4:D:14:ARG:CA	2.20	0.54
5:E:9:ILE:CD1	5:E:53:PRO:HD3	2.38	0.54
9:I:50:THR:HG23	9:I:52:ILE:HG12	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:567:LYS:CG	1:A:568:PRO:CD	2.85	0.54
1:A:774:ARG:CZ	1:A:797:LYS:HB2	2.38	0.54
1:A:1215:ARG:O	1:A:1219:THR:N	2.34	0.54
1:A:1293:SER:HB3	1:A:1297:GLU:OE1	2.07	0.54
1:A:1345:ARG:HG2	1:A:1372:VAL:HG12	1.88	0.54
2:B:215:GLN:OE1	2:B:499:ASN:HB3	2.08	0.54
2:B:1152:MET:C	2:B:1157:ALA:HB2	2.33	0.54
3:C:112:ASN:CB	3:C:114:TYR:CE1	2.91	0.54
4:D:52:LEU:O	4:D:54:GLU:N	2.40	0.54
5:E:10:SER:O	5:E:14:ARG:HG3	2.07	0.54
5:E:38:PRO:HG2	5:E:41:ASP:CG	2.33	0.54
5:E:154:ILE:HG22	5:E:155:ARG:O	2.07	0.54
7:G:20:PRO:CD	7:G:21:ARG:H	2.20	0.54
8:H:44:VAL:HG13	8:H:48:PRO:HA	1.90	0.54
1:A:1144:LYS:HB2	1:A:1268:LEU:O	2.08	0.54
3:C:17:ASN:H	3:C:240:VAL:HG11	1.68	0.54
9:I:101:PHE:HD1	9:I:101:PHE:H	1.56	0.54
1:A:440:ASP:O	1:A:460:VAL:HG23	2.08	0.54
1:A:600:PRO:CG	1:A:601:LYS:H	2.18	0.54
1:A:934:LYS:HB2	1:A:934:LYS:NZ	2.22	0.54
1:A:1018:PHE:O	1:A:1021:LEU:HB3	2.07	0.54
1:A:1244:ARG:HG2	1:A:1244:ARG:O	2.06	0.54
1:A:1423:GLY:CA	1:A:1426:GLU:HG3	2.37	0.54
2:B:95:ILE:CG1	2:B:130:VAL:HG23	2.38	0.54
2:B:192:LEU:O	2:B:193:LYS:HB2	2.08	0.54
2:B:244:LEU:HD13	2:B:366:GLN:NE2	2.23	0.54
2:B:244:LEU:HD13	2:B:366:GLN:HE22	1.72	0.54
2:B:754:SER:O	2:B:806:THR:HG21	2.08	0.54
2:B:796:LEU:HD12	2:B:852:ARG:O	2.08	0.54
3:C:99:LEU:N	3:C:99:LEU:HD22	2.22	0.54
3:C:183:TRP:O	3:C:184:ASN:C	2.50	0.54
3:C:229:TYR:N	3:C:229:TYR:CD1	2.76	0.54
6:F:130:ILE:HB	6:F:148:VAL:HG21	1.89	0.54
7:G:27:LYS:HE2	7:G:54:ILE:HB	1.89	0.54
9:I:19:ASP:HB3	9:I:24:ARG:HG2	1.88	0.54
1:A:287:HIS:HA	1:A:290:GLU:HG3	1.89	0.54
1:A:384:ASN:CG	1:A:388:LEU:HD12	2.33	0.54
1:A:900:ASP:CA	1:A:926:GLN:NE2	2.69	0.54
1:A:1036:ARG:HG2	1:A:1036:ARG:HH11	1.72	0.54
1:A:1220:PHE:O	1:A:1221:LYS:HB2	2.08	0.54
2:B:260:GLY:O	2:B:267:ARG:NH1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:308:TRP:HA	2:B:311:LEU:HB2	1.91	0.54
2:B:821:GLN:HE22	2:B:851:PHE:HA	1.73	0.54
2:B:953:LEU:O	2:B:953:LEU:HD23	2.08	0.54
3:C:112:ASN:HB2	3:C:114:TYR:HE1	1.72	0.54
4:D:29:LEU:HD12	7:G:82:PHE:CE2	2.42	0.54
6:F:93:ILE:CD1	6:F:134:ILE:HD11	2.29	0.54
7:G:139:ILE:HG12	7:G:140:LYS:HG3	1.89	0.54
8:H:82:PRO:HG2	8:H:83:GLN:N	2.20	0.54
1:A:268:ASP:HB3	1:A:299:HIS:ND1	2.24	0.53
1:A:434:ARG:NH2	1:A:440:ASP:OD1	2.41	0.53
1:A:853:ASP:OD1	1:A:855:THR:CG2	2.56	0.53
1:A:932:GLU:HG2	1:A:933:TYR:N	2.22	0.53
1:A:1011:GLN:HE22	1:A:1015:VAL:HG21	1.73	0.53
2:B:92:PHE:CD2	2:B:132:VAL:HG22	2.42	0.53
2:B:108:VAL:CG1	2:B:109:THR:H	2.21	0.53
2:B:169:ARG:N	2:B:454:THR:OG1	2.42	0.53
2:B:291:ILE:N	2:B:291:ILE:CD1	2.71	0.53
2:B:309:GLN:HA	2:B:309:GLN:NE2	2.20	0.53
2:B:412:LEU:HB3	2:B:466:TRP:HE1	1.71	0.53
2:B:834:ASN:O	2:B:838:SER:O	2.26	0.53
2:B:899:ILE:HD11	2:B:911:ILE:HA	1.90	0.53
2:B:969:ARG:NH1	3:C:61:GLU:OE1	2.41	0.53
2:B:1031:LEU:HD11	2:B:1042:GLY:HA3	1.91	0.53
2:B:1099:VAL:CG1	2:B:1100:ASP:H	2.19	0.53
3:C:18:VAL:HG23	3:C:240:VAL:HB	1.90	0.53
3:C:75:MET:O	3:C:246:ARG:NH2	2.37	0.53
8:H:126:GLU:HG3	8:H:127:GLY:H	1.73	0.53
11:K:93:SER:O	11:K:97:LYS:HG3	2.09	0.53
1:A:117:GLU:H	1:A:117:GLU:CD	2.17	0.53
1:A:447:GLN:HA	1:A:448:PRO:C	2.33	0.53
1:A:476:SER:HB2	1:A:477:PRO:HD3	1.90	0.53
1:A:567:LYS:HZ2	8:H:46:LEU:CB	2.21	0.53
1:A:829:VAL:O	1:A:831:THR:N	2.41	0.53
1:A:889:SER:HA	1:A:1297:GLU:N	2.23	0.53
1:A:909:ASP:O	1:A:911:SER:N	2.41	0.53
1:A:1081:LEU:HD11	1:A:1098:VAL:N	2.18	0.53
1:A:1164:PRO:HG2	1:A:1165:GLU:H	1.72	0.53
2:B:205:ILE:O	2:B:207:GLY:N	2.41	0.53
2:B:999:MET:HB3	2:B:1007:VAL:CG2	2.39	0.53
2:B:1197:PRO:O	2:B:1200:ALA:N	2.39	0.53
3:C:66:ARG:HH12	10:J:2:ILE:CG2	2.13	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:144:ARG:HG2	7:G:168:LEU:HD23	1.89	0.53
9:I:44:TYR:HD1	9:I:44:TYR:C	2.16	0.53
12:L:28:LYS:HE3	12:L:39:SER:OG	2.07	0.53
12:L:40:LEU:HD13	12:L:44:ASP:CB	2.37	0.53
1:A:1037:LEU:HD11	1:A:1045:VAL:HG21	1.89	0.53
1:A:1038:THR:H	1:A:1041:ALA:HB3	1.73	0.53
2:B:622:LYS:HZ1	9:I:59:VAL:HG22	1.73	0.53
3:C:46:ILE:HD13	3:C:157:CYS:SG	2.47	0.53
3:C:101:LEU:O	3:C:102:GLN:HG3	2.09	0.53
5:E:213:ILE:HG12	5:E:214:CYS:N	2.23	0.53
8:H:82:PRO:CG	8:H:83:GLN:H	2.16	0.53
10:J:57:ILE:O	10:J:60:PHE:HB2	2.09	0.53
1:A:56:PRO:O	1:A:57:ARG:NH1	2.42	0.53
1:A:146:MET:C	1:A:171:GLN:HB2	2.33	0.53
1:A:265:LYS:HE2	1:A:302:THR:HG23	1.88	0.53
1:A:925:LEU:C	1:A:927:VAL:N	2.65	0.53
1:A:1286:LYS:HE3	1:A:1304:TRP:CZ2	2.44	0.53
1:A:1287:TYR:O	1:A:1302:PRO:HA	2.09	0.53
1:A:1454:MET:O	1:A:1454:MET:HG3	2.08	0.53
2:B:351:TYR:CD1	2:B:355:ILE:HD11	2.44	0.53
2:B:526:GLU:OE1	2:B:752:ALA:HB3	2.08	0.53
2:B:846:ILE:HG23	2:B:974:PRO:CG	2.35	0.53
2:B:1104:HIS:CG	2:B:1122:ARG:HB2	2.44	0.53
3:C:167:HIS:CA	11:K:6:ARG:HH12	2.20	0.53
3:C:213:PRO:HG2	3:C:214:ASN:H	1.73	0.53
3:C:252:GLN:CG	11:K:95:ILE:HG23	2.37	0.53
5:E:168:TYR:HB3	5:E:170:LEU:HG	1.90	0.53
10:J:43:ARG:N	10:J:43:ARG:HD3	2.22	0.53
10:J:47:ARG:HG2	10:J:47:ARG:HH11	1.74	0.53
1:A:382:PRO:HD3	1:A:428:TYR:CE2	2.43	0.53
1:A:523:ILE:HG12	1:A:622:VAL:HG22	1.91	0.53
1:A:768:GLN:CG	1:A:816:HIS:HA	2.26	0.53
1:A:868:TYR:CE1	1:A:1064:VAL:CG1	2.91	0.53
1:A:1111:MET:CG	1:A:1114:PRO:HB3	2.38	0.53
1:A:1342:GLU:HG3	5:E:198:ILE:HG21	1.91	0.53
2:B:603:LEU:HB3	2:B:609:ILE:HD11	1.90	0.53
2:B:708:GLU:O	2:B:709:ASP:C	2.51	0.53
2:B:1096:ARG:O	2:B:1097:HIS:CB	2.56	0.53
3:C:118:LEU:HB2	3:C:132:PRO:HG2	1.90	0.53
5:E:182:ASP:O	5:E:186:LEU:HG	2.09	0.53
8:H:84:ALA:O	8:H:85:GLY:C	2.51	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:89:LEU:CD1	8:H:91:ASP:OD1	2.56	0.53
8:H:113:ALA:HB2	8:H:126:GLU:OE2	2.08	0.53
8:H:128:ASN:ND2	8:H:131:ASN:OD1	2.41	0.53
1:A:347:PHE:H	2:B:1107:ALA:HA	1.73	0.53
1:A:709:THR:HG22	1:A:710:LEU:HD12	1.90	0.53
1:A:774:ARG:O	1:A:775:ILE:C	2.50	0.53
1:A:777:PHE:CD1	1:A:781:ASP:HA	2.44	0.53
1:A:1141:THR:HG21	1:A:1205:LYS:HD3	1.91	0.53
2:B:125:SER:O	2:B:126:SER:HB3	2.08	0.53
2:B:211:VAL:O	2:B:480:SER:HA	2.09	0.53
2:B:292:ILE:CD1	2:B:327:ARG:H	2.12	0.53
2:B:880:THR:HB	2:B:934:LYS:CG	2.37	0.53
2:B:1064:TYR:O	2:B:1065:GLN:C	2.51	0.53
5:E:64:PRO:HB2	5:E:69:ILE:HD11	1.89	0.53
5:E:80:VAL:HG12	5:E:82:PHE:CE1	2.42	0.53
6:F:118:LEU:O	6:F:118:LEU:HG	2.08	0.53
7:G:20:PRO:HD2	7:G:21:ARG:H	1.74	0.53
8:H:81:PRO:HD2	8:H:83:GLN:OE1	2.09	0.53
1:A:382:PRO:HD3	1:A:428:TYR:CD2	2.43	0.53
1:A:1011:GLN:NE2	1:A:1015:VAL:CG2	2.72	0.53
1:A:1209:MET:HE1	1:A:1236:LEU:HB3	1.91	0.53
2:B:172:ILE:CD1	2:B:178:ASN:ND2	2.71	0.53
2:B:818:PRO:HB2	2:B:1091:TYR:OH	2.08	0.53
3:C:33:LEU:O	3:C:37:MET:HG3	2.09	0.53
3:C:51:VAL:HG22	3:C:155:LEU:HD22	1.91	0.53
4:D:154:PHE:CE1	4:D:163:VAL:HG11	2.40	0.53
5:E:154:ILE:O	5:E:196:VAL:HA	2.08	0.53
7:G:1:MET:O	7:G:2:PHE:C	2.52	0.53
8:H:2:SER:HA	8:H:62:SER:HB3	1.89	0.53
8:H:118:PHE:O	8:H:119:GLY:C	2.52	0.53
9:I:88:SER:C	9:I:90:GLN:H	2.17	0.53
10:J:37:SER:OG	10:J:47:ARG:NH2	2.41	0.53
11:K:42:LEU:O	11:K:46:ILE:HG13	2.09	0.53
11:K:65:HIS:CD2	11:K:67:PHE:H	2.27	0.53
1:A:211:PHE:HD1	1:A:214:ILE:CD1	2.22	0.53
1:A:224:PHE:CD2	1:A:231:PRO:HG3	2.43	0.53
1:A:367:PRO:HG2	1:A:370:ILE:HD12	1.91	0.53
1:A:590:ARG:HG3	1:A:591:PHE:N	2.23	0.53
1:A:614:PHE:CD1	1:A:614:PHE:C	2.86	0.53
1:A:1045:VAL:O	1:A:1049:ILE:HG13	2.08	0.53
1:A:1048:ASN:HD22	1:A:1048:ASN:N	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1171:GLN:OE1	1:A:1172:LEU:N	2.41	0.53
2:B:29:ASP:HB3	2:B:658:ILE:HD13	1.89	0.53
2:B:54:PHE:HE1	2:B:414:ALA:HA	1.74	0.53
2:B:219:ALA:HB2	2:B:405:ARG:NH1	2.24	0.53
2:B:467:GLY:CA	2:B:475:SER:HB2	2.39	0.53
2:B:515:HIS:H	2:B:518:HIS:CD2	2.27	0.53
2:B:802:PRO:HG3	2:B:809:MET:HE1	1.90	0.53
2:B:1084:GLN:HG2	3:C:201:TRP:CZ2	2.43	0.53
2:B:1201:LYS:HE2	2:B:1205:GLN:CD	2.31	0.53
4:D:71:LYS:HA	4:D:74:GLN:CG	2.39	0.53
7:G:91:VAL:HG12	7:G:92:VAL:N	2.24	0.53
8:H:123:MET:CE	8:H:142:LEU:HD21	2.37	0.53
9:I:103:CYS:SG	9:I:106:CYS:SG	3.06	0.53
1:A:11:LEU:HB2	2:B:1193:GLN:HG3	1.91	0.53
1:A:96:ILE:HG22	1:A:97:ALA:N	2.23	0.53
1:A:925:LEU:C	1:A:927:VAL:H	2.17	0.53
1:A:1239:ARG:HH22	1:A:1241:ARG:HH22	1.56	0.53
2:B:562:GLY:HA3	2:B:590:HIS:ND1	2.24	0.53
2:B:603:LEU:HB3	2:B:609:ILE:CD1	2.39	0.53
2:B:822:ASN:ND2	10:J:52:THR:HG21	2.24	0.53
2:B:842:ASN:ND2	2:B:845:SER:OG	2.42	0.53
2:B:1130:PHE:HZ	2:B:1138:MET:HG2	1.74	0.53
3:C:148:ARG:NH1	10:J:64:ASN:HA	2.24	0.53
3:C:148:ARG:HG2	3:C:149:LYS:H	1.72	0.53
4:D:50:LEU:HD11	7:G:4:ILE:HD11	1.90	0.53
4:D:52:LEU:HD21	4:D:147:TYR:HE2	1.72	0.53
5:E:17:ARG:HG3	5:E:35:VAL:HG13	1.90	0.53
6:F:138:LEU:O	6:F:140:ASP:N	2.38	0.53
7:G:27:LYS:HD3	7:G:51:TYR:CE2	2.44	0.53
7:G:88:ASP:HB3	7:G:144:ARG:CA	2.35	0.53
10:J:24:LEU:HA	10:J:28:ASP:HB2	1.91	0.53
12:L:40:LEU:HB3	12:L:44:ASP:HB2	1.91	0.53
14:T:15:DG:H2'	14:T:16:DT:C7	2.39	0.53
1:A:504:LEU:HD11	6:F:91:ALA:HB2	1.90	0.53
1:A:599:SER:HB3	1:A:614:PHE:CE1	2.44	0.53
2:B:803:LEU:CD1	2:B:1032:SER:HB3	2.39	0.53
2:B:1065:GLN:NE2	2:B:1067:ARG:H	1.91	0.53
3:C:124:LEU:O	3:C:126:GLY:N	2.42	0.53
5:E:89:GLY:C	5:E:91:LYS:H	2.17	0.53
10:J:12:LYS:O	10:J:13:VAL:C	2.51	0.53
12:L:47:ARG:HD3	12:L:52:GLY:HA2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:T:11:DA:H2''	14:T:12:DG:H5'	1.90	0.53
1:A:321:PRO:O	1:A:322:VAL:HG12	2.10	0.52
1:A:323:LYS:HD2	1:A:323:LYS:N	2.22	0.52
1:A:722:LEU:HB3	1:A:799:PHE:CE1	2.44	0.52
1:A:889:SER:HB3	1:A:1297:GLU:HG3	1.90	0.52
1:A:1161:THR:HG22	1:A:1163:ILE:HG13	1.89	0.52
1:A:1315:GLU:C	1:A:1317:MET:N	2.67	0.52
1:A:1445:ILE:HD13	7:G:70:PHE:CE2	2.44	0.52
2:B:209:GLU:CD	2:B:485:ARG:HE	2.17	0.52
2:B:370:PHE:HD2	2:B:373:ARG:HD2	1.73	0.52
2:B:378:LEU:O	2:B:382:ILE:HG13	2.08	0.52
2:B:431:TYR:CD1	2:B:447:ALA:HB2	2.43	0.52
2:B:636:PRO:HG2	2:B:743:ILE:CD1	2.40	0.52
2:B:745:PRO:O	2:B:747:MET:N	2.41	0.52
2:B:1198:TYR:CD2	2:B:1198:TYR:O	2.62	0.52
5:E:124:VAL:HB	5:E:125:PRO:HD3	1.90	0.52
1:A:41:MET:HB2	1:A:48:ALA:O	2.08	0.52
1:A:528:LEU:O	1:A:531:ILE:HG22	2.09	0.52
1:A:903:ASN:ND2	1:A:905:ASP:H	2.08	0.52
2:B:120:ARG:HH12	12:L:54:ARG:NH1	2.08	0.52
2:B:287:ARG:HD3	2:B:325:GLN:HA	1.92	0.52
2:B:293:PRO:C	2:B:294:ASP:O	2.51	0.52
2:B:583:ASN:ND2	2:B:628:THR:HG22	2.20	0.52
5:E:32:GLN:O	5:E:36:GLU:HG3	2.09	0.52
5:E:50:MET:HG3	5:E:51:GLY:N	2.24	0.52
5:E:180:ARG:HB2	5:E:215:MET:OXT	2.09	0.52
11:K:68:PHE:HD2	11:K:68:PHE:N	2.06	0.52
1:A:22:PHE:CE1	2:B:1213:THR:HG22	2.44	0.52
1:A:156:ASP:HB2	1:A:160:GLN:HE22	1.74	0.52
1:A:264:PHE:CE1	1:A:317:LYS:NZ	2.78	0.52
1:A:705:LYS:HG3	1:A:713:SER:HB3	1.91	0.52
1:A:834:THR:HG21	1:A:1077:THR:CG2	2.36	0.52
1:A:1155:ASP:OD2	1:A:1161:THR:HA	2.09	0.52
2:B:29:ASP:OD1	2:B:658:ILE:HG21	2.10	0.52
2:B:227:LYS:H	2:B:395:GLN:CD	2.17	0.52
2:B:855:PHE:HD2	2:B:972:LYS:HE3	1.75	0.52
2:B:882:THR:CG2	2:B:884:ARG:N	2.72	0.52
4:D:135:GLY:C	4:D:137:ASN:H	2.16	0.52
13:N:5:DC:H2''	13:N:6:DT:OP2	2.09	0.52
1:A:388:LEU:HD22	1:A:432:VAL:CG2	2.39	0.52
1:A:868:TYR:HE1	1:A:1064:VAL:HG13	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:888:GLY:O	1:A:940:ARG:NH2	2.42	0.52
2:B:95:ILE:HG13	2:B:130:VAL:HG23	1.91	0.52
2:B:281:PRO:C	2:B:283:VAL:N	2.67	0.52
4:D:162:ALA:HA	4:D:165:GLN:NE2	2.24	0.52
7:G:137:ILE:O	7:G:138:THR:HB	2.09	0.52
1:A:69:THR:HG21	2:B:1174:LYS:NZ	2.25	0.52
1:A:549:MET:SD	1:A:577:ILE:HD12	2.50	0.52
1:A:563:PRO:HD3	8:H:79:TRP:CD1	2.45	0.52
1:A:567:LYS:HD3	8:H:95:TYR:CD2	2.45	0.52
1:A:636:GLU:OE2	1:A:962:ARG:HD2	2.10	0.52
1:A:784:LEU:HD11	1:A:815:PHE:CE2	2.44	0.52
1:A:1161:THR:C	1:A:1163:ILE:H	2.15	0.52
2:B:39:ARG:CZ	2:B:665:GLU:HG2	2.38	0.52
2:B:69:LEU:CD1	2:B:432:MET:HE1	2.39	0.52
2:B:259:TYR:N	2:B:259:TYR:CD1	2.78	0.52
2:B:307:ASP:C	2:B:309:GLN:N	2.64	0.52
2:B:416:LEU:HD22	2:B:457:LEU:HD23	1.92	0.52
2:B:579:ARG:HG2	2:B:579:ARG:NH1	2.25	0.52
2:B:801:LYS:HA	2:B:818:PRO:HB3	1.92	0.52
2:B:1113:VAL:N	15:P:1:C:C5'	2.70	0.52
2:B:1174:LYS:O	2:B:1176:ASN:N	2.43	0.52
3:C:22:LEU:HD22	3:C:230:MET:HE1	1.91	0.52
3:C:29:MET:HE2	11:K:98:LEU:HG	1.91	0.52
7:G:35:GLU:OE2	7:G:48:VAL:HG23	2.10	0.52
7:G:55:ASP:HB3	7:G:73:LYS:HB2	1.91	0.52
7:G:79:PHE:HE2	7:G:106:MET:HE2	1.74	0.52
10:J:16:ASP:OD1	10:J:17:LYS:N	2.39	0.52
12:L:34:CYS:SG	12:L:51:CYS:SG	3.07	0.52
1:A:68:GLN:OE1	1:A:70:CYS:HB3	2.09	0.52
1:A:151:ASP:OD1	1:A:163:SER:HB3	2.10	0.52
1:A:382:PRO:CA	1:A:428:TYR:HE2	2.22	0.52
1:A:767:GLN:NE2	1:A:774:ARG:HB2	2.25	0.52
1:A:767:GLN:HE21	1:A:774:ARG:CB	2.23	0.52
1:A:997:LEU:HD13	1:A:1018:PHE:CE2	2.45	0.52
2:B:39:ARG:HG2	2:B:39:ARG:NH1	2.24	0.52
2:B:54:PHE:O	2:B:58:THR:HB	2.10	0.52
2:B:311:LEU:O	2:B:312:GLU:C	2.53	0.52
2:B:434:ARG:O	2:B:436:VAL:N	2.43	0.52
2:B:516:ASN:H	2:B:516:ASN:ND2	2.07	0.52
2:B:653:VAL:HG13	2:B:657:HIS:HB2	1.91	0.52
2:B:686:ASN:C	2:B:688:GLY:H	2.17	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:707:PRO:O	2:B:708:GLU:O	2.27	0.52
2:B:1177:HIS:HB3	2:B:1179:GLN:HE21	1.74	0.52
5:E:145:THR:HG21	5:E:187:TYR:CD2	2.44	0.52
1:A:405:VAL:HG22	1:A:432:VAL:HG13	1.92	0.52
1:A:806:ARG:NH1	2:B:729:ILE:HD12	2.23	0.52
1:A:1109:LYS:HG3	1:A:1110:ASN:ND2	2.25	0.52
2:B:288:ALA:HB2	2:B:330:ALA:HB1	1.91	0.52
2:B:459:TYR:CE1	2:B:463:THR:HG21	2.45	0.52
2:B:497:ARG:HH21	2:B:775:LYS:NZ	2.07	0.52
2:B:644:GLU:OE1	2:B:644:GLU:HA	2.09	0.52
2:B:757:PRO:HG3	2:B:1028:GLU:OE2	2.09	0.52
3:C:25:VAL:HG12	3:C:26:ASP:N	2.25	0.52
3:C:31:ASN:O	3:C:35:ARG:HG3	2.09	0.52
6:F:69:LEU:C	6:F:71:GLU:HG3	2.34	0.52
9:I:75:CYS:HB2	9:I:76:PRO:CD	2.40	0.52
11:K:59:ALA:HA	11:K:74:ARG:O	2.09	0.52
1:A:53:LEU:CD2	1:A:54:ASN:N	2.56	0.52
1:A:557:ASP:OD1	1:A:559:VAL:HB	2.09	0.52
1:A:741:ASN:ND2	1:A:744:LYS:N	2.52	0.52
1:A:896:ARG:HD3	1:A:897:TYR:HE1	1.71	0.52
1:A:963:ILE:O	1:A:963:ILE:HG12	2.10	0.52
1:A:1116:LEU:N	1:A:1308:THR:CG2	2.68	0.52
1:A:1146:VAL:HG12	1:A:1201:ALA:HB1	1.91	0.52
2:B:562:GLY:O	2:B:590:HIS:ND1	2.43	0.52
2:B:744:HIS:CD2	2:B:745:PRO:CD	2.87	0.52
2:B:944:THR:HG21	2:B:1122:ARG:NH2	2.25	0.52
4:D:47:LEU:HD13	4:D:48:ILE:N	2.24	0.52
5:E:22:MET:HE1	5:E:26:ARG:NH2	2.24	0.52
6:F:111:LEU:C	6:F:113:GLY:N	2.68	0.52
7:G:34:VAL:CG1	7:G:45:ILE:HG21	2.39	0.52
8:H:26:ILE:HG12	8:H:27:GLU:N	2.24	0.52
1:A:16:GLU:OE1	4:D:13:ARG:NH2	2.40	0.52
1:A:66:LYS:CE	1:A:68:GLN:H	2.21	0.52
1:A:132:LYS:HE3	1:A:1411:GLU:OE2	2.10	0.52
1:A:514:PRO:O	1:A:515:GLN:C	2.53	0.52
1:A:679:ILE:HG12	1:A:732:LEU:HD12	1.92	0.52
1:A:714:PHE:O	1:A:718:VAL:HG23	2.10	0.52
1:A:943:LEU:C	1:A:945:GLU:H	2.18	0.52
2:B:35:SER:O	2:B:39:ARG:HG3	2.10	0.52
2:B:235:SER:OG	2:B:236:HIS:CD2	2.62	0.52
2:B:245:GLU:C	2:B:246:LYS:HG3	2.35	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:506:GLY:O	2:B:507:LYS:CB	2.58	0.52
2:B:557:PHE:CZ	2:B:603:LEU:HD21	2.45	0.52
2:B:1045:SER:O	2:B:1048:THR:HG23	2.10	0.52
2:B:1182:CYS:C	2:B:1183:LYS:HE3	2.35	0.52
3:C:242:GLN:O	3:C:244:VAL:N	2.43	0.52
4:D:154:PHE:O	4:D:160:VAL:HG22	2.10	0.52
12:L:55:ILE:O	12:L:56:LEU:HB2	2.09	0.52
1:A:34:LYS:HG2	1:A:36:ARG:NH2	2.21	0.52
1:A:93:VAL:CG2	1:A:301:ALA:HA	2.38	0.52
1:A:356:ASP:OD2	11:K:65:HIS:HE1	1.92	0.52
1:A:401:GLY:C	1:A:435:HIS:HD2	2.18	0.52
1:A:470:LEU:HD23	1:A:470:LEU:H	1.75	0.52
1:A:688:LYS:C	1:A:690:VAL:H	2.16	0.52
1:A:1127:ASP:HB3	1:A:1130:GLN:HB3	1.92	0.52
1:A:1323:ASP:CG	1:A:1325:THR:HG22	2.34	0.52
2:B:199:MET:HE2	2:B:492:LEU:HD23	1.91	0.52
2:B:431:TYR:CE1	2:B:447:ALA:HB2	2.44	0.52
2:B:842:ASN:HD21	2:B:844:SER:HB2	1.75	0.52
2:B:1124:ARG:O	2:B:1125:ASP:HB3	2.10	0.52
2:B:1147:LEU:HD23	2:B:1151:LEU:HD13	1.92	0.52
5:E:102:GLU:C	5:E:104:ASN:H	2.16	0.52
8:H:5:LEU:HD13	8:H:133:ASN:O	2.09	0.52
8:H:109:LYS:HG2	8:H:110:ASP:H	1.73	0.52
1:A:2:VAL:HG22	1:A:3:GLY:N	2.25	0.51
2:B:114:PRO:HG3	2:B:181:LEU:HD21	1.90	0.51
2:B:294:ASP:C	2:B:296:GLU:H	2.15	0.51
2:B:313:MET:HE3	2:B:386:LEU:HB3	1.91	0.51
2:B:401:PHE:HA	2:B:404:LYS:HG3	1.92	0.51
2:B:497:ARG:NH2	2:B:775:LYS:HZ3	2.08	0.51
2:B:661:LEU:C	2:B:663:ALA:N	2.68	0.51
2:B:1116:ARG:HG3	2:B:1198:TYR:CD1	2.45	0.51
2:B:1174:LYS:O	2:B:1175:LEU:C	2.52	0.51
2:B:1198:TYR:CD2	2:B:1198:TYR:C	2.88	0.51
7:G:129:SER:CB	7:G:138:THR:HB	2.39	0.51
10:J:14:VAL:HG12	10:J:50:ILE:HD11	1.91	0.51
10:J:23:ASN:O	10:J:25:LEU:N	2.43	0.51
14:T:24:DG:H2"	14:T:25:DG:OP2	2.10	0.51
1:A:186:LYS:NZ	1:A:197:PRO:HD3	2.25	0.51
1:A:794:PRO:HG2	1:A:795:GLU:OE2	2.10	0.51
1:A:901:LEU:N	1:A:926:GLN:NE2	2.35	0.51
2:B:217:ARG:HH11	2:B:217:ARG:HG2	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:510:LYS:CB	2:B:511:PRO:HD3	2.40	0.51
2:B:694:ASP:O	2:B:698:GLU:HB2	2.10	0.51
2:B:893:LEU:HD22	2:B:897:GLY:C	2.35	0.51
3:C:66:ARG:CZ	10:J:2:ILE:HG21	2.39	0.51
4:D:63:LEU:O	4:D:129:LEU:HD11	2.10	0.51
5:E:186:LEU:O	5:E:187:TYR:C	2.50	0.51
10:J:34:THR:O	10:J:35:ALA:C	2.53	0.51
1:A:266:LEU:HD21	1:A:303:TYR:CE1	2.45	0.51
1:A:316:GLN:O	1:A:317:LYS:C	2.53	0.51
1:A:699:ALA:HB3	1:A:701:LEU:HG	1.93	0.51
1:A:808:LEU:HD23	1:A:812:GLU:C	2.34	0.51
1:A:882:SER:HB3	1:A:953:ASN:OD1	2.10	0.51
1:A:1001:ARG:O	1:A:1002:GLY:O	2.28	0.51
2:B:51:PHE:O	2:B:55:VAL:HG23	2.10	0.51
2:B:303:TYR:CD2	2:B:303:TYR:N	2.78	0.51
2:B:345:LYS:HE2	2:B:349:ILE:HD11	1.92	0.51
2:B:578:THR:O	2:B:589:VAL:HG13	2.10	0.51
2:B:1000:PRO:O	2:B:1007:VAL:HG23	2.10	0.51
4:D:35:LEU:HD12	4:D:35:LEU:N	2.25	0.51
5:E:56:LYS:NZ	5:E:84:ASP:N	2.58	0.51
6:F:128:LYS:HD3	6:F:148:VAL:O	2.10	0.51
7:G:51:TYR:C	7:G:51:TYR:CD2	2.89	0.51
8:H:9:ILE:HA	8:H:55:LEU:O	2.10	0.51
8:H:15:VAL:HG22	8:H:26:ILE:CD1	2.41	0.51
8:H:109:LYS:HG2	8:H:110:ASP:OD1	2.10	0.51
1:A:65:LEU:O	1:A:66:LYS:C	2.54	0.51
1:A:536:LEU:HD23	1:A:536:LEU:N	2.14	0.51
1:A:598:LEU:O	1:A:599:SER:C	2.53	0.51
1:A:804:TYR:OH	2:B:763:GLN:HA	2.11	0.51
2:B:33:VAL:HG21	2:B:638:PHE:HZ	1.75	0.51
2:B:129:PHE:HE2	2:B:166:PHE:HB2	1.74	0.51
2:B:809:MET:O	2:B:812:LEU:N	2.41	0.51
2:B:840:ILE:HD13	2:B:994:TYR:HE1	1.75	0.51
2:B:1076:HIS:CD2	11:K:40:HIS:NE2	2.78	0.51
3:C:125:MET:HE2	3:C:127:ARG:CZ	2.40	0.51
4:D:190:GLU:O	4:D:194:LEU:HG	2.10	0.51
5:E:61:GLN:NE2	5:E:105:PHE:CZ	2.77	0.51
8:H:17:PRO:CB	8:H:24:CYS:SG	2.89	0.51
1:A:427:GLN:HB2	1:A:430:TRP:NE1	2.24	0.51
1:A:437:MET:N	1:A:440:ASP:OD2	2.28	0.51
1:A:622:VAL:HG22	1:A:622:VAL:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:883:LEU:CD1	1:A:1017:LEU:HD11	2.39	0.51
1:A:922:ASP:OD1	1:A:924:LYS:HB2	2.10	0.51
1:A:1187:GLN:HB2	1:A:1244:ARG:HH21	1.74	0.51
3:C:124:LEU:C	3:C:126:GLY:N	2.69	0.51
3:C:241:ASP:O	3:C:245:VAL:HG22	2.10	0.51
5:E:124:VAL:N	5:E:125:PRO:HD2	2.25	0.51
5:E:143:ASN:HD22	5:E:146:HIS:CE1	2.29	0.51
7:G:59:GLY:CA	7:G:70:PHE:CD2	2.94	0.51
12:L:32:ALA:H	12:L:55:ILE:CD1	2.23	0.51
1:A:79:GLY:HA3	1:A:243:PRO:HG3	1.93	0.51
1:A:230:ARG:HD2	1:A:233:TRP:CH2	2.45	0.51
1:A:386:ASP:O	1:A:387:ARG:C	2.52	0.51
1:A:427:GLN:O	1:A:428:TYR:C	2.53	0.51
1:A:457:ALA:HB3	1:A:506:ALA:HA	1.91	0.51
1:A:688:LYS:HA	1:A:691:LEU:HB3	1.92	0.51
1:A:774:ARG:HG3	1:A:797:LYS:HB3	1.92	0.51
1:A:913:LEU:HD13	1:A:981:LEU:O	2.10	0.51
2:B:52:ASN:O	2:B:56:ASP:N	2.42	0.51
2:B:173:MET:HE2	2:B:201:GLY:O	2.10	0.51
2:B:333:PHE:CG	2:B:333:PHE:O	2.63	0.51
2:B:987:LYS:H	2:B:987:LYS:HD3	1.75	0.51
2:B:1001:PHE:CE2	3:C:34:ARG:CZ	2.93	0.51
2:B:1077:THR:HG22	11:K:44:ASN:ND2	2.26	0.51
2:B:1077:THR:HG22	11:K:44:ASN:HD21	1.75	0.51
5:E:185:ALA:O	5:E:190:LEU:HG	2.10	0.51
6:F:76:LYS:CA	6:F:79:ARG:HD2	2.39	0.51
9:I:85:PHE:HD1	9:I:99:LEU:HD13	1.72	0.51
12:L:60:ARG:HH21	12:L:65:VAL:CG2	2.24	0.51
1:A:332:LYS:CA	1:A:337:ARG:NH1	2.73	0.51
1:A:596:THR:C	1:A:598:LEU:N	2.67	0.51
1:A:598:LEU:HD23	8:H:25:ARG:CZ	2.41	0.51
1:A:1166:ASP:OD2	1:A:1239:ARG:CD	2.59	0.51
1:A:1451:VAL:C	1:A:1453:TYR:H	2.17	0.51
2:B:376:PHE:HE2	2:B:569:TYR:HD2	1.58	0.51
2:B:555:ILE:HG22	2:B:556:THR:N	2.26	0.51
2:B:661:LEU:HD11	2:B:684:LEU:HD21	1.93	0.51
2:B:806:THR:CG2	2:B:809:MET:H	2.19	0.51
2:B:864:LYS:HG3	2:B:872:GLU:OE1	2.11	0.51
2:B:1102:LYS:O	2:B:1122:ARG:NH1	2.39	0.51
3:C:3:GLU:HB3	11:K:104:ASN:HD21	1.75	0.51
5:E:22:MET:CE	5:E:26:ARG:NH2	2.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:78:LEU:HD21	5:E:80:VAL:CG2	2.21	0.51
6:F:125:LEU:C	6:F:125:LEU:HD23	2.36	0.51
8:H:43:ASN:ND2	8:H:46:LEU:HD12	2.25	0.51
10:J:1:MET:O	10:J:2:ILE:O	2.28	0.51
1:A:308:ILE:HG22	1:A:309:ALA:H	1.76	0.51
1:A:316:GLN:HE21	1:A:317:LYS:NZ	2.09	0.51
1:A:774:ARG:NH2	1:A:797:LYS:HB2	2.26	0.51
1:A:1349:TYR:O	1:A:1350:LYS:C	2.52	0.51
2:B:902:GLY:O	12:L:65:VAL:HG11	2.11	0.51
4:D:17:LYS:HD2	4:D:17:LYS:C	2.35	0.51
4:D:71:LYS:CA	4:D:74:GLN:HB2	2.32	0.51
5:E:153:HIS:O	5:E:154:ILE:CG1	2.59	0.51
6:F:109:VAL:HG13	6:F:127:GLU:OE1	2.10	0.51
7:G:62:LEU:HD13	7:G:63:PRO:N	2.25	0.51
7:G:64:THR:HG23	7:G:65:ASP:N	2.25	0.51
8:H:37:LYS:H	8:H:126:GLU:HB3	1.76	0.51
1:A:388:LEU:HD22	1:A:432:VAL:HG21	1.92	0.51
1:A:698:GLN:O	9:I:98:VAL:HG13	2.11	0.51
1:A:798:GLY:HA2	1:A:815:PHE:HD1	1.75	0.51
1:A:1445:ILE:HD12	7:G:59:GLY:O	2.11	0.51
2:B:47:GLN:O	2:B:173:MET:HE1	2.11	0.51
2:B:212:LEU:HD23	2:B:480:SER:HB2	1.93	0.51
2:B:687:GLU:O	2:B:689:LEU:HG	2.10	0.51
2:B:815:ARG:HB2	2:B:815:ARG:HH11	1.74	0.51
2:B:872:GLU:OE2	2:B:914:LYS:HE3	2.11	0.51
2:B:970:THR:HG22	2:B:971:THR:N	2.26	0.51
6:F:94:LEU:HD21	6:F:122:MET:HA	1.93	0.51
11:K:13:GLY:O	11:K:14:GLU:C	2.53	0.51
1:A:543:LEU:O	1:A:544:ASP:C	2.53	0.51
1:A:546:VAL:HG12	1:A:550:LEU:HD11	1.93	0.51
1:A:590:ARG:NH2	1:A:620:LYS:HB2	2.26	0.51
1:A:592:ASP:N	1:A:595:THR:OG1	2.43	0.51
1:A:616:VAL:HG12	1:A:617:VAL:H	1.76	0.51
2:B:110:HIS:HB2	12:L:54:ARG:NH2	2.26	0.51
2:B:324:ILE:HD13	2:B:330:ALA:HA	1.92	0.51
2:B:850:LEU:HD12	2:B:850:LEU:C	2.36	0.51
2:B:1175:LEU:HD23	2:B:1175:LEU:H	1.76	0.51
3:C:133:ILE:CD1	3:C:236:GLY:C	2.84	0.51
4:D:154:PHE:CE1	4:D:163:VAL:HG21	2.42	0.51
5:E:37:LEU:C	5:E:37:LEU:HD12	2.35	0.51
5:E:162:ARG:HH11	5:E:162:ARG:HG2	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:7:LEU:CB	7:G:74:TYR:CE2	2.94	0.51
7:G:101:VAL:CG1	7:G:102:GLN:N	2.71	0.51
10:J:1:MET:H1	10:J:56:LEU:H	1.55	0.51
12:L:60:ARG:HG2	12:L:61:THR:N	2.14	0.51
1:A:1217:LYS:HA	1:A:1217:LYS:HE3	1.93	0.50
2:B:418:LYS:O	2:B:420:LEU:N	2.44	0.50
2:B:799:PRO:HD3	10:J:1:MET:HG2	1.93	0.50
2:B:1156:ASP:O	2:B:1157:ALA:O	2.28	0.50
3:C:39:ALA:CA	3:C:164:ALA:HB3	2.41	0.50
4:D:119:ARG:HD3	4:D:221:TYR:CE2	2.46	0.50
6:F:136:ARG:O	6:F:143:PHE:HA	2.12	0.50
7:G:1:MET:HE1	7:G:3:PHE:HE1	1.76	0.50
9:I:26:LEU:CD2	9:I:37:GLU:HA	2.40	0.50
11:K:40:HIS:O	11:K:41:THR:C	2.54	0.50
12:L:60:ARG:CG	12:L:61:THR:H	2.16	0.50
1:A:69:THR:C	1:A:71:GLN:N	2.66	0.50
1:A:71:GLN:C	1:A:73:GLY:H	2.20	0.50
1:A:308:ILE:HG22	1:A:309:ALA:N	2.26	0.50
1:A:512:VAL:O	1:A:512:VAL:HG12	2.10	0.50
1:A:692:ASP:C	1:A:694:THR:N	2.68	0.50
1:A:1299:VAL:HG12	1:A:1300:LYS:N	2.25	0.50
1:A:1403:GLU:OE1	14:T:16:DT:H4'	2.12	0.50
2:B:839:MET:HE3	2:B:1010:LEU:CD2	2.40	0.50
4:D:16:LYS:C	4:D:18:VAL:H	2.20	0.50
9:I:51:ASN:ND2	9:I:54:GLU:OE1	2.43	0.50
1:A:34:LYS:HD3	1:A:34:LYS:H	1.77	0.50
1:A:42:ASP:HA	1:A:46:THR:O	2.10	0.50
1:A:88:LYS:HD3	1:A:293:GLU:CD	2.36	0.50
1:A:253:ASN:HA	2:B:884:ARG:NH2	2.26	0.50
1:A:692:ASP:O	1:A:694:THR:N	2.44	0.50
1:A:973:ILE:HD13	1:A:1037:LEU:HA	1.93	0.50
1:A:1280:GLU:O	1:A:1281:ARG:C	2.54	0.50
1:A:1330:ASN:O	1:A:1332:PHE:N	2.44	0.50
2:B:59:LEU:CD1	2:B:417:PHE:CE2	2.89	0.50
2:B:126:SER:O	2:B:169:ARG:HA	2.10	0.50
2:B:222:ILE:N	2:B:240:ILE:CD1	2.75	0.50
2:B:247:GLY:C	2:B:249:ARG:H	2.19	0.50
2:B:311:LEU:O	2:B:314:LEU:N	2.43	0.50
2:B:424:LEU:O	2:B:428:ILE:HG13	2.10	0.50
2:B:521:LEU:HB3	2:B:633:VAL:HG11	1.93	0.50
2:B:579:ARG:NH1	2:B:622:LYS:O	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:882:THR:HG21	2:B:935:ARG:CA	2.35	0.50
2:B:1084:GLN:N	2:B:1084:GLN:HE21	2.09	0.50
2:B:1175:LEU:O	2:B:1176:ASN:HB2	2.11	0.50
2:B:1196:ILE:HB	2:B:1197:PRO:HD2	1.94	0.50
3:C:44:LEU:HD21	3:C:159:ALA:CB	2.41	0.50
3:C:99:LEU:HB2	3:C:157:CYS:HB2	1.93	0.50
7:G:88:ASP:HB2	7:G:171:ILE:HD11	1.93	0.50
8:H:4:THR:HG22	8:H:5:LEU:N	2.26	0.50
11:K:7:PHE:CD1	11:K:7:PHE:C	2.89	0.50
1:A:2:VAL:CG1	2:B:1157:ALA:O	2.57	0.50
1:A:53:LEU:CD2	1:A:54:ASN:H	2.14	0.50
1:A:90:VAL:CG1	1:A:297:GLN:NE2	2.73	0.50
1:A:91:PHE:CE1	1:A:204:THR:HG23	2.47	0.50
1:A:360:GLU:O	1:A:361:LEU:C	2.53	0.50
1:A:381:THR:C	1:A:383:TYR:N	2.69	0.50
1:A:388:LEU:HA	1:A:391:LEU:HD12	1.94	0.50
1:A:492:PRO:HB2	1:A:497:THR:CG2	2.41	0.50
1:A:659:HIS:O	2:B:1081:LEU:HD23	2.11	0.50
1:A:1158:PRO:HG2	1:A:1159:ARG:NE	2.26	0.50
1:A:1280:GLU:O	1:A:1281:ARG:O	2.30	0.50
2:B:560:GLU:O	2:B:561:TRP:CD1	2.65	0.50
2:B:769:TYR:CD1	2:B:987:LYS:NZ	2.79	0.50
2:B:806:THR:HG22	2:B:809:MET:N	2.21	0.50
2:B:1003:ALA:HA	3:C:178:PHE:O	2.12	0.50
3:C:35:ARG:HH12	11:K:41:THR:N	1.95	0.50
4:D:51:ASN:O	4:D:52:LEU:C	2.54	0.50
5:E:69:ILE:N	5:E:69:ILE:CD1	2.73	0.50
8:H:1:MET:O	8:H:3:ASN:N	2.41	0.50
11:K:101:LEU:O	11:K:101:LEU:HD23	2.12	0.50
1:A:49:LYS:NZ	1:A:61:ILE:N	2.59	0.50
1:A:132:LYS:HE3	1:A:1411:GLU:HG3	1.92	0.50
1:A:666:ILE:HD12	1:A:667:GLY:N	2.17	0.50
1:A:699:ALA:O	1:A:700:ASN:HB3	2.12	0.50
1:A:913:LEU:CD1	1:A:914:GLU:N	2.71	0.50
2:B:44:VAL:HG11	2:B:495:LEU:HD13	1.93	0.50
2:B:398:ARG:NH1	2:B:398:ARG:HB2	2.26	0.50
2:B:422:LYS:HA	2:B:425:THR:HB	1.93	0.50
2:B:789:MET:HE2	2:B:953:LEU:CD2	2.40	0.50
3:C:46:ILE:HG23	3:C:157:CYS:HB3	1.93	0.50
4:D:29:LEU:N	4:D:29:LEU:CD2	2.75	0.50
4:D:144:THR:O	4:D:148:LEU:HB2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:65:THR:O	5:E:69:ILE:CD1	2.60	0.50
5:E:124:VAL:HG13	5:E:132:ILE:CG1	2.41	0.50
10:J:53:HIS:CD2	10:J:54:VAL:N	2.79	0.50
14:T:16:DT:H2''	14:T:17:DT:O5'	2.12	0.50
1:A:30:ILE:HG23	2:B:1170:THR:HG23	1.94	0.50
1:A:106:VAL:HG21	1:A:214:ILE:CD1	2.40	0.50
1:A:606:LEU:HG	1:A:613:ILE:HD12	1.92	0.50
1:A:821:ARG:HD2	2:B:512:ARG:O	2.12	0.50
1:A:851:HIS:O	1:A:853:ASP:N	2.45	0.50
1:A:1062:GLU:OE2	6:F:88:TYR:OH	2.29	0.50
1:A:1164:PRO:O	1:A:1167:GLU:HB2	2.12	0.50
2:B:171:PRO:HD2	2:B:457:LEU:HD13	1.92	0.50
2:B:281:PRO:C	2:B:283:VAL:H	2.20	0.50
2:B:373:ARG:HB3	2:B:566:LEU:HD23	1.94	0.50
2:B:704:ALA:HB2	2:B:738:PHE:CD2	2.46	0.50
2:B:1167:GLY:HA3	2:B:1216:LEU:H	1.76	0.50
3:C:67:LEU:HA	3:C:70:ILE:HD12	1.94	0.50
3:C:241:ASP:OD1	3:C:242:GLN:N	2.44	0.50
4:D:66:ARG:C	4:D:68:ARG:N	2.68	0.50
5:E:56:LYS:HZ3	5:E:84:ASP:N	2.09	0.50
8:H:56:THR:O	8:H:144:ILE:HA	2.11	0.50
8:H:136:LYS:HD2	8:H:136:LYS:H	1.76	0.50
10:J:27:GLU:C	10:J:29:GLU:H	2.20	0.50
1:A:12:ARG:HB3	2:B:1218:THR:HG22	1.93	0.50
1:A:290:GLU:HA	1:A:293:GLU:HB2	1.93	0.50
1:A:974:ASP:OD2	1:A:976:THR:OG1	2.30	0.50
2:B:129:PHE:HA	2:B:165:VAL:O	2.11	0.50
2:B:254:LEU:HD22	2:B:361:LEU:HD11	1.93	0.50
2:B:287:ARG:HG3	2:B:292:ILE:HA	1.94	0.50
2:B:1002:THR:O	2:B:1004:GLU:N	2.45	0.50
3:C:22:LEU:HD11	11:K:101:LEU:HD11	1.93	0.50
3:C:239:PRO:O	3:C:242:GLN:N	2.44	0.50
5:E:171:LYS:HG2	5:E:174:GLN:CD	2.36	0.50
8:H:40:LEU:HD22	8:H:123:MET:HE3	1.94	0.50
1:A:53:LEU:HD22	1:A:54:ASN:HD22	1.76	0.50
1:A:68:GLN:OE1	1:A:68:GLN:O	2.29	0.50
1:A:399:HIS:O	1:A:400:PRO:C	2.53	0.50
1:A:420:ARG:O	1:A:424:ILE:HG13	2.12	0.50
1:A:458:HIS:NE2	1:A:478:TYR:OH	2.40	0.50
1:A:666:ILE:CD1	1:A:667:GLY:N	2.73	0.50
1:A:889:SER:HA	1:A:1297:GLU:H	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1173:HIS:CG	1:A:1227:ILE:HG23	2.47	0.50
1:A:1345:ARG:HG2	1:A:1372:VAL:CG1	2.42	0.50
2:B:187:SER:O	2:B:191:LYS:HG3	2.11	0.50
2:B:418:LYS:C	2:B:420:LEU:N	2.69	0.50
2:B:519:TRP:C	2:B:519:TRP:CD1	2.89	0.50
2:B:797:TYR:C	2:B:798:TYR:HD2	2.20	0.50
2:B:983:ARG:NH1	2:B:1091:TYR:HB3	2.27	0.50
3:C:175:ALA:CB	10:J:43:ARG:NH2	2.64	0.50
5:E:82:PHE:O	5:E:83:CYS:HB2	2.12	0.50
5:E:180:ARG:HH21	5:E:192:ARG:CB	2.20	0.50
10:J:24:LEU:O	10:J:30:LEU:HB3	2.12	0.50
12:L:38:LEU:O	12:L:39:SER:CB	2.59	0.50
1:A:351:THR:CG2	2:B:1103:ILE:HG13	2.41	0.50
1:A:728:LYS:HA	1:A:731:ARG:HH12	1.77	0.50
1:A:1264:GLU:OE2	9:I:46:HIS:CD2	2.65	0.50
1:A:1394:THR:CG2	1:A:1398:MET:SD	3.00	0.50
1:A:1444:MET:HB3	7:G:59:GLY:O	2.12	0.50
2:B:50:SER:OG	2:B:411:PRO:HD3	2.12	0.50
2:B:120:ARG:HH12	12:L:54:ARG:HD3	1.77	0.50
2:B:204:ILE:C	2:B:205:ILE:HD12	2.37	0.50
2:B:641:GLU:O	2:B:643:ASP:N	2.44	0.50
2:B:885:MET:HG2	2:B:936:ASP:HB2	1.94	0.50
2:B:1068:GLY:O	2:B:1069:PHE:O	2.30	0.50
2:B:1183:LYS:HE3	2:B:1183:LYS:O	2.12	0.50
3:C:109:SER:O	3:C:110:THR:C	2.55	0.50
4:D:204:ASP:O	4:D:208:GLU:HB2	2.12	0.50
5:E:74:ASP:OD1	5:E:74:ASP:N	2.39	0.50
5:E:114:ASN:O	5:E:115:ASN:CB	2.60	0.50
7:G:115:MET:O	7:G:164:LYS:HD3	2.12	0.50
10:J:36:LEU:HA	10:J:39:LEU:HD12	1.94	0.50
1:A:103:CYS:SG	1:A:108:MET:HE1	2.51	0.49
1:A:288:ALA:HA	1:A:291:GLU:HG3	1.93	0.49
1:A:319:GLY:HA3	2:B:471:LYS:HA	1.94	0.49
1:A:343:LYS:HD2	2:B:1155:SER:CB	2.42	0.49
1:A:456:MET:HE1	1:A:474:VAL:CG2	2.42	0.49
1:A:739:ASP:OD1	8:H:19:ARG:NH2	2.45	0.49
1:A:1206:ASP:O	1:A:1274:ARG:NH2	2.45	0.49
1:A:1269:GLU:O	1:A:1270:ASN:HB2	2.10	0.49
1:A:1316:VAL:O	1:A:1316:VAL:HG12	2.12	0.49
2:B:806:THR:CG2	2:B:809:MET:HG2	2.28	0.49
2:B:984:HIS:NE2	2:B:1025:HIS:HA	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:996:ARG:HH12	3:C:175:ALA:H	1.60	0.49
2:B:1085:ILE:HG22	2:B:1086:PHE:N	2.25	0.49
3:C:79:GLN:NE2	3:C:127:ARG:HD3	2.27	0.49
3:C:110:THR:HG22	3:C:112:ASN:HD21	1.77	0.49
4:D:23:ASN:OD1	4:D:23:ASN:N	2.45	0.49
6:F:77:ASP:O	6:F:78:GLN:CB	2.44	0.49
6:F:81:THR:OG1	6:F:144:GLU:OE1	2.27	0.49
8:H:20:TYR:O	8:H:22:LYS:N	2.45	0.49
8:H:40:LEU:CD1	8:H:123:MET:HE3	2.39	0.49
9:I:19:ASP:OD2	9:I:22:ASN:HB2	2.11	0.49
9:I:76:PRO:HD2	9:I:108:HIS:HD2	1.77	0.49
11:K:94:ILE:O	11:K:98:LEU:HG	2.11	0.49
1:A:84:ILE:O	1:A:84:ILE:HG22	2.11	0.49
1:A:316:GLN:NE2	1:A:317:LYS:HZ2	2.09	0.49
1:A:688:LYS:CG	1:A:691:LEU:HD23	2.42	0.49
1:A:889:SER:CB	1:A:1297:GLU:HG3	2.42	0.49
1:A:890:ASP:OD2	1:A:1296:GLY:HA2	2.11	0.49
1:A:1030:ARG:NH1	1:A:1035:TYR:OH	2.45	0.49
1:A:1193:LEU:HD21	1:A:1267:MET:HE2	1.94	0.49
1:A:1313:LEU:CB	1:A:1338:VAL:HG21	2.42	0.49
2:B:102:VAL:HG21	2:B:112:LEU:HD13	1.94	0.49
2:B:323:VAL:O	2:B:323:VAL:HG12	2.12	0.49
2:B:662:MET:HA	2:B:665:GLU:HB2	1.94	0.49
2:B:745:PRO:O	2:B:746:SER:C	2.54	0.49
2:B:849:GLY:O	2:B:852:ARG:HG3	2.12	0.49
3:C:233:GLU:HG2	3:C:234:SER:H	1.77	0.49
4:D:146:GLN:HA	4:D:149:THR:HG22	1.94	0.49
5:E:88:VAL:HB	5:E:116:ILE:HG12	1.93	0.49
5:E:116:ILE:HG22	5:E:117:THR:N	2.27	0.49
5:E:178:ILE:HG22	5:E:213:ILE:O	2.12	0.49
6:F:84:TYR:H	6:F:84:TYR:HD1	1.60	0.49
6:F:90:ARG:CG	6:F:91:ALA:N	2.73	0.49
7:G:61:ILE:HG22	7:G:62:LEU:O	2.11	0.49
8:H:127:GLY:HA3	8:H:129:TYR:CZ	2.47	0.49
11:K:21:ILE:HG22	11:K:31:VAL:HG11	1.94	0.49
1:A:285:PRO:O	1:A:287:HIS:N	2.45	0.49
1:A:315:LEU:HD13	1:A:319:GLY:O	2.12	0.49
1:A:472:LEU:O	1:A:475:THR:HB	2.12	0.49
1:A:648:ASN:O	1:A:649:ILE:C	2.52	0.49
1:A:1402:PHE:CG	1:A:1403:GLU:HG2	2.47	0.49
2:B:236:HIS:CE1	2:B:389:ALA:HA	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:603:LEU:HD12	2:B:609:ILE:HG23	1.92	0.49
2:B:1039:GLY:HA2	10:J:51:LEU:HD21	1.94	0.49
4:D:123:LEU:HD22	4:D:149:THR:HG21	1.94	0.49
5:E:55:ARG:C	5:E:57:MET:N	2.68	0.49
11:K:12:LEU:HD21	11:K:17:SER:CA	2.42	0.49
12:L:55:ILE:HD13	12:L:56:LEU:N	2.27	0.49
1:A:92:HIS:O	1:A:93:VAL:C	2.55	0.49
1:A:120:GLU:C	1:A:122:MET:N	2.68	0.49
1:A:265:LYS:O	1:A:269:ILE:HG13	2.11	0.49
1:A:425:GLN:CD	1:A:425:GLN:H	2.16	0.49
1:A:942:PHE:C	1:A:942:PHE:CD2	2.90	0.49
1:A:962:ARG:O	1:A:965:GLN:N	2.46	0.49
1:A:1362:TYR:CD1	1:A:1363:VAL:N	2.80	0.49
2:B:23:ALA:O	2:B:654:ARG:HB3	2.13	0.49
2:B:23:ALA:O	2:B:654:ARG:HD2	2.13	0.49
2:B:370:PHE:HD2	2:B:373:ARG:CD	2.26	0.49
2:B:400:HIS:HA	2:B:517:THR:HG21	1.93	0.49
2:B:498:THR:O	2:B:536:VAL:HA	2.13	0.49
2:B:500:THR:O	2:B:501:PRO:C	2.56	0.49
3:C:261:ALA:HA	3:C:264:GLN:OE1	2.11	0.49
5:E:31:THR:O	5:E:34:GLU:HB3	2.12	0.49
8:H:127:GLY:O	8:H:128:ASN:CB	2.59	0.49
9:I:7:CYS:HB3	9:I:14:LEU:HD21	1.94	0.49
9:I:25:LEU:HG	9:I:38:ALA:HB2	1.94	0.49
11:K:110:ASN:C	11:K:112:GLN:H	2.21	0.49
1:A:254:GLU:HB2	2:B:935:ARG:HH22	1.77	0.49
1:A:600:PRO:C	1:A:602:ASP:H	2.20	0.49
1:A:623:GLY:O	1:A:630:ILE:HD12	2.11	0.49
1:A:877:HIS:O	1:A:878:ILE:HG13	2.12	0.49
1:A:896:ARG:HB3	1:A:897:TYR:CD1	2.47	0.49
1:A:1118:VAL:HG12	1:A:1327:ILE:HG13	1.95	0.49
2:B:46:GLN:OE1	2:B:47:GLN:N	2.38	0.49
2:B:54:PHE:CE1	2:B:414:ALA:HA	2.47	0.49
2:B:62:ILE:CG2	2:B:418:LYS:HG2	2.31	0.49
2:B:185:THR:O	2:B:186:GLU:C	2.55	0.49
2:B:290:GLY:HA2	2:B:327:ARG:HD2	1.93	0.49
2:B:405:ARG:NE	2:B:632:ARG:HG2	2.27	0.49
2:B:827:ILE:HD12	2:B:1086:PHE:HD2	1.77	0.49
2:B:862:GLN:CG	2:B:963:PHE:HD1	2.25	0.49
2:B:872:GLU:OE1	2:B:914:LYS:HE3	2.13	0.49
2:B:950:ASP:O	2:B:951:GLN:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1219:ASP:C	2:B:1219:ASP:OD1	2.55	0.49
3:C:3:GLU:N	3:C:7:GLN:OE1	2.45	0.49
4:D:119:ARG:HB3	4:D:119:ARG:CZ	2.41	0.49
5:E:134:THR:C	5:E:135:PHE:CD1	2.85	0.49
7:G:1:MET:HE1	7:G:80:LYS:O	2.12	0.49
8:H:92:ASP:C	8:H:93:TYR:CD1	2.90	0.49
8:H:109:LYS:HE3	8:H:110:ASP:OD1	2.12	0.49
12:L:30:ILE:CG2	12:L:31:CYS:H	2.25	0.49
1:A:49:LYS:HZ3	1:A:61:ILE:N	2.11	0.49
1:A:316:GLN:NE2	1:A:317:LYS:NZ	2.60	0.49
1:A:475:THR:CG2	1:A:476:SER:N	2.75	0.49
1:A:565:ILE:HG23	1:A:567:LYS:CG	2.40	0.49
1:A:567:LYS:NZ	8:H:46:LEU:HB2	2.27	0.49
1:A:666:ILE:HD11	2:B:1086:PHE:CE1	2.47	0.49
1:A:709:THR:HG21	9:I:93:LYS:O	2.13	0.49
1:A:789:LYS:HE3	9:I:67:THR:HB	1.94	0.49
1:A:896:ARG:NH2	1:A:1030:ARG:CZ	2.76	0.49
2:B:25:ILE:HD11	2:B:653:VAL:O	2.12	0.49
2:B:44:VAL:O	2:B:45:SER:C	2.56	0.49
2:B:46:GLN:HB2	2:B:408:LEU:CD2	2.42	0.49
2:B:56:ASP:HB3	2:B:57:TYR:HD1	1.77	0.49
2:B:254:LEU:HD12	2:B:272:THR:O	2.12	0.49
2:B:563:MET:O	2:B:565:PRO:HD3	2.11	0.49
2:B:806:THR:HA	2:B:1045:SER:OG	2.12	0.49
2:B:877:PRO:C	2:B:878:GLN:HG3	2.38	0.49
2:B:882:THR:C	2:B:884:ARG:H	2.20	0.49
4:D:47:LEU:HD13	4:D:48:ILE:H	1.78	0.49
5:E:50:MET:HG2	5:E:52:ARG:CZ	2.42	0.49
5:E:128:PRO:HA	5:E:129:PRO:O	2.13	0.49
1:A:289:ILE:HG23	1:A:290:GLU:N	2.27	0.49
1:A:545:GLN:O	1:A:546:VAL:C	2.56	0.49
1:A:591:PHE:HA	1:A:595:THR:CG2	2.41	0.49
1:A:1157:ASP:C	1:A:1159:ARG:H	2.21	0.49
2:B:169:ARG:HD2	2:B:454:THR:CG2	2.42	0.49
2:B:810:GLU:CA	2:B:815:ARG:HH22	2.26	0.49
2:B:1115:THR:O	2:B:1116:ARG:HB2	2.13	0.49
3:C:181:ASP:CG	3:C:186:LEU:HD13	2.37	0.49
7:G:139:ILE:CG2	7:G:140:LYS:N	2.74	0.49
1:A:144:THR:O	1:A:146:MET:CE	2.60	0.49
1:A:427:GLN:HB2	1:A:430:TRP:CG	2.47	0.49
1:A:540:PHE:CE2	1:A:565:ILE:HD12	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:693:VAL:HG21	1:A:721:PHE:HE1	1.78	0.49
1:A:767:GLN:NE2	1:A:774:ARG:HB3	2.26	0.49
1:A:899:VAL:HG22	1:A:1029:ARG:HG2	1.93	0.49
1:A:1138:ILE:HG13	1:A:1139:GLU:N	2.28	0.49
1:A:1450:LEU:HD12	1:A:1450:LEU:O	2.13	0.49
2:B:313:MET:HE3	2:B:386:LEU:HD22	1.93	0.49
2:B:629:ASP:HB3	2:B:632:ARG:HD3	1.95	0.49
2:B:801:LYS:O	10:J:52:THR:HG21	2.13	0.49
3:C:164:ALA:HA	3:C:167:HIS:O	2.13	0.49
4:D:195:ILE:HG22	4:D:195:ILE:O	2.13	0.49
6:F:127:GLU:O	6:F:128:LYS:C	2.56	0.49
6:F:130:ILE:O	6:F:148:VAL:CG2	2.61	0.49
9:I:16:PRO:HD3	9:I:27:PHE:CE2	2.47	0.49
9:I:78:CYS:SG	9:I:105:SER:O	2.70	0.49
12:L:41:SER:N	12:L:44:ASP:OD2	2.45	0.49
1:A:75:ASN:O	1:A:76:GLU:CB	2.60	0.49
1:A:590:ARG:HG2	1:A:590:ARG:NH1	2.27	0.49
1:A:730:GLY:O	1:A:732:LEU:N	2.46	0.49
1:A:870:GLU:O	5:E:205:SER:HB3	2.13	0.49
1:A:1237:ILE:CG2	1:A:1238:ILE:N	2.75	0.49
2:B:345:LYS:CG	2:B:346:GLU:H	2.18	0.49
2:B:509:ALA:O	2:B:510:LYS:C	2.55	0.49
2:B:570:VAL:HG21	2:B:573:GLN:NE2	2.27	0.49
2:B:770:GLN:CD	2:B:983:ARG:HA	2.36	0.49
2:B:878:GLN:O	2:B:879:ARG:O	2.30	0.49
2:B:952:VAL:HG12	2:B:953:LEU:H	1.76	0.49
3:C:31:ASN:HA	3:C:34:ARG:HB3	1.95	0.49
4:D:12:ARG:NH1	4:D:13:ARG:C	2.70	0.49
4:D:156:ASP:O	4:D:159:THR:N	2.46	0.49
6:F:90:ARG:O	6:F:91:ALA:C	2.56	0.49
7:G:111:THR:HG23	7:G:114:LEU:HD13	1.92	0.49
1:A:153:PRO:HD3	1:A:161:LEU:CD1	2.43	0.49
1:A:700:ASN:HB2	9:I:98:VAL:HG21	1.94	0.49
1:A:723:ASN:O	1:A:724:GLU:C	2.56	0.49
1:A:794:PRO:O	1:A:796:SER:N	2.45	0.49
1:A:1259:MET:HA	1:A:1262:LYS:CE	2.42	0.49
1:A:1433:MET:HE2	2:B:1145:SER:OG	2.12	0.49
1:A:1451:VAL:CG1	1:A:1452:LYS:N	2.75	0.49
2:B:29:ASP:CB	2:B:658:ILE:HD13	2.43	0.49
2:B:115:GLN:HG2	2:B:193:LYS:HB2	1.94	0.49
2:B:465:ASN:N	2:B:465:ASN:ND2	2.55	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:562:GLY:HA3	2:B:590:HIS:CE1	2.47	0.49
2:B:801:LYS:O	10:J:52:THR:CG2	2.61	0.49
2:B:1031:LEU:HD12	2:B:1031:LEU:O	2.13	0.49
2:B:1112:GLN:HG3	15:P:1:C:H5"	1.91	0.49
5:E:110:PHE:CD1	5:E:110:PHE:C	2.91	0.49
5:E:127:ILE:N	5:E:128:PRO:CD	2.76	0.49
8:H:46:LEU:O	8:H:47:PHE:HB2	2.12	0.49
1:A:172:PRO:HD3	1:A:185:TRP:CD1	2.48	0.48
1:A:351:THR:CG2	2:B:1103:ILE:HA	2.34	0.48
1:A:722:LEU:O	1:A:723:ASN:C	2.56	0.48
1:A:751:SER:O	1:A:752:LYS:HG2	2.13	0.48
1:A:885:THR:HG22	1:A:940:ARG:HA	1.95	0.48
1:A:916:GLY:C	1:A:919:ILE:HG22	2.37	0.48
1:A:946:VAL:HG22	5:E:201:LYS:CD	2.38	0.48
1:A:1313:LEU:C	1:A:1315:GLU:N	2.70	0.48
1:A:1437:GLY:C	1:A:1439:GLY:N	2.70	0.48
2:B:241:ARG:CG	2:B:253:THR:HG22	2.43	0.48
2:B:368:GLU:O	2:B:370:PHE:N	2.45	0.48
2:B:383:ASN:HD21	2:B:387:LEU:HD12	1.75	0.48
2:B:526:GLU:OE1	2:B:752:ALA:CB	2.61	0.48
2:B:549:THR:HG22	2:B:550:ASP:N	2.19	0.48
2:B:1030:LEU:HD13	2:B:1067:ARG:O	2.13	0.48
4:D:128:VAL:C	4:D:130:LEU:N	2.71	0.48
4:D:208:GLU:O	4:D:212:LYS:HG3	2.13	0.48
5:E:67:GLU:O	5:E:70:SER:N	2.43	0.48
5:E:120:ALA:HA	5:E:123:LEU:CD1	2.43	0.48
9:I:40:SER:OG	9:I:41:PRO:HD2	2.12	0.48
9:I:82:GLU:HB3	9:I:104:LEU:HB2	1.95	0.48
10:J:21:TYR:HB2	10:J:39:LEU:CD1	2.43	0.48
12:L:40:LEU:HD11	12:L:49:LYS:HZ1	1.78	0.48
1:A:57:ARG:HB2	1:A:57:ARG:HH11	1.77	0.48
1:A:562:THR:HG22	8:H:79:TRP:HD1	1.78	0.48
1:A:590:ARG:HB3	1:A:605:MET:N	2.29	0.48
1:A:720:ARG:O	1:A:724:GLU:CB	2.61	0.48
1:A:827:THR:CG2	1:A:828:ALA:N	2.77	0.48
1:A:1035:TYR:O	1:A:1036:ARG:HB2	2.11	0.48
1:A:1199:ARG:O	1:A:1200:ALA:C	2.57	0.48
1:A:1341:ILE:HD13	1:A:1380:GLY:HA2	1.95	0.48
1:A:1443:VAL:HG11	6:F:132:LEU:HD13	1.95	0.48
2:B:48:LEU:O	2:B:49:ASP:C	2.56	0.48
2:B:240:ILE:HG23	2:B:240:ILE:O	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:275:TYR:CD1	2:B:275:TYR:N	2.81	0.48
2:B:418:LYS:HD3	2:B:422:LYS:HZ2	1.73	0.48
2:B:458:LYS:O	2:B:459:TYR:C	2.55	0.48
2:B:637:LEU:CB	2:B:693:ILE:HD11	2.39	0.48
2:B:785:TYR:CE2	2:B:795:ILE:HG12	2.49	0.48
2:B:798:TYR:CE2	3:C:62:PHE:CE2	3.00	0.48
2:B:882:THR:O	2:B:883:LEU:HB2	2.12	0.48
2:B:983:ARG:NH1	2:B:1028:GLU:OE1	2.45	0.48
2:B:1180:PHE:O	2:B:1181:GLU:O	2.31	0.48
3:C:5:GLY:O	3:C:7:GLN:NE2	2.45	0.48
3:C:115:SER:HB2	3:C:142:VAL:HB	1.95	0.48
3:C:215:GLU:O	3:C:216:GLY:C	2.56	0.48
4:D:8:PHE:CZ	4:D:37:GLN:NE2	2.81	0.48
5:E:73:PRO:O	5:E:75:MET:N	2.46	0.48
1:A:150:THR:CG2	1:A:166:GLY:HA2	2.40	0.48
1:A:315:LEU:CD1	2:B:471:LYS:HB3	2.40	0.48
1:A:700:ASN:HD22	9:I:115:LYS:HB2	1.78	0.48
1:A:923:LEU:HD12	1:A:923:LEU:H	1.78	0.48
1:A:986:ILE:HG21	1:A:1028:THR:HA	1.94	0.48
1:A:1450:LEU:CD1	6:F:108:PHE:CZ	2.97	0.48
2:B:220:GLY:O	2:B:221:ASN:C	2.56	0.48
2:B:363:HIS:CD2	2:B:585:VAL:HG22	2.48	0.48
2:B:469:GLN:O	2:B:472:ALA:HB3	2.13	0.48
2:B:520:GLY:N	2:B:748:ILE:HG22	2.27	0.48
2:B:757:PRO:HG2	2:B:984:HIS:HE1	1.77	0.48
2:B:906:SER:O	2:B:907:GLY:O	2.31	0.48
2:B:1182:CYS:O	2:B:1183:LYS:C	2.57	0.48
3:C:105:GLY:O	3:C:149:LYS:O	2.30	0.48
3:C:184:ASN:OD1	3:C:187:LYS:CA	2.61	0.48
5:E:19:VAL:HG22	5:E:140:LEU:HD12	1.95	0.48
7:G:1:MET:SD	7:G:79:PHE:CE1	3.06	0.48
8:H:110:ASP:O	8:H:128:ASN:HB2	2.12	0.48
9:I:55:THR:HG22	9:I:58:VAL:CG2	2.43	0.48
9:I:62:ILE:O	9:I:62:ILE:HG12	2.12	0.48
11:K:50:LEU:HD11	11:K:75:ILE:CD1	2.43	0.48
1:A:34:LYS:N	1:A:34:LYS:CD	2.76	0.48
1:A:132:LYS:HE3	1:A:1411:GLU:CG	2.43	0.48
1:A:224:PHE:CZ	1:A:234:MET:HE2	2.48	0.48
1:A:299:HIS:CA	1:A:302:THR:HG22	2.43	0.48
1:A:332:LYS:O	1:A:334:GLY:N	2.46	0.48
1:A:456:MET:HE2	1:A:478:TYR:CZ	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:556:TRP:CZ3	1:A:558:GLY:HA2	2.49	0.48
1:A:655:PHE:O	1:A:658:LEU:HB3	2.13	0.48
1:A:853:ASP:OD1	1:A:855:THR:CB	2.61	0.48
2:B:48:LEU:HD23	2:B:173:MET:SD	2.54	0.48
2:B:69:LEU:HD22	2:B:429:PHE:CE1	2.48	0.48
2:B:243:ALA:CB	2:B:251:ILE:HG12	2.43	0.48
2:B:273:LEU:HD21	2:B:360:PHE:CE1	2.49	0.48
2:B:661:LEU:HD23	2:B:679:TYR:O	2.13	0.48
4:D:33:PHE:CE1	7:G:80:LYS:HD3	2.48	0.48
4:D:56:ARG:CD	4:D:149:THR:HA	2.39	0.48
6:F:135:ARG:HG2	6:F:137:TYR:CE1	2.47	0.48
8:H:24:CYS:HB2	8:H:44:VAL:CG2	2.37	0.48
8:H:77:ARG:HG2	8:H:78:SER:H	1.79	0.48
1:A:409:SER:O	1:A:410:GLY:C	2.56	0.48
1:A:445:ASN:HB2	1:A:454:SER:O	2.13	0.48
1:A:986:ILE:HG22	1:A:987:VAL:N	2.28	0.48
2:B:20:ASP:C	2:B:22:SER:N	2.70	0.48
2:B:240:ILE:CG2	2:B:254:LEU:HB3	2.43	0.48
2:B:246:LYS:HA	2:B:249:ARG:CZ	2.44	0.48
2:B:408:LEU:HD11	2:B:545:ILE:CD1	2.43	0.48
2:B:521:LEU:HD22	2:B:633:VAL:HG12	1.94	0.48
2:B:615:MET:CB	2:B:626:ILE:HG12	2.27	0.48
2:B:862:GLN:HG2	2:B:963:PHE:HD1	1.79	0.48
2:B:916:THR:HB	2:B:935:ARG:HG3	1.95	0.48
4:D:191:ALA:O	4:D:193:THR:N	2.46	0.48
6:F:116:ASP:OD1	6:F:118:LEU:N	2.47	0.48
7:G:74:TYR:H	7:G:74:TYR:HD2	1.60	0.48
7:G:126:ASN:C	7:G:126:ASN:HD22	2.19	0.48
8:H:130:ARG:HA	8:H:133:ASN:HB2	1.95	0.48
1:A:257:ARG:HB3	1:A:258:GLY:H	1.39	0.48
1:A:324:SER:O	1:A:327:ALA:HB3	2.12	0.48
1:A:382:PRO:CB	1:A:428:TYR:HE2	2.27	0.48
1:A:605:MET:HE2	1:A:607:ILE:HG13	1.95	0.48
1:A:834:THR:CG2	1:A:1077:THR:HG23	2.39	0.48
1:A:1171:GLN:O	1:A:1174:PHE:HB2	2.13	0.48
1:A:1387:HIS:NE2	13:N:4:DA:H5'	2.29	0.48
2:B:266:ALA:O	2:B:268:THR:HG22	2.14	0.48
2:B:372:SER:HB3	2:B:567:GLU:OE1	2.13	0.48
2:B:418:LYS:O	2:B:419:THR:C	2.56	0.48
2:B:847:ASP:C	2:B:849:GLY:H	2.21	0.48
2:B:891:ASP:O	2:B:893:LEU:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1082:MET:HE1	3:C:187:LYS:O	2.14	0.48
2:B:1117:GLN:HE21	2:B:1199:ALA:HB2	1.78	0.48
3:C:193:TYR:C	3:C:193:TYR:HD1	2.22	0.48
8:H:39:THR:O	8:H:123:MET:HG3	2.13	0.48
8:H:77:ARG:HB2	8:H:77:ARG:NH1	2.27	0.48
8:H:129:TYR:HA	8:H:131:ASN:ND2	2.28	0.48
1:A:350:ARG:HB3	2:B:1128:LEU:CD1	2.43	0.48
1:A:783:THR:O	1:A:784:LEU:HD23	2.14	0.48
1:A:842:VAL:HG11	2:B:1136:ASP:OD2	2.13	0.48
1:A:1141:THR:HA	1:A:1205:LYS:HZ3	1.78	0.48
2:B:97:VAL:HG22	2:B:128:LEU:HD12	1.95	0.48
3:C:92:CYS:N	3:C:95:CYS:SG	2.72	0.48
4:D:53:SER:H	4:D:148:LEU:CD2	2.27	0.48
5:E:94:LYS:O	5:E:98:ILE:HG13	2.14	0.48
5:E:103:LYS:HB3	5:E:105:PHE:CE2	2.48	0.48
6:F:148:VAL:HG23	6:F:149:GLU:N	2.27	0.48
8:H:129:TYR:C	8:H:131:ASN:H	2.21	0.48
8:H:130:ARG:N	8:H:130:ARG:CD	2.65	0.48
8:H:133:ASN:O	8:H:135:LEU:N	2.47	0.48
9:I:34:TYR:HE2	9:I:36:GLU:HB3	1.79	0.48
1:A:50:ILE:C	1:A:52:GLY:N	2.69	0.48
1:A:396:PRO:HG2	1:A:397:ASN:OD1	2.14	0.48
1:A:463:ILE:HB	1:A:464:PRO:HD2	1.95	0.48
1:A:670:ILE:HG23	1:A:805:LEU:HG	1.95	0.48
1:A:899:VAL:O	1:A:929:LEU:HD12	2.13	0.48
1:A:919:ILE:HG13	1:A:925:LEU:HD12	1.95	0.48
1:A:1100:ARG:HH21	1:A:1351:GLU:CG	2.27	0.48
1:A:1334:ASP:C	1:A:1336:MET:N	2.71	0.48
2:B:313:MET:CE	2:B:386:LEU:HB3	2.44	0.48
2:B:327:ARG:NH2	2:B:371:GLU:HG2	2.29	0.48
2:B:734:HIS:O	2:B:735:ALA:CB	2.61	0.48
2:B:758:PHE:CE2	2:B:1044:ALA:CA	2.96	0.48
2:B:769:TYR:C	2:B:771:SER:N	2.70	0.48
2:B:806:THR:HG21	2:B:808:ALA:HB3	1.94	0.48
2:B:957:ASN:O	2:B:958:GLN:C	2.56	0.48
3:C:166:GLU:C	11:K:6:ARG:HH11	2.22	0.48
3:C:174:ALA:HA	10:J:10:CYS:O	2.13	0.48
5:E:64:PRO:O	5:E:69:ILE:HD11	2.14	0.48
5:E:144:ILE:HG13	5:E:145:THR:H	1.78	0.48
7:G:62:LEU:HD22	7:G:62:LEU:HA	1.73	0.48
9:I:55:THR:HG21	9:I:109:ILE:HD13	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:34:THR:C	10:J:36:LEU:N	2.70	0.48
12:L:34:CYS:CB	12:L:51:CYS:SG	3.00	0.48
1:A:22:PHE:HB2	2:B:1211:ASN:CG	2.39	0.48
1:A:156:ASP:HB2	1:A:160:GLN:NE2	2.29	0.48
1:A:446:ARG:HG2	1:A:446:ARG:HH11	1.78	0.48
1:A:886:ILE:HG21	1:A:952:ALA:HB2	1.96	0.48
1:A:961:ARG:HG2	1:A:965:GLN:HE22	1.77	0.48
2:B:167:ILE:HD12	2:B:167:ILE:N	2.28	0.48
2:B:258:LEU:HG	2:B:258:LEU:O	2.14	0.48
2:B:363:HIS:HD2	2:B:585:VAL:HG22	1.79	0.48
2:B:590:HIS:NE2	2:B:592:ASN:O	2.47	0.48
2:B:1085:ILE:N	2:B:1085:ILE:HD12	2.28	0.48
4:D:69:ALA:C	4:D:71:LYS:N	2.70	0.48
6:F:147:SER:O	6:F:148:VAL:C	2.55	0.48
7:G:145:VAL:HG12	7:G:146:LYS:N	2.28	0.48
8:H:109:LYS:CG	8:H:110:ASP:H	2.27	0.48
1:A:122:MET:CA	1:A:141:LEU:HD11	2.42	0.48
1:A:427:GLN:HG3	1:A:430:TRP:CE2	2.47	0.48
1:A:536:LEU:H	1:A:536:LEU:CD2	2.09	0.48
1:A:600:PRO:HA	8:H:25:ARG:NH1	2.29	0.48
1:A:665:GLY:O	1:A:666:ILE:HD12	2.14	0.48
1:A:700:ASN:C	1:A:701:LEU:HD23	2.39	0.48
1:A:845:LEU:HD12	1:A:1069:ALA:HB2	1.95	0.48
1:A:1348:LEU:O	1:A:1352:VAL:HG23	2.14	0.48
2:B:446:LEU:N	2:B:446:LEU:HD23	2.29	0.48
2:B:580:VAL:HG22	2:B:624:LEU:HB3	1.95	0.48
2:B:582:VAL:HG22	2:B:626:ILE:CG2	2.43	0.48
2:B:593:PRO:C	2:B:595:ARG:N	2.69	0.48
2:B:604:ARG:C	2:B:606:LYS:N	2.69	0.48
3:C:147:LEU:HD12	3:C:151:GLN:O	2.14	0.48
3:C:176:ILE:O	3:C:176:ILE:HG22	2.13	0.48
3:C:177:GLU:CG	3:C:231:ASN:HB3	2.39	0.48
5:E:67:GLU:O	5:E:70:SER:CB	2.62	0.48
6:F:69:LEU:HD13	6:F:71:GLU:OE1	2.13	0.48
6:F:106:PRO:HG3	7:G:18:PHE:O	2.13	0.48
8:H:10:PHE:N	8:H:10:PHE:CD1	2.81	0.48
9:I:22:ASN:O	9:I:23:ASN:HB2	2.12	0.48
10:J:60:PHE:O	10:J:63:TYR:HD1	1.97	0.48
12:L:33:GLU:CD	12:L:33:GLU:N	2.72	0.48
1:A:7:SER:OG	2:B:1161:HIS:CE1	2.63	0.47
1:A:11:LEU:O	1:A:11:LEU:CD2	2.56	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:THR:HG22	1:A:173:THR:O	2.13	0.47
1:A:276:LEU:HD13	1:A:293:GLU:HA	1.96	0.47
1:A:284:ALA:HB1	1:A:289:ILE:HD12	1.96	0.47
1:A:364:VAL:O	1:A:364:VAL:HG13	2.14	0.47
1:A:482:PHE:C	1:A:484:GLY:N	2.71	0.47
1:A:546:VAL:HG12	1:A:550:LEU:CD1	2.44	0.47
1:A:1100:ARG:O	1:A:1104:ILE:HG13	2.14	0.47
2:B:265:SER:O	2:B:266:ALA:HB3	2.14	0.47
2:B:636:PRO:HG2	2:B:743:ILE:HD12	1.96	0.47
2:B:977:GLY:HA3	2:B:1099:VAL:HB	1.96	0.47
2:B:1116:ARG:HG3	2:B:1198:TYR:CE1	2.49	0.47
4:D:214:LEU:O	4:D:218:GLU:HB2	2.13	0.47
6:F:97:ARG:O	6:F:101:ILE:HG13	2.13	0.47
1:A:91:PHE:HB2	1:A:297:GLN:HE22	1.78	0.47
1:A:108:MET:HB3	1:A:210:ILE:CD1	2.44	0.47
1:A:185:TRP:CZ3	1:A:200:ARG:HG2	2.49	0.47
1:A:357:PRO:HD2	2:B:833:TYR:CZ	2.49	0.47
1:A:710:LEU:H	1:A:710:LEU:CD1	2.18	0.47
1:A:710:LEU:O	1:A:714:PHE:N	2.46	0.47
1:A:973:ILE:CD1	1:A:1038:THR:HG23	2.44	0.47
1:A:982:THR:HB	1:A:985:ASP:N	2.25	0.47
1:A:1423:GLY:HA3	1:A:1426:GLU:HG3	1.95	0.47
2:B:39:ARG:HH21	2:B:665:GLU:CD	2.21	0.47
2:B:241:ARG:HA	2:B:253:THR:HG22	1.94	0.47
2:B:616:ILE:HG12	2:B:697:GLU:HA	1.96	0.47
2:B:1065:GLN:NE2	2:B:1066:SER:H	2.12	0.47
3:C:123:ASN:CG	3:C:125:MET:H	2.22	0.47
3:C:146:LYS:HB2	10:J:61:LEU:HD11	1.95	0.47
3:C:152:GLU:HG2	3:C:153:LEU:H	1.79	0.47
4:D:7:THR:HG21	4:D:32:GLU:CD	2.40	0.47
5:E:134:THR:O	5:E:135:PHE:HD1	1.96	0.47
6:F:96:THR:O	6:F:100:GLN:HG3	2.13	0.47
1:A:152:VAL:HG13	1:A:153:PRO:HD2	1.96	0.47
1:A:323:LYS:H	1:A:323:LYS:CD	2.23	0.47
1:A:406:ILE:HG22	1:A:412:ARG:HA	1.96	0.47
2:B:128:LEU:HD21	2:B:170:LEU:HB2	1.95	0.47
2:B:205:ILE:C	2:B:207:GLY:N	2.71	0.47
2:B:275:TYR:N	2:B:275:TYR:HD1	2.12	0.47
2:B:418:LYS:HD3	2:B:422:LYS:HZ1	1.78	0.47
2:B:996:ARG:NH1	3:C:174:ALA:HA	2.27	0.47
3:C:8:VAL:O	3:C:9:LYS:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:233:GLU:CG	3:C:234:SER:N	2.77	0.47
5:E:69:ILE:H	5:E:69:ILE:CD1	2.27	0.47
8:H:25:ARG:HB2	8:H:41:ASP:OD1	2.15	0.47
8:H:89:LEU:HB2	8:H:91:ASP:OD1	2.14	0.47
10:J:28:ASP:O	10:J:29:GLU:C	2.56	0.47
1:A:129:LYS:O	1:A:130:ASP:CB	2.62	0.47
1:A:311:GLN:O	1:A:312:PRO:C	2.56	0.47
1:A:375:THR:OG1	1:A:433:GLU:HB3	2.14	0.47
1:A:556:TRP:CH2	1:A:558:GLY:HA2	2.49	0.47
1:A:960:ILE:CA	1:A:963:ILE:HG22	2.39	0.47
1:A:967:ALA:HA	1:A:1044:TRP:CZ3	2.50	0.47
1:A:1039:LYS:HE3	1:A:1043:ASP:OD2	2.15	0.47
1:A:1169:ILE:HG22	1:A:1169:ILE:O	2.14	0.47
1:A:1213:GLY:O	1:A:1214:GLU:C	2.57	0.47
1:A:1451:VAL:C	1:A:1453:TYR:N	2.68	0.47
2:B:97:VAL:HG22	2:B:128:LEU:CD1	2.45	0.47
2:B:113:TYR:HB3	2:B:114:PRO:HD2	1.95	0.47
2:B:244:LEU:O	2:B:246:LYS:N	2.47	0.47
2:B:461:LEU:H	2:B:461:LEU:CD1	2.25	0.47
2:B:496:ARG:NH1	2:B:539:LEU:HB2	2.29	0.47
2:B:789:MET:HE3	2:B:965:LYS:HB3	1.95	0.47
2:B:798:TYR:CE2	3:C:62:PHE:CZ	3.01	0.47
2:B:911:ILE:HD11	2:B:941:LEU:HB2	1.96	0.47
2:B:1097:HIS:N	2:B:1098:MET:HE2	2.28	0.47
3:C:114:TYR:HB3	3:C:140:ASN:O	2.14	0.47
3:C:236:GLY:O	3:C:237:SER:C	2.57	0.47
3:C:249:ASP:O	3:C:250:THR:C	2.55	0.47
4:D:154:PHE:CD2	4:D:154:PHE:N	2.82	0.47
8:H:62:SER:OG	8:H:63:LEU:N	2.44	0.47
9:I:34:TYR:CD2	9:I:34:TYR:C	2.92	0.47
10:J:7:CYS:SG	10:J:49:MET:CE	3.02	0.47
12:L:26:THR:HG22	12:L:27:LEU:N	2.29	0.47
1:A:661:GLY:HA3	2:B:1081:LEU:HD22	1.96	0.47
1:A:663:SER:OG	1:A:664:THR:N	2.43	0.47
1:A:1017:LEU:HD12	1:A:1017:LEU:O	2.14	0.47
1:A:1040:GLN:O	1:A:1041:ALA:C	2.58	0.47
1:A:1264:GLU:HG3	1:A:1265:ASN:OD1	2.14	0.47
2:B:44:VAL:HG21	2:B:199:MET:O	2.14	0.47
2:B:114:PRO:CG	2:B:115:GLN:H	2.22	0.47
2:B:241:ARG:HG2	2:B:253:THR:HG21	1.95	0.47
2:B:295:GLY:N	2:B:298:LEU:HD23	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:352:ALA:O	2:B:353:LYS:C	2.57	0.47
2:B:593:PRO:O	2:B:594:ALA:C	2.57	0.47
2:B:603:LEU:HD12	2:B:609:ILE:CG1	2.44	0.47
2:B:616:ILE:HD12	2:B:616:ILE:H	1.78	0.47
3:C:59:ALA:O	3:C:60:ASP:C	2.57	0.47
3:C:69:LEU:H	3:C:69:LEU:CD1	2.14	0.47
3:C:99:LEU:HD12	3:C:118:LEU:HB3	1.97	0.47
4:D:206:GLU:O	4:D:210:ILE:HG13	2.13	0.47
5:E:153:HIS:C	5:E:154:ILE:HG13	2.40	0.47
14:T:25:DG:H2"	14:T:26:DT:OP2	2.15	0.47
1:A:285:PRO:CG	1:A:288:ALA:HB3	2.40	0.47
1:A:350:ARG:CB	2:B:1128:LEU:HD11	2.43	0.47
1:A:613:ILE:O	1:A:614:PHE:HB3	2.15	0.47
1:A:786:HIS:HE1	2:B:519:TRP:CZ2	2.32	0.47
1:A:858:ASN:HD21	1:A:860:LEU:H	1.58	0.47
1:A:1001:ARG:O	1:A:1002:GLY:C	2.57	0.47
2:B:199:MET:HE2	2:B:492:LEU:HD21	1.96	0.47
2:B:356:LEU:HA	2:B:360:PHE:HB2	1.97	0.47
2:B:373:ARG:HA	2:B:566:LEU:HD23	1.97	0.47
2:B:483:LEU:CD1	2:B:491:THR:HG23	2.24	0.47
2:B:750:GLY:O	2:B:751:VAL:C	2.57	0.47
3:C:144:ILE:O	3:C:145:CYS:HB3	2.15	0.47
4:D:52:LEU:O	4:D:53:SER:HB3	2.13	0.47
5:E:162:ARG:CZ	5:E:162:ARG:HB3	2.45	0.47
7:G:15:PRO:O	7:G:16:SER:C	2.56	0.47
7:G:26:LEU:CD1	7:G:56:ILE:HD11	2.28	0.47
11:K:92:ASN:O	11:K:93:SER:C	2.57	0.47
1:A:26:GLU:O	1:A:27:VAL:C	2.56	0.47
1:A:76:GLU:O	1:A:78:PRO:HD3	2.15	0.47
1:A:117:GLU:HA	1:A:123:ARG:HG3	1.97	0.47
1:A:401:GLY:C	1:A:435:HIS:CD2	2.92	0.47
1:A:451:HIS:O	1:A:452:LYS:C	2.56	0.47
1:A:658:LEU:HD12	2:B:830:TYR:CD1	2.50	0.47
1:A:666:ILE:HD11	2:B:1086:PHE:HE1	1.79	0.47
1:A:666:ILE:H	2:B:1026:LEU:HD22	1.80	0.47
1:A:777:PHE:HA	1:A:782:ARG:O	2.14	0.47
1:A:1344:GLY:O	1:A:1347:ALA:N	2.48	0.47
2:B:26:THR:O	2:B:29:ASP:HB2	2.15	0.47
2:B:36:ALA:O	2:B:39:ARG:HB2	2.15	0.47
2:B:60:GLN:O	2:B:63:ILE:HG22	2.15	0.47
2:B:98:THR:O	2:B:126:SER:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:113:TYR:CB	2:B:114:PRO:HD2	2.45	0.47
2:B:121:ASN:HA	2:B:207:GLY:HA2	1.96	0.47
2:B:168:GLY:N	2:B:450:ALA:HB1	2.12	0.47
2:B:290:GLY:O	2:B:292:ILE:HG13	2.14	0.47
2:B:293:PRO:CD	2:B:296:GLU:OE1	2.58	0.47
2:B:308:TRP:CA	2:B:311:LEU:HD12	2.44	0.47
2:B:550:ASP:CG	2:B:551:PRO:HD2	2.39	0.47
2:B:1181:GLU:H	2:B:1188:LYS:HA	1.80	0.47
2:B:1214:PRO:O	2:B:1214:PRO:HG2	2.15	0.47
3:C:6:PRO:HA	3:C:24:ASN:HD22	1.80	0.47
3:C:39:ALA:O	3:C:164:ALA:HB3	2.13	0.47
3:C:113:VAL:HG23	3:C:147:LEU:HD21	1.96	0.47
3:C:183:TRP:O	3:C:185:LYS:HG3	2.14	0.47
4:D:17:LYS:CD	4:D:18:VAL:HG13	2.42	0.47
4:D:56:ARG:HA	4:D:148:LEU:HD13	1.97	0.47
4:D:126:ILE:C	4:D:128:VAL:N	2.71	0.47
5:E:124:VAL:HG13	5:E:132:ILE:CB	2.43	0.47
7:G:34:VAL:O	7:G:37:SER:CB	2.63	0.47
9:I:14:LEU:HB3	9:I:27:PHE:HB3	1.95	0.47
15:P:2:A:H2'	15:P:3:A:O4'	2.14	0.47
1:A:72:GLU:HB3	1:A:76:GLU:CG	2.45	0.47
1:A:250:ILE:O	1:A:250:ILE:HG22	2.15	0.47
1:A:312:PRO:O	1:A:314:ALA:N	2.47	0.47
1:A:470:LEU:HD23	1:A:470:LEU:N	2.30	0.47
1:A:774:ARG:HB2	1:A:797:LYS:O	2.15	0.47
1:A:834:THR:HG21	1:A:1077:THR:CB	2.45	0.47
1:A:843:LYS:CD	1:A:846:GLU:OE2	2.61	0.47
1:A:1004:ASN:O	1:A:1008:GLN:HG2	2.15	0.47
2:B:284:ILE:HG12	2:B:324:ILE:HD12	1.96	0.47
2:B:364:ILE:O	2:B:365:THR:HB	2.15	0.47
2:B:787:VAL:O	2:B:787:VAL:HG12	2.14	0.47
2:B:882:THR:HB	2:B:934:LYS:O	2.15	0.47
2:B:954:VAL:O	12:L:55:ILE:O	2.32	0.47
3:C:22:LEU:HB2	3:C:230:MET:HE3	1.97	0.47
3:C:64:ALA:O	3:C:65:HIS:C	2.58	0.47
3:C:209:TYR:HD1	3:C:209:TYR:H	1.61	0.47
4:D:134:THR:HG22	4:D:135:GLY:N	2.30	0.47
4:D:191:ALA:C	4:D:193:THR:H	2.23	0.47
4:D:207:LEU:O	4:D:207:LEU:HD12	2.15	0.47
11:K:63:VAL:O	11:K:63:VAL:CG2	2.61	0.47
12:L:61:THR:HG22	12:L:63:ARG:H	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:61:ILE:O	1:A:62:ASP:C	2.57	0.47
1:A:273:ASN:O	1:A:274:ILE:C	2.57	0.47
1:A:567:LYS:HE3	8:H:46:LEU:HD13	1.97	0.47
1:A:1207:LEU:HD11	1:A:1273:LEU:HD23	1.96	0.47
1:A:1342:GLU:CG	5:E:198:ILE:HD13	2.45	0.47
1:A:1385:THR:HG21	1:A:1387:HIS:HD2	1.80	0.47
1:A:1407:GLU:CD	1:A:1407:GLU:N	2.73	0.47
2:B:508:LEU:HD11	2:B:510:LYS:HZ2	1.80	0.47
2:B:558:LEU:CD2	2:B:596:LEU:HD11	2.45	0.47
2:B:593:PRO:O	2:B:595:ARG:N	2.48	0.47
2:B:882:THR:HG23	2:B:884:ARG:H	1.79	0.47
2:B:955:THR:OG1	12:L:55:ILE:HA	2.15	0.47
3:C:22:LEU:HD22	3:C:230:MET:CE	2.44	0.47
4:D:147:TYR:O	4:D:148:LEU:C	2.57	0.47
5:E:11:ARG:C	5:E:13:TRP:N	2.70	0.47
5:E:106:GLN:HE22	5:E:129:PRO:HB2	1.80	0.47
5:E:121:MET:C	5:E:123:LEU:N	2.72	0.47
5:E:134:THR:O	5:E:135:PHE:CD1	2.68	0.47
6:F:76:LYS:HA	6:F:79:ARG:CD	2.42	0.47
6:F:116:ASP:OD1	6:F:116:ASP:C	2.57	0.47
9:I:8:ARG:O	9:I:10:CYS:N	2.47	0.47
12:L:30:ILE:CG2	12:L:31:CYS:N	2.77	0.47
1:A:203:SER:HB2	1:A:205:GLU:OE1	2.15	0.47
1:A:305:ASP:C	1:A:305:ASP:OD1	2.58	0.47
1:A:675:THR:HG21	1:A:736:ASN:CB	2.45	0.47
1:A:997:LEU:HD13	1:A:1018:PHE:HE2	1.80	0.47
1:A:1397:LEU:HB2	1:A:1426:GLU:OE1	2.14	0.47
2:B:280:ILE:HB	2:B:285:ILE:HD11	1.96	0.47
2:B:485:ARG:HG3	2:B:781:PHE:CD1	2.50	0.47
2:B:658:ILE:HG22	2:B:662:MET:HE2	1.97	0.47
2:B:827:ILE:HD12	2:B:1086:PHE:CD2	2.50	0.47
2:B:1007:VAL:HG22	2:B:1008:PRO:N	2.30	0.47
3:C:45:ALA:O	3:C:159:ALA:HA	2.15	0.47
3:C:236:GLY:C	3:C:238:ILE:N	2.73	0.47
8:H:33:GLN:C	8:H:35:GLN:H	2.22	0.47
8:H:44:VAL:CG1	8:H:48:PRO:HA	2.45	0.47
1:A:33:ALA:HA	1:A:57:ARG:NH1	2.30	0.46
1:A:40:THR:CG2	1:A:41:MET:HE2	2.45	0.46
1:A:202:LEU:N	1:A:202:LEU:HD23	2.30	0.46
1:A:541:ILE:HG22	1:A:546:VAL:HG23	1.97	0.46
1:A:563:PRO:HG3	1:A:572:TRP:CE2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:577:ILE:O	1:A:578:LEU:C	2.57	0.46
1:A:752:LYS:HA	1:A:752:LYS:HD3	1.66	0.46
1:A:1203:ASN:O	1:A:1204:ASP:C	2.57	0.46
2:B:235:SER:C	2:B:236:HIS:CD2	2.93	0.46
2:B:565:PRO:O	2:B:567:GLU:N	2.48	0.46
2:B:654:ARG:O	2:B:656:GLY:N	2.48	0.46
2:B:866:TYR:O	2:B:867:GLY:C	2.57	0.46
2:B:1079:LYS:HG2	2:B:1080:LYS:N	2.30	0.46
2:B:1169:MET:HE1	2:B:1201:LYS:CA	2.39	0.46
2:B:1222:ARG:O	2:B:1223:ASP:C	2.58	0.46
3:C:177:GLU:HG3	3:C:231:ASN:CB	2.38	0.46
4:D:69:ALA:CB	4:D:72:ARG:NH1	2.76	0.46
5:E:72:PHE:N	5:E:72:PHE:CD1	2.82	0.46
5:E:102:GLU:C	5:E:104:ASN:N	2.72	0.46
5:E:112:TYR:O	5:E:137:GLU:HG3	2.14	0.46
6:F:81:THR:O	6:F:82:THR:C	2.55	0.46
6:F:101:ILE:HD13	6:F:120:ILE:CG2	2.45	0.46
7:G:1:MET:SD	7:G:79:PHE:HD1	2.38	0.46
7:G:117:GLN:OE1	7:G:117:GLN:N	2.48	0.46
8:H:104:PHE:CD2	8:H:136:LYS:HG3	2.51	0.46
9:I:86:PHE:CE1	9:I:100:PHE:HB2	2.49	0.46
1:A:219:PHE:O	1:A:222:LEU:HB2	2.15	0.46
1:A:583:PRO:HG2	1:A:586:ILE:CG1	2.45	0.46
1:A:676:MET:O	1:A:679:ILE:HB	2.15	0.46
1:A:821:ARG:HH11	1:A:821:ARG:CB	2.24	0.46
1:A:836:TYR:CD2	1:A:840:ARG:HD2	2.50	0.46
1:A:867:ILE:HD11	1:A:1000:LEU:HD21	1.97	0.46
1:A:868:TYR:CE1	1:A:1064:VAL:HG11	2.50	0.46
1:A:1067:LEU:O	1:A:1068:ALA:C	2.58	0.46
1:A:1115:SER:C	1:A:1308:THR:HG22	2.40	0.46
1:A:1127:ASP:O	1:A:1128:GLN:C	2.58	0.46
2:B:35:SER:HA	2:B:811:TYR:HE2	1.80	0.46
2:B:121:ASN:HA	2:B:207:GLY:CA	2.45	0.46
2:B:200:GLY:HA2	2:B:202:TYR:CE2	2.50	0.46
2:B:278:GLN:CG	2:B:279:ASP:N	2.53	0.46
2:B:552:MET:O	2:B:553:PRO:C	2.58	0.46
2:B:637:LEU:HD21	2:B:742:GLU:OE2	2.15	0.46
2:B:865:LYS:O	2:B:866:TYR:HD1	1.97	0.46
4:D:71:LYS:HG2	4:D:74:GLN:HG3	1.97	0.46
4:D:126:ILE:HD13	4:D:145:MET:HE3	1.96	0.46
9:I:4:PHE:CZ	9:I:14:LEU:O	2.68	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:27:LEU:HD13	12:L:37:LYS:HD2	1.97	0.46
1:A:122:MET:HE3	1:A:126:LEU:HD21	1.97	0.46
1:A:254:GLU:O	1:A:256:GLN:N	2.48	0.46
1:A:709:THR:N	1:A:712:GLU:HB2	2.30	0.46
1:A:733:ALA:O	1:A:737:LEU:HG	2.14	0.46
1:A:1140:HIS:HB2	1:A:1276:VAL:O	2.15	0.46
1:A:1285:MET:O	1:A:1305:VAL:N	2.47	0.46
2:B:373:ARG:HA	2:B:566:LEU:CD2	2.45	0.46
2:B:615:MET:HA	2:B:625:LYS:O	2.16	0.46
2:B:899:ILE:HG21	2:B:949:VAL:HG21	1.97	0.46
2:B:1095:LEU:H	2:B:1095:LEU:HD12	1.80	0.46
5:E:56:LYS:HZ3	5:E:84:ASP:H	1.62	0.46
7:G:18:PHE:HA	7:G:22:MET:CE	2.44	0.46
1:A:22:PHE:CD2	1:A:27:VAL:HG22	2.49	0.46
1:A:49:LYS:CD	1:A:55:ASP:HB3	2.46	0.46
1:A:79:GLY:HA3	1:A:243:PRO:CG	2.44	0.46
1:A:106:VAL:CG1	1:A:107:CYS:N	2.78	0.46
1:A:107:CYS:HB2	1:A:114:LEU:CD2	2.46	0.46
1:A:488:ASN:OD1	1:A:488:ASN:N	2.48	0.46
1:A:523:ILE:HG13	1:A:622:VAL:HG22	1.96	0.46
1:A:573:SER:O	1:A:574:GLY:C	2.55	0.46
1:A:670:ILE:HG12	1:A:805:LEU:HD21	1.96	0.46
1:A:824:LEU:O	1:A:827:THR:HG22	2.16	0.46
1:A:914:GLU:HB2	1:A:979:SER:O	2.16	0.46
1:A:973:ILE:O	1:A:973:ILE:HG22	2.14	0.46
1:A:1076:ALA:HA	1:A:1079:MET:HE3	1.95	0.46
1:A:1206:ASP:HB2	1:A:1274:ARG:HH22	1.81	0.46
1:A:1387:HIS:CE1	13:N:4:DA:H4'	2.51	0.46
2:B:25:ILE:CD1	2:B:653:VAL:O	2.64	0.46
2:B:703:ILE:HA	2:B:740:HIS:O	2.15	0.46
3:C:89:GLU:O	3:C:90:ASP:CB	2.64	0.46
3:C:98:VAL:C	3:C:99:LEU:HD22	2.39	0.46
4:D:24:ALA:C	4:D:26:THR:H	2.24	0.46
4:D:153:ARG:HB3	4:D:154:PHE:CD2	2.50	0.46
5:E:28:TYR:C	5:E:65:THR:CG2	2.89	0.46
7:G:138:THR:OG1	7:G:139:ILE:N	2.48	0.46
1:A:153:PRO:HA	1:A:161:LEU:HA	1.98	0.46
1:A:388:LEU:HD22	1:A:432:VAL:CB	2.46	0.46
1:A:504:LEU:HD12	1:A:504:LEU:N	2.29	0.46
1:A:673:GLY:O	1:A:676:MET:HB2	2.16	0.46
1:A:1120:LEU:C	1:A:1120:LEU:HD12	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1170:ILE:HG22	1:A:1174:PHE:CZ	2.50	0.46
1:A:1173:HIS:O	1:A:1174:PHE:CD2	2.68	0.46
1:A:1308:THR:HG23	1:A:1310:GLY:H	1.80	0.46
1:A:1377:THR:O	1:A:1378:GLN:C	2.59	0.46
2:B:326:ASP:OD1	2:B:329:THR:CB	2.64	0.46
2:B:505:ASP:CG	13:N:1:DA:C8	2.91	0.46
2:B:570:VAL:CG2	2:B:573:GLN:HB3	2.46	0.46
2:B:805:THR:HG23	2:B:809:MET:CE	2.37	0.46
2:B:886:LYS:HE2	2:B:940:PRO:HD3	1.96	0.46
2:B:1070:GLU:OE1	10:J:44:TYR:OH	2.34	0.46
3:C:226:ASP:O	3:C:227:THR:CB	2.63	0.46
4:D:217:LEU:O	4:D:219:THR:N	2.48	0.46
5:E:44:ALA:O	5:E:45:LYS:HB2	2.15	0.46
6:F:90:ARG:HE	6:F:94:LEU:CD1	2.28	0.46
7:G:137:ILE:CG2	7:G:143:ILE:HD11	2.46	0.46
8:H:8:ASP:OD2	8:H:9:ILE:N	2.40	0.46
9:I:7:CYS:HB2	9:I:34:TYR:CG	2.51	0.46
10:J:63:TYR:O	10:J:64:ASN:CB	2.61	0.46
11:K:31:VAL:HG12	11:K:32:VAL:N	2.31	0.46
1:A:130:ASP:C	1:A:130:ASP:OD1	2.58	0.46
1:A:565:ILE:CG2	1:A:567:LYS:HE2	2.46	0.46
1:A:774:ARG:CZ	1:A:797:LYS:CB	2.93	0.46
1:A:852:TYR:CD1	6:F:136:ARG:HB3	2.51	0.46
2:B:37:PHE:CE2	2:B:542:MET:HA	2.42	0.46
2:B:308:TRP:N	2:B:311:LEU:HD12	2.31	0.46
2:B:398:ARG:CB	2:B:398:ARG:HH11	2.27	0.46
2:B:427:ASP:HA	2:B:430:ARG:HD2	1.97	0.46
2:B:473:MET:C	2:B:475:SER:H	2.24	0.46
4:D:40:HIS:CG	7:G:73:LYS:HD3	2.51	0.46
9:I:69:PRO:HG2	9:I:85:PHE:CE2	2.51	0.46
10:J:1:MET:N	10:J:57:ILE:HG22	2.31	0.46
12:L:34:CYS:CB	12:L:51:CYS:HG	2.29	0.46
1:A:154:SER:CB	1:A:162:VAL:HG21	2.42	0.46
1:A:567:LYS:NZ	8:H:43:ASN:HD22	2.13	0.46
1:A:794:PRO:C	1:A:796:SER:N	2.71	0.46
1:A:798:GLY:HA2	1:A:815:PHE:CD1	2.50	0.46
1:A:962:ARG:C	1:A:964:ILE:N	2.73	0.46
1:A:1293:SER:OG	1:A:1294:PRO:HD2	2.15	0.46
2:B:56:ASP:C	2:B:57:TYR:HD1	2.24	0.46
2:B:63:ILE:HG12	2:B:130:VAL:HG21	1.97	0.46
2:B:603:LEU:HD13	2:B:608:ASP:CB	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:964:VAL:HG22	2:B:965:LYS:N	2.31	0.46
3:C:116:LYS:HG3	3:C:117:ASP:N	2.30	0.46
4:D:40:HIS:CD2	7:G:73:LYS:HD3	2.50	0.46
4:D:64:VAL:C	4:D:66:ARG:H	2.23	0.46
4:D:156:ASP:O	4:D:157:GLN:C	2.59	0.46
7:G:106:MET:HE2	7:G:106:MET:HB3	1.58	0.46
9:I:98:VAL:HG11	9:I:111:THR:HG22	1.98	0.46
9:I:111:THR:CG2	9:I:113:ASP:HB2	2.46	0.46
11:K:7:PHE:C	11:K:9:LEU:H	2.24	0.46
1:A:92:HIS:O	1:A:94:GLY:N	2.48	0.46
1:A:482:PHE:CD2	1:A:482:PHE:N	2.81	0.46
1:A:647:GLY:O	1:A:648:ASN:C	2.56	0.46
1:A:686:ALA:O	1:A:690:VAL:HG23	2.15	0.46
1:A:713:SER:O	1:A:717:ASN:ND2	2.49	0.46
1:A:851:HIS:HB2	1:A:855:THR:CG2	2.46	0.46
1:A:1100:ARG:NH2	1:A:1351:GLU:HG3	2.31	0.46
1:A:1366:ARG:HG2	1:A:1366:ARG:HH11	1.80	0.46
2:B:408:LEU:HD11	2:B:545:ILE:HD12	1.97	0.46
2:B:844:SER:O	2:B:847:ASP:HB2	2.16	0.46
2:B:1096:ARG:HB2	2:B:1096:ARG:HH11	1.79	0.46
2:B:1147:LEU:O	2:B:1151:LEU:HD13	2.16	0.46
7:G:35:GLU:HG3	7:G:48:VAL:HG23	1.98	0.46
8:H:77:ARG:O	8:H:79:TRP:N	2.49	0.46
8:H:83:GLN:C	8:H:85:GLY:H	2.22	0.46
8:H:113:ALA:HB1	8:H:124:ARG:HE	1.81	0.46
9:I:55:THR:HG1	9:I:100:PHE:HD2	1.63	0.46
9:I:82:GLU:HB3	9:I:104:LEU:HD12	1.98	0.46
1:A:50:ILE:O	1:A:52:GLY:N	2.48	0.46
1:A:69:THR:O	1:A:70:CYS:C	2.59	0.46
1:A:266:LEU:O	1:A:267:ALA:C	2.57	0.46
1:A:387:ARG:O	1:A:390:GLN:HB3	2.15	0.46
2:B:126:SER:CB	2:B:172:ILE:HD11	2.46	0.46
2:B:288:ALA:HB1	2:B:331:LEU:HD12	1.98	0.46
2:B:398:ARG:NH1	2:B:398:ARG:CB	2.79	0.46
2:B:508:LEU:HD11	2:B:510:LYS:NZ	2.30	0.46
2:B:642:ASP:O	2:B:644:GLU:N	2.49	0.46
2:B:663:ALA:O	2:B:667:GLN:HG3	2.16	0.46
2:B:792:MET:O	2:B:793:ALA:HB2	2.15	0.46
2:B:803:LEU:HB2	2:B:1032:SER:OG	2.16	0.46
2:B:810:GLU:HA	2:B:815:ARG:NH2	2.31	0.46
3:C:63:ILE:O	3:C:66:ARG:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:42:PHE:CZ	5:E:58:MET:HE3	2.51	0.46
5:E:56:LYS:HZ1	5:E:85:GLU:N	2.14	0.46
5:E:110:PHE:C	5:E:110:PHE:HD1	2.22	0.46
5:E:117:THR:C	5:E:119:SER:N	2.74	0.46
9:I:6:PHE:CB	9:I:12:ASN:O	2.54	0.46
11:K:102:LYS:O	11:K:106:GLU:HG3	2.16	0.46
1:A:108:MET:O	1:A:109:HIS:CB	2.63	0.46
1:A:447:GLN:HB3	1:A:448:PRO:HA	1.97	0.46
1:A:683:ILE:HG21	1:A:801:GLU:CD	2.41	0.46
1:A:738:LYS:NZ	3:C:194:GLU:HA	2.31	0.46
1:A:1242:VAL:CG1	1:A:1243:VAL:N	2.78	0.46
1:A:1443:VAL:CG1	6:F:132:LEU:HD13	2.46	0.46
2:B:569:TYR:CE1	2:B:589:VAL:HG21	2.51	0.46
2:B:638:PHE:CD2	2:B:690:VAL:HG22	2.51	0.46
2:B:797:TYR:HE1	2:B:854:LEU:CD2	2.29	0.46
2:B:836:GLU:O	2:B:837:ASP:HB2	2.15	0.46
2:B:865:LYS:HZ1	2:B:869:SER:HA	1.81	0.46
3:C:123:ASN:HD21	3:C:125:MET:HG2	1.81	0.46
3:C:233:GLU:HG2	3:C:234:SER:N	2.31	0.46
4:D:118:THR:O	4:D:119:ARG:C	2.58	0.46
4:D:216:ASN:C	4:D:218:GLU:H	2.22	0.46
5:E:31:THR:HG1	5:E:34:GLU:H	1.59	0.46
5:E:78:LEU:CD2	5:E:80:VAL:HG23	2.23	0.46
5:E:197:LYS:NZ	5:E:199:ILE:HD11	2.31	0.46
8:H:37:LYS:H	8:H:126:GLU:CB	2.29	0.46
9:I:17:ARG:HG2	9:I:28:GLU:HG2	1.98	0.46
11:K:50:LEU:HD11	11:K:75:ILE:HD13	1.97	0.46
1:A:34:LYS:CB	1:A:36:ARG:HH21	2.29	0.45
1:A:108:MET:HE3	1:A:210:ILE:HD12	1.98	0.45
1:A:351:THR:HG22	2:B:1103:ILE:CA	2.37	0.45
1:A:445:ASN:HB3	1:A:455:MET:HE2	1.98	0.45
1:A:493:GLN:NE2	1:A:493:GLN:HA	2.31	0.45
1:A:495:GLU:O	1:A:498:ARG:HG3	2.16	0.45
1:A:500:GLU:O	1:A:504:LEU:HB2	2.16	0.45
1:A:857:ARG:NH2	6:F:139:PRO:HG3	2.30	0.45
1:A:1077:THR:HB	1:A:1078:GLN:HE21	1.80	0.45
2:B:23:ALA:HB1	2:B:24:PRO:CD	2.41	0.45
2:B:96:TYR:N	2:B:129:PHE:O	2.33	0.45
2:B:594:ALA:HA	2:B:617:ARG:NH1	2.30	0.45
2:B:842:ASN:HD22	2:B:845:SER:N	1.98	0.45
2:B:882:THR:HB	2:B:934:LYS:C	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:234:SER:OG	3:C:235:VAL:N	2.49	0.45
4:D:54:GLU:OE1	4:D:164:ILE:HD11	2.16	0.45
4:D:218:GLU:O	4:D:219:THR:C	2.59	0.45
5:E:161:LYS:C	5:E:163:GLU:N	2.73	0.45
6:F:75:PRO:HG2	6:F:77:ASP:O	2.16	0.45
8:H:27:GLU:HG2	8:H:39:THR:HA	1.97	0.45
10:J:9:SER:OG	10:J:48:ARG:NH2	2.49	0.45
11:K:5:ASP:O	11:K:6:ARG:C	2.60	0.45
11:K:67:PHE:N	11:K:67:PHE:CD2	2.85	0.45
1:A:151:ASP:HA	1:A:162:VAL:O	2.16	0.45
1:A:1141:THR:HA	1:A:1205:LYS:NZ	2.32	0.45
2:B:26:THR:CB	2:B:708:GLU:OE1	2.62	0.45
2:B:123:THR:HG21	2:B:458:LYS:HE2	1.97	0.45
2:B:226:PHE:HA	2:B:395:GLN:CG	2.46	0.45
2:B:408:LEU:HD12	2:B:408:LEU:N	2.31	0.45
2:B:411:PRO:O	2:B:414:ALA:HB3	2.16	0.45
2:B:782:LEU:HB3	2:B:784:ASN:OD1	2.16	0.45
2:B:895:ASP:C	2:B:897:GLY:N	2.74	0.45
2:B:990:ILE:HG22	2:B:991:GLY:H	1.82	0.45
2:B:1017:ILE:N	2:B:1018:PRO:CD	2.75	0.45
3:C:238:ILE:HD13	3:C:242:GLN:HB3	1.98	0.45
5:E:117:THR:C	5:E:119:SER:H	2.23	0.45
6:F:75:PRO:HG2	6:F:78:GLN:HB2	1.97	0.45
7:G:48:VAL:HG13	7:G:74:TYR:HD1	1.81	0.45
8:H:38:LEU:HD13	8:H:125:LEU:CD1	2.44	0.45
8:H:96:VAL:HG13	8:H:142:LEU:O	2.17	0.45
10:J:8:PHE:H	10:J:49:MET:CE	2.29	0.45
10:J:32:GLU:O	10:J:33:GLY:C	2.58	0.45
12:L:70:ARG:HG2	12:L:70:ARG:NH1	2.31	0.45
1:A:482:PHE:CE1	2:B:836:GLU:HB2	2.51	0.45
1:A:700:ASN:HB2	9:I:98:VAL:CG2	2.46	0.45
1:A:839:ARG:NH1	1:A:839:ARG:CG	2.77	0.45
1:A:973:ILE:CD1	1:A:1037:LEU:HA	2.46	0.45
1:A:1015:VAL:O	1:A:1016:THR:C	2.59	0.45
1:A:1399:ARG:HB3	1:A:1408:ILE:HD13	1.98	0.45
2:B:801:LYS:N	10:J:52:THR:HG22	2.31	0.45
2:B:833:TYR:C	2:B:835:GLN:H	2.24	0.45
2:B:880:THR:HG21	2:B:934:LYS:HG3	1.97	0.45
2:B:969:ARG:HG2	2:B:970:THR:N	2.30	0.45
2:B:990:ILE:CG2	2:B:991:GLY:N	2.80	0.45
3:C:10:ILE:N	11:K:108:GLU:OE1	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:16:ASP:O	3:C:17:ASN:CG	2.59	0.45
3:C:148:ARG:HG2	3:C:149:LYS:N	2.31	0.45
3:C:181:ASP:OD1	3:C:185:LYS:HB2	2.15	0.45
5:E:54:GLN:O	5:E:57:MET:HB3	2.17	0.45
7:G:13:LEU:HD21	7:G:17:PHE:CB	2.46	0.45
7:G:88:ASP:CB	7:G:144:ARG:HA	2.38	0.45
9:I:98:VAL:CG1	9:I:111:THR:HG22	2.47	0.45
11:K:54:ARG:HH11	11:K:54:ARG:HG3	1.82	0.45
1:A:135:PHE:CE1	1:A:222:LEU:HD22	2.52	0.45
1:A:153:PRO:O	1:A:154:SER:O	2.33	0.45
1:A:202:LEU:HA	1:A:206:GLU:OE1	2.17	0.45
1:A:211:PHE:HD1	1:A:214:ILE:HD12	1.81	0.45
1:A:524:VAL:CG1	1:A:525:GLN:H	2.27	0.45
1:A:645:LEU:O	1:A:646:PHE:C	2.58	0.45
1:A:688:LYS:O	1:A:690:VAL:N	2.49	0.45
1:A:852:TYR:CD2	1:A:1060:PRO:CB	2.98	0.45
1:A:1044:TRP:O	1:A:1045:VAL:C	2.58	0.45
1:A:1215:ARG:NE	1:A:1215:ARG:HA	2.31	0.45
1:A:1235:LYS:HB3	1:A:1237:ILE:HD11	1.97	0.45
1:A:1254:ALA:O	1:A:1255:GLU:CB	2.62	0.45
1:A:1313:LEU:HD23	1:A:1338:VAL:CG2	2.46	0.45
1:A:1396:ALA:O	1:A:1400:CYS:HB3	2.17	0.45
2:B:185:THR:H	2:B:188:ASP:CG	2.24	0.45
2:B:332:ASP:O	2:B:334:ILE:N	2.43	0.45
3:C:46:ILE:CD1	3:C:67:LEU:HB3	2.45	0.45
5:E:157:SER:N	5:E:160:GLU:OE1	2.47	0.45
8:H:40:LEU:HD22	8:H:123:MET:CE	2.46	0.45
9:I:61:ASP:O	9:I:63:GLY:N	2.49	0.45
1:A:107:CYS:HB2	1:A:114:LEU:HD21	1.97	0.45
1:A:115:LEU:O	1:A:122:MET:HE2	2.16	0.45
1:A:427:GLN:HB2	1:A:430:TRP:CD2	2.52	0.45
1:A:493:GLN:CA	1:A:493:GLN:HE21	2.27	0.45
1:A:527:THR:HG21	1:A:650:GLN:HA	1.98	0.45
1:A:603:ASN:O	1:A:604:GLY:C	2.59	0.45
1:A:826:ASP:O	1:A:830:LYS:N	2.41	0.45
1:A:1097:GLY:H	1:A:1355:VAL:HG23	1.80	0.45
1:A:1138:ILE:HG21	1:A:1316:VAL:HG13	1.99	0.45
1:A:1148:ILE:HD11	1:A:1198:ASP:CA	2.44	0.45
1:A:1161:THR:C	1:A:1163:ILE:N	2.69	0.45
2:B:291:ILE:HG22	2:B:297:ILE:CG1	2.46	0.45
2:B:604:ARG:O	2:B:607:GLY:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:834:ASN:HA	2:B:838:SER:O	2.15	0.45
2:B:840:ILE:HG21	2:B:994:TYR:HD1	1.81	0.45
2:B:863:GLU:O	2:B:961:LEU:HD13	2.17	0.45
2:B:866:TYR:CG	2:B:870:ILE:HB	2.51	0.45
2:B:957:ASN:O	2:B:959:ASP:N	2.49	0.45
2:B:1006:ILE:HD13	10:J:44:TYR:CE2	2.51	0.45
3:C:212:PRO:CB	3:C:213:PRO:HD2	2.45	0.45
4:D:12:ARG:NH1	4:D:14:ARG:CA	2.79	0.45
4:D:128:VAL:O	4:D:130:LEU:N	2.49	0.45
4:D:139:LYS:HG3	4:D:140:ASP:OD1	2.16	0.45
6:F:130:ILE:O	6:F:148:VAL:HG21	2.16	0.45
6:F:138:LEU:HB2	6:F:142:SER:HB2	1.98	0.45
7:G:26:LEU:O	7:G:27:LYS:C	2.60	0.45
8:H:26:ILE:O	8:H:27:GLU:HG2	2.16	0.45
8:H:100:THR:OG1	8:H:138:GLU:HG2	2.17	0.45
10:J:20:SER:O	10:J:24:LEU:HG	2.16	0.45
10:J:32:GLU:CD	10:J:32:GLU:H	2.24	0.45
11:K:53:ASP:HB3	11:K:56:VAL:CG2	2.46	0.45
1:A:122:MET:HE3	1:A:126:LEU:HD11	1.99	0.45
1:A:506:ALA:O	1:A:507:VAL:C	2.59	0.45
1:A:640:GLN:O	1:A:641:VAL:C	2.60	0.45
1:A:993:LEU:HD22	1:A:1046:LEU:CD2	2.47	0.45
1:A:1129:GLU:O	1:A:1130:GLN:C	2.59	0.45
1:A:1187:GLN:C	1:A:1244:ARG:HB2	2.42	0.45
1:A:1215:ARG:HD2	1:A:1218:GLN:HE21	1.82	0.45
1:A:1229:SER:HB2	1:A:1233:ASP:OD2	2.16	0.45
1:A:1409:LEU:O	1:A:1412:ALA:HB3	2.17	0.45
2:B:435:THR:CG2	2:B:437:GLU:HB2	2.47	0.45
2:B:591:ARG:O	2:B:592:ASN:C	2.59	0.45
2:B:604:ARG:CA	2:B:609:ILE:HG13	2.47	0.45
2:B:745:PRO:C	2:B:747:MET:N	2.73	0.45
2:B:896:ASP:OD2	12:L:58:LYS:HE3	2.17	0.45
2:B:998:ASP:OD1	3:C:35:ARG:NH2	2.49	0.45
2:B:1104:HIS:HB2	2:B:1122:ARG:HD2	1.99	0.45
2:B:1165:ILE:O	2:B:1217:TYR:OH	2.32	0.45
3:C:18:VAL:O	3:C:19:ASP:C	2.60	0.45
3:C:33:LEU:O	3:C:34:ARG:C	2.60	0.45
3:C:175:ALA:O	3:C:176:ILE:CG1	2.59	0.45
5:E:86:PRO:O	5:E:114:ASN:HB2	2.16	0.45
6:F:75:PRO:O	6:F:77:ASP:O	2.33	0.45
6:F:133:VAL:HG13	6:F:146:TRP:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:34:VAL:HG13	7:G:45:ILE:HG21	1.98	0.45
8:H:109:LYS:HG2	8:H:110:ASP:N	2.32	0.45
9:I:50:THR:HG23	9:I:51:ASN:H	1.81	0.45
11:K:43:GLY:O	11:K:44:ASN:C	2.60	0.45
11:K:52:ASN:O	11:K:54:ARG:N	2.50	0.45
1:A:41:MET:O	1:A:42:ASP:C	2.60	0.45
1:A:77:CYS:O	1:A:77:CYS:SG	2.72	0.45
1:A:215:SER:O	1:A:218:ASP:HB2	2.16	0.45
1:A:554:PRO:HD2	1:A:648:ASN:OD1	2.16	0.45
1:A:567:LYS:HZ1	8:H:43:ASN:ND2	2.13	0.45
1:A:590:ARG:HG2	1:A:590:ARG:HH11	1.82	0.45
1:A:722:LEU:HB3	1:A:799:PHE:CD1	2.51	0.45
1:A:806:ARG:O	2:B:761:HIS:HE1	1.99	0.45
1:A:1150:SER:O	1:A:1151:GLU:HG3	2.17	0.45
1:A:1393:ASN:O	1:A:1394:THR:C	2.60	0.45
2:B:174:LEU:HD21	2:B:204:ILE:HD11	1.97	0.45
2:B:258:LEU:O	2:B:258:LEU:CG	2.64	0.45
2:B:258:LEU:C	2:B:258:LEU:HD12	2.41	0.45
2:B:388:CYS:C	2:B:390:LEU:N	2.74	0.45
2:B:758:PHE:HB3	2:B:761:HIS:CD2	2.50	0.45
4:D:64:VAL:C	4:D:66:ARG:N	2.72	0.45
4:D:66:ARG:C	4:D:68:ARG:H	2.25	0.45
4:D:161:GLY:O	4:D:164:ILE:HB	2.17	0.45
5:E:89:GLY:C	5:E:91:LYS:N	2.74	0.45
5:E:211:TYR:CD1	5:E:211:TYR:N	2.84	0.45
7:G:1:MET:CE	7:G:80:LYS:O	2.65	0.45
8:H:138:GLU:O	8:H:139:ASN:C	2.60	0.45
9:I:2:THR:O	9:I:3:THR:C	2.60	0.45
11:K:55:LYS:CB	11:K:81:TYR:CD1	2.94	0.45
1:A:182:VAL:CG2	1:A:201:VAL:HG22	2.47	0.45
1:A:219:PHE:CE1	1:A:230:ARG:HG2	2.52	0.45
1:A:360:GLU:HB2	1:A:363:GLN:HG3	1.98	0.45
1:A:372:LYS:HA	1:A:435:HIS:CE1	2.51	0.45
1:A:401:GLY:CA	1:A:435:HIS:HD2	2.30	0.45
1:A:547:LEU:HD13	11:K:58:PHE:CE1	2.52	0.45
1:A:583:PRO:O	1:A:610:GLY:HA3	2.17	0.45
1:A:1037:LEU:HD12	1:A:1042:PHE:HA	1.99	0.45
1:A:1206:ASP:HB2	1:A:1274:ARG:HH12	1.81	0.45
1:A:1407:GLU:CD	1:A:1407:GLU:H	2.25	0.45
2:B:875:GLU:O	2:B:877:PRO:HD3	2.16	0.45
3:C:17:ASN:CA	3:C:240:VAL:HG11	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:66:ARG:C	3:C:68:GLY:N	2.69	0.45
3:C:186:LEU:N	3:C:186:LEU:CD1	2.80	0.45
3:C:191:TYR:HD2	3:C:201:TRP:CD1	2.35	0.45
4:D:155:ARG:C	4:D:156:ASP:OD2	2.60	0.45
5:E:22:MET:HE3	5:E:26:ARG:CZ	2.46	0.45
5:E:26:ARG:NH1	5:E:133:GLU:OE2	2.44	0.45
6:F:148:VAL:CG2	6:F:149:GLU:N	2.80	0.45
7:G:47:CYS:O	7:G:76:ALA:HB1	2.17	0.45
10:J:57:ILE:HA	10:J:60:PHE:CD2	2.35	0.45
11:K:65:HIS:HD2	11:K:67:PHE:N	2.14	0.45
12:L:32:ALA:H	12:L:55:ILE:HG13	1.81	0.45
1:A:150:THR:HA	1:A:165:GLY:O	2.17	0.45
1:A:469:ARG:NH2	2:B:991:GLY:O	2.50	0.45
1:A:903:ASN:ND2	1:A:903:ASN:C	2.69	0.45
2:B:31:TRP:O	2:B:32:ALA:C	2.59	0.45
2:B:37:PHE:CD2	2:B:542:MET:SD	3.10	0.45
2:B:51:PHE:O	2:B:54:PHE:HB3	2.16	0.45
2:B:65:GLU:HG3	2:B:66:ASP:N	2.32	0.45
2:B:288:ALA:CB	2:B:331:LEU:HD12	2.47	0.45
2:B:429:PHE:HA	2:B:432:MET:CE	2.39	0.45
2:B:435:THR:HG23	2:B:437:GLU:HB2	1.99	0.45
2:B:558:LEU:O	2:B:561:TRP:N	2.50	0.45
3:C:69:LEU:HB3	10:J:6:ARG:HD2	1.97	0.45
3:C:91:HIS:ND1	3:C:158:VAL:HG11	2.32	0.45
3:C:167:HIS:ND1	3:C:169:LYS:HG2	2.32	0.45
3:C:239:PRO:O	3:C:240:VAL:C	2.58	0.45
4:D:60:LYS:HE3	4:D:126:ILE:HD11	1.98	0.45
5:E:79:TRP:HE1	5:E:81:GLU:HB2	1.82	0.45
5:E:212:ARG:HG3	5:E:212:ARG:NH1	2.31	0.45
7:G:138:THR:O	7:G:140:LYS:N	2.50	0.45
11:K:49:GLU:C	11:K:51:LEU:N	2.74	0.45
1:A:22:PHE:HE2	1:A:30:ILE:HD12	1.82	0.45
1:A:130:ASP:O	1:A:131:SER:C	2.59	0.45
1:A:228:PHE:HE2	4:D:15:LEU:CD2	2.29	0.45
1:A:517:ASN:ND2	1:A:1364:ASN:HD22	2.15	0.45
1:A:884:ASP:O	1:A:885:THR:C	2.60	0.45
1:A:1019:CYS:O	1:A:1020:CYS:C	2.57	0.45
1:A:1033:GLN:O	1:A:1036:ARG:NH1	2.50	0.45
1:A:1140:HIS:HA	1:A:1275:GLY:HA3	1.98	0.45
1:A:1241:ARG:O	1:A:1242:VAL:CG2	2.64	0.45
1:A:1377:THR:O	1:A:1379:GLY:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1453:TYR:O	1:A:1454:MET:HB3	2.17	0.45
2:B:233:PRO:HG2	2:B:234:ILE:CD1	2.47	0.45
2:B:1040:ASN:O	2:B:1041:GLU:C	2.60	0.45
2:B:1147:LEU:HD23	2:B:1147:LEU:O	2.17	0.45
3:C:6:PRO:HB2	11:K:101:LEU:HD12	1.99	0.45
3:C:147:LEU:HA	10:J:61:LEU:HD21	1.98	0.45
5:E:191:LYS:O	5:E:192:ARG:C	2.60	0.45
8:H:33:GLN:HG2	8:H:129:TYR:CE2	2.52	0.45
12:L:27:LEU:N	12:L:27:LEU:CD2	2.79	0.45
1:A:78:PRO:HB2	2:B:1201:LYS:HE3	1.99	0.44
1:A:100:LYS:O	1:A:103:CYS:HB2	2.16	0.44
1:A:199:LEU:N	1:A:199:LEU:HD23	2.32	0.44
1:A:939:ASP:O	1:A:942:PHE:HB3	2.17	0.44
1:A:943:LEU:C	1:A:945:GLU:N	2.73	0.44
1:A:1148:ILE:O	1:A:1149:ALA:HB2	2.17	0.44
1:A:1339:LEU:CD1	5:E:147:HIS:CD2	2.99	0.44
3:C:63:ILE:O	3:C:64:ALA:C	2.60	0.44
3:C:87:PHE:N	3:C:87:PHE:CD1	2.85	0.44
4:D:191:ALA:C	4:D:193:THR:N	2.75	0.44
5:E:55:ARG:C	5:E:57:MET:H	2.24	0.44
5:E:163:GLU:O	5:E:164:LEU:C	2.59	0.44
11:K:83:PRO:O	11:K:84:LYS:C	2.59	0.44
1:A:185:TRP:CH2	1:A:200:ARG:HG2	2.52	0.44
1:A:230:ARG:O	1:A:231:PRO:C	2.60	0.44
1:A:471:ASN:O	1:A:474:VAL:HG12	2.18	0.44
1:A:546:VAL:HG13	1:A:577:ILE:HG21	1.99	0.44
1:A:566:ILE:O	1:A:567:LYS:O	2.36	0.44
1:A:593:GLU:C	1:A:595:THR:H	2.26	0.44
1:A:841:LEU:HD23	1:A:841:LEU:HA	1.77	0.44
1:A:1224:LEU:HG	1:A:1226:VAL:HG23	2.00	0.44
1:A:1394:THR:HG22	1:A:1398:MET:SD	2.57	0.44
1:A:1427:ASN:O	1:A:1431:GLY:N	2.47	0.44
2:B:34:ILE:O	2:B:37:PHE:HB3	2.16	0.44
2:B:298:LEU:HD13	2:B:314:LEU:HD13	1.98	0.44
2:B:710:LEU:O	2:B:711:GLU:HG2	2.16	0.44
2:B:871:THR:HG22	2:B:872:GLU:N	2.33	0.44
2:B:1022:THR:HG23	2:B:1022:THR:O	2.17	0.44
2:B:1197:PRO:O	2:B:1198:TYR:C	2.59	0.44
3:C:44:LEU:CD2	3:C:159:ALA:HB1	2.47	0.44
5:E:64:PRO:O	5:E:65:THR:C	2.60	0.44
5:E:116:ILE:CG2	5:E:117:THR:N	2.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:17:ARG:HG3	9:I:28:GLU:OE1	2.17	0.44
9:I:58:VAL:HG13	9:I:62:ILE:HD13	1.98	0.44
9:I:59:VAL:C	9:I:61:ASP:H	2.25	0.44
12:L:53:HIS:C	12:L:55:ILE:H	2.26	0.44
1:A:288:ALA:CA	1:A:291:GLU:HG3	2.48	0.44
1:A:463:ILE:HD11	1:A:469:ARG:HG3	1.99	0.44
1:A:722:LEU:O	1:A:725:ALA:HB3	2.17	0.44
1:A:785:PRO:C	1:A:786:HIS:HD2	2.26	0.44
1:A:809:THR:O	1:A:810:PRO:C	2.59	0.44
1:A:1383:SER:O	1:A:1388:GLY:HA3	2.18	0.44
2:B:38:PHE:HD1	2:B:811:TYR:CD2	2.36	0.44
2:B:273:LEU:CB	2:B:276:ILE:HD12	2.43	0.44
2:B:653:VAL:HG13	2:B:657:HIS:CB	2.47	0.44
2:B:791:THR:O	2:B:792:MET:O	2.35	0.44
2:B:901:PRO:HD2	12:L:59:ALA:O	2.17	0.44
2:B:904:ARG:NH1	12:L:66:GLN:O	2.51	0.44
2:B:1001:PHE:CD1	2:B:1001:PHE:C	2.95	0.44
2:B:1033:LYS:HA	2:B:1089:PRO:HD2	1.99	0.44
3:C:82:TYR:O	3:C:84:ARG:N	2.49	0.44
10:J:13:VAL:C	10:J:14:VAL:HG23	2.42	0.44
11:K:107:THR:O	11:K:111:LEU:HG	2.16	0.44
12:L:38:LEU:HG	12:L:39:SER:N	2.18	0.44
1:A:49:LYS:NZ	1:A:60:SER:HA	2.32	0.44
1:A:58:LEU:HD21	1:A:82:GLY:HA3	2.00	0.44
1:A:120:GLU:C	1:A:122:MET:H	2.25	0.44
1:A:556:TRP:C	1:A:558:GLY:H	2.25	0.44
1:A:740:LEU:HD12	1:A:741:ASN:N	2.32	0.44
1:A:1205:LYS:O	1:A:1206:ASP:C	2.60	0.44
1:A:1319:VAL:O	1:A:1322:ILE:HG12	2.18	0.44
1:A:1334:ASP:C	1:A:1336:MET:H	2.25	0.44
2:B:30:SER:HB3	2:B:743:ILE:O	2.18	0.44
2:B:307:ASP:O	2:B:309:GLN:N	2.51	0.44
2:B:364:ILE:HG22	2:B:365:THR:N	2.32	0.44
2:B:769:TYR:HD1	2:B:987:LYS:NZ	2.15	0.44
2:B:879:ARG:HH22	2:B:885:MET:CE	2.30	0.44
3:C:62:PHE:C	3:C:62:PHE:CD2	2.96	0.44
3:C:62:PHE:C	3:C:62:PHE:HD2	2.26	0.44
3:C:259:LEU:CD2	11:K:91:CYS:HB3	2.47	0.44
4:D:12:ARG:HH11	4:D:12:ARG:CG	2.28	0.44
4:D:46:GLU:HG2	4:D:47:LEU:N	2.32	0.44
5:E:33:GLU:CD	5:E:33:GLU:N	2.75	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:111:THR:CG2	7:G:114:LEU:HB2	2.46	0.44
10:J:21:TYR:HB2	10:J:39:LEU:HD11	2.00	0.44
1:A:22:PHE:HE2	1:A:30:ILE:CD1	2.30	0.44
1:A:108:MET:H	1:A:171:GLN:HE22	1.64	0.44
1:A:256:GLN:O	1:A:257:ARG:HG3	2.18	0.44
1:A:504:LEU:CD1	6:F:91:ALA:CB	2.96	0.44
1:A:555:ASP:O	1:A:556:TRP:O	2.35	0.44
1:A:667:GLY:HA3	3:C:192:TRP:CH2	2.52	0.44
1:A:1073:GLY:O	1:A:1076:ALA:HB3	2.16	0.44
1:A:1212:VAL:O	1:A:1213:GLY:C	2.60	0.44
1:A:1220:PHE:O	1:A:1221:LYS:CB	2.65	0.44
1:A:1262:LYS:C	1:A:1264:GLU:N	2.74	0.44
1:A:1387:HIS:HA	1:A:1391:ARG:HE	1.81	0.44
2:B:242:SER:HB2	2:B:362:PRO:HG2	2.00	0.44
4:D:126:ILE:HD13	4:D:145:MET:CE	2.48	0.44
5:E:124:VAL:HB	5:E:125:PRO:CD	2.46	0.44
6:F:99:LEU:O	6:F:103:MET:CG	2.59	0.44
8:H:12:VAL:HB	8:H:52:GLN:N	2.32	0.44
8:H:58:THR:HG22	8:H:59:ILE:N	2.28	0.44
9:I:85:PHE:CD2	9:I:85:PHE:N	2.74	0.44
9:I:88:SER:C	9:I:90:GLN:N	2.76	0.44
11:K:52:ASN:O	11:K:53:ASP:C	2.60	0.44
11:K:79:GLU:C	11:K:81:TYR:H	2.25	0.44
1:A:123:ARG:HA	1:A:126:LEU:HD12	1.98	0.44
1:A:219:PHE:CE2	1:A:231:PRO:HD2	2.53	0.44
1:A:226:GLU:O	1:A:226:GLU:HG2	2.16	0.44
1:A:290:GLU:C	1:A:292:ALA:H	2.24	0.44
1:A:1187:GLN:HA	1:A:1244:ARG:HB2	1.99	0.44
2:B:293:PRO:O	2:B:294:ASP:O	2.36	0.44
2:B:328:GLU:C	2:B:328:GLU:CD	2.85	0.44
2:B:843:GLN:O	2:B:844:SER:C	2.59	0.44
2:B:1065:GLN:HB3	2:B:1069:PHE:O	2.18	0.44
2:B:1107:ALA:O	2:B:1108:ARG:O	2.35	0.44
2:B:1119:VAL:HB	2:B:1124:ARG:NH2	2.32	0.44
3:C:8:VAL:HG12	3:C:9:LYS:N	2.32	0.44
3:C:59:ALA:O	3:C:62:PHE:HB3	2.17	0.44
3:C:97:VAL:HG12	3:C:99:LEU:CD2	2.48	0.44
5:E:136:ASN:OD1	5:E:137:GLU:N	2.50	0.44
5:E:144:ILE:C	5:E:146:HIS:N	2.74	0.44
7:G:44:TYR:CE2	7:G:105:PRO:HB2	2.53	0.44
8:H:40:LEU:HB2	8:H:123:MET:CE	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:28:LYS:HB3	12:L:39:SER:CB	2.47	0.44
1:A:241:VAL:O	1:A:242:PRO:C	2.60	0.44
1:A:381:THR:CG2	1:A:382:PRO:CD	2.93	0.44
1:A:390:GLN:HE21	1:A:394:ASN:ND2	2.07	0.44
1:A:493:GLN:NE2	1:A:493:GLN:CA	2.80	0.44
1:A:517:ASN:ND2	1:A:1364:ASN:HB2	2.33	0.44
1:A:969:GLN:O	1:A:969:GLN:HG3	2.16	0.44
1:A:994:GLN:O	1:A:996:ASN:N	2.51	0.44
1:A:1239:ARG:HH12	1:A:1241:ARG:HH12	1.64	0.44
2:B:113:TYR:CD2	2:B:192:LEU:HD22	2.53	0.44
2:B:192:LEU:C	2:B:194:GLU:H	2.25	0.44
2:B:446:LEU:C	2:B:448:ILE:H	2.25	0.44
2:B:857:ARG:HD2	2:B:945:GLU:OE1	2.17	0.44
3:C:44:LEU:HD13	3:C:129:ILE:HG23	1.99	0.44
4:D:189:ASP:O	4:D:190:GLU:C	2.61	0.44
5:E:26:ARG:HH22	5:E:133:GLU:CD	2.25	0.44
15:P:4:C:H2'	15:P:5:C:C6	2.52	0.44
1:A:103:CYS:C	1:A:105:CYS:H	2.25	0.44
1:A:298:PHE:CD2	1:A:299:HIS:HD2	2.36	0.44
1:A:382:PRO:HB3	1:A:428:TYR:HE2	1.82	0.44
1:A:526:ASP:O	1:A:528:LEU:N	2.51	0.44
1:A:604:GLY:O	1:A:605:MET:HB2	2.18	0.44
1:A:650:GLN:HB3	1:A:654:ASN:ND2	2.33	0.44
1:A:912:LEU:HB2	1:A:913:LEU:H	1.66	0.44
1:A:1042:PHE:CE2	1:A:1046:LEU:HD11	2.52	0.44
1:A:1167:GLU:HA	1:A:1170:ILE:HD11	1.98	0.44
2:B:31:TRP:CE3	2:B:31:TRP:HA	2.53	0.44
2:B:67:SER:HB3	2:B:92:PHE:HD1	1.83	0.44
2:B:999:MET:HE2	2:B:1011:ILE:HD11	1.99	0.44
2:B:1034:VAL:O	2:B:1035:ALA:C	2.61	0.44
2:B:1104:HIS:CD2	2:B:1122:ARG:HB2	2.52	0.44
3:C:10:ILE:HG22	3:C:11:ARG:O	2.18	0.44
4:D:32:GLU:HG3	7:G:5:LYS:CE	2.47	0.44
4:D:70:PHE:HE1	7:G:51:TYR:CE1	2.35	0.44
4:D:120:GLU:O	4:D:120:GLU:HG2	2.17	0.44
5:E:81:GLU:HG2	5:E:82:PHE:N	2.33	0.44
5:E:156:LEU:O	5:E:157:SER:C	2.61	0.44
6:F:109:VAL:HG12	6:F:123:LYS:HE3	1.94	0.44
8:H:95:TYR:CD2	8:H:95:TYR:C	2.96	0.44
10:J:1:MET:H2	10:J:57:ILE:HG22	1.83	0.44
11:K:53:ASP:HB3	11:K:56:VAL:HG23	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:ILE:HG22	1:A:52:GLY:H	1.82	0.44
1:A:321:PRO:O	1:A:322:VAL:CG1	2.66	0.44
1:A:398:GLU:O	1:A:399:HIS:O	2.36	0.44
1:A:418:SER:C	1:A:420:ARG:H	2.25	0.44
1:A:544:ASP:OD1	1:A:545:GLN:N	2.50	0.44
1:A:1110:ASN:N	1:A:1110:ASN:ND2	2.58	0.44
1:A:1436:ILE:O	1:A:1439:GLY:N	2.44	0.44
2:B:43:LEU:HD11	2:B:811:TYR:O	2.18	0.44
2:B:305:VAL:O	2:B:305:VAL:CG1	2.65	0.44
2:B:361:LEU:HD21	2:B:377:PHE:HD2	1.83	0.44
2:B:565:PRO:O	2:B:566:LEU:C	2.61	0.44
2:B:644:GLU:C	2:B:646:LEU:N	2.76	0.44
2:B:1060:ARG:HA	2:B:1060:ARG:HD2	1.77	0.44
2:B:1115:THR:HG22	2:B:1117:GLN:HB2	1.99	0.44
3:C:18:VAL:CG2	3:C:240:VAL:HB	2.47	0.44
3:C:23:SER:O	3:C:24:ASN:HB3	2.17	0.44
3:C:71:PRO:C	3:C:72:LEU:HD23	2.43	0.44
3:C:133:ILE:CD1	3:C:237:SER:N	2.79	0.44
4:D:38:ILE:CG2	4:D:42:GLY:HA2	2.48	0.44
4:D:138:ASN:HD21	7:G:35:GLU:HB3	1.82	0.44
4:D:140:ASP:O	4:D:144:THR:N	2.51	0.44
5:E:68:SER:O	5:E:72:PHE:O	2.35	0.44
5:E:124:VAL:C	5:E:126:SER:H	2.26	0.44
8:H:14:GLU:OE1	8:H:15:VAL:O	2.36	0.44
1:A:95:PHE:O	1:A:98:LYS:N	2.51	0.43
1:A:266:LEU:HD21	1:A:303:TYR:CZ	2.53	0.43
1:A:595:THR:C	1:A:596:THR:CG2	2.91	0.43
1:A:973:ILE:HD11	1:A:1041:ALA:CB	2.48	0.43
1:A:973:ILE:HD11	1:A:1041:ALA:HB2	2.00	0.43
1:A:1313:LEU:O	1:A:1314:SER:C	2.60	0.43
1:A:1344:GLY:O	1:A:1345:ARG:C	2.61	0.43
2:B:230:ALA:HB3	2:B:231:PRO:CD	2.47	0.43
2:B:615:MET:C	2:B:616:ILE:HD12	2.41	0.43
2:B:1176:ASN:H	2:B:1178:ASN:H	1.65	0.43
3:C:43:THR:CG2	3:C:44:LEU:N	2.51	0.43
3:C:52:GLU:HB2	12:L:64:LEU:HD21	1.99	0.43
3:C:181:ASP:N	3:C:182:PRO:CD	2.81	0.43
3:C:187:LYS:HD3	8:H:22:LYS:HE2	2.00	0.43
4:D:220:LEU:HD23	4:D:221:TYR:N	2.33	0.43
5:E:59:SER:HB3	5:E:79:TRP:CZ2	2.53	0.43
5:E:181:ALA:O	5:E:182:ASP:C	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:80:LYS:O	7:G:82:PHE:CD1	2.71	0.43
11:K:7:PHE:C	11:K:9:LEU:N	2.76	0.43
11:K:68:PHE:HB3	11:K:70:ARG:HH11	1.82	0.43
1:A:35:ILE:HD13	1:A:241:VAL:HG11	1.99	0.43
1:A:332:LYS:HB2	1:A:337:ARG:NH1	2.32	0.43
1:A:392:VAL:HG13	1:A:415:LEU:HD11	2.00	0.43
1:A:443:LEU:HD23	1:A:456:MET:O	2.18	0.43
1:A:786:HIS:CE1	2:B:705:MET:HE1	2.53	0.43
1:A:1143:LEU:O	1:A:1146:VAL:HG23	2.17	0.43
1:A:1402:PHE:CE1	1:A:1403:GLU:HG2	2.53	0.43
2:B:25:ILE:HG23	2:B:29:ASP:CB	2.48	0.43
2:B:189:LEU:O	2:B:190:TYR:C	2.60	0.43
2:B:232:SER:HA	14:T:11:DA:OP1	2.18	0.43
2:B:530:GLY:C	2:B:531:GLN:HG2	2.42	0.43
2:B:882:THR:CB	2:B:934:LYS:C	2.91	0.43
2:B:1072:MET:HB2	2:B:1085:ILE:HD13	2.01	0.43
3:C:29:MET:HE2	11:K:98:LEU:HD21	1.99	0.43
5:E:94:LYS:CD	5:E:98:ILE:HD11	2.47	0.43
7:G:91:VAL:CG1	7:G:92:VAL:N	2.81	0.43
7:G:115:MET:HE1	7:G:130:TYR:CE2	2.53	0.43
8:H:42:ILE:O	8:H:44:VAL:HG23	2.18	0.43
1:A:445:ASN:CB	1:A:455:MET:HG2	2.47	0.43
1:A:1134:ILE:O	1:A:1138:ILE:HG12	2.18	0.43
1:A:1219:THR:HG21	1:A:1271:ILE:HD11	2.01	0.43
2:B:830:TYR:HE2	2:B:1000:PRO:HD3	1.77	0.43
2:B:1034:VAL:O	2:B:1036:ALA:N	2.51	0.43
2:B:1084:GLN:OE1	3:C:189:THR:CG2	2.67	0.43
3:C:258:ILE:N	3:C:258:ILE:CD1	2.79	0.43
4:D:14:ARG:HH11	4:D:14:ARG:CB	2.27	0.43
4:D:29:LEU:CD1	7:G:82:PHE:CE2	3.01	0.43
5:E:79:TRP:HD1	5:E:100:ILE:HD11	1.83	0.43
5:E:82:PHE:N	5:E:82:PHE:CD1	2.87	0.43
5:E:147:HIS:CD2	5:E:149:LEU:H	2.36	0.43
6:F:111:LEU:H	6:F:111:LEU:CD1	2.29	0.43
7:G:59:GLY:HA3	7:G:70:PHE:CE2	2.53	0.43
8:H:4:THR:HG22	8:H:6:PHE:H	1.83	0.43
8:H:12:VAL:HG11	8:H:15:VAL:CG2	2.48	0.43
9:I:100:PHE:N	9:I:100:PHE:CD1	2.85	0.43
9:I:117:LYS:HD2	9:I:117:LYS:N	2.33	0.43
1:A:534:LEU:O	1:A:534:LEU:HG	2.18	0.43
1:A:545:GLN:O	1:A:548:ASN:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:758:ILE:H	1:A:758:ILE:HG13	1.55	0.43
1:A:791:ASP:C	1:A:791:ASP:OD1	2.61	0.43
1:A:894:GLU:O	1:A:898:ARG:CB	2.67	0.43
1:A:994:GLN:C	1:A:996:ASN:N	2.77	0.43
1:A:1020:CYS:O	1:A:1021:LEU:C	2.61	0.43
1:A:1035:TYR:CB	1:A:1037:LEU:HD23	2.47	0.43
1:A:1042:PHE:HE2	1:A:1046:LEU:HD11	1.83	0.43
1:A:1172:LEU:C	1:A:1174:PHE:H	2.25	0.43
1:A:1207:LEU:CD1	1:A:1273:LEU:HD23	2.48	0.43
2:B:217:ARG:HG2	2:B:217:ARG:NH1	2.33	0.43
2:B:828:ALA:HB2	2:B:1085:ILE:HG23	1.99	0.43
2:B:1115:THR:HG22	2:B:1117:GLN:CG	2.49	0.43
3:C:40:GLU:OE1	3:C:254:LYS:HE3	2.19	0.43
4:D:8:PHE:CZ	4:D:37:GLN:CD	2.96	0.43
5:E:64:PRO:CB	5:E:69:ILE:HD11	2.48	0.43
8:H:14:GLU:OE1	8:H:15:VAL:N	2.50	0.43
8:H:130:ARG:H	8:H:130:ARG:CD	2.29	0.43
11:K:12:LEU:HD12	11:K:37:LYS:HG2	1.99	0.43
14:T:13:DT:H2''	14:T:14:DA:OP2	2.18	0.43
14:T:16:DT:C1'	14:T:17:DT:H5'	2.48	0.43
1:A:125:ALA:O	1:A:127:ALA:N	2.52	0.43
1:A:325:ILE:CG2	2:B:1210:MET:HE2	2.47	0.43
1:A:417:TYR:O	1:A:418:SER:C	2.60	0.43
1:A:730:GLY:O	1:A:733:ALA:N	2.51	0.43
1:A:1029:ARG:HG3	1:A:1029:ARG:NH1	2.28	0.43
2:B:496:ARG:NH1	2:B:496:ARG:HB3	2.33	0.43
2:B:540:SER:HA	2:B:749:LEU:O	2.19	0.43
2:B:856:PHE:CD1	2:B:856:PHE:N	2.86	0.43
2:B:886:LYS:NZ	2:B:936:ASP:OD1	2.52	0.43
2:B:1001:PHE:HE2	3:C:34:ARG:CZ	2.31	0.43
2:B:1183:LYS:O	2:B:1183:LYS:CE	2.67	0.43
3:C:6:PRO:CG	11:K:101:LEU:HB2	2.43	0.43
3:C:8:VAL:HG11	11:K:105:PHE:HD1	1.83	0.43
3:C:15:LYS:O	3:C:240:VAL:HG22	2.17	0.43
4:D:120:GLU:O	4:D:123:LEU:HB2	2.18	0.43
4:D:147:TYR:CZ	7:G:103:VAL:HG13	2.52	0.43
5:E:24:LYS:HB2	5:E:30:ILE:HB	2.00	0.43
6:F:123:LYS:O	6:F:127:GLU:HG3	2.18	0.43
11:K:89:ASN:C	11:K:91:CYS:N	2.75	0.43
12:L:50:ASP:HB3	12:L:51:CYS:H	1.69	0.43
1:A:298:PHE:HD2	1:A:299:HIS:CD2	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:590:ARG:CG	1:A:591:PHE:N	2.79	0.43
1:A:672:ASP:HB3	1:A:736:ASN:HD21	1.83	0.43
1:A:1237:ILE:HG22	1:A:1238:ILE:H	1.82	0.43
2:B:29:ASP:HB3	2:B:658:ILE:HD11	2.00	0.43
2:B:363:HIS:O	2:B:364:ILE:CB	2.67	0.43
2:B:371:GLU:OE1	2:B:371:GLU:N	2.52	0.43
2:B:640:VAL:O	2:B:640:VAL:HG12	2.18	0.43
2:B:903:VAL:CG1	2:B:904:ARG:N	2.81	0.43
2:B:1117:GLN:HG3	2:B:1156:ASP:OD1	2.18	0.43
3:C:77:ILE:HD13	3:C:77:ILE:HA	1.88	0.43
4:D:35:LEU:HD12	4:D:35:LEU:H	1.83	0.43
4:D:126:ILE:O	4:D:128:VAL:N	2.52	0.43
7:G:102:GLN:HG3	7:G:106:MET:O	2.18	0.43
7:G:134:GLU:H	7:G:134:GLU:CD	2.26	0.43
12:L:53:HIS:O	12:L:55:ILE:N	2.50	0.43
1:A:108:MET:HB3	1:A:210:ILE:HD11	2.01	0.43
1:A:224:PHE:CE2	1:A:231:PRO:HG3	2.53	0.43
1:A:341:MET:CE	2:B:1135:ARG:NH1	2.73	0.43
1:A:343:LYS:HE2	2:B:1156:ASP:OD2	2.18	0.43
1:A:577:ILE:HG13	1:A:578:LEU:N	2.34	0.43
1:A:786:HIS:N	1:A:786:HIS:HD2	2.16	0.43
1:A:939:ASP:O	1:A:940:ARG:C	2.60	0.43
1:A:962:ARG:HA	1:A:965:GLN:NE2	2.34	0.43
1:A:1253:GLU:O	1:A:1254:ALA:CB	2.66	0.43
1:A:1444:MET:HB2	1:A:1444:MET:HE3	1.75	0.43
2:B:203:PHE:N	2:B:203:PHE:CD1	2.87	0.43
2:B:288:ALA:HA	2:B:331:LEU:HD12	2.01	0.43
2:B:386:LEU:C	2:B:388:CYS:N	2.75	0.43
2:B:592:ASN:OD1	2:B:595:ARG:HG2	2.18	0.43
2:B:705:MET:HE2	2:B:742:GLU:HG2	2.01	0.43
2:B:980:PHE:CD2	2:B:1094:ARG:HA	2.53	0.43
2:B:983:ARG:HH11	2:B:1091:TYR:HB3	1.83	0.43
3:C:44:LEU:HD21	3:C:159:ALA:HB1	2.01	0.43
3:C:66:ARG:HA	3:C:69:LEU:HD13	2.00	0.43
3:C:167:HIS:HA	11:K:6:ARG:NH1	2.29	0.43
4:D:29:LEU:CD2	4:D:29:LEU:H	2.32	0.43
7:G:115:MET:HB3	7:G:116:PRO:CD	2.46	0.43
7:G:123:ALA:C	7:G:125:SER:H	2.27	0.43
8:H:88:SER:O	8:H:89:LEU:HD23	2.19	0.43
9:I:55:THR:O	9:I:58:VAL:HG23	2.19	0.43
1:A:11:LEU:HB2	2:B:1193:GLN:CG	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:MET:O	1:A:42:ASP:O	2.37	0.43
1:A:353:ILE:HD11	1:A:480:ALA:HB1	2.01	0.43
1:A:618:GLU:O	1:A:619:LYS:C	2.61	0.43
1:A:808:LEU:HD23	1:A:812:GLU:O	2.19	0.43
1:A:814:PHE:O	1:A:817:ALA:HB3	2.19	0.43
1:A:853:ASP:OD1	1:A:855:THR:HB	2.18	0.43
1:A:1001:ARG:NE	6:F:83:PRO:HD3	2.34	0.43
1:A:1081:LEU:HD11	1:A:1098:VAL:HG23	2.01	0.43
1:A:1289:ARG:NH1	1:A:1326:ARG:NH1	2.66	0.43
1:A:1293:SER:HG	1:A:1295:THR:HG23	1.83	0.43
2:B:249:ARG:NH2	2:B:418:LYS:NZ	2.66	0.43
2:B:758:PHE:N	2:B:759:PRO:CD	2.82	0.43
2:B:903:VAL:HG12	2:B:904:ARG:N	2.32	0.43
2:B:1115:THR:CG2	2:B:1117:GLN:HB2	2.48	0.43
3:C:203:GLN:HG3	3:C:207:CYS:SG	2.58	0.43
4:D:23:ASN:HA	4:D:28:GLN:O	2.18	0.43
4:D:122:GLU:CA	4:D:125:SER:HB3	2.48	0.43
5:E:35:VAL:C	5:E:37:LEU:N	2.76	0.43
7:G:34:VAL:O	7:G:37:SER:HB3	2.19	0.43
7:G:137:ILE:HG22	7:G:138:THR:N	2.33	0.43
8:H:94:ASP:OD1	8:H:94:ASP:N	2.52	0.43
9:I:100:PHE:HD1	9:I:100:PHE:N	2.17	0.43
10:J:14:VAL:CG1	10:J:14:VAL:O	2.65	0.43
14:T:15:DG:C2'	14:T:16:DT:H72	2.48	0.43
1:A:114:LEU:HB2	1:A:142:CYS:HB2	2.00	0.43
1:A:353:ILE:HD13	1:A:487:MET:HE2	1.98	0.43
1:A:423:ASP:O	1:A:424:ILE:O	2.37	0.43
1:A:598:LEU:CD1	8:H:124:ARG:HB2	2.49	0.43
1:A:818:MET:HB3	1:A:818:MET:HE2	1.78	0.43
1:A:1006:ILE:CD1	5:E:163:GLU:HG3	2.35	0.43
1:A:1446:ASP:HB2	6:F:133:VAL:HG23	2.01	0.43
2:B:114:PRO:CG	2:B:181:LEU:HD11	2.48	0.43
2:B:326:ASP:O	2:B:327:ARG:C	2.62	0.43
2:B:377:PHE:C	2:B:379:GLY:N	2.75	0.43
2:B:377:PHE:O	2:B:378:LEU:C	2.62	0.43
2:B:423:LYS:O	2:B:427:ASP:HB2	2.19	0.43
2:B:553:PRO:HG2	2:B:554:ILE:HD12	2.00	0.43
2:B:611:PRO:CG	2:B:685:LEU:HD21	2.45	0.43
2:B:637:LEU:O	2:B:690:VAL:HG13	2.19	0.43
2:B:1068:GLY:O	2:B:1069:PHE:C	2.62	0.43
5:E:30:ILE:HG22	5:E:31:THR:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:59:SER:O	5:E:60:PHE:HB3	2.19	0.43
5:E:161:LYS:NZ	5:E:193:GLY:O	2.43	0.43
6:F:75:PRO:C	6:F:77:ASP:N	2.75	0.43
9:I:10:CYS:O	9:I:11:ASN:C	2.62	0.43
10:J:31:ASP:OD1	10:J:34:THR:OG1	2.34	0.43
10:J:52:THR:O	10:J:53:HIS:C	2.62	0.43
11:K:89:ASN:O	11:K:91:CYS:N	2.52	0.43
1:A:49:LYS:HD2	1:A:55:ASP:HB3	2.01	0.43
1:A:98:LYS:O	1:A:99:ILE:C	2.61	0.43
1:A:315:LEU:N	1:A:315:LEU:HD23	2.32	0.43
1:A:492:PRO:O	1:A:493:GLN:NE2	2.52	0.43
1:A:779:PHE:CD1	1:A:785:PRO:HD3	2.50	0.43
1:A:831:THR:O	1:A:834:THR:HB	2.19	0.43
1:A:1227:ILE:CG2	1:A:1228:TRP:N	2.81	0.43
2:B:241:ARG:HH11	2:B:241:ARG:CG	2.31	0.43
2:B:610:ASN:OD1	2:B:611:PRO:HD2	2.19	0.43
2:B:661:LEU:C	2:B:663:ALA:H	2.26	0.43
2:B:790:ASP:OD2	2:B:790:ASP:N	2.39	0.43
2:B:895:ASP:C	2:B:897:GLY:H	2.26	0.43
2:B:999:MET:HE3	2:B:999:MET:CA	2.33	0.43
3:C:140:ASN:O	3:C:141:GLY:O	2.36	0.43
5:E:120:ALA:O	5:E:123:LEU:CG	2.59	0.43
6:F:127:GLU:O	6:F:129:LYS:N	2.52	0.43
7:G:111:THR:O	7:G:112:LYS:C	2.60	0.43
9:I:102:VAL:HG22	9:I:109:ILE:HG12	2.00	0.43
1:A:185:TRP:HE3	1:A:185:TRP:H	1.66	0.42
1:A:224:PHE:N	1:A:224:PHE:CD1	2.85	0.42
1:A:486:GLU:OE1	2:B:1102:LYS:HD3	2.19	0.42
1:A:547:LEU:HA	1:A:550:LEU:HD12	2.00	0.42
1:A:688:LYS:O	1:A:689:LYS:C	2.60	0.42
1:A:855:THR:CG2	1:A:857:ARG:HE	2.16	0.42
1:A:856:THR:O	1:A:856:THR:HG22	2.18	0.42
1:A:1007:ILE:O	1:A:1008:GLN:C	2.61	0.42
1:A:1061:GLY:O	1:A:1062:GLU:C	2.62	0.42
1:A:1259:MET:SD	1:A:1262:LYS:HD2	2.58	0.42
2:B:350:GLN:O	2:B:351:TYR:C	2.61	0.42
2:B:457:LEU:HD23	2:B:457:LEU:HA	1.91	0.42
2:B:1165:ILE:HG22	2:B:1166:CYS:N	2.33	0.42
3:C:39:ALA:HA	3:C:164:ALA:HB3	2.00	0.42
3:C:80:LEU:HD12	3:C:81:GLU:N	2.31	0.42
5:E:58:MET:O	5:E:59:SER:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:89:GLU:O	6:F:90:ARG:C	2.62	0.42
1:A:207:ILE:O	1:A:208:LEU:C	2.62	0.42
1:A:239:LEU:HA	1:A:240:PRO:HD2	1.88	0.42
1:A:497:THR:CG2	1:A:498:ARG:N	2.81	0.42
1:A:984:LYS:HG2	1:A:988:LEU:HD12	2.01	0.42
1:A:1119:TYR:CE1	1:A:1326:ARG:O	2.73	0.42
1:A:1163:ILE:CG2	1:A:1164:PRO:HD2	2.49	0.42
1:A:1215:ARG:HD2	1:A:1218:GLN:NE2	2.34	0.42
1:A:1424:VAL:HG11	2:B:1139:ILE:CD1	2.46	0.42
2:B:354:ASP:O	2:B:357:GLN:N	2.50	0.42
2:B:589:VAL:CG1	2:B:590:HIS:N	2.81	0.42
2:B:615:MET:HB3	2:B:626:ILE:CG1	2.30	0.42
2:B:797:TYR:C	2:B:798:TYR:CD2	2.97	0.42
2:B:1079:LYS:N	3:C:27:LEU:HD21	2.33	0.42
2:B:1110:PRO:HG2	2:B:1119:VAL:HG22	2.01	0.42
2:B:1223:ASP:HB3	2:B:1224:PHE:H	1.64	0.42
3:C:75:MET:HE1	3:C:239:PRO:HG2	2.01	0.42
5:E:67:GLU:O	5:E:70:SER:HB3	2.19	0.42
5:E:106:GLN:NE2	5:E:130:ALA:HA	2.34	0.42
7:G:9:LEU:HD12	7:G:10:ASN:N	2.31	0.42
7:G:34:VAL:O	7:G:35:GLU:C	2.60	0.42
10:J:47:ARG:HH11	10:J:47:ARG:CG	2.30	0.42
11:K:19:LEU:HD23	11:K:19:LEU:HA	1.90	0.42
1:A:69:THR:C	1:A:71:GLN:H	2.27	0.42
1:A:304:MET:O	1:A:324:SER:HB2	2.19	0.42
1:A:414:ASP:OD1	1:A:416:ARG:CG	2.64	0.42
1:A:483:ASP:O	2:B:979:LYS:CE	2.68	0.42
1:A:549:MET:CE	1:A:656:TRP:HD1	2.32	0.42
1:A:811:GLN:H	1:A:811:GLN:CD	2.27	0.42
1:A:942:PHE:HE2	1:A:946:VAL:HG21	1.85	0.42
1:A:1074:GLU:N	1:A:1075:PRO:HD2	2.34	0.42
1:A:1203:ASN:C	1:A:1205:LYS:N	2.75	0.42
2:B:446:LEU:N	2:B:446:LEU:CD2	2.82	0.42
2:B:657:HIS:CE1	2:B:689:LEU:HD11	2.54	0.42
2:B:941:LEU:O	2:B:942:ARG:C	2.62	0.42
2:B:996:ARG:NH1	3:C:175:ALA:H	2.16	0.42
3:C:91:HIS:C	3:C:91:HIS:CD2	2.97	0.42
4:D:40:HIS:CE1	7:G:7:LEU:O	2.72	0.42
4:D:151:PHE:CD1	4:D:151:PHE:N	2.87	0.42
4:D:180:LEU:HD23	4:D:180:LEU:HA	1.88	0.42
5:E:178:ILE:HG13	5:E:182:ASP:OD2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:4:THR:HG22	8:H:5:LEU:H	1.83	0.42
9:I:70:ARG:HA	9:I:83:ASN:O	2.20	0.42
11:K:30:ALA:CB	11:K:76:GLN:HB2	2.49	0.42
1:A:12:ARG:HH21	2:B:1192:TYR:HE2	1.64	0.42
1:A:339:ASN:O	1:A:343:LYS:HE3	2.19	0.42
1:A:600:PRO:C	1:A:602:ASP:N	2.76	0.42
1:A:692:ASP:O	1:A:693:VAL:C	2.63	0.42
1:A:709:THR:CG2	9:I:94:ASP:HA	2.44	0.42
1:A:742:ASN:O	1:A:743:VAL:C	2.62	0.42
1:A:868:TYR:OH	1:A:1366:ARG:HD3	2.20	0.42
1:A:920:LEU:HD23	1:A:920:LEU:C	2.44	0.42
1:A:986:ILE:O	1:A:987:VAL:C	2.62	0.42
2:B:64:CYS:O	2:B:65:GLU:HB3	2.18	0.42
2:B:69:LEU:HD13	2:B:429:PHE:HD1	1.83	0.42
2:B:290:GLY:O	2:B:292:ILE:N	2.52	0.42
2:B:616:ILE:HG23	2:B:700:SER:OG	2.20	0.42
2:B:637:LEU:HD11	2:B:703:ILE:HD13	2.01	0.42
2:B:638:PHE:HD2	2:B:690:VAL:HG22	1.84	0.42
2:B:800:GLN:HB3	10:J:52:THR:HG22	1.99	0.42
2:B:805:THR:CG2	2:B:806:THR:H	2.27	0.42
2:B:1017:ILE:HB	2:B:1018:PRO:HD3	2.02	0.42
2:B:1107:ALA:O	2:B:1108:ARG:HB3	2.20	0.42
2:B:1165:ILE:HD12	2:B:1187:ASN:HD22	1.84	0.42
3:C:61:GLU:HG2	3:C:62:PHE:N	2.34	0.42
4:D:67:ARG:N	4:D:133:THR:HG21	2.35	0.42
4:D:141:LEU:O	4:D:145:MET:HG2	2.20	0.42
5:E:177:ARG:C	5:E:212:ARG:HD3	2.44	0.42
1:A:66:LYS:O	1:A:67:CYS:HB2	2.19	0.42
1:A:225:ASN:ND2	1:A:228:PHE:N	2.53	0.42
1:A:260:ASP:OD1	1:A:262:LEU:N	2.45	0.42
1:A:305:ASP:OD1	1:A:306:ASN:N	2.53	0.42
1:A:326:ARG:HG2	1:A:326:ARG:NH1	2.31	0.42
1:A:497:THR:HG22	1:A:498:ARG:N	2.35	0.42
1:A:1036:ARG:HG2	1:A:1036:ARG:NH1	2.35	0.42
1:A:1144:LYS:HD2	1:A:1269:GLU:HG3	2.01	0.42
2:B:67:SER:O	2:B:68:THR:O	2.38	0.42
2:B:69:LEU:HD13	2:B:432:MET:CE	2.47	0.42
2:B:287:ARG:NE	2:B:292:ILE:O	2.52	0.42
2:B:303:TYR:HH	2:B:586:TRP:HH2	1.63	0.42
2:B:332:ASP:C	2:B:334:ILE:N	2.76	0.42
2:B:557:PHE:HZ	2:B:603:LEU:HD21	1.80	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:624:LEU:HD12	2:B:624:LEU:HA	1.67	0.42
2:B:638:PHE:HB3	2:B:651:LEU:HD22	2.00	0.42
2:B:803:LEU:HD13	2:B:1032:SER:O	2.19	0.42
2:B:1002:THR:HG22	2:B:1072:MET:HG2	2.01	0.42
2:B:1134:GLU:H	2:B:1134:GLU:CD	2.28	0.42
2:B:1187:ASN:HB3	2:B:1188:LYS:H	1.61	0.42
4:D:119:ARG:NH1	4:D:119:ARG:CB	2.80	0.42
4:D:155:ARG:HE	4:D:219:THR:HG21	1.85	0.42
5:E:73:PRO:C	5:E:75:MET:H	2.27	0.42
7:G:15:PRO:O	7:G:18:PHE:HD1	2.03	0.42
9:I:71:SER:C	9:I:73:ARG:H	2.26	0.42
10:J:5:VAL:O	10:J:6:ARG:O	2.37	0.42
10:J:41:LEU:HD11	10:J:50:ILE:HG13	2.02	0.42
11:K:23:PRO:CA	11:K:31:VAL:HG13	2.47	0.42
12:L:38:LEU:HD22	12:L:48:CYS:HA	1.99	0.42
1:A:197:PRO:HG2	1:A:199:LEU:HD21	2.01	0.42
1:A:380:VAL:CG2	1:A:426:LEU:HD13	2.50	0.42
1:A:446:ARG:HD3	1:A:480:ALA:HB2	2.02	0.42
1:A:544:ASP:CG	1:A:545:GLN:N	2.78	0.42
1:A:949:ASP:OD2	1:A:949:ASP:C	2.63	0.42
1:A:1445:ILE:HD11	7:G:68:ALA:HB1	2.02	0.42
2:B:129:PHE:CD2	2:B:166:PHE:HA	2.55	0.42
2:B:168:GLY:HA2	2:B:450:ALA:O	2.19	0.42
2:B:244:LEU:O	2:B:245:GLU:C	2.62	0.42
2:B:309:GLN:CA	2:B:309:GLN:NE2	2.82	0.42
2:B:821:GLN:O	2:B:1091:TYR:HA	2.20	0.42
3:C:66:ARG:O	3:C:68:GLY:N	2.52	0.42
3:C:152:GLU:HG2	3:C:153:LEU:N	2.34	0.42
3:C:260:LEU:O	3:C:260:LEU:HD12	2.20	0.42
5:E:117:THR:HG22	5:E:120:ALA:H	1.83	0.42
6:F:131:PRO:O	6:F:132:LEU:HD23	2.19	0.42
6:F:138:LEU:C	6:F:140:ASP:H	2.26	0.42
9:I:79:HIS:O	9:I:81:ARG:HD2	2.19	0.42
9:I:86:PHE:CD1	9:I:86:PHE:C	2.98	0.42
10:J:24:LEU:HD13	10:J:38:ARG:CG	2.49	0.42
11:K:8:GLU:O	11:K:37:LYS:HD2	2.19	0.42
11:K:19:LEU:HD22	11:K:33:ILE:CG2	2.50	0.42
1:A:18:GLN:HB3	2:B:1215:ARG:HG3	2.01	0.42
1:A:40:THR:CG2	1:A:41:MET:HG3	2.33	0.42
1:A:64:ASN:O	1:A:65:LEU:C	2.63	0.42
1:A:120:GLU:HB2	1:A:123:ARG:NH2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:565:ILE:HG21	1:A:567:LYS:HE2	2.01	0.42
1:A:833:GLU:O	1:A:837:ILE:HG13	2.20	0.42
1:A:1095:THR:HG21	1:A:1112:LYS:HD2	2.01	0.42
1:A:1155:ASP:O	1:A:1190:PRO:O	2.38	0.42
1:A:1449:SER:C	1:A:1451:VAL:H	2.28	0.42
1:A:1450:LEU:O	1:A:1450:LEU:CG	2.67	0.42
2:B:26:THR:O	2:B:27:ALA:C	2.62	0.42
2:B:205:ILE:C	2:B:207:GLY:H	2.28	0.42
2:B:616:ILE:CG2	2:B:700:SER:OG	2.68	0.42
2:B:847:ASP:C	2:B:849:GLY:N	2.78	0.42
2:B:1197:PRO:C	2:B:1199:ALA:N	2.75	0.42
4:D:130:LEU:O	4:D:134:THR:HB	2.19	0.42
5:E:29:PHE:O	5:E:30:ILE:HG13	2.19	0.42
8:H:80:ARG:HB3	8:H:83:GLN:OE1	2.20	0.42
9:I:82:GLU:HB3	9:I:104:LEU:CG	2.50	0.42
11:K:53:ASP:OD2	11:K:81:TYR:OH	2.32	0.42
1:A:92:HIS:CG	1:A:304:MET:HE1	2.55	0.42
1:A:356:ASP:OD1	1:A:358:ASN:HB2	2.19	0.42
1:A:533:LYS:HZ1	1:A:745:GLN:HE22	1.65	0.42
1:A:608:ILE:HB	1:A:613:ILE:HD11	2.01	0.42
1:A:1146:VAL:HG11	1:A:1207:LEU:HD12	2.02	0.42
2:B:102:VAL:O	2:B:109:THR:HA	2.20	0.42
2:B:303:TYR:OH	2:B:586:TRP:HH2	2.03	0.42
2:B:309:GLN:OE1	9:I:52:ILE:CD1	2.66	0.42
2:B:466:TRP:N	2:B:475:SER:OG	2.53	0.42
2:B:706:GLN:NE2	2:B:730:ARG:HD2	2.35	0.42
2:B:860:MET:HB2	2:B:965:LYS:HG2	2.01	0.42
2:B:1098:MET:O	2:B:1099:VAL:C	2.61	0.42
4:D:29:LEU:O	4:D:30:GLY:O	2.37	0.42
4:D:122:GLU:O	4:D:125:SER:HB3	2.19	0.42
5:E:48:ASP:CG	5:E:49:SER:N	2.72	0.42
11:K:56:VAL:HG22	11:K:77:THR:HG22	2.01	0.42
12:L:33:GLU:OE1	12:L:53:HIS:CB	2.68	0.42
1:A:115:LEU:CD1	1:A:142:CYS:HB3	2.50	0.42
1:A:207:ILE:HG22	1:A:211:PHE:CD2	2.54	0.42
1:A:207:ILE:CG2	1:A:211:PHE:CE2	3.02	0.42
1:A:423:ASP:HB3	1:A:424:ILE:H	1.55	0.42
1:A:666:ILE:O	1:A:667:GLY:C	2.60	0.42
1:A:875:ALA:HA	1:A:878:ILE:HD12	2.02	0.42
1:A:929:LEU:CD1	1:A:929:LEU:O	2.67	0.42
1:A:966:ASN:O	1:A:967:ALA:C	2.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1029:ARG:NH1	1:A:1029:ARG:CG	2.83	0.42
1:A:1277:GLU:C	1:A:1279:ILE:N	2.78	0.42
2:B:47:GLN:HB3	2:B:173:MET:CE	2.50	0.42
2:B:120:ARG:CG	2:B:955:THR:HG21	2.46	0.42
2:B:283:VAL:HG21	2:B:317:CYS:O	2.20	0.42
2:B:613:VAL:HG13	2:B:627:PHE:C	2.42	0.42
2:B:640:VAL:HG23	2:B:740:HIS:HA	2.00	0.42
2:B:711:GLU:HB2	2:B:712:PRO:CD	2.50	0.42
3:C:29:MET:HE2	11:K:98:LEU:CG	2.50	0.42
3:C:213:PRO:O	3:C:214:ASN:CB	2.68	0.42
3:C:258:ILE:HG12	11:K:42:LEU:HD21	2.02	0.42
4:D:149:THR:HG23	4:D:150:ASN:N	2.35	0.42
5:E:197:LYS:HG3	5:E:211:TYR:CE2	2.54	0.42
6:F:82:THR:CG2	6:F:84:TYR:H	2.26	0.42
8:H:91:ASP:C	8:H:93:TYR:N	2.78	0.42
8:H:138:GLU:C	8:H:138:GLU:OE1	2.63	0.42
10:J:36:LEU:C	10:J:38:ARG:N	2.75	0.42
14:T:15:DG:C2'	14:T:16:DT:C7	2.97	0.42
1:A:53:LEU:HD23	1:A:54:ASN:CB	2.49	0.42
1:A:332:LYS:O	1:A:333:GLU:CB	2.60	0.42
1:A:356:ASP:C	1:A:358:ASN:H	2.27	0.42
1:A:504:LEU:HD21	6:F:88:TYR:CD2	2.55	0.42
1:A:784:LEU:C	1:A:786:HIS:H	2.27	0.42
1:A:1112:LYS:O	1:A:1114:PRO:CD	2.68	0.42
1:A:1152:ILE:HG23	1:A:1260:LEU:HD22	2.02	0.42
1:A:1299:VAL:CG1	1:A:1300:LYS:N	2.83	0.42
2:B:235:SER:HB3	2:B:258:LEU:HG	2.01	0.42
2:B:294:ASP:C	2:B:296:GLU:N	2.76	0.42
2:B:705:MET:HA	2:B:705:MET:CE	2.38	0.42
2:B:840:ILE:HG21	2:B:994:TYR:CD1	2.55	0.42
2:B:845:SER:HB3	2:B:850:LEU:HD23	2.02	0.42
2:B:1001:PHE:CZ	2:B:1073:TYR:HB2	2.55	0.42
2:B:1031:LEU:HD11	2:B:1042:GLY:CA	2.50	0.42
3:C:166:GLU:O	11:K:6:ARG:NH1	2.53	0.42
5:E:85:GLU:C	5:E:87:SER:N	2.78	0.42
5:E:90:VAL:CA	5:E:120:ALA:HB2	2.50	0.42
7:G:122:ASN:HD22	7:G:131:GLN:HE21	1.67	0.42
7:G:138:THR:HG23	7:G:139:ILE:HG22	2.01	0.42
8:H:93:TYR:CD1	8:H:93:TYR:N	2.87	0.42
8:H:117:SER:HB2	8:H:122:LEU:CD2	2.50	0.42
9:I:85:PHE:CE1	9:I:99:LEU:HD13	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:30:LEU:HD23	10:J:31:ASP:N	2.33	0.42
13:N:2:DC:C6	13:N:3:DT:H72	2.54	0.42
1:A:31:SER:OG	1:A:82:GLY:HA2	2.20	0.41
1:A:53:LEU:HD23	1:A:54:ASN:HB3	2.02	0.41
1:A:102:VAL:CG1	1:A:211:PHE:HE1	2.33	0.41
1:A:537:ARG:O	1:A:540:PHE:CE1	2.73	0.41
1:A:556:TRP:CE3	1:A:558:GLY:HA2	2.56	0.41
1:A:857:ARG:NH2	6:F:139:PRO:CG	2.83	0.41
1:A:882:SER:HA	1:A:952:ALA:O	2.20	0.41
1:A:1121:GLU:HB2	1:A:1321:GLY:O	2.20	0.41
1:A:1151:GLU:HB3	1:A:1153:TYR:HE1	1.85	0.41
2:B:405:ARG:HA	2:B:631:GLY:O	2.19	0.41
2:B:455:SER:O	2:B:456:GLY:C	2.63	0.41
2:B:487:THR:HG22	2:B:488:TYR:N	2.35	0.41
2:B:498:THR:HG23	2:B:537:LYS:H	1.85	0.41
2:B:648:HIS:CG	2:B:649:LYS:N	2.86	0.41
2:B:705:MET:HE3	2:B:742:GLU:HB2	2.01	0.41
2:B:855:PHE:HZ	2:B:857:ARG:NH1	2.18	0.41
2:B:1017:ILE:H	2:B:1018:PRO:HD3	1.83	0.41
3:C:100:THR:HG22	3:C:101:LEU:N	2.35	0.41
3:C:262:LEU:HD23	3:C:262:LEU:HA	1.91	0.41
4:D:65:GLU:O	4:D:68:ARG:HB3	2.20	0.41
6:F:120:ILE:O	6:F:124:GLU:HG3	2.19	0.41
7:G:21:ARG:CD	7:G:24:GLN:HB2	2.46	0.41
8:H:6:PHE:CD2	8:H:6:PHE:C	2.98	0.41
11:K:65:HIS:CD2	11:K:65:HIS:C	2.98	0.41
12:L:30:ILE:HD11	12:L:59:ALA:HB2	2.02	0.41
1:A:49:LYS:NZ	1:A:61:ILE:HG13	2.22	0.41
1:A:80:HIS:H	1:A:243:PRO:HB3	1.86	0.41
1:A:135:PHE:HD1	1:A:222:LEU:HD22	1.86	0.41
1:A:279:LEU:HD12	1:A:289:ILE:HA	2.01	0.41
1:A:1198:ASP:OD2	1:A:1200:ALA:HB3	2.19	0.41
2:B:296:GLU:O	2:B:299:GLU:HB2	2.20	0.41
2:B:308:TRP:CZ3	9:I:45:ARG:HG2	2.54	0.41
2:B:579:ARG:HA	2:B:589:VAL:HG13	2.00	0.41
2:B:637:LEU:HD12	2:B:693:ILE:CD1	2.50	0.41
2:B:642:ASP:C	2:B:644:GLU:N	2.78	0.41
2:B:835:GLN:O	2:B:836:GLU:HB2	2.21	0.41
2:B:874:PHE:HB3	2:B:896:ASP:O	2.20	0.41
2:B:973:ILE:HG23	2:B:974:PRO:CD	2.49	0.41
2:B:980:PHE:CE2	2:B:1094:ARG:HG3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:984:HIS:O	2:B:985:GLY:C	2.63	0.41
2:B:1007:VAL:CG2	2:B:1008:PRO:CD	2.98	0.41
2:B:1180:PHE:CB	2:B:1191:ILE:HD12	2.40	0.41
3:C:131:HIS:HA	3:C:132:PRO:HD3	1.90	0.41
4:D:139:LYS:HD3	4:D:143:ASN:ND2	2.28	0.41
4:D:220:LEU:HD23	4:D:221:TYR:C	2.45	0.41
5:E:37:LEU:CD1	5:E:41:ASP:HB2	2.50	0.41
7:G:29:LYS:HD2	7:G:32:GLU:OE1	2.20	0.41
8:H:12:VAL:CG1	8:H:15:VAL:HG22	2.50	0.41
8:H:135:LEU:CB	8:H:137:GLN:HG2	2.49	0.41
9:I:75:CYS:HB2	9:I:76:PRO:HD2	2.02	0.41
11:K:49:GLU:CG	11:K:94:ILE:HG13	2.43	0.41
11:K:106:GLU:O	11:K:107:THR:C	2.63	0.41
12:L:47:ARG:NH2	12:L:54:ARG:HE	2.18	0.41
1:A:75:ASN:O	1:A:76:GLU:HB2	2.20	0.41
1:A:154:SER:HB3	1:A:162:VAL:CG2	2.45	0.41
1:A:1002:GLY:HA3	1:A:1007:ILE:HG21	2.02	0.41
1:A:1017:LEU:HD23	5:E:204:THR:O	2.20	0.41
1:A:1106:ASN:O	1:A:1107:VAL:HB	2.21	0.41
1:A:1127:ASP:CG	1:A:1130:GLN:CB	2.91	0.41
2:B:29:ASP:O	2:B:30:SER:C	2.63	0.41
2:B:113:TYR:CE2	2:B:192:LEU:HD22	2.56	0.41
2:B:244:LEU:HG	2:B:250:PHE:H	1.84	0.41
2:B:316:PRO:HG2	2:B:317:CYS:H	1.85	0.41
2:B:387:LEU:O	2:B:392:ARG:HB2	2.20	0.41
2:B:593:PRO:HG2	2:B:617:ARG:HH21	1.80	0.41
2:B:657:HIS:ND1	2:B:679:TYR:OH	2.46	0.41
2:B:843:GLN:HB3	2:B:995:ARG:HG3	2.02	0.41
2:B:1102:LYS:C	2:B:1122:ARG:NH1	2.78	0.41
3:C:112:ASN:N	3:C:112:ASN:ND2	2.68	0.41
3:C:131:HIS:O	3:C:133:ILE:N	2.53	0.41
3:C:142:VAL:O	3:C:142:VAL:HG12	2.19	0.41
3:C:233:GLU:OE1	10:J:12:LYS:HG3	2.21	0.41
4:D:14:ARG:NH1	4:D:16:LYS:NZ	2.68	0.41
5:E:17:ARG:O	5:E:18:THR:C	2.62	0.41
5:E:37:LEU:HG	5:E:37:LEU:O	2.20	0.41
5:E:182:ASP:O	5:E:185:ALA:HB3	2.20	0.41
6:F:147:SER:C	6:F:149:GLU:N	2.72	0.41
7:G:26:LEU:O	7:G:29:LYS:N	2.53	0.41
9:I:75:CYS:SG	9:I:79:HIS:N	2.93	0.41
11:K:65:HIS:CD2	11:K:67:PHE:HB2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:337:ARG:HE	1:A:839:ARG:HH22	1.55	0.41
1:A:399:HIS:CG	1:A:400:PRO:N	2.86	0.41
1:A:446:ARG:HG2	1:A:446:ARG:NH1	2.36	0.41
1:A:698:GLN:NE2	9:I:99:LEU:HD21	2.35	0.41
1:A:752:LYS:HG3	2:B:1015:HIS:O	2.20	0.41
1:A:868:TYR:HD2	1:A:1058:VAL:HG21	1.80	0.41
1:A:898:ARG:HD3	1:A:933:TYR:CE1	2.56	0.41
1:A:909:ASP:C	1:A:911:SER:H	2.27	0.41
2:B:179:CYS:O	2:B:180:TYR:C	2.64	0.41
2:B:410:GLY:O	2:B:413:LEU:HB2	2.21	0.41
2:B:622:LYS:HE2	9:I:59:VAL:HG21	2.01	0.41
2:B:792:MET:HA	2:B:856:PHE:O	2.20	0.41
2:B:879:ARG:N	2:B:879:ARG:CZ	2.83	0.41
2:B:889:THR:HG23	2:B:891:ASP:H	1.85	0.41
2:B:936:ASP:OD1	2:B:936:ASP:C	2.63	0.41
2:B:1113:VAL:N	15:P:1:C:H5'	2.35	0.41
3:C:31:ASN:O	3:C:32:SER:C	2.63	0.41
3:C:110:THR:HG22	3:C:112:ASN:ND2	2.36	0.41
5:E:65:THR:O	5:E:66:GLU:C	2.63	0.41
5:E:162:ARG:HH11	5:E:162:ARG:CG	2.33	0.41
7:G:56:ILE:O	7:G:57:GLN:HB2	2.19	0.41
8:H:95:TYR:C	8:H:95:TYR:HD2	2.28	0.41
9:I:7:CYS:C	9:I:8:ARG:O	2.61	0.41
10:J:45:CYS:O	10:J:48:ARG:HG3	2.20	0.41
10:J:64:ASN:HD22	10:J:65:PRO:HD3	1.86	0.41
11:K:91:CYS:O	11:K:94:ILE:HB	2.20	0.41
1:A:319:GLY:CA	2:B:471:LYS:HA	2.50	0.41
1:A:335:ARG:NH1	2:B:1206:GLU:OE2	2.46	0.41
1:A:719:VAL:O	1:A:720:ARG:C	2.63	0.41
1:A:758:ILE:HA	1:A:761:MET:HE2	2.02	0.41
1:A:877:HIS:O	1:A:878:ILE:CG1	2.68	0.41
1:A:947:PHE:CE1	1:A:954:TRP:CD1	3.09	0.41
1:A:1134:ILE:HG13	1:A:1134:ILE:H	1.48	0.41
1:A:1187:GLN:HA	1:A:1244:ARG:HE	1.85	0.41
1:A:1263:ILE:O	1:A:1267:MET:HG3	2.19	0.41
2:B:68:THR:HG22	2:B:91:SER:HB3	2.02	0.41
2:B:254:LEU:HD22	2:B:361:LEU:HD12	2.03	0.41
2:B:292:ILE:HD13	2:B:326:ASP:HA	2.03	0.41
2:B:314:LEU:O	2:B:318:VAL:HG23	2.21	0.41
2:B:405:ARG:CD	2:B:631:GLY:O	2.68	0.41
2:B:731:VAL:CG1	2:B:732:SER:N	2.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:809:MET:O	2:B:811:TYR:N	2.53	0.41
2:B:916:THR:HG22	2:B:935:ARG:HD2	2.03	0.41
2:B:1084:GLN:HE21	2:B:1084:GLN:H	1.67	0.41
3:C:120:ILE:HD11	3:C:130:GLY:O	2.21	0.41
3:C:200:GLU:O	3:C:202:PRO:HD3	2.20	0.41
3:C:249:ASP:O	3:C:252:GLN:CB	2.69	0.41
5:E:52:ARG:HA	5:E:53:PRO:HD2	1.85	0.41
5:E:143:ASN:O	5:E:146:HIS:HB2	2.21	0.41
6:F:116:ASP:O	6:F:119:ARG:HB2	2.20	0.41
7:G:14:HIS:HD2	7:G:16:SER:N	2.14	0.41
7:G:17:PHE:C	7:G:19:GLY:N	2.76	0.41
7:G:96:GLN:HA	7:G:121:PHE:CE2	2.54	0.41
8:H:19:ARG:O	8:H:20:TYR:CD2	2.74	0.41
8:H:51:ALA:O	8:H:52:GLN:HB2	2.20	0.41
10:J:30:LEU:HD11	10:J:38:ARG:NH1	2.35	0.41
15:P:2:A:H8	15:P:2:A:O5'	2.03	0.41
1:A:27:VAL:O	1:A:28:ARG:C	2.61	0.41
1:A:213:HIS:O	1:A:214:ILE:C	2.61	0.41
1:A:346:ASP:HB3	2:B:1108:ARG:H	1.84	0.41
1:A:818:MET:HA	2:B:514:LEU:HB3	2.01	0.41
1:A:1104:ILE:C	1:A:1106:ASN:N	2.78	0.41
1:A:1187:GLN:HA	1:A:1244:ARG:NE	2.36	0.41
2:B:123:THR:CB	2:B:458:LYS:HE2	2.50	0.41
2:B:449:ASN:OD1	2:B:451:LYS:HB3	2.20	0.41
2:B:640:VAL:HB	2:B:738:PHE:O	2.20	0.41
2:B:653:VAL:N	2:B:689:LEU:HD22	2.36	0.41
2:B:703:ILE:HG22	2:B:704:ALA:N	2.35	0.41
2:B:785:TYR:CD1	2:B:785:TYR:C	2.98	0.41
2:B:816:GLU:O	2:B:817:LEU:HD23	2.20	0.41
2:B:1064:TYR:O	2:B:1065:GLN:O	2.39	0.41
2:B:1181:GLU:HB2	2:B:1188:LYS:HG2	2.02	0.41
3:C:10:ILE:HG13	11:K:108:GLU:HB3	2.02	0.41
3:C:33:LEU:HD12	3:C:33:LEU:C	2.43	0.41
3:C:101:LEU:HD12	3:C:101:LEU:HA	1.87	0.41
4:D:29:LEU:HD22	4:D:29:LEU:H	1.84	0.41
4:D:60:LYS:O	4:D:64:VAL:HG23	2.19	0.41
5:E:58:MET:O	5:E:59:SER:O	2.38	0.41
7:G:96:GLN:HA	7:G:121:PHE:CD2	2.55	0.41
8:H:138:GLU:O	8:H:139:ASN:O	2.38	0.41
12:L:55:ILE:O	12:L:56:LEU:CB	2.69	0.41
1:A:38:PRO:HG2	1:A:39:GLU:OE2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:67:CYS:O	1:A:68:GLN:CG	2.68	0.41
1:A:141:LEU:HD23	1:A:141:LEU:HA	1.90	0.41
1:A:178:GLY:O	1:A:179:LEU:HD23	2.21	0.41
1:A:290:GLU:C	1:A:292:ALA:N	2.77	0.41
1:A:382:PRO:CD	1:A:428:TYR:CE2	3.04	0.41
1:A:413:ILE:HG21	1:A:424:ILE:HD11	2.01	0.41
1:A:540:PHE:HE2	1:A:565:ILE:HD12	1.85	0.41
1:A:577:ILE:O	1:A:580:VAL:HG23	2.20	0.41
1:A:605:MET:HE1	1:A:612:ILE:HG23	2.03	0.41
1:A:896:ARG:HH22	1:A:1030:ARG:NH2	2.16	0.41
1:A:898:ARG:HA	1:A:933:TYR:CD1	2.55	0.41
2:B:114:PRO:O	2:B:115:GLN:C	2.63	0.41
2:B:364:ILE:O	2:B:365:THR:CB	2.69	0.41
2:B:398:ARG:HH11	2:B:398:ARG:HB3	1.85	0.41
2:B:420:LEU:O	2:B:423:LYS:N	2.54	0.41
2:B:485:ARG:HG3	2:B:781:PHE:HD1	1.84	0.41
2:B:571:PRO:O	2:B:574:SER:O	2.38	0.41
2:B:595:ARG:O	2:B:596:LEU:C	2.63	0.41
2:B:604:ARG:CB	2:B:609:ILE:HG13	2.48	0.41
2:B:970:THR:CG2	2:B:971:THR:N	2.84	0.41
2:B:1082:MET:HA	3:C:189:THR:HA	2.03	0.41
3:C:66:ARG:C	3:C:68:GLY:H	2.28	0.41
3:C:80:LEU:HD11	3:C:95:CYS:CA	2.51	0.41
3:C:241:ASP:HB3	11:K:109:TRP:CE2	2.56	0.41
5:E:93:MET:C	5:E:95:THR:N	2.76	0.41
5:E:182:ASP:HB3	5:E:185:ALA:HB2	2.01	0.41
8:H:104:PHE:CD2	8:H:114:VAL:HG12	2.56	0.41
1:A:196:GLU:HG2	1:A:197:PRO:CD	2.48	0.41
1:A:541:ILE:HG22	1:A:546:VAL:CG2	2.50	0.41
1:A:557:ASP:O	1:A:559:VAL:HG23	2.21	0.41
1:A:567:LYS:HE3	8:H:46:LEU:HB3	2.02	0.41
1:A:1356:ILE:HD12	1:A:1368:MET:SD	2.61	0.41
2:B:46:GLN:HB2	2:B:408:LEU:HD21	2.01	0.41
2:B:123:THR:OG1	2:B:458:LYS:HE2	2.20	0.41
2:B:263:GLY:O	2:B:264:SER:C	2.63	0.41
2:B:448:ILE:HG13	2:B:448:ILE:H	1.74	0.41
2:B:492:LEU:HB2	2:B:751:VAL:HG11	2.01	0.41
2:B:500:THR:HA	2:B:501:PRO:HD2	1.76	0.41
2:B:507:LYS:O	2:B:508:LEU:C	2.63	0.41
2:B:882:THR:CB	2:B:934:LYS:O	2.69	0.41
2:B:911:ILE:CG2	2:B:966:VAL:HG11	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:41:ILE:HA	3:C:42:PRO:HD3	1.91	0.41
7:G:126:ASN:HA	7:G:127:PRO:HA	1.98	0.41
11:K:19:LEU:HD21	11:K:35:PHE:CE2	2.56	0.41
14:T:16:DT:H2''	14:T:17:DT:C5'	2.50	0.41
1:A:114:LEU:O	1:A:115:LEU:HG	2.21	0.41
1:A:252:PHE:O	1:A:256:GLN:NE2	2.53	0.41
1:A:332:LYS:H	1:A:337:ARG:HB2	1.84	0.41
1:A:418:SER:C	1:A:420:ARG:N	2.79	0.41
1:A:592:ASP:HB2	1:A:604:GLY:H	1.85	0.41
1:A:608:ILE:C	1:A:610:GLY:N	2.77	0.41
1:A:629:LEU:CD1	1:A:645:LEU:HD21	2.51	0.41
1:A:709:THR:H	1:A:712:GLU:HB2	1.86	0.41
1:A:719:VAL:HG13	1:A:723:ASN:HD21	1.84	0.41
1:A:757:ASN:O	1:A:761:MET:HG3	2.21	0.41
1:A:785:PRO:HG2	1:A:786:HIS:CD2	2.56	0.41
1:A:848:ILE:HD13	1:A:1370:LEU:HD11	2.03	0.41
1:A:860:LEU:C	1:A:862:ASN:H	2.29	0.41
1:A:943:LEU:O	1:A:945:GLU:N	2.54	0.41
1:A:1120:LEU:HD23	1:A:1304:TRP:O	2.20	0.41
1:A:1147:THR:HA	1:A:1197:LEU:HD23	2.01	0.41
1:A:1262:LYS:C	1:A:1264:GLU:H	2.29	0.41
1:A:1325:THR:CG2	1:A:1326:ARG:HG3	2.50	0.41
1:A:1341:ILE:CD1	1:A:1380:GLY:HA2	2.51	0.41
1:A:1365:TYR:O	1:A:1366:ARG:C	2.63	0.41
2:B:47:GLN:HB3	2:B:173:MET:HE1	2.02	0.41
2:B:110:HIS:O	2:B:112:LEU:N	2.54	0.41
2:B:291:ILE:HG12	2:B:300:HIS:CD2	2.56	0.41
2:B:379:GLY:O	2:B:382:ILE:N	2.54	0.41
2:B:504:ARG:C	2:B:506:GLY:H	2.28	0.41
2:B:563:MET:HE1	2:B:580:VAL:HB	2.03	0.41
2:B:594:ALA:HB2	2:B:617:ARG:HH12	1.85	0.41
2:B:911:ILE:HD11	2:B:941:LEU:CD1	2.49	0.41
2:B:961:LEU:HD23	2:B:961:LEU:HA	1.89	0.41
2:B:1072:MET:HE3	2:B:1085:ILE:CB	2.21	0.41
2:B:1103:ILE:O	2:B:1103:ILE:CG2	2.68	0.41
2:B:1132:GLU:O	2:B:1133:MET:C	2.63	0.41
2:B:1137:CYS:O	2:B:1140:ALA:HB3	2.21	0.41
2:B:1138:MET:HE2	2:B:1146:PHE:HD2	1.77	0.41
3:C:148:ARG:CG	3:C:149:LYS:N	2.84	0.41
4:D:12:ARG:HH12	4:D:14:ARG:N	2.19	0.41
4:D:12:ARG:NH1	4:D:14:ARG:N	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:90:VAL:HG23	5:E:120:ALA:HA	2.01	0.41
5:E:93:MET:HG2	5:E:120:ALA:O	2.21	0.41
6:F:97:ARG:HA	6:F:97:ARG:HD2	1.81	0.41
7:G:26:LEU:HD23	7:G:26:LEU:HA	1.87	0.41
7:G:39:THR:O	7:G:43:GLY:HA2	2.21	0.41
7:G:145:VAL:CG1	7:G:146:LYS:N	2.84	0.41
8:H:13:SER:N	8:H:27:GLU:O	2.54	0.41
9:I:13:MET:HG2	9:I:14:LEU:N	2.35	0.41
9:I:118:ARG:NH1	9:I:118:ARG:HB3	2.36	0.41
10:J:21:TYR:CE1	10:J:36:LEU:HD21	2.56	0.41
11:K:67:PHE:N	11:K:67:PHE:HD2	2.18	0.41
11:K:87:LEU:O	11:K:88:LYS:C	2.64	0.41
12:L:27:LEU:O	12:L:28:LYS:HB2	2.20	0.41
12:L:59:ALA:O	12:L:60:ARG:O	2.38	0.41
1:A:4:GLN:O	1:A:5:GLN:O	2.39	0.41
1:A:51:GLY:C	1:A:56:PRO:HB3	2.44	0.41
1:A:83:HIS:O	1:A:84:ILE:HG13	2.21	0.41
1:A:89:PRO:C	1:A:204:THR:HG21	2.46	0.41
1:A:204:THR:O	1:A:205:GLU:C	2.63	0.41
1:A:384:ASN:OD1	1:A:388:LEU:HD12	2.21	0.41
1:A:441:PRO:O	1:A:441:PRO:HG2	2.21	0.41
1:A:691:LEU:O	1:A:694:THR:HB	2.20	0.41
1:A:894:GLU:O	1:A:898:ARG:HB2	2.21	0.41
1:A:1111:MET:HE3	1:A:1111:MET:HB2	1.87	0.41
1:A:1144:LYS:HZ2	1:A:1269:GLU:CD	2.28	0.41
1:A:1325:THR:OG1	5:E:146:HIS:O	2.38	0.41
2:B:170:LEU:O	2:B:171:PRO:C	2.64	0.41
2:B:384:ARG:HE	2:B:384:ARG:HB3	1.58	0.41
2:B:653:VAL:HA	2:B:689:LEU:HD22	2.03	0.41
2:B:769:TYR:HD1	2:B:987:LYS:HZ3	1.69	0.41
2:B:785:TYR:HD1	2:B:786:ASN:N	2.19	0.41
4:D:35:LEU:O	4:D:46:GLU:HA	2.21	0.41
4:D:195:ILE:C	4:D:197:SER:H	2.28	0.41
5:E:29:PHE:N	5:E:65:THR:HG22	2.36	0.41
5:E:63:ASN:HB3	5:E:64:PRO:HD2	2.02	0.41
5:E:161:LYS:O	5:E:162:ARG:C	2.64	0.41
8:H:107:VAL:O	8:H:108:SER:O	2.39	0.41
1:A:25:GLU:O	1:A:26:GLU:C	2.64	0.40
1:A:102:VAL:HB	1:A:211:PHE:CZ	2.56	0.40
1:A:306:ASN:O	1:A:306:ASN:CG	2.64	0.40
1:A:350:ARG:HA	1:A:468:PHE:HE1	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:556:TRP:CZ2	1:A:558:GLY:HA2	2.56	0.40
1:A:658:LEU:CD1	2:B:830:TYR:CD1	3.04	0.40
1:A:666:ILE:HG23	2:B:1026:LEU:HB3	2.03	0.40
1:A:809:THR:N	1:A:812:GLU:HB2	2.35	0.40
1:A:947:PHE:CE1	1:A:954:TRP:CE2	3.10	0.40
2:B:115:GLN:HE21	2:B:119:LEU:CD1	2.35	0.40
2:B:312:GLU:O	2:B:315:LYS:HB2	2.21	0.40
2:B:350:GLN:O	2:B:353:LYS:N	2.54	0.40
2:B:365:THR:CG2	2:B:367:LEU:HB2	2.51	0.40
2:B:500:THR:O	2:B:500:THR:HG22	2.21	0.40
2:B:558:LEU:O	2:B:559:SER:C	2.65	0.40
2:B:622:LYS:CE	9:I:59:VAL:HG22	2.50	0.40
2:B:637:LEU:HA	2:B:637:LEU:HD23	1.83	0.40
2:B:871:THR:O	2:B:917:PRO:HG3	2.21	0.40
2:B:996:ARG:HH12	3:C:174:ALA:CA	2.29	0.40
3:C:116:LYS:O	3:C:118:LEU:N	2.54	0.40
4:D:128:VAL:C	4:D:130:LEU:H	2.29	0.40
5:E:33:GLU:N	5:E:33:GLU:OE1	2.54	0.40
5:E:179:GLN:HA	5:E:179:GLN:OE1	2.20	0.40
11:K:50:LEU:HD13	11:K:75:ILE:HG12	2.03	0.40
1:A:145:LYS:HE3	1:A:145:LYS:CA	2.32	0.40
1:A:524:VAL:CG1	1:A:525:GLN:N	2.80	0.40
1:A:574:GLY:O	1:A:575:LYS:C	2.64	0.40
1:A:666:ILE:HD11	2:B:1067:ARG:O	2.20	0.40
1:A:760:GLN:OE1	2:B:1021:MET:HE1	2.21	0.40
1:A:820:GLY:O	1:A:823:GLY:N	2.54	0.40
1:A:1142:THR:O	1:A:1145:SER:OG	2.32	0.40
1:A:1208:THR:O	1:A:1212:VAL:HG23	2.21	0.40
2:B:52:ASN:O	2:B:53:GLN:C	2.64	0.40
2:B:273:LEU:HB2	2:B:276:ILE:CD1	2.46	0.40
2:B:310:MET:HB2	2:B:310:MET:HE3	1.96	0.40
2:B:521:LEU:HB3	2:B:633:VAL:CG1	2.51	0.40
2:B:549:THR:CG2	2:B:550:ASP:H	2.22	0.40
2:B:610:ASN:HA	2:B:611:PRO:HD3	1.86	0.40
2:B:648:HIS:CD2	2:B:649:LYS:O	2.73	0.40
2:B:654:ARG:NH1	2:B:654:ARG:CG	2.83	0.40
2:B:736:THR:O	2:B:736:THR:HG22	2.21	0.40
2:B:1039:GLY:HA2	10:J:51:LEU:CD2	2.52	0.40
2:B:1096:ARG:CB	2:B:1096:ARG:NH1	2.84	0.40
2:B:1202:LEU:O	2:B:1203:LEU:C	2.64	0.40
3:C:11:ARG:HD3	3:C:21:ILE:CD1	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:66:ARG:NH2	10:J:5:VAL:HG23	2.36	0.40
3:C:82:TYR:O	3:C:85:ASP:N	2.38	0.40
4:D:8:PHE:CE2	7:G:6:ASP:HB2	2.56	0.40
4:D:193:THR:O	4:D:196:PRO:HD3	2.21	0.40
7:G:121:PHE:HB2	7:G:130:TYR:CE2	2.56	0.40
8:H:26:ILE:HG21	8:H:42:ILE:HD12	2.01	0.40
9:I:69:PRO:HG2	9:I:85:PHE:CD2	2.56	0.40
14:T:10:DA:C2	14:T:11:DA:C6	3.09	0.40
1:A:112:LYS:HG2	1:A:113:LEU:N	2.36	0.40
1:A:215:SER:HB3	1:A:218:ASP:OD2	2.22	0.40
1:A:350:ARG:NH1	1:A:488:ASN:OD1	2.44	0.40
1:A:754:SER:O	1:A:755:PHE:C	2.64	0.40
1:A:856:THR:HG21	1:A:1370:LEU:HD21	2.03	0.40
1:A:1057:VAL:HG12	1:A:1058:VAL:N	2.37	0.40
1:A:1098:VAL:N	1:A:1099:PRO:HD2	2.36	0.40
1:A:1259:MET:HE3	1:A:1263:ILE:CD1	2.41	0.40
1:A:1368:MET:O	1:A:1369:ALA:C	2.64	0.40
1:A:1424:VAL:HG13	1:A:1436:ILE:HD12	2.03	0.40
2:B:216:GLU:HA	2:B:406:LEU:HD23	2.04	0.40
2:B:294:ASP:N	9:I:12:ASN:HD22	2.18	0.40
3:C:82:TYR:C	3:C:84:ARG:N	2.79	0.40
3:C:133:ILE:HD12	3:C:237:SER:CA	2.51	0.40
3:C:163:ILE:O	3:C:170:TRP:HB2	2.22	0.40
3:C:168:ALA:O	3:C:170:TRP:N	2.54	0.40
3:C:238:ILE:HG22	3:C:243:VAL:HG22	2.03	0.40
6:F:152:ILE:CG2	6:F:153:VAL:N	2.83	0.40
8:H:130:ARG:HH11	8:H:130:ARG:H	1.70	0.40
9:I:20:LYS:O	9:I:21:GLU:C	2.64	0.40
10:J:13:VAL:O	10:J:14:VAL:HG23	2.22	0.40
13:N:3:DT:H2"	13:N:4:DA:C8	2.57	0.40
1:A:68:GLN:O	1:A:70:CYS:N	2.52	0.40
1:A:77:CYS:C	1:A:78:PRO:O	2.61	0.40
1:A:278:THR:O	1:A:282:ASN:HB2	2.21	0.40
1:A:407:ARG:HB3	1:A:430:TRP:CE2	2.55	0.40
1:A:445:ASN:OD1	1:A:445:ASN:C	2.61	0.40
1:A:711:ARG:HD2	9:I:95:THR:O	2.22	0.40
1:A:1193:LEU:HB2	1:A:1260:LEU:HD21	2.03	0.40
2:B:205:ILE:O	2:B:206:ASN:C	2.64	0.40
2:B:241:ARG:CB	2:B:253:THR:HG22	2.51	0.40
2:B:326:ASP:OD1	2:B:329:THR:OG1	2.35	0.40
2:B:326:ASP:C	2:B:328:GLU:N	2.77	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:365:THR:O	2:B:365:THR:HG22	2.22	0.40
2:B:798:TYR:CD2	2:B:798:TYR:N	2.89	0.40
2:B:916:THR:HB	2:B:935:ARG:CG	2.52	0.40
2:B:955:THR:HG22	2:B:956:THR:N	2.34	0.40
2:B:1079:LYS:HA	3:C:27:LEU:HD21	2.02	0.40
3:C:34:ARG:HG2	3:C:35:ARG:N	2.36	0.40
3:C:61:GLU:O	3:C:62:PHE:C	2.62	0.40
3:C:168:ALA:O	3:C:169:LYS:C	2.62	0.40
4:D:24:ALA:C	4:D:26:THR:N	2.80	0.40
5:E:3:GLN:HG3	5:E:4:GLU:N	2.37	0.40
5:E:112:TYR:HB3	5:E:116:ILE:HD11	2.03	0.40
5:E:192:ARG:HH11	5:E:192:ARG:HG3	1.85	0.40
6:F:114:GLU:C	6:F:115:THR:HG23	2.46	0.40
9:I:88:SER:HB3	9:I:95:THR:HG21	2.03	0.40
1:A:241:VAL:HA	1:A:242:PRO:HD2	1.98	0.40
1:A:559:VAL:O	1:A:560:ILE:C	2.65	0.40
1:A:606:LEU:CG	1:A:613:ILE:HD12	2.51	0.40
1:A:665:GLY:O	1:A:666:ILE:C	2.65	0.40
1:A:779:PHE:HD2	1:A:779:PHE:HA	1.77	0.40
1:A:994:GLN:O	1:A:995:GLU:C	2.65	0.40
1:A:1035:TYR:CD2	1:A:1035:TYR:N	2.88	0.40
1:A:1189:SER:OG	1:A:1191:TRP:HB2	2.21	0.40
2:B:175:ARG:HH11	2:B:175:ARG:HG2	1.85	0.40
2:B:189:LEU:CD1	2:B:196:PRO:HA	2.51	0.40
2:B:247:GLY:C	2:B:249:ARG:N	2.79	0.40
2:B:261:ARG:O	2:B:262:GLU:C	2.64	0.40
2:B:505:ASP:O	2:B:506:GLY:O	2.40	0.40
2:B:606:LYS:HD2	2:B:608:ASP:OD2	2.21	0.40
2:B:644:GLU:OE2	2:B:646:LEU:HB2	2.22	0.40
2:B:875:GLU:O	2:B:877:PRO:CD	2.69	0.40
3:C:91:HIS:CD2	3:C:91:HIS:O	2.75	0.40
3:C:235:VAL:HG13	10:J:13:VAL:HG13	2.04	0.40
3:C:238:ILE:CG2	3:C:243:VAL:HG22	2.51	0.40
4:D:146:GLN:O	4:D:147:TYR:C	2.63	0.40
4:D:216:ASN:O	4:D:218:GLU:N	2.55	0.40
6:F:90:ARG:HG3	6:F:91:ALA:H	1.81	0.40
7:G:9:LEU:HD22	7:G:34:VAL:HG23	2.04	0.40
7:G:22:MET:O	7:G:23:LYS:C	2.65	0.40
7:G:48:VAL:HG13	7:G:74:TYR:CD1	2.56	0.40
8:H:61:SER:HB3	8:H:139:ASN:CG	2.47	0.40
8:H:83:GLN:HE22	11:K:57:LEU:HD21	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:99:GLY:HA3	8:H:118:PHE:CD2	2.56	0.40
11:K:113:THR:O	11:K:114:LEU:CB	2.70	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1407/1733 (81%)	977 (69%)	291 (21%)	139 (10%)	0	5
2	B	1097/1224 (90%)	736 (67%)	235 (21%)	126 (12%)	0	3
3	C	264/347 (76%)	182 (69%)	50 (19%)	32 (12%)	0	3
4	D	174/221 (79%)	116 (67%)	41 (24%)	17 (10%)	0	5
5	E	212/215 (99%)	141 (66%)	51 (24%)	20 (9%)	0	5
6	F	85/155 (55%)	66 (78%)	15 (18%)	4 (5%)	2	15
7	G	169/171 (99%)	138 (82%)	23 (14%)	8 (5%)	2	15
8	H	131/146 (90%)	84 (64%)	21 (16%)	26 (20%)	0	1
9	I	117/122 (96%)	80 (68%)	26 (22%)	11 (9%)	0	5
10	J	63/70 (90%)	39 (62%)	12 (19%)	12 (19%)	0	1
11	K	112/120 (93%)	82 (73%)	25 (22%)	5 (4%)	2	15
12	L	44/70 (63%)	25 (57%)	7 (16%)	12 (27%)	0	0
All	All	3875/4594 (84%)	2666 (69%)	797 (21%)	412 (11%)	0	4

All (412) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	GLN
1	A	5	GLN

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Mol	Chain	Res	Type
1	A	54	ASN
1	A	58	LEU
1	A	62	ASP
1	A	63	ARG
1	A	67	CYS
1	A	70	CYS
1	A	74	MET
1	A	76	GLU
1	A	130	ASP
1	A	154	SER
1	A	255	SER
1	A	257	ARG
1	A	286	HIS
1	A	311	GLN
1	A	312	PRO
1	A	318	SER
1	A	322	VAL
1	A	332	LYS
1	A	399	HIS
1	A	410	GLY
1	A	424	ILE
1	A	466	SER
1	A	526	ASP
1	A	543	LEU
1	A	556	TRP
1	A	567	LYS
1	A	666	ILE
1	A	780	VAL
1	A	821	ARG
1	A	891	ALA
1	A	963	ILE
1	A	986	ILE
1	A	1002	GLY
1	A	1120	LEU
1	A	1122	PRO
1	A	1124	HIS
1	A	1223	ASP
1	A	1233	ASP
1	A	1242	VAL
1	A	1255	GLU
1	A	1270	ASN
1	A	1281	ARG

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Mol	Chain	Res	Type
1	A	1309	ASP
1	A	1405	THR
1	A	1438	THR
2	B	21	GLU
2	B	27	ALA
2	B	58	THR
2	B	67	SER
2	B	68	THR
2	B	108	VAL
2	B	206	ASN
2	B	259	TYR
2	B	282	ILE
2	B	291	ILE
2	B	294	ASP
2	B	367	LEU
2	B	369	GLY
2	B	391	ASP
2	B	435	THR
2	B	449	ASN
2	B	467	GLY
2	B	501	PRO
2	B	502	ILE
2	B	508	LEU
2	B	509	ALA
2	B	629	ASP
2	B	643	ASP
2	B	708	GLU
2	B	709	ASP
2	B	728	ARG
2	B	731	VAL
2	B	735	ALA
2	B	749	LEU
2	B	792	MET
2	B	810	GLU
2	B	879	ARG
2	B	906	SER
2	B	907	GLY
2	B	958	GLN
2	B	1046	PRO
2	B	1069	PHE
2	B	1103	ILE
2	B	1176	ASN

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Mol	Chain	Res	Type
2	B	1181	GLU
2	B	1222	ARG
2	B	1223	ASP
3	C	60	ASP
3	C	141	GLY
3	C	142	VAL
3	C	149	LYS
3	C	161	LYS
3	C	172	PRO
3	C	176	ILE
3	C	209	TYR
3	C	215	GLU
3	C	216	GLY
3	C	237	SER
4	D	5	THR
4	D	8	PHE
4	D	17	LYS
4	D	19	GLU
4	D	52	LEU
4	D	119	ARG
4	D	157	GLN
4	D	198	LEU
4	D	218	GLU
5	E	36	GLU
5	E	45	LYS
5	E	74	ASP
5	E	115	ASN
5	E	129	PRO
6	F	128	LYS
7	G	139	ILE
8	H	21	ASN
8	H	47	PHE
8	H	82	PRO
8	H	95	TYR
8	H	108	SER
8	H	128	ASN
8	H	140	ALA
10	J	2	ILE
10	J	6	ARG
10	J	42	LYS
10	J	64	ASN
12	L	50	ASP

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Mol	Chain	Res	Type
12	L	53	HIS
12	L	54	ARG
12	L	55	ILE
12	L	59	ALA
12	L	60	ARG
1	A	41	MET
1	A	43	GLU
1	A	48	ALA
1	A	57	ARG
1	A	73	GLY
1	A	93	VAL
1	A	96	ILE
1	A	128	ILE
1	A	167	CYS
1	A	169	ASN
1	A	219	PHE
1	A	250	ILE
1	A	400	PRO
1	A	423	ASP
1	A	439	ASN
1	A	465	TYR
1	A	517	ASN
1	A	597	LEU
1	A	604	GLY
1	A	619	LYS
1	A	683	ILE
1	A	731	ARG
1	A	753	GLY
1	A	755	PHE
1	A	795	GLU
1	A	830	LYS
1	A	846	GLU
1	A	875	ALA
1	A	885	THR
1	A	926	GLN
1	A	1064	VAL
1	A	1169	ILE
1	A	1206	ASP
1	A	1221	LYS
1	A	1254	ALA
1	A	1314	SER
1	A	1316	VAL

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Mol	Chain	Res	Type
1	A	1377	THR
1	A	1378	GLN
2	B	24	PRO
2	B	43	LEU
2	B	45	SER
2	B	65	GLU
2	B	186	GLU
2	B	221	ASN
2	B	245	GLU
2	B	257	LYS
2	B	258	LEU
2	B	260	GLY
2	B	295	GLY
2	B	333	PHE
2	B	365	THR
2	B	409	ALA
2	B	466	TRP
2	B	506	GLY
2	B	507	LYS
2	B	566	LEU
2	B	591	ARG
2	B	642	ASP
2	B	655	LYS
2	B	729	ILE
2	B	734	HIS
2	B	746	SER
2	B	751	VAL
2	B	864	LYS
2	B	881	ASN
2	B	884	ARG
2	B	1003	ALA
2	B	1065	GLN
2	B	1075	GLY
2	B	1108	ARG
2	B	1171	VAL
2	B	1175	LEU
3	C	11	ARG
3	C	90	ASP
3	C	110	THR
3	C	125	MET
3	C	126	GLY
3	C	184	ASN

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Mol	Chain	Res	Type
3	C	213	PRO
3	C	231	ASN
4	D	30	GLY
4	D	192	LYS
5	E	59	SER
5	E	76	GLY
5	E	130	ALA
5	E	158	SER
5	E	167	ARG
7	G	156	SER
8	H	2	SER
8	H	12	VAL
8	H	17	PRO
8	H	32	THR
8	H	59	ILE
8	H	62	SER
8	H	78	SER
8	H	89	LEU
8	H	90	ALA
8	H	139	ASN
9	I	9	ASP
9	I	11	ASN
9	I	57	GLY
9	I	106	CYS
10	J	17	LYS
10	J	24	LEU
10	J	28	ASP
10	J	29	GLU
12	L	28	LYS
1	A	51	GLY
1	A	61	ILE
1	A	86	LEU
1	A	313	GLN
1	A	331	GLY
1	A	479	ASN
1	A	527	THR
1	A	583	PRO
1	A	591	PHE
1	A	852	TYR
1	A	910	PRO
1	A	995	GLU
1	A	1139	GLU

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Mol	Chain	Res	Type
1	A	1244	ARG
1	A	1365	TYR
2	B	114	PRO
2	B	277	LYS
2	B	511	PRO
2	B	541	LEU
2	B	575	PRO
2	B	619	ILE
2	B	641	GLU
2	B	711	GLU
2	B	738	PHE
2	B	850	LEU
2	B	894	ASP
2	B	1017	ILE
2	B	1035	ALA
2	B	1082	MET
2	B	1097	HIS
2	B	1155	SER
2	B	1157	ALA
2	B	1214	PRO
3	C	117	ASP
3	C	132	PRO
4	D	21	GLU
4	D	129	LEU
4	D	199	ASN
4	D	219	THR
5	E	51	GLY
5	E	65	THR
5	E	73	PRO
5	E	104	ASN
6	F	78	GLN
7	G	2	PHE
8	H	77	ARG
8	H	81	PRO
8	H	134	ASN
9	I	8	ARG
9	I	16	PRO
9	I	56	ALA
9	I	78	CYS
10	J	13	VAL
10	J	14	VAL
11	K	53	ASP

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Mol	Chain	Res	Type
12	L	35	SER
12	L	37	LYS
12	L	39	SER
1	A	42	ASP
1	A	126	LEU
1	A	131	SER
1	A	226	GLU
1	A	276	LEU
1	A	592	ASP
1	A	722	LEU
1	A	789	LYS
1	A	1231	ASP
1	A	1308	THR
1	A	1403	GLU
2	B	125	SER
2	B	249	ARG
2	B	347	LYS
2	B	418	LYS
2	B	419	THR
2	B	436	VAL
2	B	448	ILE
2	B	474	SER
2	B	483	LEU
2	B	594	ALA
2	B	744	HIS
2	B	1041	GLU
2	B	1099	VAL
2	B	1188	LYS
3	C	17	ASN
3	C	56	THR
3	C	148	ARG
3	C	169	LYS
3	C	214	ASN
4	D	147	TYR
4	D	169	SER
5	E	48	ASP
5	E	64	PRO
5	E	83	CYS
6	F	139	PRO
6	F	149	GLU
7	G	20	PRO
7	G	154	VAL

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Mol	Chain	Res	Type
8	H	8	ASP
8	H	83	GLN
8	H	107	VAL
11	K	6	ARG
11	K	90	ALA
12	L	56	LEU
1	A	35	ILE
1	A	253	ASN
1	A	525	GLN
1	A	536	LEU
1	A	693	VAL
1	A	944	ARG
1	A	958	VAL
1	A	975	HIS
1	A	1016	THR
2	B	28	GLU
2	B	111	ALA
2	B	126	SER
2	B	309	GLN
2	B	323	VAL
2	B	468	GLU
2	B	543	SER
2	B	636	PRO
2	B	707	PRO
2	B	764	SER
2	B	793	ALA
2	B	951	GLN
2	B	1156	ASP
3	C	10	ILE
3	C	208	GLU
3	C	243	VAL
5	E	95	THR
5	E	106	GLN
7	G	63	PRO
7	G	124	GLY
8	H	44	VAL
8	H	63	LEU
9	I	47	GLU
10	J	33	GLY
11	K	12	LEU
11	K	14	GLU
1	A	77	CYS

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Mol	Chain	Res	Type
1	A	138	ILE
1	A	141	LEU
1	A	730	GLY
1	A	763	ALA
1	A	1158	PRO
1	A	1369	ALA
2	B	421	PHE
2	B	892	LYS
3	C	129	ILE
5	E	92	THR
8	H	92	ASP
12	L	45	ALA
1	A	554	PRO
1	A	987	VAL
2	B	100	PRO
3	C	240	VAL
9	I	59	VAL
10	J	57	ILE
1	A	599	SER
1	A	647	GLY
3	C	182	PRO
7	G	92	VAL
9	I	62	ILE
1	A	244	PRO
1	A	718	VAL
1	A	1114	PRO
2	B	1006	ILE
1	A	600	PRO
1	A	1212	VAL
1	A	1335	ILE
2	B	1034	VAL
1	A	1049	ILE

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	1240/1520 (82%)	1096 (88%)	144 (12%)	5	23
2	B	965/1061 (91%)	826 (86%)	139 (14%)	3	16
3	C	234/299 (78%)	202 (86%)	32 (14%)	3	18
4	D	160/200 (80%)	138 (86%)	22 (14%)	3	18
5	E	196/197 (100%)	174 (89%)	22 (11%)	6	24
6	F	77/137 (56%)	68 (88%)	9 (12%)	5	23
7	G	152/152 (100%)	133 (88%)	19 (12%)	4	20
8	H	118/128 (92%)	98 (83%)	20 (17%)	2	12
9	I	113/116 (97%)	97 (86%)	16 (14%)	3	17
10	J	60/65 (92%)	55 (92%)	5 (8%)	10	33
11	K	99/102 (97%)	90 (91%)	9 (9%)	9	31
12	L	40/57 (70%)	36 (90%)	4 (10%)	7	28
All	All	3454/4034 (86%)	3013 (87%)	441 (13%)	4	20

All (441) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LEU
1	A	18	GLN
1	A	32	VAL
1	A	34	LYS
1	A	39	GLU
1	A	41	MET
1	A	57	ARG
1	A	68	GLN
1	A	70	CYS
1	A	84	ILE
1	A	93	VAL
1	A	96	ILE
1	A	121	LEU
1	A	141	LEU
1	A	145	LYS
1	A	160	GLN
1	A	161	LEU
1	A	162	VAL
1	A	173	THR
1	A	182	VAL
1	A	196	GLU
1	A	199	LEU

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Mol	Chain	Res	Type
1	A	200	ARG
1	A	202	LEU
1	A	205	GLU
1	A	208	LEU
1	A	215	SER
1	A	227	VAL
1	A	245	PRO
1	A	252	PHE
1	A	268	ASP
1	A	277	GLU
1	A	290	GLU
1	A	297	GLN
1	A	312	PRO
1	A	317	LYS
1	A	320	ARG
1	A	321	PRO
1	A	322	VAL
1	A	337	ARG
1	A	344	ARG
1	A	345	VAL
1	A	354	SER
1	A	385	ILE
1	A	394	ASN
1	A	396	PRO
1	A	407	ARG
1	A	408	ASP
1	A	412	ARG
1	A	425	GLN
1	A	438	ASP
1	A	442	VAL
1	A	443	LEU
1	A	445	ASN
1	A	449	SER
1	A	451	HIS
1	A	455	MET
1	A	461	LYS
1	A	462	VAL
1	A	475	THR
1	A	476	SER
1	A	479	ASN
1	A	481	ASP
1	A	483	ASP

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Mol	Chain	Res	Type
1	A	486	GLU
1	A	493	GLN
1	A	497	THR
1	A	505	CYS
1	A	512	VAL
1	A	527	THR
1	A	536	LEU
1	A	547	LEU
1	A	565	ILE
1	A	571	LEU
1	A	595	THR
1	A	599	SER
1	A	618	GLU
1	A	666	ILE
1	A	669	THR
1	A	670	ILE
1	A	685	GLU
1	A	691	LEU
1	A	701	LEU
1	A	710	LEU
1	A	740	LEU
1	A	764	CYS
1	A	768	GLN
1	A	774	ARG
1	A	779	PHE
1	A	786	HIS
1	A	805	LEU
1	A	821	ARG
1	A	827	THR
1	A	839	ARG
1	A	858	ASN
1	A	929	LEU
1	A	934	LYS
1	A	941	LYS
1	A	969	GLN
1	A	970	THR
1	A	987	VAL
1	A	1009	ASN
1	A	1029	ARG
1	A	1030	ARG
1	A	1037	LEU
1	A	1048	ASN

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Mol	Chain	Res	Type
1	A	1067	LEU
1	A	1077	THR
1	A	1110	ASN
1	A	1116	LEU
1	A	1122	PRO
1	A	1124	HIS
1	A	1129	GLU
1	A	1134	ILE
1	A	1146	VAL
1	A	1163	ILE
1	A	1170	ILE
1	A	1171	GLN
1	A	1187	GLN
1	A	1193	LEU
1	A	1195	LEU
1	A	1217	LYS
1	A	1230	GLU
1	A	1232	ASN
1	A	1255	GLU
1	A	1260	LEU
1	A	1264	GLU
1	A	1288	ASP
1	A	1291	VAL
1	A	1295	THR
1	A	1297	GLU
1	A	1308	THR
1	A	1333	ILE
1	A	1345	ARG
1	A	1353	TYR
1	A	1370	LEU
1	A	1394	THR
1	A	1400	CYS
1	A	1426	GLU
1	A	1436	ILE
1	A	1438	THR
1	A	1445	ILE
1	A	1447	GLU
1	A	1451	VAL
2	B	21	GLU
2	B	46	GLN
2	B	57	TYR
2	B	63	ILE

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Mol	Chain	Res	Type
2	B	64	CYS
2	B	67	SER
2	B	97	VAL
2	B	101	MET
2	B	104	GLU
2	B	128	LEU
2	B	134	LYS
2	B	167	ILE
2	B	194	GLU
2	B	217	ARG
2	B	222	ILE
2	B	225	VAL
2	B	244	LEU
2	B	249	ARG
2	B	250	PHE
2	B	258	LEU
2	B	261	ARG
2	B	262	GLU
2	B	272	THR
2	B	275	TYR
2	B	276	ILE
2	B	286	PHE
2	B	289	LEU
2	B	291	ILE
2	B	299	GLU
2	B	303	TYR
2	B	309	GLN
2	B	313	MET
2	B	325	GLN
2	B	364	ILE
2	B	365	THR
2	B	371	GLU
2	B	387	LEU
2	B	393	LYS
2	B	394	ASP
2	B	396	ASP
2	B	404	LYS
2	B	424	LEU
2	B	425	THR
2	B	429	PHE
2	B	446	LEU
2	B	452	THR

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Mol	Chain	Res	Type
2	B	465	ASN
2	B	466	TRP
2	B	468	GLU
2	B	485	ARG
2	B	487	THR
2	B	496	ARG
2	B	505	ASP
2	B	508	LEU
2	B	510	LYS
2	B	516	ASN
2	B	537	LYS
2	B	554	ILE
2	B	555	ILE
2	B	557	PHE
2	B	563	MET
2	B	576	ASP
2	B	580	VAL
2	B	582	VAL
2	B	598	GLU
2	B	601	ARG
2	B	603	LEU
2	B	609	ILE
2	B	615	MET
2	B	616	ILE
2	B	622	LYS
2	B	628	THR
2	B	635	ARG
2	B	636	PRO
2	B	640	VAL
2	B	644	GLU
2	B	680	THR
2	B	693	ILE
2	B	705	MET
2	B	737	THR
2	B	748	ILE
2	B	766	ARG
2	B	780	VAL
2	B	786	ASN
2	B	790	ASP
2	B	791	THR
2	B	805	THR
2	B	806	THR

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Mol	Chain	Res	Type
2	B	811	TYR
2	B	815	ARG
2	B	825	VAL
2	B	830	TYR
2	B	837	ASP
2	B	839	MET
2	B	878	GLN
2	B	879	ARG
2	B	882	THR
2	B	884	ARG
2	B	887	HIS
2	B	889	THR
2	B	895	ASP
2	B	909	ASP
2	B	915	THR
2	B	939	THR
2	B	944	THR
2	B	955	THR
2	B	956	THR
2	B	957	ASN
2	B	959	ASP
2	B	983	ARG
2	B	992	ILE
2	B	997	GLU
2	B	999	MET
2	B	1000	PRO
2	B	1006	ILE
2	B	1046	PRO
2	B	1049	ASP
2	B	1053	GLU
2	B	1058	LEU
2	B	1060	ARG
2	B	1067	ARG
2	B	1069	PHE
2	B	1084	GLN
2	B	1087	PHE
2	B	1095	LEU
2	B	1098	MET
2	B	1103	ILE
2	B	1122	ARG
2	B	1150	ARG
2	B	1155	SER

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Mol	Chain	Res	Type
2	B	1156	ASP
2	B	1159	ARG
2	B	1160	VAL
2	B	1163	CYS
2	B	1175	LEU
2	B	1183	LYS
2	B	1202	LEU
2	B	1214	PRO
2	B	1218	THR
3	C	3	GLU
3	C	7	GLN
3	C	11	ARG
3	C	53	THR
3	C	55	THR
3	C	56	THR
3	C	58	LEU
3	C	73	GLN
3	C	76	ASP
3	C	77	ILE
3	C	78	GLU
3	C	99	LEU
3	C	106	GLU
3	C	108	GLU
3	C	117	ASP
3	C	129	ILE
3	C	138	GLU
3	C	145	CYS
3	C	147	LEU
3	C	166	GLU
3	C	177	GLU
3	C	186	LEU
3	C	194	GLU
3	C	200	GLU
3	C	203	GLN
3	C	226	ASP
3	C	238	ILE
3	C	240	VAL
3	C	245	VAL
3	C	259	LEU
3	C	265	MET
3	C	268	ASP
4	D	11	ARG

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Mol	Chain	Res	Type
4	D	14	ARG
4	D	15	LEU
4	D	17	LYS
4	D	22	GLU
4	D	23	ASN
4	D	29	LEU
4	D	47	LEU
4	D	57	LEU
4	D	63	LEU
4	D	65	GLU
4	D	123	LEU
4	D	124	GLU
4	D	138	ASN
4	D	139	LYS
4	D	150	ASN
4	D	154	PHE
4	D	155	ARG
4	D	158	GLU
4	D	160	VAL
4	D	187	THR
4	D	200	ASN
5	E	24	LYS
5	E	31	THR
5	E	33	GLU
5	E	34	GLU
5	E	37	LEU
5	E	40	GLU
5	E	50	MET
5	E	52	ARG
5	E	69	ILE
5	E	72	PHE
5	E	74	ASP
5	E	78	LEU
5	E	99	HIS
5	E	107	THR
5	E	119	SER
5	E	123	LEU
5	E	127	ILE
5	E	132	ILE
5	E	134	THR
5	E	140	LEU
5	E	191	LYS

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Mol	Chain	Res	Type
5	E	207	ARG
6	F	77	ASP
6	F	79	ARG
6	F	84	TYR
6	F	112	GLU
6	F	116	ASP
6	F	119	ARG
6	F	125	LEU
6	F	147	SER
6	F	155	LEU
7	G	1	MET
7	G	8	SER
7	G	12	THR
7	G	13	LEU
7	G	21	ARG
7	G	24	GLN
7	G	26	LEU
7	G	45	ILE
7	G	48	VAL
7	G	49	LEU
7	G	53	ASN
7	G	62	LEU
7	G	63	PRO
7	G	74	TYR
7	G	93	SER
7	G	101	VAL
7	G	111	THR
7	G	133	SER
7	G	134	GLU
8	H	3	ASN
8	H	10	PHE
8	H	14	GLU
8	H	15	VAL
8	H	20	TYR
8	H	31	THR
8	H	33	GLN
8	H	39	THR
8	H	53	ASP
8	H	61	SER
8	H	64	ASN
8	H	86	ASP
8	H	89	LEU

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Mol	Chain	Res	Type
8	H	94	ASP
8	H	102	TYR
8	H	107	VAL
8	H	129	TYR
8	H	130	ARG
8	H	138	GLU
8	H	143	LEU
9	I	8	ARG
9	I	28	GLU
9	I	31	THR
9	I	44	TYR
9	I	49	ILE
9	I	50	THR
9	I	51	ASN
9	I	52	ILE
9	I	59	VAL
9	I	72	ASP
9	I	74	GLU
9	I	85	PHE
9	I	93	LYS
9	I	101	PHE
9	I	106	CYS
9	I	111	THR
10	J	22	LEU
10	J	26	GLN
10	J	34	THR
10	J	43	ARG
10	J	44	TYR
11	K	25	THR
11	K	47	ARG
11	K	51	LEU
11	K	68	PHE
11	K	94	ILE
11	K	107	THR
11	K	111	LEU
11	K	113	THR
11	K	114	LEU
12	L	27	LEU
12	L	54	ARG
12	L	55	ILE
12	L	68	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (141)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
1	A	75	ASN
1	A	160	GLN
1	A	169	ASN
1	A	171	GLN
1	A	213	HIS
1	A	225	ASN
1	A	256	GLN
1	A	281	HIS
1	A	282	ASN
1	A	297	GLN
1	A	299	HIS
1	A	316	GLN
1	A	339	ASN
1	A	394	ASN
1	A	435	HIS
1	A	447	GLN
1	A	451	HIS
1	A	490	HIS
1	A	493	GLN
1	A	515	GLN
1	A	517	ASN
1	A	589	GLN
1	A	611	GLN
1	A	640	GLN
1	A	654	ASN
1	A	700	ASN
1	A	706	HIS
1	A	723	ASN
1	A	736	ASN
1	A	741	ASN
1	A	745	GLN
1	A	757	ASN
1	A	767	GLN
1	A	768	GLN
1	A	786	HIS
1	A	858	ASN
1	A	903	ASN
1	A	926	GLN
1	A	935	GLN
1	A	959	ASN
1	A	965	GLN

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Mol	Chain	Res	Type
1	A	1048	ASN
1	A	1052	GLN
1	A	1078	GLN
1	A	1110	ASN
1	A	1187	GLN
1	A	1203	ASN
1	A	1218	GLN
1	A	1278	ASN
1	A	1312	ASN
1	A	1354	ASN
1	A	1378	GLN
1	A	1390	ASN
1	A	1427	ASN
1	A	1432	GLN
2	B	103	ASN
2	B	115	GLN
2	B	178	ASN
2	B	236	HIS
2	B	255	GLN
2	B	366	GLN
2	B	383	ASN
2	B	433	GLN
2	B	465	ASN
2	B	515	HIS
2	B	516	ASN
2	B	518	HIS
2	B	587	HIS
2	B	686	ASN
2	B	706	GLN
2	B	744	HIS
2	B	761	HIS
2	B	794	ASN
2	B	821	GLN
2	B	842	ASN
2	B	862	GLN
2	B	887	HIS
2	B	957	ASN
2	B	975	GLN
2	B	984	HIS
2	B	986	GLN
2	B	1062	HIS
2	B	1065	GLN

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Mol	Chain	Res	Type
2	B	1097	HIS
2	B	1117	GLN
2	B	1141	HIS
2	B	1161	HIS
2	B	1179	GLN
2	B	1193	GLN
3	C	7	GLN
3	C	24	ASN
3	C	65	HIS
3	C	79	GLN
3	C	102	GLN
3	C	112	ASN
3	C	123	ASN
3	C	135	GLN
3	C	151	GLN
3	C	195	GLN
3	C	231	ASN
4	D	9	GLN
4	D	34	GLN
4	D	39	ASN
4	D	40	HIS
4	D	41	GLN
4	D	132	GLN
4	D	138	ASN
4	D	143	ASN
4	D	150	ASN
4	D	165	GLN
4	D	179	GLN
4	D	200	ASN
5	E	54	GLN
5	E	101	GLN
5	E	104	ASN
5	E	106	GLN
5	E	143	ASN
5	E	146	HIS
5	E	147	HIS
6	F	104	ASN
7	G	10	ASN
7	G	14	HIS
7	G	24	GLN
7	G	53	ASN
7	G	102	GLN

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Mol	Chain	Res	Type
7	G	126	ASN
7	G	131	GLN
7	G	158	HIS
8	H	43	ASN
8	H	128	ASN
8	H	131	ASN
8	H	139	ASN
9	I	12	ASN
9	I	46	HIS
9	I	51	ASN
9	I	108	HIS
10	J	53	HIS
11	K	29	ASN
11	K	44	ASN
11	K	65	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	P	10/18 (55%)	1 (10%)	1 (10%)

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
15	P	2	A

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
15	P	1	C

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
14	BRU	T	23	15,14	18,21,22	3.90	1 (5%)	25,30,33	1.03	1 (4%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
14	BRU	T	23	15,14	-	0/7/21/22	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	T	23	BRU	BR-C5	-16.43	1.50	1.88

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	T	23	BRU	C6-C5-C4	-2.86	117.77	120.67

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	T	23	BRU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	1417/1733 (81%)	0.08	35 (2%) 58 35	18, 67, 100, 123	0
2	B	1113/1224 (90%)	0.37	55 (4%) 35 21	21, 77, 109, 121	0
3	C	266/347 (76%)	0.00	1 (0%) 88 71	34, 66, 93, 107	0
4	D	178/221 (80%)	0.39	12 (6%) 24 16	46, 76, 106, 111	0
5	E	214/215 (99%)	0.44	7 (3%) 49 29	43, 88, 108, 117	0
6	F	87/155 (56%)	-0.28	2 (2%) 61 36	16, 44, 74, 84	0
7	G	171/171 (100%)	0.07	0 100 100	47, 63, 94, 101	0
8	H	135/146 (92%)	0.68	11 (8%) 18 13	71, 94, 110, 116	0
9	I	119/122 (97%)	0.62	7 (5%) 28 18	59, 92, 110, 119	0
10	J	65/70 (92%)	0.03	0 100 100	45, 62, 87, 98	0
11	K	114/120 (95%)	-0.23	1 (0%) 81 57	28, 67, 85, 96	0
12	L	46/70 (65%)	0.92	8 (17%) 4 4	51, 94, 110, 115	0
13	N	7/12 (58%)	2.24	4 (57%) 0 0	120, 125, 135, 137	0
14	T	17/26 (65%)	1.87	9 (52%) 0 0	99, 119, 135, 136	0
15	P	11/18 (61%)	1.75	3 (27%) 1 2	115, 119, 129, 139	0
All	All	3960/4650 (85%)	0.23	155 (3%) 43 26	16, 73, 107, 139	0

All (155) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	471	LYS	5.8
2	B	883	LEU	5.6
2	B	506	GLY	4.8
4	D	18	VAL	4.7
2	B	472	ALA	4.6
2	B	70	ILE	4.6
2	B	250	PHE	4.4

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Mol	Chain	Res	Type	RSRZ
4	D	17	LYS	4.4
15	P	1	C	4.3
9	I	116	ASN	4.3
1	A	1081	LEU	4.2
2	B	715	ALA	4.1
1	A	3	GLY	4.0
1	A	69	THR	3.9
1	A	483	ASP	3.8
2	B	470	LYS	3.8
2	B	446	LEU	3.7
4	D	136	GLY	3.7
1	A	252	PHE	3.6
1	A	2	VAL	3.5
8	H	84	ALA	3.5
4	D	24	ALA	3.4
11	K	114	LEU	3.4
12	L	27	LEU	3.3
13	N	5	DC	3.3
1	A	1254	ALA	3.2
1	A	65	LEU	3.2
2	B	468	GLU	3.2
2	B	502	ILE	3.1
2	B	710	LEU	3.1
2	B	882	THR	3.1
2	B	436	VAL	3.1
2	B	431	TYR	3.1
1	A	51	GLY	3.1
5	E	50	MET	3.0
2	B	262	GLU	3.0
13	N	7	DT	3.0
2	B	734	HIS	3.0
2	B	507	LYS	3.0
1	A	255	SER	3.0
8	H	135	LEU	2.9
9	I	53	GLY	2.9
2	B	108	VAL	2.9
8	H	1	MET	2.9
2	B	723	VAL	2.9
2	B	731	VAL	2.9
4	D	25	ALA	2.8
2	B	24	PRO	2.8
4	D	20	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
2	B	134	LYS	2.8
5	E	90	VAL	2.8
4	D	4	SER	2.8
2	B	577	ALA	2.8
1	A	1092	LYS	2.7
12	L	26	THR	2.7
6	F	69	LEU	2.7
2	B	467	GLY	2.7
1	A	159	THR	2.7
1	A	186	LYS	2.7
2	B	712	PRO	2.7
4	D	3	VAL	2.6
1	A	1080	THR	2.6
14	T	27	DC	2.6
12	L	43	THR	2.6
2	B	725	PRO	2.6
14	T	11	DA	2.6
2	B	249	ARG	2.6
1	A	66	LYS	2.6
2	B	933	SER	2.6
8	H	108	SER	2.6
2	B	241	ARG	2.6
4	D	11	ARG	2.5
1	A	1198	ASP	2.5
2	B	668	ASP	2.5
1	A	56	PRO	2.5
14	T	13	DT	2.5
8	H	35	GLN	2.5
9	I	117	LYS	2.5
9	I	120	GLN	2.5
2	B	879	ARG	2.5
1	A	158	PRO	2.4
2	B	709	ASP	2.4
5	E	93	MET	2.4
2	B	934	LYS	2.4
1	A	1217	LYS	2.4
12	L	52	GLY	2.4
2	B	266	ALA	2.4
12	L	25	ALA	2.4
2	B	733	HIS	2.3
2	B	504	ARG	2.3
4	D	19	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
4	D	137	ASN	2.3
2	B	164	LYS	2.3
8	H	83	GLN	2.3
12	L	53	HIS	2.3
2	B	473	MET	2.3
12	L	49	LYS	2.3
2	B	866	TYR	2.3
13	N	1	DA	2.3
1	A	1110	ASN	2.3
14	T	10	DA	2.2
2	B	868	MET	2.2
5	E	192	ARG	2.2
14	T	24	DG	2.2
8	H	139	ASN	2.2
1	A	1378	GLN	2.2
2	B	115	GLN	2.2
2	B	242	SER	2.2
5	E	179	GLN	2.2
14	T	12	DG	2.2
14	T	25	DG	2.2
8	H	64	ASN	2.2
2	B	561	TRP	2.2
15	P	7	G	2.2
12	L	68	GLU	2.2
14	T	15	DG	2.2
2	B	532	ALA	2.1
1	A	160	GLN	2.1
13	N	6	DT	2.1
2	B	736	THR	2.1
9	I	60	GLN	2.1
1	A	153	PRO	2.1
1	A	1245	PRO	2.1
2	B	265	SER	2.1
2	B	263	GLY	2.1
5	E	215	MET	2.1
8	H	76	THR	2.1
9	I	119	THR	2.1
1	A	1187	GLN	2.1
6	F	76	LYS	2.1
1	A	1455	PRO	2.1
4	D	165	GLN	2.1
14	T	14	DA	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	59	GLY	2.1
1	A	1380	GLY	2.1
2	B	101	MET	2.1
2	B	133	LYS	2.1
2	B	594	ALA	2.1
1	A	1173	HIS	2.0
8	H	85	GLY	2.0
5	E	41	ASP	2.0
9	I	3	THR	2.0
1	A	567	LYS	2.0
1	A	975	HIS	2.0
3	C	218	PRO	2.0
8	H	129	TYR	2.0
2	B	880	THR	2.0
1	A	1255	GLU	2.0
2	B	505	ASP	2.0
1	A	154	SER	2.0
1	A	50	ILE	2.0
1	A	1158	PRO	2.0
2	B	935	ARG	2.0
2	B	475	SER	2.0
15	P	10	U	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
14	BRU	T	23	20/21	0.73	0.20	105,113,118,121	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
17	MG	A	2458	1/1	0.86	0.13	151,151,151,151	0
16	ZN	I	1122	1/1	0.95	0.08	131,131,131,131	0
16	ZN	L	1071	1/1	0.98	0.04	106,106,106,106	0
16	ZN	C	1269	1/1	0.99	0.11	40,40,40,40	0
16	ZN	A	2456	1/1	0.99	0.03	87,87,87,87	0
16	ZN	B	2225	1/1	1.00	0.02	42,42,42,42	0
16	ZN	J	1066	1/1	1.00	0.03	47,47,47,47	0
16	ZN	A	2457	1/1	1.00	0.08	42,42,42,42	0
16	ZN	I	1121	1/1	1.00	0.02	79,79,79,79	0

6.5 Other polymers [i](#)

There are no such residues in this entry.