



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:38 PM UTC

PDB ID : 1WZ2 / pdb_00001wz2
Title : The crystal structure of Leucyl-tRNA synthetase and tRNA(leucine) complex
Authors : Fukunaga, R.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2005-02-21
Resolution : 3.21 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

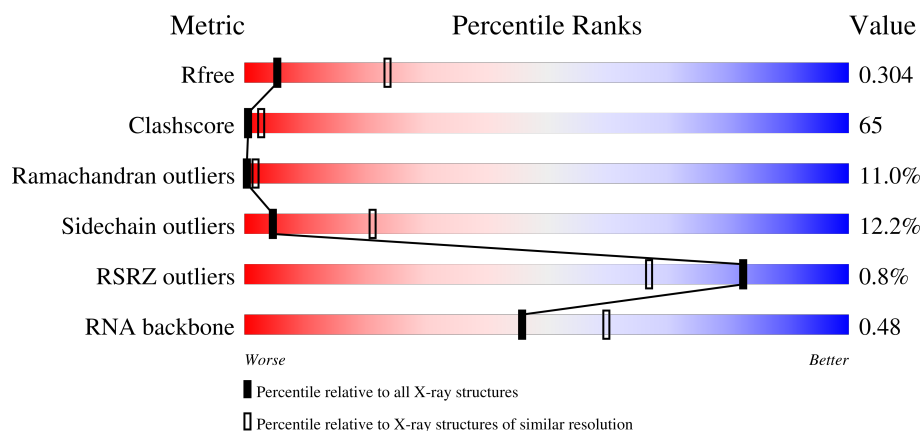
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.21 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	1768 (3.24-3.20)
Clashscore	190562	1879 (3.24-3.20)
Ramachandran outliers	187476	1844 (3.24-3.20)
Sidechain outliers	187428	1843 (3.24-3.20)
RSRZ outliers	180081	1768 (3.24-3.20)
RNA backbone	3983	1055 (3.50-2.94)

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	C	88	28% 42% 20% 9%
1	D	88	2% 38% 38% 18% 7%
2	A	967	19% 58% 19% ..
2	B	967	20% 59% 18% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 19578 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 RNA chain called tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	88	Total	C	N	O	P	0	0	0
			1880	836	339	617	88			
1	D	88	Total	C	N	O	P	0	0	0
			1880	836	339	617	88			

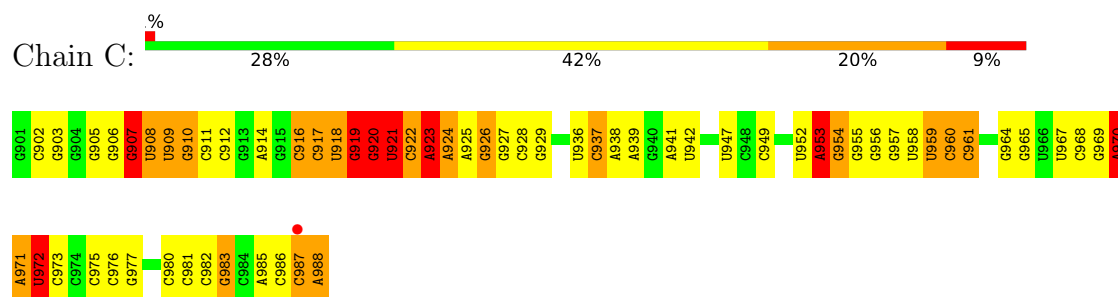
- Molecule 2 is a protein called Leucyl-tRNA synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	948	Total	C	N	O	S	0	0	0
			7909	5132	1323	1430	24			
2	B	948	Total	C	N	O	S	0	0	0
			7909	5132	1323	1430	24			

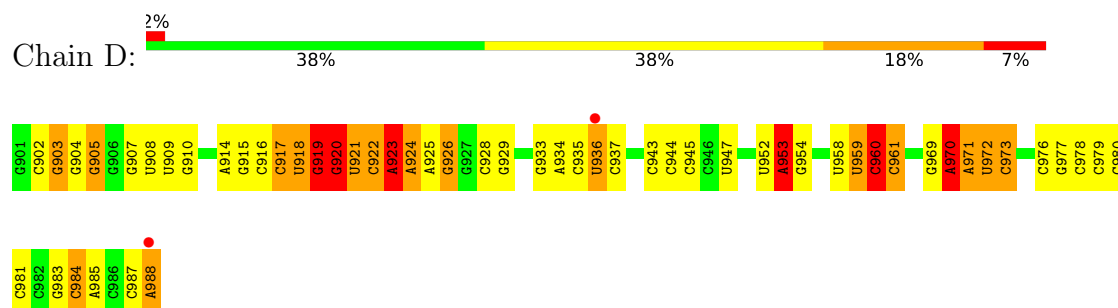
3 Residue-property plots

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.

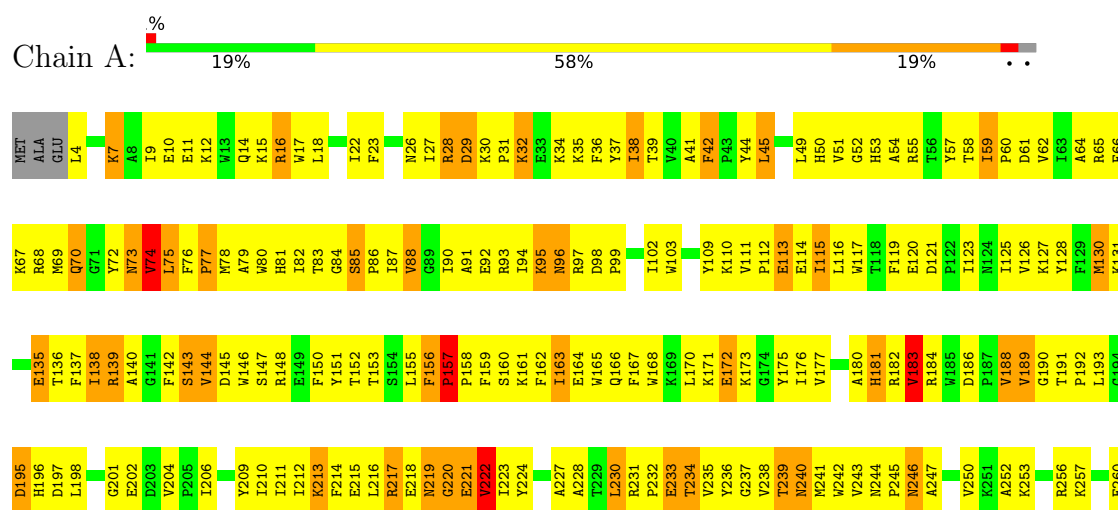
• Molecule 1: tRNA

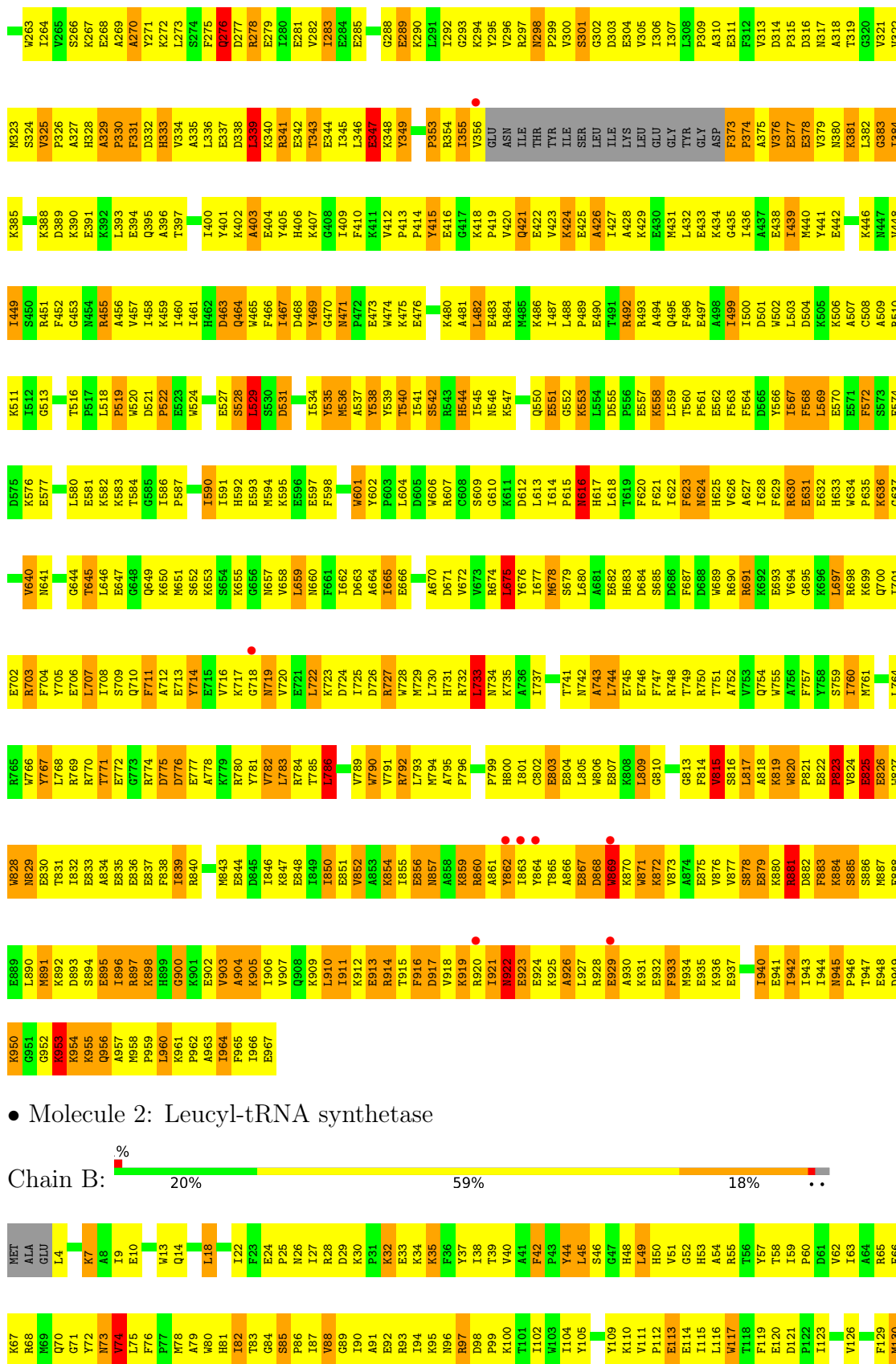


• Molecule 1: tRNA



• Molecule 2: Leucyl-tRNA synthetase





D949	S886	V824	W762	I701	E632	F563	L503	M440	N380	V321	K259	L193	K131
K950	M887	E825	D763	E702	H633	F564	D504	T441	K381	V322	E260	H196	A132
G951	E888	E826	L764	R703	D565	E442	K506	F443	L382	E443	E261	D197	E135
G952	E889	W827	R765	F704	P635	Y566	K507	F443	G383	V323	W262	L198	T136
K953	L890	W828	W766	Y705	K636	I567	C508	K446	L384	V324	W263	M199	F137
K954	M891	N829	Y767	E706	G637	F568	A509	M447	K385	V325	W264	E200	L138
K955	K892	E830	L768	L707	L569	E570	A509	V448	S386	P326	W265	G201	R139
Q956	D893	R831	R769	I708	E571	E570	K510	V448	Q387	A327	S266	E202	A140
A957	S894	I832	R770	S709	E571	E571	K511	S450	K388	H328	K267	D203	G141
M958	E895	E833	F770	F572	F572	F572	G513	R451	D389	A329	E268	D204	F142
P959	I896	A834	S573	S573	S573	S573	G514	S451	K390	P330	A269	V204	F142
L960	R897	G644	G644	G644	G644	G644	L514	F452	E391	F331	A270	P205	S143
K961	D774	T645	G453	G453	G453	G453	G515	F452	K392	D332	Y271	P206	V144
P962	D775	A712	E454	E454	E454	E454	T516	N454	L393	H383	K272	I206	D145
A963	D776	E577	E577	E577	E577	E577	P517	A456	E394	V334	K273	I210	W146
P964	E777	L580	L580	L580	L580	L580	L518	A456	A335	A335	S274	I211	S147
F965	E778	E581	E581	E581	E581	E581	P519	A456	Q395	G336	S275	I212	R148
I966	G718	K650	K650	K650	K650	K650	W520	K459	A396	L336	Q276	K213	E149
E967	G719	M651	M651	M651	M651	M651	D521	I460	T397	E337	D277	F214	F150
	R780	S652	S652	S652	S652	S652	P622	I461	K398	L338	R278	E215	Y151
	W821	K653	K653	K653	K653	K653	E523	H462	T399	L339	K279	L216	T152
	L722	S654	S654	S654	S654	S654	W524	Q463	Y401	R341	E280	K217	T153
	K723	P587	P587	P587	P587	P587	V525	Q464	K402	E342	E281	E218	S154
	D724						I526		A403	T343	V282	N219	L155
	I725	V658	V658	V658	V658	V658	E527	I467	E404	E344	I283	G220	F156
	D726	L659	L659	L659	L659	L659	E528	D463	Y405	L345	E284	E221	E167
	R727	N660	N660	N660	N660	N660	L529	Y469	H406	L346	E285	V222	F158
	W728	F661	F661	F661	F661	F661	S530	G470	E347	K348	F286	I223	F159
	M729	E593	E593	E593	E593	E593	W531	N471	G408	Y349	K287	Y224	S160
	R730	K595	K595	K595	K595	K595	S532	P472	I409	K349	G288	L225	K161
	H731	E596	E596	E596	E596	E596	T533	K473	F410	P350	E289	P226	F162
	R732	E597	E597	E597	E597	E597	I534	W474	K411	P352	K290	A227	I163
	L733	F598	F598	F598	F598	F598	Y535	K475	W412	P353	I292	A228	E164
	W734	E599	E599	E599	E599	E599	M536	E476	P414	R354	G293	W165	Q166
	K735	W601	W601	W601	W601	W601	E477	K477	P414	I355	K294	R231	F167
	A736	D671	D671	D671	D671	D671	Y538	A478	Y415	V356	Y295	P232	W168
	I737						Y539	R479	E416		V296	E233	K169
	K738	R674	R674	R674	R674	R674	T540	K480	G417	GLU	V297	E234	L170
	E739	L675	L675	L675	L675	L675	I541	A481	K418	ASN	R297	T234	K171
	T740	Y676	Y676	Y676	Y676	Y676	S542	L482	P419	ILE	N298	V235	E172
	T741	I677	I677	I677	I677	I677	R543	E483	W420	THR	P299	V236	K173
	N742	M678	M678	M678	M678	M678	H544	R484	Q421	TYR	V300	G237	K173
	A743	S679	S679	S679	S679	S679	I545	M485	E422	ILE	S301	V238	G174
	L744	L680	L680	L680	L680	L680	N546	K486	W423	SER	G302	T239	Y175
	E745	A681	A681	A681	A681	A681	K547	I487	K424	LEU	D303	N240	I176
	E746	E882	E882	E882	E882	E882	L548	P489	E425	ILE	E304	M241	
	F747	H683	H683	H683	H683	H683	R549	A426	A426	LYS	V305	W242	
	R748	D684	D684	D684	D684	D684	Q550	E490	I427	LEU	I306	V243	
	T749						F620	T491	A428	GLU	I307	N244	
	R750	F687	F687	F687	F687	F687	E551	R492	K429	GLY	I308	P245	
	T751	D688	D688	D688	D688	D688	G552	R492	E430	TYR	P309	N246	
	A752	W689	W689	W689	W689	W689	K553	R493	M431	GLY	A310		
	W753	R690	R690	R690	R690	R690	L554	A494	K431	GLY	A310		
	Q754						D555	Q495	L432	ASP	E311	V250	
	W755	E693	E693	E693	E693	E693	H625	F496	E433	F373	F312	K251	
	A756	V694	V694	V694	V694	V694	E557	E497	K434	P374	G312	A252	
	F757	G695	G695	G695	G695	G695	W626	I427	E435	A375	D314	K253	
	W758	K696	K696	K696	K696	K696	K558	I499	I436	V376	P315	V188	
	S759	P629	P629	P629	P629	P629	L559	I500	A437	E377	D316	G190	
	I760	R630	R630	R630	R630	R630	E561	D501	E438	E378	K257	T191	
	M761	E631	E631	E631	E631	E631	E562	W502	I439	V379	A318	P192	

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	120.55Å 231.13Å 118.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.99 – 3.21 14.99 – 3.21	Depositor EDS
% Data completeness (in resolution range)	90.7 (14.99-3.21) 89.8 (14.99-3.21)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.22 (at 3.19Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.241 , 0.305 0.243 , 0.304	Depositor DCC
R_{free} test set	5012 reflections (10.06%)	wwPDB-VP
Wilson B-factor (Å ²)	75.5	Xtriage
Anisotropy	0.463	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 66.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.046 for l,-k,h	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	19578	wwPDB-VP
Average B, all atoms (Å ²)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.28% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	C	0.42	0/2099	0.82	9/3270 (0.3%)
1	D	0.40	0/2099	0.82	6/3270 (0.2%)
2	A	0.67	1/8115 (0.0%)	1.10	45/10953 (0.4%)
2	B	0.48	0/8115	1.04	44/10953 (0.4%)
All	All	0.55	1/20428 (0.0%)	1.02	104/28446 (0.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	6
1	D	0	5
2	A	0	2
All	All	0	13

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	144	VAL	CA-CB	-6.15	1.47	1.54

All (104) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	815	VAL	CB-CA-C	-11.83	96.17	112.14
2	B	680	LEU	N-CA-C	10.80	125.84	112.23
2	A	680	LEU	N-CA-C	10.67	125.68	112.23
2	A	904	ALA	N-CA-C	-10.66	99.95	113.16
2	B	904	ALA	N-CA-C	-10.58	100.05	113.16
2	A	956	GLN	N-CA-C	-9.15	99.81	112.25
2	B	956	GLN	N-CA-C	-8.84	100.23	112.25
2	B	189	VAL	N-CA-C	-8.76	104.62	113.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	786	LEU	N-CA-C	-8.63	101.84	111.07
2	A	469	TYR	N-CA-C	-8.54	101.10	112.72
2	A	189	VAL	N-CA-C	-8.48	104.91	113.47
2	B	156	PHE	CA-C-N	8.40	129.04	120.38
2	B	156	PHE	C-N-CA	8.40	129.04	120.38
2	A	144	VAL	N-CA-C	8.24	120.10	109.30
2	B	601	TRP	N-CA-C	8.21	121.15	111.71
2	A	786	LEU	N-CA-C	-8.20	102.29	111.07
2	B	469	TYR	N-CA-C	-8.11	101.69	112.72
1	C	919	G	N9-C1'-C2'	8.06	124.10	112.00
2	A	156	PHE	CA-C-N	8.03	128.65	120.38
2	A	156	PHE	C-N-CA	8.03	128.65	120.38
2	B	144	VAL	N-CA-C	8.02	119.80	109.30
2	A	74	VAL	N-CA-C	7.72	125.39	109.34
2	A	476	GLU	N-CA-C	-7.70	102.69	112.93
1	D	960	C	C2'-C3'-O3'	7.62	120.93	109.50
2	B	683	HIS	CB-CA-C	-7.59	106.91	117.23
2	A	601	TRP	N-CA-C	7.52	121.56	112.38
2	B	130	MET	N-CA-C	-7.46	103.23	111.36
2	B	476	GLU	N-CA-C	-7.42	103.07	112.93
2	B	74	VAL	N-CA-C	7.34	124.61	109.34
2	A	270	ALA	N-CA-C	-7.09	103.48	111.14
2	A	426	ALA	N-CA-C	-7.09	105.25	114.04
2	A	130	MET	N-CA-C	-7.05	103.67	111.36
2	B	270	ALA	N-CA-C	-7.03	103.55	111.14
2	B	426	ALA	N-CA-C	-6.88	105.51	114.04
2	A	157	PRO	N-CA-C	6.87	119.08	110.70
2	B	846	ILE	CB-CA-C	-6.85	103.12	111.88
2	A	896	ILE	N-CA-C	-6.78	106.42	112.12
2	A	675	LEU	CA-CB-CG	6.48	138.97	116.30
2	B	157	PRO	N-CA-C	6.45	118.57	110.70
1	D	953	A	N9-C1'-C2'	6.43	123.64	114.00
2	A	733	LEU	N-CA-C	-6.39	104.00	110.97
1	C	920	G	N9-C1'-C2'	6.29	121.43	112.00
2	A	383	GLY	N-CA-C	-6.25	107.56	115.31
1	C	907	G	N9-C1'-C2'	6.22	123.33	114.00
2	B	733	LEU	N-CA-C	-6.21	104.20	110.97
2	A	897	ARG	N-CA-C	-6.20	104.98	112.54
1	C	909	U	C2'-C3'-O3'	-6.12	104.53	113.70
1	D	920	G	N9-C1'-C2'	6.10	123.15	114.00
2	A	221	GLU	N-CA-C	6.09	116.05	108.19
2	B	896	ILE	N-CA-C	-6.08	106.82	111.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	923	A	C2'-C3'-O3'	6.07	118.61	109.50
2	B	383	GLY	N-CA-C	-6.07	107.78	115.31
2	A	325	VAL	CA-C-N	6.07	125.69	119.56
2	A	325	VAL	C-N-CA	6.07	125.69	119.56
2	A	572	PHE	N-CA-C	6.07	118.33	108.63
2	B	897	ARG	N-CA-C	-6.06	105.14	112.54
2	B	325	VAL	CA-C-N	5.96	125.58	119.56
2	B	325	VAL	C-N-CA	5.96	125.58	119.56
2	B	221	GLU	N-CA-C	5.96	115.87	108.19
2	B	538	TYR	N-CA-C	-5.87	104.80	111.14
2	B	926	ALA	N-CA-C	-5.84	105.25	112.38
2	A	926	ALA	N-CA-C	-5.76	105.36	112.38
2	B	572	PHE	N-CA-C	5.75	117.82	108.63
2	A	665	ILE	CB-CA-C	-5.70	104.44	112.14
2	A	59	ILE	CA-C-N	-5.70	113.01	119.28
2	A	59	ILE	C-N-CA	-5.70	113.01	119.28
1	C	970	A	C2'-C3'-O3'	5.63	117.94	109.50
2	A	538	TYR	N-CA-C	-5.61	105.08	111.14
2	A	32	LYS	N-CA-C	5.59	117.46	111.36
2	B	298	ASN	CA-C-N	5.55	125.02	119.24
2	B	298	ASN	C-N-CA	5.55	125.02	119.24
1	C	953	A	N9-C1'-C2'	5.53	122.30	114.00
2	A	803	GLU	N-CA-C	-5.51	105.38	111.71
2	A	95	LYS	N-CA-C	-5.48	104.99	110.97
2	B	877	VAL	N-CA-C	-5.45	105.06	110.62
1	C	923	A	C2'-C3'-O3'	5.44	117.66	109.50
2	B	467	ILE	N-CA-C	-5.41	98.15	107.24
2	A	952	GLY	N-CA-C	-5.34	106.32	115.08
2	B	803	GLU	N-CA-C	-5.32	105.59	111.71
2	A	905	LYS	N-CA-C	-5.30	105.92	112.38
2	A	467	ILE	N-CA-C	-5.29	98.35	107.24
2	A	298	ASN	CA-C-N	5.27	124.72	119.24
2	A	298	ASN	C-N-CA	5.27	124.72	119.24
2	A	697	LEU	N-CA-C	-5.25	105.73	111.82
2	A	222	VAL	N-CA-C	5.25	120.26	109.34
2	A	628	ILE	N-CA-C	5.24	120.24	109.34
2	B	32	LYS	N-CA-C	5.24	117.07	111.36
1	D	970	A	C2'-C3'-O3'	5.22	117.33	109.50
2	B	876	VAL	N-CA-C	-5.19	107.76	112.12
2	A	622	ILE	CB-CA-C	-5.17	105.24	112.02
1	D	919	G	N9-C1'-C2'	5.15	119.72	112.00
2	A	859	LYS	N-CA-C	5.14	115.32	108.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	628	ILE	N-CA-C	5.13	120.02	109.34
2	B	140	ALA	N-CA-C	-5.13	105.92	113.61
2	B	905	LYS	N-CA-C	-5.13	106.12	112.38
1	C	920	G	C4'-C3'-O3'	-5.12	105.33	113.00
2	B	827	TRP	N-CA-C	-5.12	99.90	110.80
2	B	859	LYS	N-CA-C	5.11	115.28	108.38
2	B	405	TYR	N-CA-C	-5.10	105.28	112.12
2	B	222	VAL	N-CA-C	5.10	119.94	109.34
1	C	972	U	N1-C1'-C2'	5.09	121.63	114.00
2	B	436	ILE	N-CA-C	-5.09	106.95	112.80
2	A	439	ILE	N-CA-C	5.05	115.12	107.80
2	B	697	LEU	N-CA-C	-5.04	105.98	111.82

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	535	TYR	Sidechain
2	A	767	TYR	Sidechain
1	C	907	G	Sidechain
1	C	919	G	Sidechain
1	C	920	G	Sidechain
1	C	921	U	Sidechain
1	C	926	G	Sidechain
1	C	959	U	Sidechain
1	D	919	G	Sidechain
1	D	920	G	Sidechain
1	D	926	G	Sidechain
1	D	953	A	Sidechain
1	D	959	U	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	C	1880	0	956	88	0
1	D	1880	0	956	64	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	7909	0	7908	1212	0
2	B	7909	0	7908	1091	0
All	All	19578	0	17728	2425	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 65.

All (2425) 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:A:866:ALA:N	2:A:955:LYS:HZ3	1.39	1.18
2:A:30:LYS:HB2	2:A:73:ASN:HD22	1.11	1.13
2:A:170:LEU:HB3	2:A:176:ILE:HD11	1.23	1.09
2:A:616:ASN:HD22	2:A:617:HIS:N	1.51	1.08
2:A:68:ARG:HH22	2:A:143:SER:HB3	1.15	1.07
2:A:924:GLU:HB3	2:A:928:ARG:HH21	1.12	1.07
2:B:920:ARG:HE	2:B:920:ARG:HA	1.12	1.06
2:B:26:ASN:HB3	2:B:28:ARG:NH2	1.70	1.06
2:A:480:LYS:HE2	2:A:484:ARG:HH22	1.17	1.05
2:A:921:ILE:HD12	2:A:928:ARG:HH12	1.20	1.05
2:A:922:ASN:HD22	2:A:923:GLU:N	1.53	1.05
2:B:703:ARG:HB2	2:B:703:ARG:HH11	1.18	1.05
2:A:724:ASP:HA	2:A:727:ARG:HG3	1.33	1.04
2:A:771:THR:HG21	2:A:774:ARG:HH11	1.18	1.04
2:B:198:LEU:HB2	2:B:202:GLU:HG2	1.40	1.02
2:A:924:GLU:HB3	2:A:928:ARG:NH2	1.75	1.02
2:B:733:LEU:HD11	2:B:789:VAL:HG11	1.41	1.02
2:B:866:ALA:N	2:B:955:LYS:HZ3	1.58	1.01
2:A:922:ASN:HD22	2:A:922:ASN:C	1.68	1.01
2:B:866:ALA:H	2:B:955:LYS:NZ	1.58	1.01
2:A:616:ASN:ND2	2:A:617:HIS:H	1.57	1.01
2:B:558:LYS:HB3	2:B:584:THR:HA	1.43	1.01
2:B:860:ARG:NH1	2:B:943:ILE:H	1.59	1.01
2:B:650:LYS:HE2	2:B:651:MET:H	1.22	1.00
2:A:529:LEU:H	2:A:529:LEU:HD12	1.27	1.00
2:A:163:ILE:HD12	2:A:531:ASP:HB2	1.40	1.00
2:A:722:LEU:H	2:A:722:LEU:HD22	1.22	1.00
2:A:87:ILE:HG13	2:A:88:VAL:H	1.24	0.99
2:B:703:ARG:HB2	2:B:703:ARG:NH1	1.77	0.99
2:A:188:VAL:HG23	2:A:189:VAL:H	1.28	0.99
1:D:904:G:H2'	1:D:905:G:H5''	1.45	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:848:GLU:O	2:A:852:VAL:HG23	1.63	0.98
2:A:235:VAL:HA	2:A:323:MET:HE1	1.42	0.98
2:B:227:ALA:HA	2:B:321:VAL:HG23	1.45	0.98
2:A:567:ILE:HA	2:A:595:LYS:HD2	1.44	0.97
1:C:916:C:H5'	1:C:917:C:C5	1.99	0.97
2:A:227:ALA:HA	2:A:321:VAL:HG23	1.46	0.97
2:A:426:ALA:HA	2:A:429:LYS:HE2	1.45	0.97
2:A:690:ARG:NH1	2:A:693:GLU:HG3	1.79	0.96
2:B:62:VAL:HG21	2:B:678:MET:HE2	1.44	0.96
2:A:68:ARG:NH2	2:A:143:SER:HB3	1.79	0.96
2:A:890:LEU:HD12	2:A:906:ILE:HD11	1.48	0.96
1:C:986:C:H4'	1:C:987:C:H5''	1.47	0.95
2:A:345:ILE:HG12	2:A:346:LEU:H	1.29	0.95
2:B:88:VAL:HG21	2:B:513:GLY:HA2	1.48	0.95
2:A:68:ARG:HH22	2:A:143:SER:CB	1.80	0.95
2:A:558:LYS:HB3	2:A:584:THR:HA	1.48	0.94
2:B:860:ARG:HH11	2:B:943:ILE:N	1.66	0.94
2:A:792:ARG:HH21	2:A:792:ARG:HG3	1.30	0.94
2:A:660:ASN:HB2	2:A:663:ASP:HB3	1.50	0.93
2:B:958:MET:HE3	2:B:959:PRO:HD2	1.50	0.93
2:A:860:ARG:NH1	2:A:861:ALA:HA	1.84	0.93
2:A:771:THR:HG21	2:A:774:ARG:NH1	1.82	0.93
2:B:429:LYS:O	2:B:433:GLU:HG2	1.67	0.92
2:A:182:ARG:HD2	2:A:206:ILE:HG21	1.49	0.92
2:A:28:ARG:H	2:A:28:ARG:HE	1.01	0.92
2:A:139:ARG:HH11	2:A:139:ARG:HG3	1.34	0.92
2:A:860:ARG:NH1	2:A:943:ILE:H	1.66	0.92
2:A:866:ALA:H	2:A:955:LYS:HZ3	0.98	0.92
2:B:784:ARG:HH22	2:B:810:GLY:H	1.15	0.92
2:B:826:GLU:C	2:B:828:TRP:H	1.70	0.91
2:A:770:ARG:HD2	2:A:933:PHE:CE2	2.06	0.91
2:B:927:LEU:HD12	2:B:944:ILE:HD12	1.50	0.91
2:B:82:ILE:HG21	2:B:126:VAL:HG13	1.50	0.91
2:A:480:LYS:HE2	2:A:484:ARG:NH2	1.84	0.91
2:A:866:ALA:H	2:A:955:LYS:NZ	1.69	0.91
2:B:49:LEU:H	2:B:49:LEU:HD12	1.34	0.91
2:B:233:GLU:HA	2:B:427:ILE:HD12	1.51	0.91
2:B:734:ASN:HD21	2:B:824:VAL:H	1.12	0.91
2:B:355:ILE:HG22	2:B:356:VAL:H	1.36	0.91
2:A:210:ILE:HD11	2:A:232:PRO:HG3	1.54	0.90
2:B:860:ARG:HH11	2:B:943:ILE:H	0.99	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:882:ASP:CG	2:B:883:PHE:H	1.79	0.90
2:B:26:ASN:HB3	2:B:28:ARG:HH22	1.34	0.90
2:A:826:GLU:C	2:A:828:TRP:H	1.70	0.89
2:B:167:PHE:HA	2:B:170:LEU:HD12	1.55	0.89
2:A:567:ILE:HG22	2:A:595:LYS:HB2	1.51	0.89
2:A:49:LEU:H	2:A:49:LEU:HD12	1.35	0.89
2:A:198:LEU:HB2	2:A:202:GLU:HG2	1.52	0.89
2:B:920:ARG:HA	2:B:920:ARG:NE	1.85	0.89
2:A:771:THR:CG2	2:A:774:ARG:HH11	1.86	0.89
2:A:496:PHE:CE1	2:A:614:ILE:HG12	2.08	0.89
2:A:230:LEU:H	2:A:230:LEU:HD23	1.37	0.88
2:A:730:LEU:HB3	2:A:827:TRP:NE1	1.88	0.88
2:B:870:LYS:HE3	2:B:905:LYS:HE3	1.55	0.88
2:A:111:VAL:HG22	2:A:128:TYR:HE2	1.39	0.88
2:A:343:THR:HG23	2:A:344:GLU:H	1.37	0.88
1:D:983:G:H2'	1:D:984:C:H5''	1.53	0.88
2:B:83:THR:HG22	2:B:515:GLY:HA2	1.56	0.88
2:B:675:LEU:HD23	2:B:697:LEU:HD21	1.54	0.87
1:D:922:C:H4'	1:D:923:A:O5'	1.72	0.87
2:B:567:ILE:HG22	2:B:595:LYS:HB2	1.55	0.87
2:A:489:PRO:HG3	2:A:684:ASP:OD2	1.75	0.87
2:B:555:ASP:HB3	2:B:558:LYS:HG2	1.55	0.87
2:A:471:ASN:OD1	2:A:473:GLU:HG2	1.73	0.87
2:B:714:TYR:H	2:B:714:TYR:HD2	1.21	0.87
2:A:219:ASN:ND2	2:A:220:GLY:H	1.72	0.87
2:B:188:VAL:HG23	2:B:189:VAL:H	1.40	0.87
2:A:921:ILE:HB	2:A:928:ARG:HH22	1.40	0.87
1:C:902:C:H2'	1:C:903:G:O4'	1.74	0.86
2:A:211:ILE:HG22	2:A:228:ALA:HB2	1.57	0.86
2:A:482:LEU:O	2:A:482:LEU:HD23	1.75	0.86
2:B:44:TYR:HE1	2:B:87:ILE:HD11	1.39	0.86
2:A:496:PHE:HE1	2:A:614:ILE:HG12	1.40	0.86
2:A:541:ILE:HB	2:A:594:MET:HE2	1.55	0.86
2:B:351:ILE:H	2:B:351:ILE:HD12	1.39	0.86
2:A:836:GLU:O	2:A:840:ARG:HG3	1.74	0.86
2:A:204:VAL:HG21	2:A:448:VAL:CG2	2.05	0.86
2:B:342:GLU:HG2	2:B:343:THR:H	1.40	0.86
2:A:829:ASN:OD1	2:A:832:ILE:HG13	1.77	0.85
2:B:587:PRO:HB2	2:B:590:ILE:HG12	1.56	0.85
2:B:182:ARG:HD2	2:B:206:ILE:HG21	1.59	0.84
2:B:413:PRO:HB2	2:B:414:PRO:HD3	1.57	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:819:LYS:H	2:A:819:LYS:HE3	1.43	0.84
2:A:803:GLU:HA	2:A:815:VAL:CG2	2.07	0.84
2:B:446:LYS:N	2:B:446:LYS:HD2	1.92	0.84
1:C:928:C:H2'	1:C:929:G:C8	2.13	0.84
2:B:703:ARG:HD2	2:B:707:LEU:HD11	1.60	0.84
1:C:928:C:H2'	1:C:929:G:H8	1.42	0.83
2:A:145:ASP:OD1	2:A:147:SER:HB3	1.78	0.83
2:A:731:HIS:HE1	2:A:833:GLU:OE1	1.60	0.83
2:B:705:TYR:CE2	2:B:805:LEU:HD21	2.13	0.83
2:A:671:ASP:OD2	2:A:800:HIS:HB2	1.78	0.83
2:A:867:GLU:H	2:A:867:GLU:CD	1.86	0.83
2:B:4:LEU:O	2:B:4:LEU:HD23	1.79	0.83
2:B:866:ALA:H	2:B:955:LYS:HZ3	0.83	0.83
2:A:966:ILE:O	2:A:967:GLU:HB2	1.79	0.83
2:B:186:ASP:HB2	2:B:193:LEU:HD11	1.59	0.83
2:A:770:ARG:HD2	2:A:933:PHE:HE2	1.41	0.83
2:B:86:PRO:O	2:B:90:ILE:HG12	1.78	0.83
2:A:732:ARG:HH11	2:A:735:LYS:HD3	1.45	0.82
2:A:826:GLU:C	2:A:828:TRP:N	2.34	0.82
2:A:28:ARG:H	2:A:28:ARG:NE	1.76	0.82
2:B:935:GLU:OE1	2:B:941:GLU:HA	1.80	0.82
1:D:923:A:H4'	1:D:924:A:O5'	1.79	0.82
2:A:51:VAL:O	2:A:54:ALA:HB3	1.80	0.82
2:B:13:TRP:CE2	2:B:803:GLU:HB3	2.15	0.82
2:A:238:VAL:HG11	2:A:298:ASN:HD22	1.45	0.81
2:A:345:ILE:HG12	2:A:346:LEU:N	1.94	0.81
2:A:384:ILE:HG22	2:A:385:LYS:H	1.45	0.81
2:A:887:MET:HE2	2:A:891:MET:HG2	1.61	0.81
2:A:859:LYS:HB3	2:A:941:GLU:HB3	1.63	0.81
1:C:922:C:H4'	1:C:923:A:O5'	1.78	0.81
2:A:355:ILE:HG22	2:A:356:VAL:H	1.45	0.81
2:B:230:LEU:HD23	2:B:230:LEU:H	1.45	0.81
2:A:722:LEU:HD22	2:A:722:LEU:N	1.95	0.81
2:B:826:GLU:C	2:B:828:TRP:N	2.34	0.81
2:B:340:LYS:NZ	2:B:341:ARG:HH12	1.79	0.81
2:B:860:ARG:HB3	2:B:966:ILE:HG22	1.61	0.81
2:A:895:GLU:OE1	2:A:898:LYS:HD2	1.81	0.81
2:A:690:ARG:HH11	2:A:693:GLU:HG3	1.45	0.80
2:B:268:GLU:HG3	2:B:316:ASP:HA	1.63	0.80
2:B:641:ASN:HA	2:B:683:HIS:O	1.80	0.80
2:B:170:LEU:HB2	2:B:176:ILE:HD11	1.62	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:660:ASN:HB2	2:A:663:ASP:CB	2.10	0.80
2:B:186:ASP:HB3	2:B:191:THR:HG23	1.61	0.80
2:A:412:VAL:HG23	2:A:414:PRO:HD2	1.64	0.80
1:C:986:C:N3	2:A:506:LYS:HG2	1.97	0.80
2:A:922:ASN:C	2:A:922:ASN:ND2	2.34	0.80
2:B:384:ILE:HG22	2:B:385:LYS:H	1.47	0.80
2:A:73:ASN:O	2:A:601:TRP:HH2	1.64	0.80
2:A:39:THR:HG23	2:A:604:LEU:HD11	1.63	0.79
1:D:904:G:C2'	1:D:905:G:H5''	2.11	0.79
2:A:931:LYS:O	2:A:935:GLU:HG3	1.80	0.79
2:B:860:ARG:HE	2:B:942:ILE:HA	1.48	0.79
2:B:863:ILE:HB	2:B:953:LYS:HD3	1.64	0.79
1:C:911:C:H2'	1:C:912:C:H6	1.47	0.79
2:B:157:PRO:HB2	2:B:158:PRO:HD3	1.65	0.79
2:A:82:ILE:HG13	2:A:153:THR:HG23	1.63	0.79
2:A:170:LEU:CB	2:A:176:ILE:HD11	2.11	0.79
2:A:732:ARG:NH1	2:A:735:LYS:HD3	1.98	0.79
2:A:922:ASN:ND2	2:A:923:GLU:N	2.30	0.79
2:B:116:LEU:HD12	2:B:119:PHE:CD2	2.17	0.79
2:B:547:LYS:HA	2:B:547:LYS:HE2	1.63	0.79
2:B:919:LYS:O	2:B:922:ASN:HB2	1.82	0.79
2:A:297:ARG:HG2	2:A:304:GLU:HG2	1.63	0.79
2:A:487:ILE:HG22	2:A:489:PRO:O	1.82	0.79
2:B:297:ARG:HG2	2:B:304:GLU:HG2	1.63	0.79
1:D:902:C:H3'	1:D:903:G:H5''	1.64	0.79
2:A:924:GLU:CB	2:A:928:ARG:HH21	1.94	0.78
2:A:186:ASP:HB3	2:A:191:THR:HG23	1.65	0.78
2:A:882:ASP:CG	2:A:883:PHE:H	1.92	0.78
2:B:343:THR:HG23	2:B:344:GLU:H	1.47	0.78
2:B:345:ILE:HG12	2:B:346:LEU:H	1.47	0.78
2:B:464:GLN:HA	2:B:524:TRP:CH2	2.18	0.78
1:C:986:C:H4'	1:C:987:C:C5'	2.14	0.78
2:A:204:VAL:HG21	2:A:448:VAL:HG22	1.66	0.78
2:B:51:VAL:O	2:B:54:ALA:HB3	1.84	0.78
2:B:722:LEU:H	2:B:722:LEU:CD2	1.97	0.78
2:B:949:ASP:HB2	2:B:954:LYS:HE2	1.64	0.78
2:A:348:LYS:NZ	2:A:348:LYS:HB3	1.99	0.78
2:A:871:TRP:CZ3	2:A:918:VAL:HG13	2.18	0.78
2:B:867:GLU:H	2:B:867:GLU:CD	1.92	0.78
2:B:55:ARG:O	2:B:59:ILE:HG13	1.83	0.78
2:B:471:ASN:ND2	2:B:473:GLU:HG2	1.99	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:87:ILE:HG13	2:A:88:VAL:N	1.98	0.78
2:A:393:LEU:HD12	2:A:396:ALA:HB3	1.66	0.78
2:A:482:LEU:HD12	2:A:500:ILE:HD11	1.66	0.78
2:B:45:LEU:HD11	2:B:80:TRP:HB3	1.64	0.78
2:B:333:HIS:HA	2:B:336:LEU:HB2	1.66	0.78
2:A:482:LEU:HD11	2:A:496:PHE:HB3	1.66	0.77
2:A:650:LYS:HD2	2:A:651:MET:H	1.48	0.77
2:B:540:THR:HG23	2:B:541:ILE:HG23	1.64	0.77
2:B:731:HIS:CD2	2:B:829:ASN:H	2.02	0.77
2:B:801:ILE:O	2:B:805:LEU:HG	1.84	0.77
2:A:529:LEU:H	2:A:529:LEU:CD1	1.96	0.77
2:A:209:TYR:HE1	2:A:317:ASN:HD21	1.30	0.77
1:C:985:A:H61	2:A:504:ASP:HB2	1.47	0.77
2:A:860:ARG:HB3	2:A:966:ILE:HG22	1.64	0.77
2:A:871:TRP:CD1	2:A:959:PRO:HG3	2.18	0.77
1:C:986:C:N3	2:A:507:ALA:N	2.32	0.77
2:A:242:TRP:HH2	2:A:332:ASP:HA	1.50	0.77
2:B:446:LYS:HD2	2:B:446:LYS:H	1.47	0.77
2:B:834:ALA:HA	2:B:837:GLU:OE2	1.83	0.77
2:A:819:LYS:H	2:A:819:LYS:CE	1.97	0.77
2:B:678:MET:HE3	2:B:749:THR:HG21	1.66	0.77
2:A:722:LEU:H	2:A:722:LEU:CD2	1.98	0.77
2:B:150:PHE:HD1	2:B:151:TYR:O	1.68	0.77
2:A:770:ARG:NH1	2:A:933:PHE:HD2	1.81	0.76
2:A:919:LYS:HD2	2:A:960:LEU:CD1	2.16	0.76
2:B:845:ASP:O	2:B:849:ILE:HG13	1.84	0.76
2:B:880:LYS:HG3	2:B:885:SER:HB2	1.67	0.76
2:A:198:LEU:HB2	2:A:202:GLU:CG	2.14	0.76
2:B:631:GLU:HA	2:B:634:TRP:CE2	2.20	0.76
2:A:27:ILE:N	2:A:28:ARG:HH21	1.83	0.76
2:B:914:ARG:HH21	2:B:915:THR:HG23	1.51	0.76
2:A:28:ARG:HE	2:A:28:ARG:N	1.81	0.76
2:A:488:LEU:HD12	2:A:606:TRP:CH2	2.21	0.76
2:A:88:VAL:HG21	2:A:513:GLY:HA2	1.66	0.76
2:A:731:HIS:CE1	2:A:833:GLU:OE1	2.39	0.76
2:A:928:ARG:O	2:A:930:ALA:N	2.18	0.76
2:B:82:ILE:HG21	2:B:126:VAL:CG1	2.16	0.76
2:B:887:MET:SD	2:B:906:ILE:HD12	2.26	0.76
2:B:931:LYS:O	2:B:935:GLU:HG3	1.86	0.76
1:D:929:G:H1	1:D:947:U:H3	1.35	0.75
2:B:165:TRP:CD1	2:B:561:PRO:HA	2.21	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:238:VAL:CG1	2:A:298:ASN:HD22	1.98	0.75
2:A:703:ARG:HG2	2:A:761:MET:HE1	1.67	0.75
2:A:949:ASP:HB2	2:A:954:LYS:HE2	1.69	0.75
2:A:641:ASN:HA	2:A:683:HIS:O	1.85	0.75
2:B:767:TYR:HE2	2:B:783:LEU:HD11	1.49	0.75
2:B:678:MET:HB3	2:B:749:THR:HB	1.68	0.75
2:A:492:ARG:HH11	2:A:492:ARG:CG	1.99	0.75
2:A:17:TRP:CH2	2:A:800:HIS:HD2	2.04	0.75
2:A:957:ALA:HB2	2:A:963:ALA:HB2	1.67	0.75
2:B:846:ILE:HG12	2:B:964:ILE:CD1	2.16	0.75
2:A:139:ARG:HG3	2:A:139:ARG:NH1	1.95	0.74
2:A:624:ASN:HD22	2:A:624:ASN:H	1.35	0.74
2:B:211:ILE:HG22	2:B:228:ALA:HB2	1.68	0.74
2:A:213:LYS:HD2	2:A:435:GLY:O	1.87	0.74
2:B:631:GLU:HA	2:B:634:TRP:NE1	2.01	0.74
2:A:551:GLU:O	2:A:553:LYS:HG2	1.86	0.74
2:B:89:GLY:O	2:B:93:ARG:HG3	1.87	0.74
2:B:681:ALA:HA	2:B:750:ARG:HG3	1.68	0.74
2:A:755:TRP:O	2:A:759:SER:HB3	1.87	0.74
2:A:645:THR:HG22	2:A:650:LYS:HA	1.68	0.74
1:C:908:U:H5'	1:C:961:C:OP2	1.88	0.74
1:D:902:C:C3'	1:D:903:G:H5''	2.17	0.74
2:A:354:ARG:HD2	2:A:376:VAL:CG1	2.17	0.74
2:A:432:LEU:HD11	2:A:439:ILE:HG13	1.70	0.74
2:B:836:GLU:O	2:B:840:ARG:HG3	1.87	0.74
2:A:30:LYS:HB2	2:A:73:ASN:ND2	1.96	0.73
2:A:230:LEU:H	2:A:230:LEU:CD2	2.01	0.73
2:B:26:ASN:CB	2:B:28:ARG:HH22	2.01	0.73
2:B:928:ARG:O	2:B:930:ALA:N	2.21	0.73
2:A:566:TYR:HA	2:A:570:GLU:HB2	1.70	0.73
2:A:766:TRP:CH2	2:A:770:ARG:HD3	2.23	0.73
2:B:703:ARG:HH11	2:B:703:ARG:CB	2.00	0.73
2:B:859:LYS:HB3	2:B:941:GLU:HB3	1.69	0.73
2:A:345:ILE:HG23	2:A:346:LEU:HD13	1.71	0.73
2:B:198:LEU:CB	2:B:202:GLU:HG2	2.19	0.73
2:B:544:HIS:O	2:B:548:LEU:HG	1.87	0.73
2:B:857:ASN:ND2	2:B:967:GLU:HG2	2.03	0.73
2:B:957:ALA:HB2	2:B:963:ALA:HB2	1.67	0.73
1:C:982:C:H2'	1:C:983:G:C8	2.24	0.73
2:A:413:PRO:HB2	2:A:414:PRO:HD3	1.70	0.73
2:A:537:ALA:O	2:A:540:THR:HG22	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:691:ARG:O	2:A:694:VAL:HG12	1.88	0.73
2:B:920:ARG:C	2:B:922:ASN:H	1.97	0.73
2:A:42:PHE:CD1	2:A:81:HIS:HB2	2.24	0.73
2:A:233:GLU:HB3	2:A:423:VAL:HG23	1.68	0.73
2:B:882:ASP:CG	2:B:883:PHE:N	2.47	0.73
2:A:792:ARG:HG3	2:A:792:ARG:NH2	2.04	0.73
2:A:832:ILE:HA	2:A:835:GLU:HG3	1.71	0.73
2:A:920:ARG:C	2:A:922:ASN:H	1.96	0.73
2:A:17:TRP:CH2	2:A:800:HIS:CD2	2.76	0.73
2:A:373:PHE:CD1	2:A:374:PRO:HD3	2.24	0.73
2:B:95:LYS:C	2:B:97:ARG:H	1.96	0.72
2:B:865:THR:HG1	2:B:871:TRP:CD1	2.07	0.72
2:A:250:VAL:HG12	2:A:285:GLU:HA	1.70	0.72
2:A:342:GLU:HG2	2:A:343:THR:H	1.54	0.72
2:A:803:GLU:CD	2:A:815:VAL:HG23	2.14	0.72
2:A:558:LYS:HD2	2:A:583:LYS:O	1.89	0.72
2:A:860:ARG:NH2	2:A:862:TYR:HB3	2.04	0.72
2:B:734:ASN:HD21	2:B:824:VAL:N	1.86	0.72
2:B:803:GLU:OE2	2:B:815:VAL:N	2.23	0.72
2:B:925:LYS:HA	2:B:928:ARG:HG2	1.68	0.72
2:A:75:LEU:C	2:A:75:LEU:HD12	2.14	0.72
2:A:771:THR:HG22	2:A:774:ARG:HD3	1.70	0.72
2:B:695:GLY:O	2:B:698:ARG:HB3	1.90	0.72
2:B:848:GLU:O	2:B:852:VAL:HG23	1.89	0.72
2:A:82:ILE:H	2:A:152:THR:HG1	1.35	0.72
2:A:488:LEU:HD12	2:A:606:TRP:CZ3	2.24	0.72
2:A:239:THR:CG2	2:A:326:PRO:HD2	2.20	0.72
2:B:757:PHE:HD1	2:B:794:MET:SD	2.12	0.72
2:A:423:VAL:C	2:A:425:GLU:H	1.95	0.72
2:B:480:LYS:HA	2:B:483:GLU:OE1	1.89	0.72
2:B:167:PHE:HA	2:B:170:LEU:CD1	2.19	0.72
2:B:467:ILE:HG13	2:B:508:CYS:SG	2.30	0.72
2:A:863:ILE:HB	2:A:953:LYS:HD3	1.70	0.71
2:B:423:VAL:C	2:B:425:GLU:H	1.97	0.71
2:A:95:LYS:C	2:A:97:ARG:H	1.96	0.71
2:A:119:PHE:CD1	2:A:125:ILE:HG12	2.24	0.71
2:A:59:ILE:HG12	2:A:678:MET:HE1	1.71	0.71
2:A:690:ARG:HD3	2:A:693:GLU:OE2	1.89	0.71
2:B:32:LYS:HG2	2:B:600:TYR:CD1	2.25	0.71
2:B:729:MET:HE2	2:B:729:MET:HA	1.71	0.71
2:A:860:ARG:HH22	2:A:862:TYR:N	1.87	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:22:ILE:HG13	2:B:817:LEU:HD21	1.73	0.71
2:B:784:ARG:NH2	2:B:810:GLY:H	1.88	0.71
2:B:957:ALA:HB2	2:B:963:ALA:CB	2.21	0.71
2:A:219:ASN:HD22	2:A:220:GLY:H	1.37	0.71
2:A:731:HIS:CD2	2:A:829:ASN:H	2.08	0.71
2:A:770:ARG:NH1	2:A:933:PHE:CD2	2.59	0.71
2:A:717:LYS:HD3	2:A:717:LYS:C	2.15	0.71
2:A:957:ALA:HB2	2:A:963:ALA:CB	2.20	0.71
2:A:67:LYS:HD3	2:A:70:GLN:HE21	1.54	0.71
2:A:734:ASN:OD1	2:A:823:PRO:HA	1.91	0.71
2:B:30:LYS:HE3	2:B:71:GLY:O	1.90	0.71
2:B:890:LEU:HD12	2:B:906:ILE:HD11	1.73	0.71
2:A:730:LEU:HB3	2:A:827:TRP:HE1	1.54	0.70
2:A:198:LEU:HD22	2:A:202:GLU:HA	1.73	0.70
2:A:631:GLU:HA	2:A:634:TRP:CE2	2.26	0.70
2:B:282:VAL:HG12	2:B:283:ILE:N	2.07	0.70
2:A:276:GLN:HA	2:A:460:ILE:HD13	1.71	0.70
2:A:342:GLU:HG2	2:A:343:THR:N	2.04	0.70
2:A:419:PRO:HG2	2:A:422:GLU:HG3	1.71	0.70
2:A:857:ASN:O	2:A:940:ILE:HD11	1.90	0.70
2:B:471:ASN:HD21	2:B:473:GLU:HG2	1.55	0.70
2:B:826:GLU:O	2:B:827:TRP:HB3	1.91	0.70
1:C:970:A:H4'	1:C:971:A:OP1	1.91	0.70
2:A:198:LEU:HB2	2:A:202:GLU:CD	2.15	0.70
2:A:824:VAL:HG11	2:A:827:TRP:HE3	1.56	0.70
2:B:487:ILE:HG22	2:B:489:PRO:O	1.91	0.70
2:A:613:LEU:O	2:A:618:LEU:HB2	1.91	0.70
2:A:140:ALA:HB2	2:A:665:ILE:HD11	1.72	0.70
2:B:235:VAL:HA	2:B:323:MET:HE1	1.73	0.70
2:A:204:VAL:HG21	2:A:448:VAL:HG21	1.74	0.70
2:A:333:HIS:HA	2:A:336:LEU:HB2	1.73	0.70
2:A:795:ALA:HB3	2:A:796:PRO:HD3	1.72	0.70
2:A:826:GLU:O	2:A:827:TRP:HB3	1.90	0.70
2:A:12:LYS:NZ	2:A:16:ARG:HH12	1.90	0.70
2:B:803:GLU:OE2	2:B:815:VAL:HG12	1.91	0.70
2:A:866:ALA:N	2:A:955:LYS:NZ	2.27	0.69
2:A:919:LYS:O	2:A:922:ASN:HB2	1.92	0.69
2:B:297:ARG:HB3	2:B:297:ARG:NH2	2.07	0.69
2:B:927:LEU:CD1	2:B:944:ILE:HD12	2.23	0.69
1:C:920:G:H5''	1:C:921:U:H5	1.57	0.69
2:A:62:VAL:HG21	2:A:678:MET:HE2	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:339:LEU:HD22	2:A:340:LYS:N	2.08	0.69
2:A:374:PRO:HG2	2:A:379:VAL:HG21	1.74	0.69
2:B:660:ASN:HB2	2:B:663:ASP:CB	2.22	0.69
2:B:690:ARG:HB3	2:B:690:ARG:NH1	2.06	0.69
2:A:22:ILE:HG23	2:A:23:PHE:CD1	2.27	0.69
2:A:165:TRP:HD1	2:A:561:PRO:HA	1.58	0.69
2:B:741:THR:HG1	2:B:820:TRP:HZ3	1.41	0.69
1:C:923:A:H4'	1:C:924:A:O5'	1.91	0.69
2:A:91:ALA:O	2:A:94:ILE:HG13	1.91	0.69
2:B:400:ILE:HD12	2:B:401:TYR:N	2.06	0.69
2:B:770:ARG:HD2	2:B:933:PHE:CE2	2.27	0.69
2:A:577:GLU:OE2	2:A:592:HIS:HB2	1.92	0.69
2:B:7:LYS:HB2	2:B:7:LYS:NZ	2.07	0.69
2:B:675:LEU:CD2	2:B:697:LEU:HD21	2.22	0.69
2:B:675:LEU:HD22	2:B:701:ILE:HD11	1.74	0.69
2:A:163:ILE:CD1	2:A:531:ASP:HB2	2.22	0.69
2:A:449:ILE:N	2:A:449:ILE:HD12	2.08	0.69
2:A:863:ILE:HG22	2:A:953:LYS:HG2	1.74	0.69
2:B:33:GLU:CD	2:B:33:GLU:H	2.00	0.69
2:B:35:LYS:HB2	2:B:601:TRP:CZ3	2.28	0.69
2:A:45:LEU:HD11	2:A:80:TRP:HB3	1.75	0.69
2:A:10:GLU:O	2:A:14:GLN:HG3	1.93	0.69
2:A:930:ALA:HB1	2:A:934:MET:HE2	1.75	0.69
2:A:480:LYS:CE	2:A:484:ARG:HH22	1.99	0.68
2:A:730:LEU:HB3	2:A:827:TRP:CD1	2.28	0.68
2:B:341:ARG:HD3	2:B:341:ARG:N	2.07	0.68
2:B:14:GLN:O	2:B:18:LEU:HB2	1.93	0.68
2:B:566:TYR:HA	2:B:570:GLU:HB3	1.75	0.68
2:A:30:LYS:CB	2:A:73:ASN:HD22	1.98	0.68
2:A:198:LEU:CB	2:A:202:GLU:HG2	2.23	0.68
2:A:239:THR:HG23	2:A:326:PRO:HD2	1.74	0.68
2:B:65:ARG:HA	2:B:68:ARG:NH1	2.08	0.68
2:B:650:LYS:HE2	2:B:651:MET:N	2.03	0.68
2:B:871:TRP:NE1	2:B:959:PRO:HB3	2.09	0.68
2:A:629:PHE:O	2:A:631:GLU:N	2.25	0.68
2:B:116:LEU:HD12	2:B:119:PHE:HD2	1.59	0.68
2:B:276:GLN:O	2:B:460:ILE:HD12	1.92	0.68
2:B:767:TYR:CE2	2:B:783:LEU:HD11	2.27	0.68
2:A:717:LYS:HD3	2:A:717:LYS:O	1.94	0.68
2:B:28:ARG:HH11	2:B:28:ARG:HG3	1.59	0.68
2:A:82:ILE:HG21	2:A:126:VAL:HG13	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:652:SER:OG	2:A:655:LYS:HB2	1.94	0.68
2:A:722:LEU:N	2:A:722:LEU:CD2	2.55	0.68
2:A:924:GLU:CD	2:A:927:LEU:HD13	2.19	0.68
2:B:770:ARG:HA	2:B:933:PHE:HE2	1.58	0.68
2:B:26:ASN:HB2	2:B:29:ASP:OD2	1.93	0.68
2:B:198:LEU:H	2:B:198:LEU:HD12	1.59	0.68
2:B:734:ASN:ND2	2:B:823:PRO:HA	2.07	0.68
1:C:929:G:H1	1:C:947:U:H3	1.42	0.68
1:C:988:A:H5''	2:A:528:SER:OG	1.94	0.68
2:A:221:GLU:OE2	2:A:221:GLU:HA	1.93	0.68
2:B:237:GLY:O	2:B:325:VAL:HG13	1.94	0.68
2:B:300:VAL:HG13	2:B:301:SER:H	1.59	0.68
2:B:185:TRP:CZ2	2:B:190:GLY:HA2	2.29	0.67
2:B:345:ILE:HG12	2:B:346:LEU:N	2.09	0.67
2:B:826:GLU:CD	2:B:826:GLU:N	2.52	0.67
1:D:920:G:H5''	1:D:921:U:H5	1.59	0.67
2:B:894:SER:C	2:B:896:ILE:H	2.03	0.67
2:B:92:GLU:O	2:B:95:LYS:HB3	1.94	0.67
2:B:555:ASP:HB3	2:B:558:LYS:CG	2.24	0.67
2:B:795:ALA:HB3	2:B:796:PRO:HD3	1.77	0.67
2:A:919:LYS:H	2:A:919:LYS:CE	2.07	0.67
2:B:26:ASN:CB	2:B:28:ARG:NH2	2.55	0.67
1:D:977:G:H2'	1:D:978:C:C6	2.30	0.67
2:A:404:GLU:O	2:A:420:VAL:HG21	1.95	0.67
2:A:872:LYS:O	2:A:876:VAL:HG23	1.94	0.67
2:A:894:SER:C	2:A:896:ILE:H	2.02	0.67
2:B:26:ASN:HB2	2:B:29:ASP:CG	2.19	0.67
2:A:242:TRP:CH2	2:A:332:ASP:HA	2.29	0.67
2:B:218:GLU:CD	2:B:219:ASN:HD22	2.03	0.67
2:B:614:ILE:N	2:B:615:PRO:HD2	2.09	0.67
2:A:139:ARG:NH2	2:A:666:GLU:OE1	2.27	0.67
2:A:870:LYS:HE2	2:A:905:LYS:HE3	1.77	0.67
2:A:933:PHE:CD1	2:A:933:PHE:C	2.72	0.67
1:C:916:C:OP1	1:C:916:C:H4'	1.93	0.66
2:A:428:ALA:O	2:A:432:LEU:HD23	1.95	0.66
2:B:729:MET:HE1	2:B:763:ASP:C	2.18	0.66
2:A:891:MET:SD	2:A:897:ARG:HG3	2.35	0.66
2:B:57:TYR:O	2:B:60:PRO:HG2	1.95	0.66
2:B:741:THR:OG1	2:B:820:TRP:HZ3	1.78	0.66
2:A:529:LEU:HD12	2:A:529:LEU:N	2.06	0.66
2:A:536:MET:SD	2:A:607:ARG:NH1	2.69	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:682:GLU:OE1	2:A:748:ARG:HB3	1.95	0.66
2:B:136:THR:HG22	2:B:661:PHE:HD2	1.60	0.66
2:B:326:PRO:HA	2:B:332:ASP:HB2	1.77	0.66
2:A:266:SER:HB2	2:A:269:ALA:HB2	1.78	0.66
2:A:488:LEU:HD22	2:A:683:HIS:CE1	2.31	0.66
2:A:741:THR:HG1	2:A:820:TRP:HZ3	1.42	0.66
2:B:935:GLU:HG2	2:B:942:ILE:HD13	1.78	0.66
2:A:703:ARG:HG3	2:A:707:LEU:HD12	1.78	0.66
2:B:871:TRP:CZ3	2:B:918:VAL:HG13	2.30	0.66
2:B:636:LYS:HZ2	2:B:636:LYS:HB3	1.60	0.66
2:B:793:LEU:CD2	2:B:821:PRO:HG2	2.25	0.66
2:B:921:ILE:HB	2:B:928:ARG:NH2	2.09	0.66
2:A:188:VAL:HG23	2:A:189:VAL:N	2.06	0.66
2:A:434:LYS:HB3	2:A:436:ILE:HG12	1.77	0.66
2:A:921:ILE:HD12	2:A:928:ARG:NH1	2.03	0.66
2:B:171:LYS:HG2	2:B:176:ILE:HD12	1.78	0.66
2:B:459:LYS:NZ	2:B:461:ILE:HD13	2.11	0.66
2:B:690:ARG:HB3	2:B:690:ARG:CZ	2.25	0.66
2:A:947:THR:HG23	2:A:948:GLU:N	2.11	0.66
2:B:256:ARG:HG3	2:B:257:LYS:H	1.61	0.66
2:A:784:ARG:HH22	2:A:810:GLY:H	1.45	0.65
2:B:139:ARG:HG3	2:B:139:ARG:HH11	1.60	0.65
1:D:983:G:C2'	1:D:984:C:H5''	2.25	0.65
2:A:860:ARG:NH1	2:A:943:ILE:N	2.41	0.65
2:B:197:ASP:HB3	2:B:451:ARG:HB2	1.78	0.65
2:B:650:LYS:CE	2:B:651:MET:H	2.05	0.65
2:A:83:THR:HG23	2:A:152:THR:HB	1.78	0.65
2:B:198:LEU:HB2	2:B:202:GLU:CG	2.20	0.65
2:B:537:ALA:HB2	2:B:602:TYR:CZ	2.31	0.65
2:A:354:ARG:HD2	2:A:376:VAL:HG12	1.78	0.65
2:A:914:ARG:NH2	2:A:915:THR:HG23	2.11	0.65
2:A:82:ILE:HG21	2:A:126:VAL:CG1	2.26	0.65
2:A:730:LEU:HD22	2:A:827:TRP:CZ2	2.31	0.65
2:A:210:ILE:CD1	2:A:232:PRO:HG3	2.24	0.65
2:A:297:ARG:HG2	2:A:304:GLU:CG	2.25	0.65
1:C:967:U:H2'	1:C:969:G:N7	2.11	0.65
2:A:86:PRO:O	2:A:90:ILE:HG13	1.95	0.65
2:A:109:TYR:OH	2:A:653:LYS:HE2	1.96	0.65
2:A:590:ILE:O	2:A:594:MET:HG3	1.97	0.65
2:A:647:GLU:OE2	2:A:690:ARG:HA	1.97	0.65
2:A:767:TYR:HE2	2:A:783:LEU:CD1	2.09	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:914:ARG:HH21	2:A:915:THR:HG23	1.62	0.65
2:B:50:HIS:CE1	2:B:52:GLY:HA3	2.31	0.65
2:B:616:ASN:ND2	2:B:617:HIS:H	1.93	0.65
2:A:233:GLU:HA	2:A:427:ILE:HD12	1.77	0.65
2:B:678:MET:HE3	2:B:749:THR:CG2	2.27	0.65
2:A:4:LEU:O	2:A:4:LEU:HD23	1.97	0.65
2:B:87:ILE:HD13	2:B:126:VAL:CG2	2.27	0.65
2:B:540:THR:CG2	2:B:541:ILE:HG23	2.25	0.65
2:A:197:ASP:HB3	2:A:451:ARG:HB2	1.78	0.64
2:A:650:LYS:HD2	2:A:651:MET:N	2.11	0.64
2:B:39:THR:HG22	2:B:40:VAL:H	1.60	0.64
2:B:300:VAL:HG13	2:B:301:SER:N	2.12	0.64
2:B:924:GLU:O	2:B:928:ARG:N	2.28	0.64
2:B:924:GLU:HB3	2:B:928:ARG:HH21	1.62	0.64
2:B:922:ASN:HD22	2:B:923:GLU:N	1.96	0.64
2:A:345:ILE:CG1	2:A:346:LEU:H	2.06	0.64
2:B:27:ILE:HG13	2:B:28:ARG:N	2.13	0.64
2:B:198:LEU:HD22	2:B:202:GLU:HA	1.78	0.64
2:B:724:ASP:HA	2:B:727:ARG:HG3	1.79	0.64
2:B:880:LYS:CG	2:B:885:SER:HB2	2.28	0.64
2:A:139:ARG:HH11	2:A:139:ARG:CG	2.09	0.64
2:A:467:ILE:HG13	2:A:508:CYS:HB3	1.80	0.64
2:B:563:PHE:CD1	2:B:584:THR:HG21	2.33	0.64
2:B:632:GLU:HG3	2:B:633:HIS:ND1	2.13	0.64
2:A:313:VAL:HG12	2:A:322:VAL:HG21	1.78	0.64
2:A:890:LEU:CD1	2:A:906:ILE:HD11	2.27	0.64
2:B:289:GLU:O	2:B:292:ILE:HB	1.98	0.64
2:B:570:GLU:OE1	2:B:576:LYS:HE2	1.98	0.64
1:C:920:G:H5''	1:C:921:U:C5	2.33	0.64
1:D:977:G:H2'	1:D:978:C:H6	1.62	0.64
2:A:492:ARG:HH11	2:A:492:ARG:HG2	1.63	0.64
2:A:871:TRP:HH2	2:A:919:LYS:HE3	1.61	0.64
2:B:660:ASN:HB2	2:B:663:ASP:HB3	1.80	0.64
1:D:943:C:H2'	1:D:944:C:C6	2.33	0.64
2:A:212:ILE:HD13	2:A:235:VAL:CG1	2.27	0.64
2:A:475:LYS:NZ	2:A:503:LEU:O	2.31	0.64
2:B:860:ARG:HB3	2:B:966:ILE:HA	1.78	0.64
2:B:866:ALA:N	2:B:955:LYS:NZ	2.31	0.64
2:A:136:THR:HG23	2:A:662:ILE:HB	1.80	0.64
2:A:49:LEU:HD12	2:A:49:LEU:N	2.10	0.63
2:A:92:GLU:O	2:A:95:LYS:HB3	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:73:ASN:O	2:B:601:TRP:HH2	1.81	0.63
2:B:78:MET:HE3	2:B:137:PHE:HE2	1.62	0.63
2:B:641:ASN:C	2:B:641:ASN:HD22	2.06	0.63
2:A:342:GLU:CG	2:A:343:THR:H	2.11	0.63
2:A:924:GLU:O	2:A:928:ARG:N	2.28	0.63
2:B:373:PHE:N	2:B:374:PRO:HD2	2.14	0.63
2:B:213:LYS:HD2	2:B:435:GLY:O	1.99	0.63
2:B:256:ARG:HH11	2:B:278:ARG:HG3	1.63	0.63
2:B:958:MET:CE	2:B:959:PRO:HD2	2.27	0.63
2:A:272:LYS:HE3	2:A:442:GLU:OE1	1.98	0.63
2:A:343:THR:HG23	2:A:344:GLU:N	2.12	0.63
2:B:755:TRP:O	2:B:759:SER:HB3	1.99	0.63
2:B:909:LYS:NZ	2:B:914:ARG:O	2.29	0.63
2:A:616:ASN:ND2	2:A:617:HIS:N	2.24	0.63
2:B:10:GLU:O	2:B:14:GLN:HG3	1.97	0.63
2:A:85:SER:H	2:A:86:PRO:CD	2.12	0.63
2:A:724:ASP:HA	2:A:727:ARG:CG	2.19	0.63
2:B:139:ARG:HG3	2:B:139:ARG:NH1	2.13	0.63
2:B:681:ALA:CA	2:B:750:ARG:HG3	2.28	0.63
2:B:428:ALA:O	2:B:432:LEU:HD23	1.98	0.63
2:B:87:ILE:HD13	2:B:126:VAL:HG22	1.79	0.63
2:B:495:GLN:HE21	2:B:614:ILE:HG21	1.63	0.63
2:A:282:VAL:HG12	2:A:283:ILE:H	1.64	0.63
2:A:631:GLU:HA	2:A:634:TRP:NE1	2.14	0.63
2:A:728:TRP:HE3	2:A:729:MET:N	1.97	0.63
2:A:924:GLU:O	2:A:927:LEU:HB3	1.99	0.63
2:B:45:LEU:HD11	2:B:80:TRP:CB	2.29	0.63
2:A:268:GLU:OE1	2:A:268:GLU:N	2.26	0.62
2:A:544:HIS:H	2:A:544:HIS:CD2	2.15	0.62
2:B:332:ASP:O	2:B:333:HIS:HB2	1.99	0.62
1:C:918:U:H5''	1:C:919:G:OP1	1.98	0.62
2:A:180:ALA:O	2:A:181:HIS:HB2	1.99	0.62
2:B:216:LEU:HD11	2:B:294:LYS:HB3	1.80	0.62
2:B:273:LEU:HG	2:B:440:MET:HE3	1.80	0.62
2:B:764:LEU:HD13	2:B:786:LEU:HD13	1.80	0.62
2:A:235:VAL:HB	2:A:300:VAL:HG11	1.79	0.62
2:A:482:LEU:HD23	2:A:482:LEU:C	2.24	0.62
2:A:862:TYR:C	2:A:862:TYR:CD2	2.77	0.62
2:B:51:VAL:HG11	2:B:689:TRP:CE3	2.33	0.62
2:A:41:ALA:HA	2:A:607:ARG:NH2	2.15	0.62
2:A:126:VAL:HG12	2:A:126:VAL:O	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:724:ASP:CA	2:A:727:ARG:HG3	2.20	0.62
2:A:730:LEU:CB	2:A:827:TRP:HE1	2.12	0.62
2:A:860:ARG:C	2:A:860:ARG:NE	2.57	0.62
1:C:911:C:H2'	1:C:912:C:C6	2.33	0.62
2:A:544:HIS:HB2	2:A:594:MET:HE3	1.81	0.62
2:A:733:LEU:O	2:A:737:ILE:HG13	1.99	0.62
2:A:94:ILE:HD12	2:A:95:LYS:N	2.14	0.62
2:A:145:ASP:OD1	2:A:145:ASP:C	2.43	0.62
2:A:168:TRP:CH2	2:A:520:TRP:HB3	2.34	0.62
2:A:306:ILE:HG12	2:A:307:ILE:N	2.14	0.62
2:A:540:THR:OG1	2:A:598:PHE:HA	2.00	0.62
2:A:7:LYS:HB2	2:A:7:LYS:NZ	2.15	0.62
2:B:181:HIS:ND1	2:B:464:GLN:HG2	2.14	0.62
2:B:531:ASP:OD2	2:B:532:SER:N	2.32	0.62
2:A:213:LYS:HB2	2:A:224:TYR:CD2	2.35	0.62
2:B:68:ARG:NH2	2:B:143:SER:HB3	2.14	0.62
2:B:85:SER:H	2:B:86:PRO:HD3	1.64	0.62
2:B:126:VAL:O	2:B:126:VAL:HG12	1.99	0.62
2:B:212:ILE:HD13	2:B:235:VAL:HG12	1.82	0.62
2:B:277:ASP:O	2:B:278:ARG:HG3	1.99	0.62
1:C:914:A:H1'	1:C:925:A:C6	2.35	0.62
2:A:186:ASP:HB2	2:A:193:LEU:HD11	1.82	0.62
2:A:702:GLU:O	2:A:706:GLU:HG3	2.00	0.62
2:B:234:THR:HG22	2:B:325:VAL:HG11	1.80	0.62
2:A:709:SER:O	2:A:712:ALA:HB3	1.99	0.62
2:A:776:ASP:OD2	2:A:778:ALA:HB3	1.99	0.62
2:A:860:ARG:HH11	2:A:943:ILE:H	1.48	0.62
2:B:140:ALA:O	2:B:674:ARG:NH1	2.31	0.62
2:B:709:SER:O	2:B:712:ALA:HB3	2.00	0.62
1:D:970:A:H2'	1:D:972:U:OP2	2.00	0.61
2:A:906:ILE:O	2:A:910:LEU:HB2	2.00	0.61
2:B:49:LEU:HD12	2:B:49:LEU:N	2.13	0.61
2:B:793:LEU:HD21	2:B:821:PRO:HG2	1.81	0.61
2:A:297:ARG:NH2	2:A:297:ARG:CB	2.63	0.61
2:B:745:GLU:HA	2:B:745:GLU:OE2	1.99	0.61
2:B:928:ARG:C	2:B:930:ALA:H	2.09	0.61
1:C:986:C:C2	2:A:507:ALA:HB3	2.36	0.61
2:A:11:GLU:O	2:A:15:LYS:HG3	2.00	0.61
2:A:102:ILE:HD12	2:A:103:TRP:N	2.15	0.61
2:A:882:ASP:CG	2:A:883:PHE:N	2.56	0.61
2:B:44:TYR:CE1	2:B:87:ILE:HD11	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:264:ILE:HG21	2:B:291:LEU:HD21	1.81	0.61
2:A:326:PRO:HA	2:A:332:ASP:HB2	1.81	0.61
2:A:803:GLU:HA	2:A:815:VAL:HG23	1.82	0.61
2:B:44:TYR:OH	2:B:87:ILE:HG13	2.00	0.61
2:B:401:TYR:O	2:B:405:TYR:HB2	2.00	0.61
2:B:920:ARG:HE	2:B:920:ARG:CA	2.01	0.61
2:A:864:TYR:CZ	2:A:922:ASN:OD1	2.53	0.61
2:B:57:TYR:C	2:B:60:PRO:HD2	2.26	0.61
2:B:91:ALA:O	2:B:94:ILE:HG13	1.99	0.61
2:B:345:ILE:CG1	2:B:346:LEU:H	2.13	0.61
2:B:723:LYS:HG3	2:B:724:ASP:H	1.66	0.61
2:A:26:ASN:O	2:A:29:ASP:HB2	2.01	0.61
2:A:297:ARG:NH2	2:A:297:ARG:HB3	2.15	0.61
2:A:857:ASN:ND2	2:A:967:GLU:HG2	2.16	0.61
2:A:924:GLU:OE2	2:A:927:LEU:HD13	2.01	0.61
2:B:729:MET:HE3	2:B:767:TYR:HB2	1.82	0.61
2:B:879:GLU:O	2:B:880:LYS:HD2	2.00	0.61
2:A:618:LEU:O	2:A:621:PHE:HB3	2.00	0.61
2:B:277:ASP:OD1	2:B:462:HIS:NE2	2.33	0.61
2:B:867:GLU:CD	2:B:867:GLU:N	2.57	0.61
2:B:890:LEU:CD1	2:B:906:ILE:HD11	2.31	0.61
2:A:893:ASP:OD1	2:A:894:SER:O	2.19	0.61
2:A:919:LYS:HD2	2:A:960:LEU:HD11	1.82	0.61
2:B:145:ASP:OD1	2:B:147:SER:HB3	1.99	0.61
2:B:914:ARG:NE	2:B:915:THR:O	2.34	0.61
2:A:235:VAL:HG11	2:A:431:MET:HE1	1.82	0.61
2:A:928:ARG:C	2:A:930:ALA:H	2.08	0.61
2:B:28:ARG:NH1	2:B:28:ARG:H	1.98	0.61
1:D:970:A:H4'	1:D:971:A:OP1	2.01	0.61
2:A:866:ALA:CA	2:A:955:LYS:HZ3	2.11	0.61
2:B:770:ARG:HA	2:B:933:PHE:CE2	2.35	0.61
2:A:94:ILE:HD11	2:A:120:GLU:N	2.15	0.60
2:A:492:ARG:HD2	2:A:614:ILE:CD1	2.30	0.60
2:A:123:ILE:O	2:A:127:LYS:HB2	2.00	0.60
2:A:241:MET:HB2	2:A:307:ILE:HA	1.81	0.60
2:A:567:ILE:O	2:A:568:PHE:CG	2.54	0.60
2:A:803:GLU:OE2	2:A:814:PHE:HB3	2.01	0.60
2:B:448:VAL:HG12	2:B:456:ALA:HB3	1.82	0.60
2:B:730:LEU:HB3	2:B:827:TRP:NE1	2.16	0.60
2:A:45:LEU:HD11	2:A:80:TRP:CB	2.31	0.60
2:A:427:ILE:O	2:A:431:MET:HG3	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:860:ARG:NE	2:A:860:ARG:O	2.35	0.60
2:A:381:LYS:HB3	2:A:382:LEU:HD12	1.83	0.60
2:A:594:MET:O	2:A:597:GLU:HB2	2.01	0.60
2:B:748:ARG:HB3	2:B:748:ARG:HH11	1.67	0.60
2:B:935:GLU:CD	2:B:942:ILE:H	2.09	0.60
2:A:210:ILE:HG22	2:A:439:ILE:HG12	1.83	0.60
2:A:234:THR:HG22	2:A:325:VAL:HG11	1.83	0.60
2:A:461:ILE:CG2	2:A:464:GLN:HB2	2.32	0.60
2:B:166:GLN:O	2:B:170:LEU:HG	2.01	0.60
2:B:186:ASP:HB3	2:B:191:THR:CG2	2.32	0.60
1:C:976:C:O2'	1:C:977:G:H5'	2.01	0.60
1:C:953:A:H5'	1:C:954:G:OP1	2.02	0.60
2:A:12:LYS:HZ3	2:A:16:ARG:HH12	1.50	0.60
2:A:266:SER:HB2	2:A:269:ALA:CB	2.32	0.60
2:A:297:ARG:HG2	2:A:304:GLU:CD	2.27	0.60
2:A:919:LYS:H	2:A:919:LYS:HE3	1.66	0.60
2:A:919:LYS:NZ	2:A:960:LEU:HD11	2.16	0.60
2:B:32:LYS:HG2	2:B:600:TYR:HD1	1.65	0.60
2:B:85:SER:H	2:B:86:PRO:CD	2.14	0.60
2:B:266:SER:HB3	2:B:269:ALA:HB2	1.83	0.60
1:D:979:C:H2'	1:D:980:C:C6	2.37	0.60
2:A:412:VAL:CG2	2:A:414:PRO:HD2	2.32	0.60
2:A:468:ASP:C	2:A:470:GLY:H	2.08	0.60
2:B:468:ASP:C	2:B:470:GLY:H	2.09	0.60
2:B:781:TYR:CE2	2:B:785:THR:HG21	2.37	0.60
2:B:781:TYR:O	2:B:785:THR:HG23	2.02	0.60
2:A:95:LYS:C	2:A:97:ARG:N	2.58	0.60
2:A:560:THR:HB	2:A:561:PRO:HD2	1.84	0.60
2:A:767:TYR:CZ	2:A:782:VAL:HG11	2.37	0.60
2:B:79:ALA:HB1	2:B:150:PHE:O	2.01	0.60
2:B:282:VAL:HG12	2:B:283:ILE:H	1.66	0.60
2:A:857:ASN:OD1	2:A:967:GLU:HA	2.02	0.59
2:B:725:ILE:HG21	2:B:771:THR:CG2	2.31	0.59
2:A:17:TRP:HH2	2:A:800:HIS:CD2	2.20	0.59
2:A:142:PHE:C	2:A:144:VAL:H	2.11	0.59
2:A:297:ARG:HH21	2:A:297:ARG:HB2	1.67	0.59
2:A:354:ARG:HD2	2:A:376:VAL:HG13	1.82	0.59
2:A:915:THR:OG1	2:A:916:PHE:N	2.31	0.59
2:B:540:THR:OG1	2:B:598:PHE:HA	2.01	0.59
2:B:569:LEU:HA	2:B:630:ARG:HD3	1.85	0.59
2:B:746:GLU:HB2	2:B:748:ARG:HD2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:678:MET:HB3	2:A:749:THR:HB	1.84	0.59
2:A:895:GLU:OE1	2:A:898:LYS:CD	2.50	0.59
2:A:960:LEU:N	2:A:960:LEU:HD22	2.17	0.59
2:B:142:PHE:C	2:B:144:VAL:H	2.10	0.59
2:B:860:ARG:C	2:B:860:ARG:CZ	2.75	0.59
2:A:711:PHE:HA	2:A:714:TYR:CD2	2.38	0.59
2:A:914:ARG:NE	2:A:915:THR:O	2.35	0.59
2:A:933:PHE:C	2:A:933:PHE:HD1	2.08	0.59
2:B:339:LEU:HD22	2:B:340:LYS:N	2.17	0.59
2:B:475:LYS:HG2	2:B:479:ARG:NH2	2.18	0.59
2:B:864:TYR:HH	2:B:871:TRP:HZ2	1.49	0.59
2:B:935:GLU:OE1	2:B:942:ILE:N	2.34	0.59
2:A:75:LEU:HD23	2:A:601:TRP:CD2	2.37	0.59
2:A:79:ALA:HB1	2:A:150:PHE:O	2.01	0.59
2:A:182:ARG:O	2:A:183:VAL:HB	2.02	0.59
2:A:824:VAL:HG11	2:A:827:TRP:CE3	2.37	0.59
2:A:860:ARG:CB	2:A:966:ILE:HG22	2.33	0.59
2:B:100:LYS:HE2	2:B:104:ILE:HD11	1.83	0.59
2:B:241:MET:HB2	2:B:307:ILE:HA	1.84	0.59
2:B:471:ASN:CG	2:B:473:GLU:HG2	2.28	0.59
2:B:711:PHE:CD1	2:B:783:LEU:HB3	2.38	0.59
1:C:986:C:C2	2:A:506:LYS:HG2	2.37	0.59
2:A:152:THR:HG22	2:A:159:PHE:HE1	1.67	0.59
2:A:560:THR:O	2:A:563:PHE:HB3	2.03	0.59
2:A:819:LYS:N	2:A:819:LYS:HD2	2.17	0.59
2:A:921:ILE:HB	2:A:928:ARG:NH2	2.16	0.59
2:B:112:PRO:O	2:B:114:GLU:N	2.36	0.59
2:B:594:MET:O	2:B:597:GLU:HB2	2.02	0.59
2:B:618:LEU:O	2:B:621:PHE:HB3	2.03	0.59
1:D:916:C:O2'	1:D:972:U:H4'	2.03	0.59
2:A:242:TRP:CE3	2:A:324:SER:HB2	2.38	0.59
2:A:401:TYR:O	2:A:405:TYR:HB2	2.03	0.59
2:A:741:THR:OG1	2:A:820:TRP:HZ3	1.85	0.59
2:B:94:ILE:HD12	2:B:95:LYS:N	2.18	0.59
2:A:231:ARG:HB3	2:A:233:GLU:OE2	2.02	0.59
2:B:227:ALA:CA	2:B:321:VAL:HG23	2.26	0.59
2:B:233:GLU:HB3	2:B:423:VAL:HG23	1.84	0.59
2:B:250:VAL:O	2:B:264:ILE:HA	2.02	0.59
2:A:211:ILE:CG2	2:A:228:ALA:HB2	2.30	0.59
2:A:297:ARG:CB	2:A:297:ARG:HH21	2.16	0.59
2:B:50:HIS:H	2:B:53:HIS:CD2	2.21	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:404:GLU:HA	2:B:407:LYS:O	2.03	0.59
2:B:921:ILE:HD12	2:B:928:ARG:HH22	1.68	0.59
2:B:943:ILE:HG22	2:B:946:PRO:HG3	1.84	0.59
2:B:966:ILE:O	2:B:967:GLU:HB2	2.03	0.59
2:A:66:PHE:CD1	2:A:744:LEU:HD12	2.37	0.58
2:A:250:VAL:O	2:A:264:ILE:HA	2.04	0.58
2:A:378:GLU:HA	2:A:378:GLU:OE2	2.02	0.58
2:A:393:LEU:HG	2:A:397:THR:OG1	2.03	0.58
2:A:547:LYS:O	2:A:550:GLN:HB3	2.03	0.58
2:A:847:LYS:O	2:A:851:GLU:HG3	2.03	0.58
2:B:355:ILE:HG22	2:B:356:VAL:N	2.12	0.58
2:B:722:LEU:H	2:B:722:LEU:HD23	1.68	0.58
1:D:904:G:C3'	1:D:905:G:H5''	2.33	0.58
2:A:75:LEU:HD12	2:A:77:PRO:HD3	1.85	0.58
2:A:966:ILE:O	2:A:967:GLU:CB	2.50	0.58
2:B:49:LEU:H	2:B:49:LEU:CD1	2.12	0.58
2:B:105:TYR:O	2:B:111:VAL:HG23	2.03	0.58
2:A:216:LEU:HG	2:A:216:LEU:O	2.03	0.58
2:A:263:TRP:HH2	2:A:438:GLU:OE1	1.86	0.58
2:A:923:GLU:N	2:A:923:GLU:CD	2.61	0.58
2:A:420:VAL:C	2:A:422:GLU:H	2.12	0.58
2:A:819:LYS:N	2:A:819:LYS:CD	2.66	0.58
2:A:860:ARG:HH22	2:A:862:TYR:HB3	1.68	0.58
2:A:860:ARG:HH11	2:A:943:ILE:N	2.01	0.58
2:A:920:ARG:O	2:A:922:ASN:N	2.36	0.58
2:B:733:LEU:HD13	2:B:737:ILE:HG13	1.85	0.58
2:B:857:ASN:O	2:B:940:ILE:HD11	2.03	0.58
2:A:27:ILE:H	2:A:28:ARG:NH2	2.01	0.58
2:A:488:LEU:HA	2:A:489:PRO:C	2.27	0.58
2:A:729:MET:SD	2:A:764:LEU:HA	2.44	0.58
2:B:901:LYS:O	2:B:901:LYS:HD3	2.03	0.58
2:A:410:PHE:O	2:A:416:GLU:HB3	2.03	0.58
2:A:944:ILE:HG22	2:A:945:ASN:N	2.18	0.58
2:B:429:LYS:HB3	2:B:429:LYS:NZ	2.19	0.58
2:B:660:ASN:HB2	2:B:663:ASP:HB2	1.86	0.58
2:B:60:PRO:HB2	2:B:76:PHE:CE1	2.39	0.58
2:B:342:GLU:HG2	2:B:343:THR:N	2.15	0.58
2:B:804:GLU:O	2:B:807:GLU:HB3	2.03	0.58
2:A:867:GLU:CD	2:A:867:GLU:N	2.58	0.58
2:A:923:GLU:CD	2:A:923:GLU:H	2.11	0.58
2:B:50:HIS:HE1	2:B:52:GLY:HA3	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:238:VAL:HA	2:B:325:VAL:HG22	1.85	0.58
2:B:488:LEU:HA	2:B:489:PRO:C	2.29	0.58
2:A:239:THR:O	2:A:240:ASN:HB3	2.03	0.58
2:A:566:TYR:O	2:A:595:LYS:HD2	2.04	0.58
2:A:710:GLN:O	2:A:712:ALA:N	2.37	0.58
2:B:495:GLN:O	2:B:499:ILE:HG12	2.04	0.58
2:B:652:SER:OG	2:B:655:LYS:HB2	2.04	0.58
2:B:682:GLU:OE1	2:B:748:ARG:HB3	2.03	0.58
2:B:713:GLU:HA	2:B:713:GLU:OE2	2.04	0.58
2:A:167:PHE:O	2:A:170:LEU:HB2	2.04	0.58
2:B:211:ILE:HG12	2:B:438:GLU:O	2.03	0.58
2:B:377:GLU:OE2	2:B:380:ASN:HB2	2.04	0.58
2:B:410:PHE:O	2:B:416:GLU:HB3	2.04	0.58
2:B:835:GLU:OE1	2:B:921:ILE:HG13	2.03	0.58
1:C:937:C:O5'	1:C:937:C:H6	1.87	0.57
2:A:871:TRP:HZ3	2:A:918:VAL:HG22	1.69	0.57
2:B:467:ILE:HG13	2:B:508:CYS:HB3	1.85	0.57
2:B:860:ARG:CZ	2:B:860:ARG:O	2.52	0.57
2:A:112:PRO:O	2:A:114:GLU:N	2.37	0.57
2:A:355:ILE:HG23	2:A:412:VAL:CG1	2.34	0.57
2:B:180:ALA:O	2:B:181:HIS:HB2	2.04	0.57
2:B:459:LYS:HZ3	2:B:461:ILE:HD13	1.70	0.57
2:B:629:PHE:O	2:B:631:GLU:N	2.29	0.57
2:A:404:GLU:HA	2:A:407:LYS:O	2.05	0.57
2:A:614:ILE:N	2:A:615:PRO:HD2	2.19	0.57
2:A:646:LEU:O	2:A:647:GLU:HB2	2.04	0.57
2:A:751:THR:O	2:A:752:ALA:C	2.48	0.57
2:B:44:TYR:CD1	2:B:44:TYR:C	2.82	0.57
2:B:563:PHE:CE1	2:B:584:THR:HG21	2.39	0.57
2:B:675:LEU:HD13	2:B:794:MET:HE1	1.86	0.57
2:B:727:ARG:HG2	2:B:727:ARG:HH11	1.69	0.57
2:B:751:THR:O	2:B:752:ALA:C	2.47	0.57
2:B:831:THR:O	2:B:835:GLU:HG3	2.05	0.57
1:D:943:C:H2'	1:D:944:C:H6	1.66	0.57
1:C:941:A:O3'	2:A:699:LYS:NZ	2.32	0.57
2:A:42:PHE:O	2:A:42:PHE:HD1	1.87	0.57
2:B:95:LYS:C	2:B:97:ARG:N	2.58	0.57
2:B:687:PHE:C	2:B:687:PHE:CD2	2.82	0.57
2:B:784:ARG:O	2:B:784:ARG:HD3	2.05	0.57
2:A:348:LYS:HB3	2:A:348:LYS:HZ3	1.70	0.57
2:A:920:ARG:C	2:A:922:ASN:N	2.58	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:631:GLU:HA	2:B:634:TRP:CD1	2.40	0.57
2:A:757:PHE:HD1	2:A:794:MET:SD	2.27	0.57
2:A:860:ARG:CB	2:A:966:ILE:HA	2.34	0.57
2:B:116:LEU:HD12	2:B:119:PHE:CE2	2.40	0.57
2:B:541:ILE:O	2:B:545:ILE:HG12	2.05	0.57
2:B:793:LEU:CD2	2:B:821:PRO:CG	2.82	0.57
2:A:331:PHE:O	2:A:334:VAL:HG23	2.04	0.57
2:A:559:LEU:HD22	2:A:563:PHE:CE2	2.40	0.57
2:A:770:ARG:HD2	2:A:933:PHE:CD2	2.39	0.57
2:B:32:LYS:O	2:B:35:LYS:HG3	2.04	0.57
2:B:410:PHE:CE2	2:B:423:VAL:HG11	2.40	0.57
2:B:846:ILE:HG12	2:B:964:ILE:HD13	1.86	0.57
1:D:928:C:OP1	2:B:696:LYS:HE3	2.04	0.57
2:A:233:GLU:HA	2:A:427:ILE:CD1	2.34	0.57
2:A:253:LYS:HD3	2:A:260:GLU:OE1	2.04	0.57
2:A:551:GLU:O	2:A:553:LYS:N	2.37	0.57
2:A:804:GLU:O	2:A:807:GLU:HB3	2.05	0.57
2:B:242:TRP:CH2	2:B:332:ASP:HA	2.40	0.57
2:B:420:VAL:C	2:B:422:GLU:H	2.12	0.57
2:B:624:ASN:HD22	2:B:624:ASN:H	1.51	0.57
2:B:697:LEU:O	2:B:701:ILE:HG12	2.05	0.57
2:A:171:LYS:HE2	2:A:520:TRP:CE2	2.40	0.57
2:A:745:GLU:HA	2:A:745:GLU:OE2	2.05	0.57
2:B:151:TYR:CD1	2:B:156:PHE:HB2	2.40	0.57
2:A:83:THR:HG22	2:A:153:THR:HG22	1.87	0.56
2:A:256:ARG:HH11	2:A:278:ARG:HD3	1.70	0.56
2:B:239:THR:O	2:B:240:ASN:HB3	2.04	0.56
2:B:662:ILE:HG23	2:B:663:ASP:H	1.70	0.56
2:A:840:ARG:O	2:A:844:GLU:HG3	2.04	0.56
2:B:161:LYS:HD2	2:B:559:LEU:O	2.05	0.56
2:B:212:ILE:HD13	2:B:235:VAL:CG1	2.35	0.56
2:B:705:TYR:CD2	2:B:805:LEU:HD21	2.40	0.56
2:B:870:LYS:HE2	2:B:957:ALA:O	2.05	0.56
2:A:93:ARG:HG2	2:A:451:ARG:NH2	2.21	0.56
2:A:196:HIS:CD2	2:A:197:ASP:H	2.22	0.56
2:A:864:TYR:HD2	2:A:962:PRO:HB3	1.70	0.56
2:A:877:VAL:HG22	2:A:906:ILE:HG23	1.85	0.56
2:B:24:GLU:CD	2:B:147:SER:HB2	2.30	0.56
2:B:44:TYR:C	2:B:44:TYR:HD1	2.14	0.56
2:B:135:GLU:O	2:B:138:ILE:HG22	2.06	0.56
2:B:389:ASP:O	2:B:390:LYS:HD3	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:432:LEU:HD11	2:B:439:ILE:HG13	1.87	0.56
2:B:609:SER:O	2:B:640:VAL:HA	2.05	0.56
2:B:918:VAL:HG11	2:B:920:ARG:HD2	1.87	0.56
2:A:93:ARG:HD3	2:A:451:ARG:NH2	2.20	0.56
2:A:481:ALA:O	2:A:484:ARG:N	2.34	0.56
2:B:44:TYR:HE1	2:B:87:ILE:CD1	2.16	0.56
2:B:165:TRP:HD1	2:B:561:PRO:HA	1.70	0.56
2:B:725:ILE:HD13	2:B:770:ARG:NH2	2.21	0.56
2:B:743:ALA:HB2	2:B:751:THR:HG22	1.87	0.56
2:B:884:LYS:O	2:B:887:MET:N	2.38	0.56
2:A:325:VAL:N	2:A:332:ASP:OD2	2.39	0.56
2:A:662:ILE:HG23	2:A:663:ASP:N	2.19	0.56
2:B:53:HIS:O	2:B:57:TYR:HD2	1.89	0.56
2:B:920:ARG:O	2:B:922:ASN:N	2.37	0.56
1:D:979:C:H2'	1:D:980:C:H6	1.71	0.56
2:A:16:ARG:CG	2:A:16:ARG:HH11	2.19	0.56
2:A:45:LEU:HD21	2:A:80:TRP:HB3	1.87	0.56
2:A:384:ILE:HG22	2:A:385:LYS:N	2.18	0.56
2:A:789:VAL:O	2:A:790:TRP:C	2.49	0.56
2:A:825:GLU:HG2	2:A:826:GLU:HG2	1.87	0.56
2:B:98:ASP:O	2:B:102:ILE:HG23	2.06	0.56
2:B:236:TYR:CE2	2:B:414:PRO:HG2	2.41	0.56
2:B:272:LYS:HE2	2:B:442:GLU:OE1	2.05	0.56
2:B:708:ILE:HB	2:B:805:LEU:HD13	1.87	0.56
2:B:742:ASN:HD22	2:B:742:ASN:N	2.03	0.56
2:A:27:ILE:N	2:A:28:ARG:NH2	2.53	0.56
2:A:771:THR:CG2	2:A:774:ARG:HD3	2.35	0.56
2:A:831:THR:O	2:A:835:GLU:HG3	2.06	0.56
2:A:884:LYS:O	2:A:887:MET:N	2.38	0.56
2:B:374:PRO:HG3	2:B:379:VAL:HG21	1.88	0.56
2:B:475:LYS:HG2	2:B:475:LYS:O	2.06	0.56
2:B:779:LYS:O	2:B:783:LEU:HD13	2.04	0.56
2:B:797:PHE:CD2	2:B:797:PHE:N	2.73	0.56
2:A:102:ILE:HD12	2:A:102:ILE:C	2.30	0.56
2:A:355:ILE:HD12	2:A:412:VAL:HG11	1.88	0.56
2:A:706:GLU:O	2:A:709:SER:HB2	2.06	0.56
2:A:953:LYS:NZ	2:A:953:LYS:HB3	2.19	0.56
2:B:789:VAL:O	2:B:790:TRP:C	2.49	0.56
2:A:67:LYS:CE	2:A:70:GLN:NE2	2.69	0.56
2:A:212:ILE:HD13	2:A:235:VAL:HG12	1.88	0.56
2:A:690:ARG:HH12	2:A:693:GLU:HG3	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:860:ARG:HH22	2:A:862:TYR:CB	2.18	0.56
2:B:567:ILE:HD13	2:B:594:MET:HE3	1.88	0.56
2:B:767:TYR:HE2	2:B:783:LEU:CD1	2.19	0.56
1:C:905:G:H2'	1:C:906:G:O4'	2.06	0.56
2:A:82:ILE:HG13	2:A:153:THR:CG2	2.33	0.56
2:A:268:GLU:H	2:A:268:GLU:CD	2.12	0.56
2:A:545:ILE:HG12	2:A:594:MET:HE1	1.87	0.56
2:A:708:ILE:HD12	2:A:791:VAL:HG23	1.87	0.56
2:A:866:ALA:HB3	2:A:955:LYS:NZ	2.21	0.56
2:B:551:GLU:O	2:B:553:LYS:N	2.39	0.56
2:B:744:LEU:HD23	2:B:752:ALA:HB2	1.87	0.56
2:B:852:VAL:O	2:B:852:VAL:HG12	2.06	0.55
2:A:675:LEU:HD12	2:A:697:LEU:HD21	1.88	0.55
2:A:728:TRP:O	2:A:731:HIS:N	2.38	0.55
2:A:863:ILE:HG13	2:A:945:ASN:OD1	2.05	0.55
2:B:613:LEU:O	2:B:618:LEU:HB2	2.06	0.55
2:B:742:ASN:O	2:B:743:ALA:C	2.49	0.55
2:B:746:GLU:O	2:B:748:ARG:HG3	2.06	0.55
2:B:868:ASP:O	2:B:870:LYS:N	2.39	0.55
2:A:112:PRO:HG2	2:A:115:ILE:HD12	1.87	0.55
2:A:331:PHE:HD1	2:A:334:VAL:HG21	1.72	0.55
2:B:167:PHE:O	2:B:170:LEU:HB2	2.06	0.55
2:B:727:ARG:HG2	2:B:727:ARG:NH1	2.21	0.55
1:C:920:G:H4'	1:C:920:G:OP1	2.06	0.55
2:A:198:LEU:H	2:A:198:LEU:HD12	1.70	0.55
2:A:631:GLU:HA	2:A:634:TRP:CD1	2.42	0.55
2:B:555:ASP:OD2	2:B:558:LYS:HE2	2.07	0.55
1:D:980:C:O2'	1:D:981:C:H5'	2.06	0.55
2:A:84:GLY:O	2:A:513:GLY:HA3	2.07	0.55
2:A:349:TYR:H	2:A:349:TYR:HD1	1.55	0.55
2:A:423:VAL:C	2:A:425:GLU:N	2.64	0.55
2:A:767:TYR:HE2	2:A:783:LEU:HD13	1.70	0.55
2:A:859:LYS:CB	2:A:941:GLU:HB3	2.33	0.55
2:A:868:ASP:O	2:A:870:LYS:N	2.40	0.55
2:B:210:ILE:C	2:B:210:ILE:HD12	2.31	0.55
2:B:878:SER:CB	2:B:915:THR:HG22	2.36	0.55
2:A:381:LYS:NZ	2:A:381:LYS:C	2.64	0.55
2:B:314:ASP:HB3	2:B:317:ASN:HB3	1.88	0.55
2:B:835:GLU:O	2:B:838:PHE:HB3	2.07	0.55
2:B:847:LYS:O	2:B:851:GLU:HG3	2.06	0.55
2:A:884:LYS:O	2:A:886:SER:N	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:235:VAL:HB	2:B:300:VAL:HG11	1.88	0.55
2:B:884:LYS:HG2	2:B:888:GLU:OE1	2.07	0.55
2:A:66:PHE:CE2	2:A:70:GLN:NE2	2.69	0.55
2:A:231:ARG:HB3	2:A:233:GLU:CD	2.32	0.55
2:A:354:ARG:HE	2:A:375:ALA:C	2.13	0.55
2:A:469:TYR:HB3	2:A:503:LEU:HD23	1.89	0.55
2:A:567:ILE:HA	2:A:595:LYS:CD	2.28	0.55
2:A:869:TRP:CD1	2:A:869:TRP:H	2.25	0.55
2:B:508:CYS:O	2:B:509:ALA:HB2	2.06	0.55
2:A:555:ASP:OD2	2:A:558:LYS:HG2	2.07	0.55
2:A:733:LEU:HD11	2:A:789:VAL:HG21	1.89	0.55
2:B:489:PRO:HG3	2:B:684:ASP:OD2	2.06	0.55
2:B:537:ALA:O	2:B:540:THR:HG22	2.07	0.55
2:A:58:THR:O	2:A:62:VAL:HG23	2.07	0.54
2:A:342:GLU:CG	2:A:343:THR:N	2.68	0.54
2:A:377:GLU:CD	2:A:377:GLU:C	2.75	0.54
2:A:714:TYR:CD1	2:A:780:ARG:HG2	2.42	0.54
2:A:766:TRP:CH2	2:A:836:GLU:OE1	2.60	0.54
2:B:84:GLY:O	2:B:513:GLY:HA3	2.07	0.54
2:B:139:ARG:HH11	2:B:139:ARG:CG	2.19	0.54
2:B:864:TYR:HD2	2:B:962:PRO:HB3	1.72	0.54
1:D:933:G:O2'	1:D:934:A:H5'	2.07	0.54
2:A:152:THR:HG22	2:A:159:PHE:CE1	2.43	0.54
2:B:136:THR:HG22	2:B:661:PHE:CD2	2.41	0.54
2:B:219:ASN:OD1	2:B:220:GLY:N	2.41	0.54
2:A:388:LYS:HD3	2:A:389:ASP:N	2.21	0.54
2:A:393:LEU:C	2:A:395:GLN:H	2.15	0.54
2:A:480:LYS:CE	2:A:484:ARG:NH2	2.64	0.54
2:A:784:ARG:CZ	2:A:809:LEU:HD23	2.37	0.54
2:B:423:VAL:C	2:B:425:GLU:N	2.66	0.54
2:B:432:LEU:HD13	2:B:437:ALA:O	2.06	0.54
1:C:986:C:C5	2:A:181:HIS:NE2	2.72	0.54
2:A:27:ILE:H	2:A:28:ARG:HH21	1.54	0.54
2:A:49:LEU:H	2:A:49:LEU:CD1	2.13	0.54
2:A:75:LEU:HD12	2:A:76:PHE:N	2.22	0.54
2:A:78:MET:HE3	2:A:137:PHE:CE2	2.42	0.54
2:A:922:ASN:HD22	2:A:923:GLU:CA	2.18	0.54
2:B:536:MET:N	2:B:536:MET:SD	2.81	0.54
2:B:728:TRP:O	2:B:731:HIS:N	2.38	0.54
2:B:753:VAL:HG23	2:B:797:PHE:CE1	2.42	0.54
2:B:910:LEU:C	2:B:910:LEU:HD13	2.32	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:67:LYS:HE2	2:A:70:GLN:NE2	2.23	0.54
2:A:282:VAL:HG12	2:A:283:ILE:N	2.22	0.54
2:A:623:PHE:O	2:A:626:VAL:HG22	2.08	0.54
2:A:964:ILE:HD12	2:A:965:PHE:N	2.23	0.54
2:B:173:LYS:HB3	2:B:175:TYR:CE2	2.43	0.54
2:B:298:ASN:HD22	2:B:299:PRO:HD2	1.71	0.54
2:B:730:LEU:HD22	2:B:827:TRP:CZ2	2.42	0.54
2:A:98:ASP:O	2:A:102:ILE:HG23	2.07	0.54
2:A:343:THR:HG23	2:A:344:GLU:HG2	1.89	0.54
2:A:377:GLU:O	2:A:378:GLU:HB2	2.07	0.54
2:A:734:ASN:OD1	2:A:823:PRO:CA	2.56	0.54
2:B:206:ILE:O	2:B:206:ILE:HG22	2.08	0.54
2:B:275:PHE:O	2:B:277:ASP:N	2.39	0.54
2:B:567:ILE:O	2:B:568:PHE:CG	2.60	0.54
2:B:729:MET:O	2:B:729:MET:HG3	2.07	0.54
2:B:757:PHE:CD1	2:B:794:MET:SD	2.99	0.54
1:D:914:A:H4'	2:B:750:ARG:HH22	1.72	0.54
1:D:960:C:O2'	1:D:961:C:OP2	2.16	0.54
2:A:51:VAL:HG23	2:A:52:GLY:N	2.23	0.54
2:A:75:LEU:HD23	2:A:601:TRP:CG	2.42	0.54
2:A:560:THR:HB	2:A:561:PRO:CD	2.38	0.54
2:A:724:ASP:HB2	2:A:929:GLU:OE2	2.07	0.54
2:A:894:SER:C	2:A:896:ILE:N	2.65	0.54
2:B:48:HIS:HB2	2:B:109:TYR:HD1	1.73	0.54
2:B:50:HIS:ND1	2:B:52:GLY:N	2.56	0.54
2:B:213:LYS:NZ	2:B:213:LYS:HB3	2.21	0.54
2:B:226:PRO:HG3	2:B:263:TRP:CE3	2.43	0.54
2:B:343:THR:HG23	2:B:344:GLU:N	2.21	0.54
2:B:413:PRO:CB	2:B:414:PRO:HD3	2.33	0.54
2:A:67:LYS:CD	2:A:70:GLN:HE21	2.18	0.54
2:B:45:LEU:HD13	2:B:130:MET:CB	2.38	0.54
2:B:347:GLU:OE1	2:B:348:LYS:N	2.39	0.54
2:B:467:ILE:HG13	2:B:508:CYS:CB	2.37	0.54
2:B:475:LYS:HA	2:B:623:PHE:HE1	1.72	0.54
2:A:388:LYS:HD3	2:A:389:ASP:HB2	1.89	0.54
2:A:860:ARG:NH2	2:A:862:TYR:N	2.56	0.54
2:B:51:VAL:HG23	2:B:659:LEU:HB3	1.89	0.54
2:B:188:VAL:HG23	2:B:189:VAL:N	2.16	0.54
2:B:393:LEU:HD12	2:B:396:ALA:HB3	1.88	0.54
2:B:776:ASP:OD2	2:B:778:ALA:HB3	2.08	0.54
2:B:838:PHE:O	2:B:842:VAL:HG23	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:955:G:OP1	2:A:961:LYS:NZ	2.39	0.54
2:A:62:VAL:HG21	2:A:678:MET:CE	2.38	0.54
2:A:150:PHE:HD1	2:A:151:TYR:O	1.91	0.54
2:A:420:VAL:HG12	2:A:424:LYS:NZ	2.23	0.54
2:A:495:GLN:HG2	2:A:614:ILE:HG21	1.90	0.54
2:A:609:SER:O	2:A:640:VAL:HA	2.08	0.54
2:A:824:VAL:CG1	2:A:827:TRP:HE3	2.20	0.54
2:B:243:VAL:HG12	2:B:321:VAL:HG12	1.90	0.54
1:C:985:A:H2'	1:C:986:C:C4	2.43	0.53
2:A:15:LYS:NZ	2:A:15:LYS:HB3	2.23	0.53
2:A:216:LEU:HB2	2:A:296:VAL:HG12	1.91	0.53
2:A:393:LEU:HG	2:A:397:THR:HG1	1.73	0.53
2:A:508:CYS:O	2:A:509:ALA:HB2	2.07	0.53
2:A:826:GLU:CD	2:A:826:GLU:N	2.63	0.53
2:A:953:LYS:HB3	2:A:953:LYS:HZ3	1.72	0.53
2:B:55:ARG:HD2	2:B:687:PHE:CE1	2.44	0.53
2:B:62:VAL:CG2	2:B:678:MET:HE2	2.27	0.53
2:B:710:GLN:O	2:B:712:ALA:N	2.41	0.53
2:B:860:ARG:HH22	2:B:861:ALA:C	2.16	0.53
2:B:871:TRP:CD1	2:B:959:PRO:HB3	2.42	0.53
2:A:12:LYS:NZ	2:A:16:ARG:NH1	2.55	0.53
2:A:59:ILE:CG1	2:A:678:MET:HE1	2.38	0.53
2:A:193:LEU:HG	2:A:197:ASP:HB2	1.90	0.53
2:A:237:GLY:C	2:A:325:VAL:HG22	2.33	0.53
2:B:199:MET:HE3	2:B:451:ARG:O	2.08	0.53
2:B:616:ASN:HA	2:B:620:PHE:CE1	2.44	0.53
2:B:725:ILE:HD13	2:B:770:ARG:HH21	1.72	0.53
2:B:733:LEU:CD1	2:B:789:VAL:HG11	2.28	0.53
2:B:868:ASP:O	2:B:869:TRP:C	2.52	0.53
2:A:233:GLU:HB3	2:A:423:VAL:CG2	2.36	0.53
2:A:263:TRP:CH2	2:A:438:GLU:OE1	2.62	0.53
2:A:555:ASP:OD2	2:A:558:LYS:HE2	2.09	0.53
2:A:730:LEU:O	2:A:827:TRP:NE1	2.42	0.53
2:B:66:PHE:CG	2:B:744:LEU:HD12	2.43	0.53
2:B:182:ARG:O	2:B:183:VAL:HB	2.07	0.53
2:B:235:VAL:HG23	2:B:236:TYR:N	2.23	0.53
2:B:240:ASN:HA	2:B:305:VAL:HB	1.90	0.53
2:B:834:ALA:O	2:B:837:GLU:CD	2.52	0.53
2:B:855:ILE:O	2:B:856:GLU:HB2	2.07	0.53
2:A:39:THR:HG23	2:A:604:LEU:CD1	2.36	0.53
2:A:382:LEU:C	2:A:384:ILE:H	2.15	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:826:GLU:O	2:A:828:TRP:N	2.40	0.53
2:A:860:ARG:HB3	2:A:966:ILE:HA	1.90	0.53
2:B:42:PHE:O	2:B:42:PHE:HD1	1.91	0.53
2:B:166:GLN:NE2	2:B:534:ILE:HG12	2.23	0.53
2:B:389:ASP:C	2:B:390:LYS:HD3	2.33	0.53
2:B:475:LYS:O	2:B:479:ARG:NH1	2.41	0.53
2:B:966:ILE:O	2:B:967:GLU:CB	2.57	0.53
2:A:78:MET:HE3	2:A:137:PHE:HE2	1.74	0.53
2:A:242:TRP:CD1	2:A:310:ALA:HB2	2.44	0.53
2:A:242:TRP:HZ3	2:A:332:ASP:CG	2.17	0.53
2:A:336:LEU:O	2:A:338:ASP:N	2.42	0.53
2:A:459:LYS:HG2	2:A:460:ILE:N	2.22	0.53
2:A:871:TRP:C	2:A:875:GLU:OE2	2.52	0.53
2:B:35:LYS:HD2	2:B:35:LYS:C	2.34	0.53
2:B:275:PHE:C	2:B:277:ASP:H	2.17	0.53
2:B:393:LEU:C	2:B:395:GLN:H	2.16	0.53
2:B:461:ILE:CG2	2:B:464:GLN:HB2	2.39	0.53
2:A:256:ARG:NH1	2:A:278:ARG:HD3	2.24	0.53
2:A:733:LEU:HD11	2:A:789:VAL:CB	2.38	0.53
2:A:884:LYS:NZ	2:A:884:LYS:HB2	2.23	0.53
2:B:253:LYS:NZ	2:B:283:ILE:HD11	2.23	0.53
2:B:340:LYS:HZ2	2:B:341:ARG:HH12	1.55	0.53
2:B:681:ALA:N	2:B:750:ARG:HG3	2.23	0.53
2:B:775:ASP:C	2:B:775:ASP:OD1	2.51	0.53
2:B:797:PHE:H	2:B:797:PHE:HD2	1.56	0.53
2:A:742:ASN:O	2:A:743:ALA:C	2.51	0.53
2:B:39:THR:HG22	2:B:40:VAL:N	2.23	0.53
2:B:79:ALA:HB2	2:B:539:TYR:HE2	1.73	0.53
2:B:336:LEU:O	2:B:338:ASP:N	2.42	0.53
2:B:620:PHE:N	2:B:620:PHE:CD1	2.76	0.53
1:C:985:A:H2'	1:C:986:C:C5	2.44	0.53
2:A:173:LYS:HD3	2:A:175:TYR:CE2	2.44	0.53
2:A:198:LEU:HD13	2:A:202:GLU:OE1	2.09	0.53
2:B:66:PHE:CE2	2:B:744:LEU:HB3	2.44	0.53
2:B:171:LYS:HD2	2:B:520:TRP:CZ3	2.44	0.53
2:B:384:ILE:HG22	2:B:385:LYS:N	2.20	0.53
2:B:395:GLN:HG3	2:B:396:ALA:N	2.24	0.53
2:B:860:ARG:NE	2:B:942:ILE:HA	2.20	0.53
2:B:884:LYS:O	2:B:886:SER:N	2.41	0.53
2:A:51:VAL:HG13	2:A:659:LEU:HB3	1.90	0.53
2:A:676:TYR:HB2	2:A:697:LEU:HD23	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:860:ARG:C	2:A:860:ARG:CZ	2.82	0.53
2:B:471:ASN:ND2	2:B:471:ASN:C	2.66	0.53
2:B:860:ARG:HA	2:B:966:ILE:HA	1.90	0.53
1:C:988:A:C5'	2:A:528:SER:OG	2.57	0.53
1:D:902:C:C2'	1:D:903:G:H5''	2.38	0.53
2:A:150:PHE:CE2	2:A:538:TYR:HD2	2.27	0.53
2:A:868:ASP:O	2:A:869:TRP:C	2.52	0.53
2:B:54:ALA:HB1	2:B:661:PHE:CE1	2.44	0.53
2:B:623:PHE:O	2:B:624:ASN:C	2.52	0.53
2:A:17:TRP:CZ3	2:A:800:HIS:CD2	2.97	0.52
2:A:136:THR:CG2	2:A:662:ILE:HB	2.39	0.52
2:A:860:ARG:NH2	2:A:861:ALA:C	2.67	0.52
2:B:112:PRO:O	2:B:113:GLU:C	2.52	0.52
2:A:241:MET:HG3	2:A:296:VAL:HG21	1.90	0.52
2:A:528:SER:OG	2:A:529:LEU:HD12	2.09	0.52
2:A:644:GLY:O	2:A:650:LYS:NZ	2.38	0.52
2:A:716:VAL:O	2:A:716:VAL:HG12	2.09	0.52
2:A:766:TRP:CZ3	2:A:836:GLU:OE1	2.63	0.52
2:A:801:ILE:O	2:A:805:LEU:HG	2.10	0.52
2:B:568:PHE:C	2:B:569:LEU:HD12	2.34	0.52
2:B:733:LEU:O	2:B:737:ILE:HG13	2.09	0.52
2:B:761:MET:SD	2:B:790:TRP:HH2	2.32	0.52
2:B:781:TYR:CZ	2:B:785:THR:HG21	2.44	0.52
2:A:662:ILE:HG23	2:A:663:ASP:H	1.74	0.52
2:A:826:GLU:N	2:A:826:GLU:OE2	2.42	0.52
2:A:877:VAL:C	2:A:879:GLU:H	2.16	0.52
2:B:703:ARG:HD2	2:B:707:LEU:CD1	2.37	0.52
2:B:782:VAL:HG12	2:B:783:LEU:HD12	1.91	0.52
1:D:988:A:C8	2:B:529:LEU:HD21	2.44	0.52
2:A:188:VAL:CG2	2:A:189:VAL:H	2.07	0.52
2:B:82:ILE:HG13	2:B:153:THR:HG23	1.91	0.52
2:B:83:THR:HG23	2:B:152:THR:HB	1.91	0.52
2:B:277:ASP:O	2:B:277:ASP:CG	2.50	0.52
2:B:297:ARG:NH2	2:B:297:ARG:CB	2.72	0.52
2:B:486:LYS:H	2:B:637:GLY:HA2	1.74	0.52
2:B:624:ASN:HD22	2:B:624:ASN:N	2.08	0.52
2:B:625:HIS:CD2	2:B:635:PRO:HD3	2.44	0.52
2:B:720:VAL:HG12	2:B:777:GLU:HG2	1.91	0.52
2:A:112:PRO:O	2:A:113:GLU:C	2.53	0.52
2:A:292:ILE:HD13	2:A:307:ILE:HG22	1.91	0.52
2:A:318:ALA:O	2:A:440:MET:HE1	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:482:LEU:CD1	2:A:500:ILE:HD11	2.38	0.52
2:A:854:LYS:HE2	2:A:967:GLU:CD	2.34	0.52
2:B:223:ILE:HD11	2:B:264:ILE:HG13	1.92	0.52
2:B:382:LEU:C	2:B:384:ILE:H	2.16	0.52
2:B:661:PHE:CE2	2:B:665:ILE:HD11	2.44	0.52
2:B:722:LEU:H	2:B:722:LEU:HD22	1.71	0.52
2:B:723:LYS:HG3	2:B:724:ASP:N	2.24	0.52
2:A:14:GLN:O	2:A:18:LEU:HB2	2.08	0.52
2:A:234:THR:O	2:A:325:VAL:HG21	2.10	0.52
2:A:752:ALA:O	2:A:755:TRP:N	2.43	0.52
2:A:860:ARG:O	2:A:860:ARG:CZ	2.58	0.52
2:B:100:LYS:O	2:B:104:ILE:HG13	2.10	0.52
2:B:356:VAL:HG21	2:B:411:LYS:HB2	1.91	0.52
2:B:764:LEU:O	2:B:768:LEU:HG	2.08	0.52
2:A:342:GLU:N	2:A:342:GLU:OE2	2.41	0.52
2:A:355:ILE:HG22	2:A:356:VAL:N	2.21	0.52
2:A:710:GLN:C	2:A:712:ALA:N	2.68	0.52
2:B:400:ILE:HD12	2:B:400:ILE:C	2.34	0.52
2:B:803:GLU:HG2	2:B:815:VAL:HG12	1.92	0.52
2:A:323:MET:HG3	2:A:323:MET:O	2.08	0.52
2:A:942:ILE:C	2:A:943:ILE:HG13	2.35	0.52
2:B:671:ASP:OD1	2:B:799:PRO:HD2	2.10	0.52
2:B:826:GLU:O	2:B:828:TRP:N	2.42	0.52
2:A:37:TYR:HD2	2:A:38:ILE:H	1.58	0.52
2:B:241:MET:HG3	2:B:296:VAL:HG21	1.91	0.52
2:B:345:ILE:CG1	2:B:346:LEU:N	2.73	0.52
2:B:676:TYR:O	2:B:679:SER:HB3	2.10	0.52
2:A:480:LYS:HG2	2:A:484:ARG:NH2	2.24	0.52
2:B:232:PRO:HD2	2:B:424:LYS:HG3	1.92	0.52
2:B:233:GLU:OE2	2:B:234:THR:N	2.42	0.52
2:B:433:GLU:HA	2:B:433:GLU:OE2	2.10	0.52
2:B:558:LYS:O	2:B:584:THR:HG22	2.10	0.52
2:A:177:VAL:HG23	2:A:466:PHE:HB2	1.92	0.51
2:A:864:TYR:CG	2:A:865:THR:N	2.77	0.51
2:B:266:SER:HB3	2:B:269:ALA:CB	2.41	0.51
2:B:728:TRP:C	2:B:730:LEU:N	2.67	0.51
2:B:956:GLN:O	2:B:956:GLN:HG2	2.09	0.51
2:A:44:TYR:OH	2:A:87:ILE:HG12	2.09	0.51
2:A:326:PRO:HA	2:A:332:ASP:CB	2.40	0.51
2:A:347:GLU:C	2:A:347:GLU:CD	2.78	0.51
2:A:373:PHE:HD1	2:A:374:PRO:HD3	1.68	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:486:LYS:H	2:A:637:GLY:HA2	1.75	0.51
2:A:496:PHE:HE1	2:A:614:ILE:CG1	2.18	0.51
2:A:728:TRP:C	2:A:730:LEU:N	2.68	0.51
2:A:860:ARG:CZ	2:A:861:ALA:HA	2.39	0.51
2:B:35:LYS:HB2	2:B:601:TRP:HZ3	1.75	0.51
2:B:273:LEU:HA	2:B:276:GLN:HG3	1.92	0.51
2:B:834:ALA:O	2:B:837:GLU:OE2	2.29	0.51
2:B:915:THR:O	2:B:916:PHE:HD2	1.93	0.51
2:A:36:PHE:O	2:A:36:PHE:CD2	2.64	0.51
2:A:65:ARG:O	2:A:68:ARG:N	2.44	0.51
2:A:555:ASP:HB3	2:A:558:LYS:HG2	1.93	0.51
2:A:631:GLU:C	2:A:633:HIS:H	2.16	0.51
2:A:672:VAL:HG21	2:A:698:ARG:HG3	1.93	0.51
2:B:164:GLU:O	2:B:165:TRP:C	2.54	0.51
2:B:427:ILE:HG22	2:B:431:MET:SD	2.50	0.51
2:B:679:SER:O	2:B:750:ARG:HG2	2.10	0.51
2:B:863:ILE:HG22	2:B:953:LYS:HG2	1.92	0.51
2:A:148:ARG:NH1	2:A:597:GLU:OE1	2.43	0.51
2:A:275:PHE:C	2:A:277:ASP:H	2.18	0.51
2:B:235:VAL:HG23	2:B:236:TYR:H	1.76	0.51
2:A:164:GLU:O	2:A:165:TRP:C	2.53	0.51
2:A:488:LEU:HD22	2:A:683:HIS:HE1	1.75	0.51
2:A:722:LEU:HD23	2:A:722:LEU:O	2.10	0.51
2:A:768:LEU:O	2:A:769:ARG:C	2.53	0.51
2:A:928:ARG:C	2:A:930:ALA:N	2.68	0.51
2:B:913:GLU:O	2:B:914:ARG:O	2.29	0.51
2:B:933:PHE:CD1	2:B:933:PHE:C	2.89	0.51
2:B:946:PRO:HG2	2:B:953:LYS:HE2	1.92	0.51
2:A:53:HIS:O	2:A:57:TYR:HD2	1.93	0.51
2:A:150:PHE:CD1	2:A:150:PHE:C	2.88	0.51
2:A:268:GLU:O	2:A:271:TYR:HB3	2.11	0.51
2:A:306:ILE:CG1	2:A:307:ILE:N	2.74	0.51
2:A:630:ARG:O	2:A:632:GLU:N	2.38	0.51
2:B:44:TYR:OH	2:B:86:PRO:HD2	2.11	0.51
2:B:67:LYS:HE3	2:B:72:TYR:CE1	2.45	0.51
2:B:297:ARG:CB	2:B:297:ARG:HH21	2.24	0.51
2:B:391:GLU:HG3	2:B:394:GLU:HB2	1.93	0.51
2:B:717:LYS:O	2:B:717:LYS:HD3	2.11	0.51
2:A:480:LYS:HA	2:A:483:GLU:OE1	2.11	0.51
2:A:803:GLU:OE1	2:A:815:VAL:HG23	2.11	0.51
2:B:547:LYS:O	2:B:550:GLN:HB3	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:636:LYS:HB3	2:B:636:LYS:NZ	2.25	0.51
2:B:870:LYS:O	2:B:872:LYS:N	2.43	0.51
1:C:916:C:O2'	1:C:972:U:H1'	2.10	0.51
1:D:961:C:O2	1:D:961:C:H2'	2.10	0.51
2:A:51:VAL:O	2:A:54:ALA:CB	2.56	0.51
2:A:860:ARG:CZ	2:A:861:ALA:CA	2.89	0.51
2:A:913:GLU:O	2:A:914:ARG:O	2.29	0.51
2:B:45:LEU:HD13	2:B:130:MET:HA	1.92	0.51
2:B:793:LEU:HD23	2:B:821:PRO:HG3	1.93	0.51
1:C:949:C:C2	1:C:957:G:N2	2.79	0.51
2:A:93:ARG:HG3	2:A:93:ARG:HH11	1.74	0.51
2:A:95:LYS:O	2:A:97:ARG:N	2.44	0.51
2:A:112:PRO:CG	2:A:115:ILE:HD12	2.41	0.51
2:A:168:TRP:NE1	2:A:519:PRO:HB2	2.25	0.51
2:A:239:THR:HG21	2:A:326:PRO:HD2	1.92	0.51
2:A:690:ARG:HH11	2:A:693:GLU:CG	2.20	0.51
2:A:838:PHE:HE2	2:A:922:ASN:ND2	2.09	0.51
2:B:630:ARG:O	2:B:632:GLU:N	2.41	0.51
2:A:819:LYS:H	2:A:819:LYS:CD	2.24	0.51
2:A:871:TRP:NE1	2:A:959:PRO:HB3	2.26	0.51
2:A:873:VAL:CG1	2:A:906:ILE:HG12	2.40	0.51
2:B:200:GLU:HG2	2:B:201:GLY:N	2.26	0.51
2:B:860:ARG:CB	2:B:966:ILE:HA	2.41	0.51
1:D:902:C:H2'	1:D:903:G:H5''	1.92	0.50
2:A:332:ASP:O	2:A:333:HIS:HB2	2.11	0.50
2:A:490:GLU:OE1	2:A:493:ARG:HB2	2.11	0.50
2:A:751:THR:O	2:A:754:GLN:N	2.43	0.50
2:A:919:LYS:HD2	2:A:960:LEU:HD13	1.93	0.50
2:B:328:HIS:O	2:B:329:ALA:C	2.53	0.50
2:B:824:VAL:O	2:B:825:GLU:C	2.53	0.50
2:B:839:ILE:C	2:B:839:ILE:HD12	2.36	0.50
2:B:877:VAL:C	2:B:879:GLU:H	2.18	0.50
2:B:915:THR:OG1	2:B:916:PHE:N	2.44	0.50
2:A:217:ARG:HH21	2:A:222:VAL:CG1	2.24	0.50
2:A:269:ALA:O	2:A:273:LEU:HD12	2.10	0.50
2:A:880:LYS:HG3	2:A:886:SER:HA	1.92	0.50
2:A:950:LYS:H	2:A:953:LYS:NZ	2.10	0.50
2:B:51:VAL:CG2	2:B:659:LEU:HB3	2.41	0.50
2:B:160:SER:O	2:B:164:GLU:HG3	2.11	0.50
2:B:743:ALA:HB2	2:B:751:THR:CG2	2.41	0.50
2:A:135:GLU:O	2:A:138:ILE:HG22	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:676:TYR:HA	2:A:697:LEU:CD2	2.41	0.50
2:A:793:LEU:HD23	2:A:821:PRO:CG	2.41	0.50
2:A:809:LEU:O	2:A:810:GLY:C	2.54	0.50
2:B:51:VAL:CG2	2:B:659:LEU:HD23	2.40	0.50
2:B:51:VAL:HG21	2:B:659:LEU:HD23	1.92	0.50
2:B:148:ARG:HB3	2:B:542:SER:HB3	1.93	0.50
2:B:540:THR:HG21	2:B:598:PHE:HD1	1.76	0.50
2:B:730:LEU:HB3	2:B:827:TRP:CD1	2.46	0.50
2:A:41:ALA:HA	2:A:607:ARG:HH22	1.75	0.50
2:A:172:GLU:OE1	2:A:172:GLU:N	2.45	0.50
2:A:183:VAL:O	2:A:184:ARG:C	2.54	0.50
2:A:240:ASN:O	2:A:324:SER:HB3	2.11	0.50
2:A:275:PHE:O	2:A:277:ASP:N	2.39	0.50
2:A:871:TRP:CD2	2:A:920:ARG:NH2	2.78	0.50
2:A:884:LYS:HG3	2:A:888:GLU:HG3	1.93	0.50
2:B:94:ILE:HD11	2:B:120:GLU:N	2.27	0.50
2:B:242:TRP:HH2	2:B:332:ASP:HA	1.75	0.50
2:B:395:GLN:O	2:B:399:THR:HG23	2.10	0.50
2:A:235:VAL:HG23	2:A:236:TYR:N	2.26	0.50
2:A:328:HIS:O	2:A:329:ALA:C	2.54	0.50
2:B:495:GLN:HG2	2:B:614:ILE:HG21	1.92	0.50
2:B:782:VAL:HG12	2:B:783:LEU:N	2.26	0.50
2:A:61:ASP:OD1	2:A:143:SER:N	2.25	0.50
2:A:72:TYR:O	2:A:74:VAL:HG23	2.11	0.50
2:A:413:PRO:CB	2:A:414:PRO:HD3	2.42	0.50
2:B:244:ASN:HB2	2:B:313:VAL:HG23	1.94	0.50
2:B:327:ALA:HB2	2:B:353:PRO:O	2.12	0.50
2:B:393:LEU:C	2:B:395:GLN:N	2.70	0.50
2:B:928:ARG:C	2:B:930:ALA:N	2.69	0.50
2:A:98:ASP:OD2	2:A:99:PRO:HD2	2.11	0.50
2:A:155:LEU:C	2:A:157:PRO:HD3	2.37	0.50
2:A:235:VAL:HG11	2:A:431:MET:CE	2.42	0.50
2:A:389:ASP:O	2:A:390:LYS:HD3	2.12	0.50
2:A:781:TYR:O	2:A:785:THR:HG23	2.12	0.50
2:A:817:LEU:N	2:A:817:LEU:HD23	2.27	0.50
2:A:862:TYR:OH	2:A:926:ALA:HB1	2.11	0.50
2:A:863:ILE:CB	2:A:953:LYS:HD3	2.41	0.50
2:B:196:HIS:CD2	2:B:197:ASP:H	2.30	0.50
2:B:482:LEU:HD11	2:B:496:PHE:HB3	1.94	0.50
2:B:587:PRO:HB2	2:B:590:ILE:CG1	2.35	0.50
2:A:235:VAL:HG23	2:A:236:TYR:H	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:300:VAL:HG13	2:A:301:SER:N	2.27	0.50
2:A:425:GLU:O	2:A:429:LYS:HD3	2.11	0.50
2:A:541:ILE:HB	2:A:594:MET:CE	2.34	0.50
2:A:569:LEU:N	2:A:569:LEU:HD12	2.26	0.50
2:A:860:ARG:HA	2:A:966:ILE:HA	1.93	0.50
2:A:931:LYS:HE2	2:A:942:ILE:HG22	1.92	0.50
2:A:947:THR:HG23	2:A:948:GLU:H	1.77	0.50
2:B:411:LYS:HA	2:B:416:GLU:CD	2.37	0.50
1:C:909:U:H5''	1:C:910:G:OP2	2.12	0.50
2:A:232:PRO:HD2	2:A:424:LYS:HG3	1.93	0.50
2:A:252:ALA:HB2	2:A:282:VAL:HA	1.94	0.50
2:A:292:ILE:HG13	2:A:309:PRO:HB3	1.94	0.50
2:A:474:TRP:NE1	2:A:627:ALA:HB2	2.27	0.50
2:A:713:GLU:O	2:A:714:TYR:C	2.53	0.50
2:A:717:LYS:C	2:A:717:LYS:CD	2.83	0.50
2:A:855:ILE:HG23	2:A:855:ILE:O	2.10	0.50
2:B:631:GLU:C	2:B:633:HIS:H	2.17	0.50
2:B:866:ALA:HB3	2:B:869:TRP:CD1	2.47	0.50
1:C:916:C:C5'	1:C:917:C:C5	2.86	0.49
2:A:79:ALA:HB2	2:A:539:TYR:HE2	1.76	0.49
2:A:85:SER:H	2:A:86:PRO:HD3	1.78	0.49
2:A:568:PHE:HD1	2:A:598:PHE:CE2	2.30	0.49
2:B:49:LEU:HA	2:B:53:HIS:HD2	1.77	0.49
2:B:231:ARG:HB3	2:B:233:GLU:CD	2.37	0.49
2:B:268:GLU:OE2	2:B:315:PRO:HB2	2.11	0.49
2:B:330:PRO:CD	2:B:400:ILE:HG12	2.42	0.49
2:B:871:TRP:CE3	2:B:920:ARG:NH1	2.80	0.49
2:B:921:ILE:HD12	2:B:928:ARG:NH2	2.27	0.49
2:A:45:LEU:HD13	2:A:130:MET:HB2	1.94	0.49
2:A:142:PHE:O	2:A:144:VAL:N	2.45	0.49
2:A:870:LYS:O	2:A:872:LYS:N	2.44	0.49
2:A:914:ARG:HE	2:A:915:THR:C	2.20	0.49
2:A:924:GLU:OE1	2:A:927:LEU:HD22	2.13	0.49
2:B:175:TYR:CE1	2:B:474:TRP:HB2	2.47	0.49
2:B:185:TRP:CD1	2:B:186:ASP:N	2.81	0.49
2:B:587:PRO:O	2:B:591:ILE:HG12	2.12	0.49
2:B:717:LYS:HD3	2:B:717:LYS:C	2.36	0.49
2:B:966:ILE:O	2:B:966:ILE:HG13	2.12	0.49
2:A:41:ALA:HB2	2:A:607:ARG:HH21	1.76	0.49
2:A:111:VAL:HG22	2:A:128:TYR:CE2	2.31	0.49
2:A:482:LEU:C	2:A:482:LEU:CD2	2.85	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:697:LEU:O	2:A:701:ILE:HG12	2.12	0.49
2:A:878:SER:CB	2:A:915:THR:HG22	2.42	0.49
2:B:196:HIS:HD2	2:B:197:ASP:H	1.58	0.49
2:B:282:VAL:CG1	2:B:283:ILE:N	2.72	0.49
2:B:662:ILE:HG23	2:B:663:ASP:N	2.25	0.49
2:A:119:PHE:C	2:A:121:ASP:N	2.69	0.49
2:A:616:ASN:HB2	2:A:620:PHE:CE2	2.47	0.49
2:A:717:LYS:HD2	2:A:777:GLU:OE2	2.12	0.49
2:B:42:PHE:O	2:B:42:PHE:CD1	2.65	0.49
2:B:95:LYS:O	2:B:97:ARG:N	2.45	0.49
2:B:297:ARG:HB3	2:B:297:ARG:CZ	2.41	0.49
2:B:354:ARG:HD2	2:B:376:VAL:HG12	1.95	0.49
2:B:455:ARG:HG2	2:B:455:ARG:HH11	1.78	0.49
2:B:713:GLU:O	2:B:714:TYR:C	2.55	0.49
2:B:746:GLU:OE1	2:B:748:ARG:HD2	2.13	0.49
2:B:846:ILE:HD12	2:B:938:LEU:HD21	1.94	0.49
2:B:907:VAL:O	2:B:910:LEU:HB3	2.12	0.49
1:C:958:U:H6	1:C:958:U:H3'	1.78	0.49
2:A:467:ILE:HG21	2:A:469:TYR:CZ	2.47	0.49
2:A:691:ARG:HH11	2:A:691:ARG:CG	2.26	0.49
2:A:800:HIS:C	2:A:802:CYS:H	2.21	0.49
2:A:902:GLU:C	2:A:904:ALA:H	2.21	0.49
2:B:185:TRP:HZ2	2:B:190:GLY:HA2	1.75	0.49
2:B:273:LEU:HB3	2:B:280:ILE:HD11	1.94	0.49
2:A:26:ASN:C	2:A:28:ARG:HH21	2.20	0.49
2:A:393:LEU:C	2:A:395:GLN:N	2.69	0.49
2:A:463:ASP:O	2:A:464:GLN:C	2.55	0.49
2:B:79:ALA:O	2:B:80:TRP:CE3	2.65	0.49
2:B:488:LEU:HD12	2:B:606:TRP:CZ3	2.46	0.49
2:B:724:ASP:HB2	2:B:929:GLU:OE2	2.11	0.49
2:B:741:THR:HA	2:B:820:TRP:CH2	2.47	0.49
2:A:66:PHE:CZ	2:A:70:GLN:OE1	2.66	0.49
2:A:214:PHE:CE2	2:A:298:ASN:HA	2.48	0.49
2:A:240:ASN:HA	2:A:305:VAL:HB	1.93	0.49
2:A:703:ARG:CG	2:A:761:MET:HE1	2.39	0.49
2:A:730:LEU:HD22	2:A:827:TRP:HZ2	1.78	0.49
2:A:947:THR:CG2	2:A:948:GLU:N	2.75	0.49
2:B:298:ASN:HD22	2:B:299:PRO:CD	2.25	0.49
2:B:809:LEU:O	2:B:810:GLY:C	2.56	0.49
2:B:889:GLU:HG3	2:B:889:GLU:O	2.11	0.49
2:B:902:GLU:C	2:B:904:ALA:H	2.21	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:910:G:C6	1:C:911:C:N4	2.81	0.49
1:C:941:A:H2'	1:C:942:U:C6	2.48	0.49
2:A:184:ARG:NH1	2:A:195:ASP:OD2	2.46	0.49
2:A:184:ARG:NH2	2:A:202:GLU:O	2.45	0.49
2:A:400:ILE:C	2:A:400:ILE:HD12	2.37	0.49
2:A:691:ARG:NH1	2:A:691:ARG:HG2	2.26	0.49
2:A:871:TRP:CZ3	2:A:918:VAL:HA	2.47	0.49
2:B:22:ILE:CG1	2:B:817:LEU:HD21	2.42	0.49
2:B:150:PHE:CD1	2:B:150:PHE:C	2.90	0.49
2:B:151:TYR:CE1	2:B:156:PHE:HD1	2.30	0.49
2:B:163:ILE:O	2:B:166:GLN:HB3	2.13	0.49
2:B:474:TRP:CZ2	2:B:623:PHE:HB3	2.47	0.49
2:B:490:GLU:C	2:B:492:ARG:H	2.21	0.49
1:D:935:C:H5'	1:D:936:U:H5''	1.95	0.49
2:A:218:GLU:HG3	2:A:219:ASN:N	2.28	0.49
2:A:227:ALA:CA	2:A:321:VAL:HG23	2.31	0.49
2:A:931:LYS:NZ	2:A:935:GLU:OE2	2.42	0.49
2:B:172:GLU:OE1	2:B:172:GLU:N	2.46	0.49
2:B:540:THR:HG21	2:B:598:PHE:HB2	1.93	0.49
2:B:751:THR:O	2:B:754:GLN:N	2.45	0.49
2:B:922:ASN:O	2:B:925:LYS:N	2.44	0.49
2:A:196:HIS:CD2	2:A:197:ASP:N	2.81	0.49
2:A:311:GLU:HG2	2:A:389:ASP:OD2	2.12	0.49
2:A:840:ARG:O	2:A:843:MET:HB2	2.12	0.49
2:B:37:TYR:HD2	2:B:38:ILE:H	1.60	0.49
2:B:45:LEU:HD13	2:B:130:MET:HB2	1.95	0.49
2:B:760:ILE:HD12	2:B:790:TRP:CD1	2.48	0.49
2:B:768:LEU:O	2:B:769:ARG:C	2.55	0.49
2:A:355:ILE:HD12	2:A:412:VAL:CG1	2.43	0.48
2:A:570:GLU:O	2:A:595:LYS:HE2	2.13	0.48
2:A:782:VAL:HG12	2:A:783:LEU:N	2.28	0.48
2:A:836:GLU:HA	2:A:839:ILE:HD11	1.94	0.48
2:B:65:ARG:O	2:B:68:ARG:N	2.46	0.48
2:B:166:GLN:CG	2:B:534:ILE:HD11	2.43	0.48
2:B:256:ARG:CZ	2:B:277:ASP:OD2	2.61	0.48
2:B:676:TYR:CZ	2:B:680:LEU:HD11	2.48	0.48
1:D:953:A:O2'	2:B:849:ILE:HG23	2.12	0.48
2:A:65:ARG:HG2	2:A:143:SER:OG	2.13	0.48
2:A:165:TRP:CD1	2:A:561:PRO:HA	2.44	0.48
2:A:880:LYS:HG3	2:A:886:SER:HB3	1.95	0.48
2:A:933:PHE:HD1	2:A:933:PHE:O	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:67:LYS:HD2	2:B:70:GLN:NE2	2.28	0.48
2:B:218:GLU:CD	2:B:219:ASN:ND2	2.70	0.48
2:B:282:VAL:CG1	2:B:283:ILE:H	2.25	0.48
2:B:375:ALA:O	2:B:377:GLU:N	2.40	0.48
2:B:463:ASP:O	2:B:464:GLN:C	2.56	0.48
2:B:894:SER:C	2:B:896:ILE:N	2.66	0.48
2:A:126:VAL:CG1	2:A:126:VAL:O	2.60	0.48
2:A:289:GLU:O	2:A:292:ILE:HB	2.13	0.48
2:A:388:LYS:CD	2:A:389:ASP:HB2	2.42	0.48
2:A:467:ILE:HG13	2:A:508:CYS:CB	2.43	0.48
2:A:488:LEU:CD1	2:A:606:TRP:CH2	2.92	0.48
2:A:931:LYS:HE2	2:A:942:ILE:O	2.13	0.48
2:B:496:PHE:CE1	2:B:614:ILE:HG23	2.49	0.48
2:B:614:ILE:N	2:B:615:PRO:CD	2.75	0.48
2:B:741:THR:O	2:B:745:GLU:HG2	2.13	0.48
1:C:954:G:N2	2:A:961:LYS:HG3	2.29	0.48
2:A:42:PHE:CD1	2:A:42:PHE:O	2.66	0.48
2:A:170:LEU:O	2:A:176:ILE:HG12	2.13	0.48
2:A:227:ALA:HA	2:A:321:VAL:O	2.12	0.48
2:A:256:ARG:HG3	2:A:257:LYS:H	1.78	0.48
2:A:501:ASP:O	2:A:503:LEU:N	2.39	0.48
2:A:725:ILE:CD1	2:A:770:ARG:HE	2.26	0.48
2:A:784:ARG:HH22	2:A:810:GLY:N	2.11	0.48
2:A:871:TRP:CG	2:A:920:ARG:HH22	2.31	0.48
2:B:42:PHE:CD1	2:B:81:HIS:HB2	2.49	0.48
2:B:79:ALA:N	2:B:539:TYR:OH	2.46	0.48
2:B:256:ARG:HG3	2:B:257:LYS:N	2.28	0.48
2:B:340:LYS:HB3	2:B:341:ARG:HH11	1.77	0.48
2:B:351:ILE:H	2:B:351:ILE:CD1	2.16	0.48
2:B:429:LYS:O	2:B:433:GLU:CG	2.52	0.48
2:B:505:LYS:H	2:B:505:LYS:HD2	1.78	0.48
2:B:601:TRP:HA	2:B:601:TRP:CE3	2.48	0.48
2:B:677:ILE:HG22	2:B:678:MET:N	2.28	0.48
2:B:869:TRP:CD1	2:B:869:TRP:H	2.31	0.48
1:C:916:C:H2'	1:C:972:U:O3'	2.12	0.48
2:A:725:ILE:HD13	2:A:770:ARG:HE	1.78	0.48
2:A:855:ILE:HG13	2:A:856:GLU:HG2	1.95	0.48
2:A:964:ILE:HD11	2:A:966:ILE:HG23	1.96	0.48
2:B:37:TYR:CD2	2:B:38:ILE:N	2.82	0.48
2:B:327:ALA:HB1	2:B:354:ARG:CB	2.44	0.48
2:B:500:ILE:HG23	2:B:623:PHE:CZ	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:501:ASP:O	2:B:503:LEU:N	2.41	0.48
2:B:752:ALA:O	2:B:755:TRP:N	2.46	0.48
1:D:917:C:H6	1:D:917:C:O5'	1.96	0.48
2:A:41:ALA:CA	2:A:607:ARG:NH2	2.77	0.48
2:A:162:PHE:HA	2:A:564:PHE:CE2	2.49	0.48
2:A:198:LEU:HD22	2:A:202:GLU:CA	2.43	0.48
2:A:490:GLU:C	2:A:492:ARG:H	2.22	0.48
2:A:705:TYR:CD2	2:A:805:LEU:HD11	2.48	0.48
2:B:126:VAL:CG1	2:B:126:VAL:O	2.61	0.48
2:B:354:ARG:HD2	2:B:376:VAL:CG1	2.42	0.48
2:B:377:GLU:O	2:B:378:GLU:HB2	2.13	0.48
2:B:464:GLN:NE2	2:B:507:ALA:HB1	2.28	0.48
2:B:732:ARG:HB3	2:B:732:ARG:HH11	1.77	0.48
2:A:449:ILE:N	2:A:449:ILE:CD1	2.75	0.48
2:A:892:LYS:O	2:A:892:LYS:HG2	2.13	0.48
1:C:920:G:H1'	1:C:969:G:H21	1.78	0.48
1:D:958:U:O5'	1:D:958:U:H6	1.97	0.48
2:A:623:PHE:O	2:A:624:ASN:C	2.56	0.48
2:B:48:HIS:HB2	2:B:109:TYR:CD1	2.48	0.48
2:B:171:LYS:CG	2:B:176:ILE:HD12	2.42	0.48
2:B:345:ILE:O	2:B:346:LEU:HB2	2.13	0.48
2:B:356:VAL:HB	2:B:409:ILE:O	2.14	0.48
2:B:423:VAL:HA	2:B:426:ALA:HB3	1.95	0.48
1:C:941:A:H4'	2:A:699:LYS:NZ	2.29	0.48
1:D:970:A:O2'	1:D:971:A:O5'	2.32	0.48
2:A:792:ARG:HH21	2:A:792:ARG:CG	2.15	0.48
2:A:800:HIS:C	2:A:802:CYS:N	2.70	0.48
2:B:53:HIS:O	2:B:57:TYR:CD2	2.67	0.48
2:B:198:LEU:HD23	2:B:448:VAL:HG13	1.95	0.48
2:B:420:VAL:HG12	2:B:424:LYS:NZ	2.28	0.48
2:B:560:THR:HB	2:B:561:PRO:HD2	1.95	0.48
2:B:732:ARG:HB3	2:B:732:ARG:NH1	2.29	0.48
2:B:894:SER:O	2:B:896:ILE:N	2.47	0.48
2:A:953:LYS:NZ	2:A:953:LYS:CB	2.76	0.48
2:A:956:GLN:O	2:A:956:GLN:HG2	2.14	0.48
2:B:183:VAL:O	2:B:184:ARG:C	2.57	0.48
2:B:710:GLN:O	2:B:713:GLU:HG2	2.13	0.48
2:A:55:ARG:O	2:A:59:ILE:HG13	2.14	0.47
2:A:94:ILE:HD12	2:A:94:ILE:C	2.39	0.47
2:A:188:VAL:HG23	2:A:190:GLY:H	1.79	0.47
2:A:419:PRO:O	2:A:422:GLU:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:846:ILE:O	2:A:850:ILE:HG13	2.14	0.47
2:B:276:GLN:O	2:B:277:ASP:HB3	2.14	0.47
2:B:729:MET:HE1	2:B:763:ASP:O	2.14	0.47
2:B:793:LEU:HD23	2:B:821:PRO:CG	2.44	0.47
1:C:958:U:H3'	1:C:958:U:C6	2.49	0.47
1:D:984:C:H6	1:D:984:C:H5'	1.79	0.47
2:A:279:GLU:OE1	2:A:281:GLU:OE1	2.32	0.47
2:A:671:ASP:OD1	2:A:799:PRO:HD2	2.13	0.47
2:A:717:LYS:HD2	2:A:718:GLY:O	2.14	0.47
2:A:770:ARG:CD	2:A:933:PHE:HE2	2.19	0.47
2:A:827:TRP:O	2:A:827:TRP:HD1	1.95	0.47
2:B:212:ILE:HD13	2:B:431:MET:HE1	1.95	0.47
2:B:233:GLU:HA	2:B:427:ILE:CD1	2.33	0.47
2:B:646:LEU:HD12	2:B:689:TRP:HB3	1.96	0.47
2:B:704:PHE:HE1	2:B:790:TRP:CD2	2.31	0.47
2:B:953:LYS:O	2:B:954:LYS:C	2.57	0.47
1:C:986:C:H5	2:A:181:HIS:HE2	1.56	0.47
2:A:42:PHE:CE1	2:A:81:HIS:HB2	2.48	0.47
2:A:375:ALA:O	2:A:377:GLU:N	2.40	0.47
2:A:714:TYR:HD1	2:A:780:ARG:CG	2.27	0.47
2:A:746:GLU:O	2:A:748:ARG:HG3	2.14	0.47
2:A:767:TYR:CE2	2:A:782:VAL:HG11	2.49	0.47
2:B:68:ARG:HB2	2:B:74:VAL:HG11	1.96	0.47
2:B:340:LYS:CB	2:B:341:ARG:HH11	2.28	0.47
2:B:701:ILE:O	2:B:704:PHE:HB3	2.13	0.47
1:C:922:C:H4'	1:C:923:A:C5'	2.44	0.47
2:A:37:TYR:HD2	2:A:38:ILE:N	2.12	0.47
2:A:53:HIS:O	2:A:57:TYR:CD2	2.67	0.47
2:A:145:ASP:OD1	2:A:145:ASP:O	2.32	0.47
2:A:238:VAL:HA	2:A:325:VAL:HG22	1.96	0.47
2:A:381:LYS:HZ2	2:A:382:LEU:HD12	1.79	0.47
2:A:470:GLY:O	2:A:471:ASN:C	2.57	0.47
2:A:568:PHE:HB2	2:A:569:LEU:HD12	1.96	0.47
2:A:695:GLY:O	2:A:698:ARG:HB3	2.15	0.47
2:B:40:VAL:CG1	2:B:78:MET:HE1	2.44	0.47
2:B:326:PRO:HA	2:B:332:ASP:CB	2.44	0.47
2:B:680:LEU:C	2:B:750:ARG:HG3	2.39	0.47
2:B:725:ILE:CD1	2:B:770:ARG:HE	2.27	0.47
2:B:734:ASN:HD21	2:B:823:PRO:HA	1.75	0.47
2:A:198:LEU:CD2	2:A:202:GLU:HA	2.44	0.47
2:A:609:SER:OG	2:A:610:GLY:N	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:786:LEU:C	2:A:786:LEU:HD23	2.40	0.47
2:A:959:PRO:C	2:A:960:LEU:CD2	2.87	0.47
2:A:964:ILE:CD1	2:A:966:ILE:HG23	2.45	0.47
2:A:12:LYS:HZ2	2:A:16:ARG:NH1	2.12	0.47
2:A:267:LYS:O	2:A:270:ALA:HB3	2.14	0.47
2:A:546:ASN:O	2:A:550:GLN:HB2	2.14	0.47
2:A:871:TRP:CH2	2:A:919:LYS:HE3	2.47	0.47
2:A:922:ASN:O	2:A:925:LYS:N	2.47	0.47
2:A:944:ILE:HG22	2:A:945:ASN:H	1.78	0.47
2:B:45:LEU:HD13	2:B:130:MET:CA	2.45	0.47
2:B:85:SER:N	2:B:86:PRO:CD	2.77	0.47
2:B:830:GLU:HG3	2:B:831:THR:N	2.29	0.47
2:A:75:LEU:CD1	2:A:77:PRO:HD3	2.44	0.47
2:A:99:PRO:O	2:A:102:ILE:HG13	2.14	0.47
2:A:218:GLU:O	2:A:219:ASN:C	2.57	0.47
2:A:318:ALA:HA	2:A:440:MET:SD	2.55	0.47
2:A:518:LEU:HD12	2:A:524:TRP:CB	2.44	0.47
2:A:541:ILE:CB	2:A:594:MET:HE2	2.36	0.47
2:A:835:GLU:O	2:A:838:PHE:HB3	2.15	0.47
2:A:866:ALA:HB3	2:A:955:LYS:HZ1	1.78	0.47
2:A:877:VAL:CG2	2:A:906:ILE:HG23	2.45	0.47
2:A:884:LYS:C	2:A:886:SER:N	2.72	0.47
2:A:894:SER:O	2:A:896:ILE:N	2.47	0.47
2:B:59:ILE:HA	2:B:678:MET:HE1	1.97	0.47
2:B:83:THR:CG2	2:B:153:THR:HG22	2.44	0.47
2:B:119:PHE:C	2:B:121:ASP:N	2.70	0.47
2:B:150:PHE:CD1	2:B:151:TYR:O	2.58	0.47
2:B:212:ILE:CD1	2:B:235:VAL:CG1	2.93	0.47
2:B:216:LEU:CD1	2:B:294:LYS:HB3	2.43	0.47
2:B:218:GLU:O	2:B:219:ASN:C	2.56	0.47
2:B:256:ARG:CG	2:B:257:LYS:H	2.23	0.47
2:B:393:LEU:HG	2:B:397:THR:OG1	2.14	0.47
2:B:395:GLN:HG3	2:B:396:ALA:H	1.80	0.47
2:B:540:THR:HG21	2:B:598:PHE:CD1	2.50	0.47
2:B:554:LEU:HD12	2:B:586:ILE:HD11	1.97	0.47
2:B:838:PHE:O	2:B:841:SER:OG	2.28	0.47
2:B:860:ARG:NH1	2:B:861:ALA:HA	2.30	0.47
2:B:862:TYR:HB3	2:B:964:ILE:HB	1.95	0.47
2:B:864:TYR:CG	2:B:865:THR:N	2.82	0.47
2:B:884:LYS:O	2:B:885:SER:C	2.57	0.47
2:B:951:GLY:HA3	2:B:965:PHE:CE1	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:919:G:C6	1:C:969:G:C6	3.03	0.47
1:C:957:G:O2'	1:C:958:U:H5'	2.15	0.47
2:A:195:ASP:C	2:A:202:GLU:OE1	2.57	0.47
2:A:241:MET:HG3	2:A:296:VAL:CG2	2.45	0.47
2:A:348:LYS:HB3	2:A:348:LYS:HZ2	1.77	0.47
2:A:423:VAL:HA	2:A:426:ALA:HB3	1.96	0.47
2:A:558:LYS:HB3	2:A:584:THR:CA	2.34	0.47
2:A:767:TYR:HE2	2:A:783:LEU:HD11	1.79	0.47
2:A:830:GLU:HG3	2:A:831:THR:N	2.30	0.47
2:B:135:GLU:HA	2:B:138:ILE:HG22	1.97	0.47
2:B:519:PRO:HG2	2:B:520:TRP:CE3	2.49	0.47
2:B:690:ARG:HB2	2:B:693:GLU:HG3	1.97	0.47
1:D:914:A:H2'	1:D:915:G:O4'	2.15	0.47
2:A:16:ARG:CG	2:A:16:ARG:NH1	2.77	0.47
2:A:59:ILE:HB	2:A:60:PRO:CD	2.45	0.47
2:A:210:ILE:HG22	2:A:439:ILE:HG23	1.97	0.47
2:A:314:ASP:HB3	2:A:317:ASN:HB3	1.95	0.47
2:A:327:ALA:HB2	2:A:353:PRO:O	2.15	0.47
2:A:461:ILE:HG21	2:A:464:GLN:HB2	1.97	0.47
2:A:747:PHE:N	2:A:747:PHE:CD1	2.83	0.47
2:A:825:GLU:OE2	2:A:825:GLU:O	2.33	0.47
2:A:860:ARG:NH1	2:A:860:ARG:O	2.47	0.47
2:A:880:LYS:HG3	2:A:886:SER:CA	2.45	0.47
2:B:402:LYS:O	2:B:405:TYR:HB3	2.15	0.47
2:B:470:GLY:O	2:B:471:ASN:C	2.58	0.47
2:B:641:ASN:C	2:B:641:ASN:ND2	2.69	0.47
2:B:793:LEU:HD21	2:B:821:PRO:CG	2.43	0.47
2:A:93:ARG:O	2:A:98:ASP:HB2	2.15	0.47
2:A:168:TRP:CE2	2:A:519:PRO:HB2	2.49	0.47
2:A:215:GLU:O	2:A:296:VAL:HA	2.15	0.47
2:A:354:ARG:HH11	2:A:354:ARG:HG3	1.80	0.47
2:A:544:HIS:H	2:A:544:HIS:HD2	1.59	0.47
2:A:576:LYS:O	2:A:580:LEU:HD13	2.15	0.47
2:A:800:HIS:O	2:A:802:CYS:N	2.48	0.47
2:B:63:ILE:O	2:B:67:LYS:HG2	2.15	0.47
2:B:167:PHE:HA	2:B:170:LEU:CG	2.44	0.47
2:B:521:ASP:N	2:B:522:PRO:HD3	2.30	0.47
2:B:890:LEU:C	2:B:892:LYS:N	2.71	0.47
1:D:980:C:H2'	1:D:981:C:H6	1.79	0.46
2:A:75:LEU:HD23	2:A:601:TRP:CE2	2.50	0.46
2:A:243:VAL:HG22	2:A:292:ILE:HD11	1.95	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:331:PHE:CD1	2:A:334:VAL:HG21	2.51	0.46
2:A:587:PRO:O	2:A:591:ILE:HG12	2.15	0.46
2:A:890:LEU:C	2:A:892:LYS:N	2.72	0.46
2:B:259:LYS:HE2	2:B:261:GLU:OE1	2.15	0.46
2:B:482:LEU:CD1	2:B:496:PHE:HB3	2.45	0.46
1:D:953:A:C2	2:B:966:ILE:HG12	2.50	0.46
2:A:196:HIS:HD2	2:A:197:ASP:H	1.64	0.46
2:A:213:LYS:NZ	2:A:213:LYS:HB3	2.30	0.46
2:A:238:VAL:HG11	2:A:298:ASN:HB2	1.97	0.46
2:A:268:GLU:HG3	2:A:316:ASP:HA	1.97	0.46
2:A:402:LYS:O	2:A:403:ALA:C	2.58	0.46
2:A:457:VAL:HG23	2:A:458:ILE:N	2.31	0.46
2:A:544:HIS:O	2:A:547:LYS:HB3	2.14	0.46
2:A:626:VAL:HG12	2:A:634:TRP:CE2	2.50	0.46
2:A:772:GLU:OE1	2:A:936:LYS:HE3	2.15	0.46
2:B:45:LEU:CD1	2:B:80:TRP:HB3	2.40	0.46
2:B:495:GLN:HE21	2:B:614:ILE:CG2	2.27	0.46
2:B:558:LYS:HG3	2:B:584:THR:O	2.14	0.46
2:B:698:ARG:HH11	2:B:698:ARG:HG3	1.80	0.46
2:B:733:LEU:CD1	2:B:737:ILE:HD11	2.45	0.46
2:B:766:TRP:HH2	2:B:836:GLU:OE1	1.97	0.46
2:B:860:ARG:CB	2:B:966:ILE:HG22	2.40	0.46
2:A:42:PHE:CE1	2:A:81:HIS:CG	3.04	0.46
2:A:382:LEU:C	2:A:384:ILE:N	2.74	0.46
2:A:544:HIS:HE1	2:A:593:GLU:CD	2.23	0.46
2:B:67:LYS:O	2:B:72:TYR:HD1	1.99	0.46
2:B:418:LYS:HB3	2:B:419:PRO:HD2	1.97	0.46
2:B:436:ILE:HG22	2:B:436:ILE:O	2.16	0.46
2:B:546:ASN:O	2:B:550:GLN:HB2	2.15	0.46
2:B:616:ASN:HD22	2:B:617:HIS:H	1.60	0.46
2:B:829:ASN:OD1	2:B:832:ILE:HG13	2.16	0.46
2:B:834:ALA:CA	2:B:837:GLU:OE2	2.60	0.46
2:A:204:VAL:HG23	2:A:204:VAL:O	2.16	0.46
2:A:297:ARG:HB3	2:A:297:ARG:CZ	2.45	0.46
2:A:355:ILE:HG23	2:A:412:VAL:HG11	1.97	0.46
2:A:412:VAL:HG23	2:A:414:PRO:CD	2.39	0.46
2:A:717:LYS:NZ	2:A:719:ASN:HB2	2.29	0.46
2:A:824:VAL:O	2:A:825:GLU:C	2.57	0.46
2:A:933:PHE:HE1	2:A:937:GLU:HB2	1.81	0.46
2:B:418:LYS:HG3	2:B:422:GLU:OE2	2.16	0.46
2:B:803:GLU:CD	2:B:815:VAL:HG12	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:210:ILE:HD11	2:A:232:PRO:CG	2.37	0.46
2:A:381:LYS:C	2:A:381:LYS:HZ3	2.24	0.46
2:A:455:ARG:HD3	2:A:456:ALA:N	2.30	0.46
2:A:728:TRP:CE3	2:A:729:MET:N	2.80	0.46
2:A:918:VAL:HG11	2:A:920:ARG:HD2	1.97	0.46
2:B:238:VAL:HG13	2:B:238:VAL:O	2.15	0.46
1:C:956:G:O2'	1:C:957:G:H5'	2.16	0.46
2:A:50:HIS:H	2:A:53:HIS:CD2	2.34	0.46
2:A:327:ALA:HB1	2:A:354:ARG:CB	2.46	0.46
2:A:710:GLN:O	2:A:711:PHE:C	2.57	0.46
2:A:724:ASP:C	2:A:726:ASP:N	2.73	0.46
2:A:860:ARG:NH1	2:A:861:ALA:CA	2.69	0.46
2:A:911:ILE:O	2:A:911:ILE:HG13	2.15	0.46
2:B:204:VAL:HG11	2:B:443:PHE:HB3	1.97	0.46
2:B:722:LEU:HG	2:B:727:ARG:NH1	2.31	0.46
1:D:954:G:O6	2:B:963:ALA:HA	2.16	0.46
2:A:62:VAL:CG2	2:A:678:MET:HE2	2.44	0.46
2:A:356:VAL:HB	2:A:409:ILE:O	2.16	0.46
2:A:678:MET:N	2:A:678:MET:SD	2.88	0.46
2:A:872:LYS:HA	2:A:875:GLU:OE2	2.15	0.46
2:B:710:GLN:C	2:B:712:ALA:N	2.69	0.46
2:B:734:ASN:ND2	2:B:824:VAL:H	1.94	0.46
2:B:789:VAL:O	2:B:791:VAL:N	2.49	0.46
2:B:789:VAL:O	2:B:792:ARG:N	2.49	0.46
2:A:93:ARG:HG2	2:A:451:ARG:HH21	1.80	0.46
2:A:183:VAL:HG13	2:A:184:ARG:O	2.16	0.46
2:A:424:LYS:NZ	2:A:424:LYS:HB2	2.31	0.46
2:A:806:TRP:CB	2:A:815:VAL:HG22	2.45	0.46
2:A:863:ILE:HG22	2:A:953:LYS:CG	2.44	0.46
2:B:65:ARG:O	2:B:68:ARG:HB3	2.16	0.46
2:B:459:LYS:HZ2	2:B:461:ILE:CD1	2.29	0.46
2:B:557:GLU:O	2:B:559:LEU:N	2.49	0.46
2:B:722:LEU:HD23	2:B:722:LEU:N	2.30	0.46
2:B:918:VAL:CG1	2:B:920:ARG:HD2	2.46	0.46
2:A:64:ALA:O	2:A:68:ARG:HB2	2.16	0.46
2:A:232:PRO:HG2	2:A:428:ALA:HB2	1.98	0.46
2:A:731:HIS:HD2	2:A:828:TRP:HA	1.80	0.46
2:B:476:GLU:OE1	2:B:476:GLU:HA	2.16	0.46
2:B:567:ILE:CD1	2:B:594:MET:HE3	2.45	0.46
2:B:880:LYS:O	2:B:881:ARG:C	2.59	0.46
2:B:920:ARG:C	2:B:922:ASN:N	2.60	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:116:LEU:C	2:A:116:LEU:HD23	2.41	0.46
2:A:159:PHE:O	2:A:162:PHE:HB3	2.16	0.46
2:A:173:LYS:HB3	2:A:175:TYR:CE2	2.51	0.46
2:A:230:LEU:CD2	2:A:230:LEU:N	2.76	0.46
2:A:382:LEU:HD12	2:A:382:LEU:N	2.31	0.46
2:A:395:GLN:HG3	2:A:396:ALA:H	1.81	0.46
2:A:489:PRO:HD3	2:A:683:HIS:HB3	1.98	0.46
2:A:624:ASN:HD22	2:A:624:ASN:N	2.07	0.46
2:A:660:ASN:HB2	2:A:663:ASP:HB2	1.94	0.46
2:A:884:LYS:O	2:A:885:SER:C	2.58	0.46
2:B:70:GLN:HB3	2:B:72:TYR:CD1	2.51	0.46
2:B:234:THR:O	2:B:325:VAL:HG21	2.16	0.46
2:B:471:ASN:C	2:B:471:ASN:HD22	2.23	0.46
2:B:516:THR:O	2:B:526:ILE:HG13	2.15	0.46
1:C:949:C:C2	1:C:957:G:C2	3.04	0.45
2:A:297:ARG:O	2:A:299:PRO:HD3	2.16	0.45
2:A:393:LEU:O	2:A:395:GLN:N	2.49	0.45
2:A:903:VAL:HG12	2:A:906:ILE:HG13	1.97	0.45
2:B:231:ARG:HB3	2:B:233:GLU:OE2	2.17	0.45
2:B:749:THR:O	2:B:750:ARG:C	2.57	0.45
2:A:51:VAL:CG2	2:A:52:GLY:N	2.79	0.45
2:A:741:THR:O	2:A:745:GLU:HG2	2.17	0.45
2:A:855:ILE:O	2:A:856:GLU:HB2	2.15	0.45
2:A:882:ASP:C	2:A:883:PHE:HD1	2.24	0.45
2:B:292:ILE:HG13	2:B:309:PRO:HB3	1.98	0.45
2:B:505:LYS:HD2	2:B:505:LYS:N	2.30	0.45
2:B:914:ARG:HE	2:B:915:THR:N	2.13	0.45
1:D:919:G:H1'	1:D:970:A:C2	2.52	0.45
2:A:23:PHE:CD2	2:A:143:SER:HA	2.51	0.45
2:A:166:GLN:HB2	2:A:534:ILE:HD11	1.97	0.45
2:A:186:ASP:HB3	2:A:191:THR:CG2	2.41	0.45
2:A:950:LYS:HG2	2:A:953:LYS:HZ1	1.82	0.45
2:B:9:ILE:HD13	2:B:804:GLU:HG2	1.97	0.45
2:B:412:VAL:O	2:B:413:PRO:C	2.60	0.45
2:B:535:TYR:CE1	2:B:536:MET:SD	3.10	0.45
2:B:786:LEU:HD23	2:B:786:LEU:C	2.41	0.45
2:B:890:LEU:C	2:B:892:LYS:H	2.25	0.45
1:C:918:U:H2'	1:C:918:U:O2	2.15	0.45
1:D:905:G:H5'	1:D:905:G:H8	1.82	0.45
2:A:61:ASP:OD2	2:A:674:ARG:NH2	2.45	0.45
2:A:211:ILE:HG21	2:A:319:THR:CG2	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:464:GLN:NE2	2:A:465:TRP:O	2.49	0.45
2:A:742:ASN:O	2:A:744:LEU:N	2.50	0.45
2:A:872:LYS:HA	2:A:875:GLU:CD	2.41	0.45
2:B:136:THR:CG2	2:B:661:PHE:HD2	2.26	0.45
2:B:155:LEU:C	2:B:157:PRO:HD3	2.42	0.45
2:B:412:VAL:H	2:B:416:GLU:HG2	1.82	0.45
2:B:485:MET:SD	2:B:635:PRO:HB2	2.57	0.45
2:A:9:ILE:O	2:A:10:GLU:C	2.60	0.45
2:A:17:TRP:CZ2	2:A:803:GLU:HG3	2.52	0.45
2:A:914:ARG:HH21	2:A:915:THR:C	2.25	0.45
2:B:266:SER:O	2:B:269:ALA:HB3	2.16	0.45
2:B:381:LYS:HD2	2:B:381:LYS:C	2.40	0.45
2:B:676:TYR:HA	2:B:697:LEU:CD2	2.46	0.45
2:B:953:LYS:HB3	2:B:953:LYS:NZ	2.30	0.45
1:D:944:C:H2'	1:D:945:C:H6	1.81	0.45
2:A:294:LYS:N	2:A:294:LYS:HD2	2.32	0.45
2:A:544:HIS:CD2	2:A:544:HIS:N	2.85	0.45
2:A:582:LYS:H	2:A:582:LYS:HD2	1.81	0.45
2:A:838:PHE:HE2	2:A:922:ASN:HD21	1.63	0.45
2:B:142:PHE:O	2:B:144:VAL:N	2.49	0.45
2:B:306:ILE:HG12	2:B:307:ILE:N	2.31	0.45
2:B:342:GLU:N	2:B:342:GLU:OE2	2.50	0.45
2:B:393:LEU:CD1	2:B:396:ALA:HB3	2.46	0.45
2:B:678:MET:CE	2:B:749:THR:HG21	2.40	0.45
2:B:711:PHE:HE1	2:B:783:LEU:HD23	1.82	0.45
2:B:713:GLU:OE2	2:B:713:GLU:CA	2.65	0.45
2:B:882:ASP:O	2:B:883:PHE:HB3	2.15	0.45
1:C:960:C:H4'	1:C:961:C:OP2	2.17	0.45
2:A:80:TRP:CD1	2:A:130:MET:HG3	2.51	0.45
2:A:468:ASP:C	2:A:470:GLY:N	2.74	0.45
2:A:557:GLU:O	2:A:559:LEU:N	2.49	0.45
2:A:953:LYS:O	2:A:954:LYS:C	2.59	0.45
2:B:55:ARG:HD2	2:B:687:PHE:CD1	2.51	0.45
2:B:83:THR:HG22	2:B:153:THR:HG22	1.97	0.45
2:B:123:ILE:HD11	2:B:155:LEU:CD1	2.47	0.45
2:B:232:PRO:HG2	2:B:428:ALA:HB2	1.99	0.45
2:B:252:ALA:HB2	2:B:282:VAL:HA	1.99	0.45
2:B:482:LEU:HD23	2:B:482:LEU:C	2.41	0.45
2:B:718:GLY:O	2:B:719:ASN:C	2.60	0.45
2:B:730:LEU:HD23	2:B:730:LEU:HA	1.84	0.45
2:B:742:ASN:O	2:B:745:GLU:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:780:ARG:O	2:B:781:TYR:C	2.59	0.45
2:B:921:ILE:HB	2:B:928:ARG:HH22	1.77	0.45
2:A:93:ARG:HG3	2:A:93:ARG:NH1	2.32	0.45
2:A:112:PRO:HB2	2:A:115:ILE:HG13	1.99	0.45
2:A:210:ILE:O	2:A:210:ILE:HG13	2.16	0.45
2:A:211:ILE:HG21	2:A:319:THR:HG21	1.99	0.45
2:A:211:ILE:HA	2:A:227:ALA:O	2.17	0.45
2:A:218:GLU:OE2	2:A:294:LYS:HE2	2.16	0.45
2:A:277:ASP:HB2	2:A:460:ILE:HB	1.99	0.45
2:A:341:ARG:HG2	2:A:341:ARG:HH11	1.81	0.45
2:A:426:ALA:HA	2:A:429:LYS:CE	2.31	0.45
2:B:51:VAL:O	2:B:54:ALA:CB	2.62	0.45
2:B:54:ALA:CB	2:B:661:PHE:CD1	3.00	0.45
2:B:382:LEU:C	2:B:384:ILE:N	2.75	0.45
2:B:864:TYR:CE1	2:B:922:ASN:CG	2.95	0.45
1:C:916:C:H5'	1:C:917:C:H5	1.66	0.45
1:C:939:A:H4'	1:C:939:A:OP1	2.16	0.45
1:D:921:U:OP2	1:D:922:C:H3'	2.17	0.45
2:A:61:ASP:OD2	2:A:674:ARG:NH1	2.48	0.45
2:A:256:ARG:O	2:A:257:LYS:C	2.60	0.45
2:A:266:SER:O	2:A:269:ALA:HB3	2.17	0.45
2:A:749:THR:O	2:A:750:ARG:C	2.59	0.45
2:A:831:THR:O	2:A:835:GLU:CG	2.65	0.45
2:A:840:ARG:HE	2:A:840:ARG:HB3	1.60	0.45
2:B:7:LYS:HB2	2:B:7:LYS:HZ3	1.81	0.45
2:B:227:ALA:HA	2:B:321:VAL:O	2.15	0.45
2:B:245:PRO:O	2:B:288:GLY:HA3	2.17	0.45
2:B:387:GLN:HE21	2:B:387:GLN:HA	1.82	0.45
2:B:387:GLN:HG3	2:B:388:LYS:N	2.32	0.45
2:B:731:HIS:HE1	2:B:833:GLU:OE1	2.00	0.45
2:B:766:TRP:HZ3	2:B:836:GLU:CG	2.30	0.45
2:B:950:LYS:H	2:B:953:LYS:NZ	2.15	0.45
2:A:250:VAL:HG12	2:A:285:GLU:HG3	1.99	0.45
2:A:518:LEU:C	2:A:520:TRP:H	2.24	0.45
2:A:568:PHE:CB	2:A:569:LEU:HD12	2.46	0.45
2:A:728:TRP:HE3	2:A:729:MET:CA	2.29	0.45
2:B:28:ARG:HG3	2:B:28:ARG:NH1	2.30	0.45
2:B:117:TRP:CD1	2:B:117:TRP:H	2.35	0.45
2:B:347:GLU:C	2:B:349:TYR:N	2.75	0.45
2:B:682:GLU:OE1	2:B:748:ARG:NH1	2.49	0.45
2:B:800:HIS:C	2:B:802:CYS:N	2.72	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:890:LEU:O	2:B:892:LYS:N	2.50	0.45
2:B:911:ILE:O	2:B:911:ILE:HG13	2.16	0.45
1:D:960:C:H4'	1:D:961:C:H5''	1.98	0.44
2:A:94:ILE:HD11	2:A:120:GLU:CA	2.46	0.44
2:A:130:MET:HE1	2:A:151:TYR:HD2	1.81	0.44
2:A:242:TRP:CZ3	2:A:332:ASP:CG	2.95	0.44
2:A:518:LEU:HD12	2:A:524:TRP:HB3	1.98	0.44
2:A:553:LYS:NZ	2:A:553:LYS:HB3	2.32	0.44
2:A:916:PHE:HB3	2:A:917:ASP:H	1.67	0.44
2:B:373:PHE:N	2:B:374:PRO:CD	2.80	0.44
2:B:860:ARG:HB3	2:B:966:ILE:CG2	2.40	0.44
2:A:67:LYS:HE2	2:A:70:GLN:HE22	1.82	0.44
2:A:786:LEU:C	2:A:786:LEU:CD2	2.90	0.44
2:B:42:PHE:CD1	2:B:42:PHE:N	2.85	0.44
2:B:215:GLU:O	2:B:296:VAL:HA	2.17	0.44
2:B:429:LYS:HB3	2:B:429:LYS:HZ2	1.82	0.44
2:B:511:LYS:HE3	2:B:524:TRP:CE2	2.51	0.44
2:B:714:TYR:CD2	2:B:714:TYR:N	2.73	0.44
2:A:31:PRO:HD2	2:A:34:LYS:HG3	1.98	0.44
2:A:69:MET:HB3	2:A:818:ALA:O	2.17	0.44
2:A:85:SER:N	2:A:86:PRO:CD	2.77	0.44
2:A:156:PHE:C	2:A:158:PRO:HD2	2.43	0.44
2:A:482:LEU:O	2:A:493:ARG:NH1	2.50	0.44
2:A:768:LEU:O	2:A:770:ARG:N	2.49	0.44
2:B:57:TYR:O	2:B:60:PRO:CG	2.62	0.44
2:B:170:LEU:CB	2:B:176:ILE:HD11	2.41	0.44
2:B:211:ILE:O	2:B:211:ILE:HG13	2.16	0.44
2:B:234:THR:HA	2:B:355:ILE:CD1	2.47	0.44
2:B:476:GLU:HA	2:B:479:ARG:NH1	2.32	0.44
2:B:860:ARG:NH1	2:B:860:ARG:O	2.50	0.44
2:A:234:THR:HB	2:A:325:VAL:HG21	1.99	0.44
2:A:432:LEU:HD11	2:A:439:ILE:CG1	2.45	0.44
2:A:616:ASN:HD22	2:A:616:ASN:C	2.20	0.44
2:A:730:LEU:CA	2:A:827:TRP:HE1	2.30	0.44
2:A:766:TRP:O	2:A:770:ARG:N	2.47	0.44
2:B:186:ASP:OD2	2:B:188:VAL:HG13	2.18	0.44
2:B:518:LEU:HD22	2:B:520:TRP:CZ2	2.52	0.44
2:B:742:ASN:N	2:B:742:ASN:ND2	2.65	0.44
2:A:219:ASN:O	2:A:220:GLY:C	2.60	0.44
2:A:617:HIS:O	2:A:618:LEU:C	2.61	0.44
2:A:872:LYS:HA	2:A:872:LYS:HZ2	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:878:SER:HB2	2:A:914:ARG:HB2	1.99	0.44
2:A:933:PHE:CE1	2:A:937:GLU:HB2	2.51	0.44
2:B:340:LYS:HG2	2:B:341:ARG:NH1	2.32	0.44
2:B:679:SER:HA	2:B:753:VAL:HG11	2.00	0.44
2:B:718:GLY:O	2:B:720:VAL:HG13	2.18	0.44
2:B:750:ARG:HE	2:B:750:ARG:HB3	1.50	0.44
2:B:783:LEU:HD12	2:B:783:LEU:N	2.33	0.44
2:B:846:ILE:HG12	2:B:964:ILE:HD12	1.94	0.44
1:D:902:C:H2'	1:D:903:G:C4'	2.47	0.44
1:D:972:U:H5''	1:D:973:C:OP2	2.18	0.44
2:A:112:PRO:C	2:A:114:GLU:N	2.76	0.44
2:A:518:LEU:HD22	2:A:520:TRP:CZ2	2.53	0.44
2:A:569:LEU:O	2:A:570:GLU:C	2.60	0.44
2:A:789:VAL:O	2:A:791:VAL:N	2.50	0.44
2:B:145:ASP:OD1	2:B:145:ASP:C	2.60	0.44
2:B:216:LEU:O	2:B:216:LEU:HG	2.17	0.44
2:B:330:PRO:HD3	2:B:400:ILE:HG12	2.00	0.44
2:B:393:LEU:O	2:B:395:GLN:N	2.51	0.44
2:B:725:ILE:HG21	2:B:771:THR:HG21	1.99	0.44
2:B:800:HIS:C	2:B:802:CYS:H	2.25	0.44
1:C:957:G:C2	1:C:958:U:C2	3.06	0.44
2:A:50:HIS:CE1	2:A:53:HIS:CE1	3.06	0.44
2:A:244:ASN:HB2	2:A:313:VAL:HG23	1.99	0.44
2:A:862:TYR:HB2	2:A:964:ILE:HA	1.99	0.44
2:B:256:ARG:O	2:B:257:LYS:C	2.60	0.44
2:B:261:GLU:HB2	2:B:263:TRP:HE1	1.81	0.44
2:B:339:LEU:HD13	2:B:339:LEU:N	2.33	0.44
2:B:449:ILE:HG23	2:B:454:ASN:O	2.18	0.44
2:B:884:LYS:C	2:B:886:SER:N	2.73	0.44
2:B:908:GLN:HE22	2:B:958:MET:HG3	1.83	0.44
1:D:937:C:O2	1:D:937:C:H2'	2.18	0.44
2:A:130:MET:HE1	2:A:151:TYR:CD2	2.53	0.44
2:A:863:ILE:CG2	2:A:953:LYS:HD3	2.48	0.44
2:A:955:LYS:C	2:A:957:ALA:H	2.26	0.44
2:B:75:LEU:HD22	2:B:601:TRP:CD1	2.53	0.44
2:B:104:ILE:HG21	2:B:653:LYS:HD3	1.99	0.44
2:B:168:TRP:NE1	2:B:519:PRO:HB2	2.33	0.44
2:B:250:VAL:HG12	2:B:285:GLU:HG3	2.00	0.44
2:B:710:GLN:O	2:B:711:PHE:C	2.61	0.44
2:B:733:LEU:HD13	2:B:733:LEU:C	2.43	0.44
2:B:794:MET:HB3	2:B:794:MET:HE3	1.67	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:953:A:HI'	2:B:849:ILE:CG2	2.48	0.44
2:A:243:VAL:HG23	2:A:244:ASN:N	2.33	0.44
2:A:744:LEU:C	2:A:746:GLU:N	2.75	0.44
2:A:803:GLU:HA	2:A:815:VAL:HG21	1.98	0.44
2:B:58:THR:HA	2:B:142:PHE:HE1	1.83	0.44
2:B:79:ALA:HB2	2:B:539:TYR:CE2	2.51	0.44
2:B:112:PRO:C	2:B:114:GLU:N	2.76	0.44
2:B:331:PHE:O	2:B:334:VAL:HG23	2.17	0.44
2:B:388:LYS:HD3	2:B:388:LYS:C	2.43	0.44
2:B:739:GLU:HB3	2:B:755:TRP:CD1	2.53	0.44
1:C:937:C:H2'	1:C:938:A:O4'	2.18	0.43
1:C:958:U:C6	1:C:958:U:C3'	3.01	0.43
1:C:972:U:H5'	1:C:973:C:OP2	2.18	0.43
1:D:923:A:HO2'	1:D:924:A:P	2.40	0.43
2:A:49:LEU:HD22	2:A:137:PHE:HE1	1.83	0.43
2:A:238:VAL:HG13	2:A:238:VAL:O	2.16	0.43
2:A:245:PRO:O	2:A:288:GLY:HA3	2.18	0.43
2:A:636:LYS:HB3	2:A:636:LYS:NZ	2.32	0.43
2:A:703:ARG:HG3	2:A:707:LEU:CD1	2.47	0.43
2:A:767:TYR:CE2	2:A:783:LEU:HD11	2.52	0.43
2:A:824:VAL:CG1	2:A:827:TRP:CE3	3.00	0.43
2:A:959:PRO:C	2:A:961:LYS:H	2.26	0.43
2:A:966:ILE:O	2:A:966:ILE:HG13	2.17	0.43
2:B:57:TYR:O	2:B:60:PRO:HD2	2.17	0.43
2:B:267:LYS:O	2:B:270:ALA:HB3	2.18	0.43
2:B:459:LYS:HZ2	2:B:461:ILE:HD13	1.82	0.43
2:B:711:PHE:CE1	2:B:783:LEU:HD23	2.53	0.43
2:B:724:ASP:OD2	2:B:928:ARG:HD3	2.18	0.43
2:B:738:LYS:NZ	2:B:738:LYS:HB3	2.33	0.43
2:A:81:HIS:HD2	2:A:152:THR:HG21	1.83	0.43
2:A:83:THR:O	2:A:528:SER:HB3	2.17	0.43
2:A:272:LYS:HD3	2:A:442:GLU:CD	2.43	0.43
2:A:675:LEU:CD1	2:A:697:LEU:HD21	2.48	0.43
2:A:677:ILE:HD11	2:A:689:TRP:HZ3	1.83	0.43
2:A:701:ILE:O	2:A:704:PHE:HB3	2.16	0.43
2:A:890:LEU:O	2:A:892:LYS:N	2.51	0.43
2:A:921:ILE:O	2:A:924:GLU:HB3	2.17	0.43
2:A:958:MET:HE3	2:A:959:PRO:HD2	1.99	0.43
2:B:331:PHE:HD1	2:B:334:VAL:HG21	1.83	0.43
2:B:355:ILE:HG23	2:B:412:VAL:CG1	2.49	0.43
2:B:742:ASN:O	2:B:744:LEU:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:58:THR:HG22	2:A:62:VAL:CG2	2.49	0.43
2:A:166:GLN:NE2	2:A:534:ILE:HG12	2.33	0.43
2:A:235:VAL:CA	2:A:323:MET:HE1	2.30	0.43
2:A:244:ASN:HD22	2:A:313:VAL:HG23	1.82	0.43
2:A:662:ILE:C	2:A:664:ALA:N	2.76	0.43
2:A:824:VAL:HB	2:A:827:TRP:CE3	2.53	0.43
2:A:868:ASP:C	2:A:870:LYS:N	2.75	0.43
2:B:9:ILE:O	2:B:10:GLU:C	2.59	0.43
2:B:188:VAL:HG23	2:B:190:GLY:H	1.84	0.43
2:B:339:LEU:HD22	2:B:340:LYS:HG3	2.00	0.43
2:B:449:ILE:HG22	2:B:450:SER:N	2.33	0.43
2:B:618:LEU:HD23	2:B:618:LEU:HA	1.88	0.43
2:B:911:ILE:O	2:B:912:LYS:HG3	2.18	0.43
2:B:944:ILE:O	2:B:945:ASN:C	2.61	0.43
1:C:985:A:H61	2:A:504:ASP:CB	2.24	0.43
1:D:917:C:C2	1:D:918:U:C5	3.06	0.43
2:A:919:LYS:H	2:A:919:LYS:HE2	1.82	0.43
2:B:152:THR:C	2:B:153:THR:HG23	2.43	0.43
2:B:163:ILE:HD13	2:B:163:ILE:HA	1.92	0.43
2:B:210:ILE:HG22	2:B:439:ILE:HG12	1.99	0.43
2:B:373:PHE:N	2:B:373:PHE:CD1	2.86	0.43
2:B:412:VAL:HG23	2:B:414:PRO:HD2	2.00	0.43
2:B:577:GLU:OE1	2:B:592:HIS:HB2	2.18	0.43
2:B:644:GLY:HA2	2:B:687:PHE:O	2.18	0.43
2:B:860:ARG:HH12	2:B:861:ALA:HA	1.83	0.43
2:B:877:VAL:HG22	2:B:906:ILE:HG23	2.01	0.43
1:C:988:A:N7	2:A:529:LEU:HD21	2.33	0.43
2:A:412:VAL:O	2:A:413:PRO:C	2.60	0.43
2:A:446:LYS:H	2:A:446:LYS:HD2	1.84	0.43
2:A:460:ILE:N	2:A:460:ILE:HD12	2.33	0.43
2:A:890:LEU:C	2:A:892:LYS:H	2.25	0.43
2:B:32:LYS:C	2:B:34:LYS:H	2.26	0.43
2:B:310:ALA:HB1	2:B:312:PHE:CE1	2.53	0.43
1:C:964:G:O2'	1:C:965:G:H5'	2.18	0.43
2:A:27:ILE:HG12	2:A:28:ARG:CZ	2.49	0.43
2:A:45:LEU:CD1	2:A:80:TRP:HB3	2.47	0.43
2:A:183:VAL:O	2:A:183:VAL:CG1	2.65	0.43
2:A:330:PRO:CD	2:A:400:ILE:HG12	2.48	0.43
2:A:395:GLN:C	2:A:397:THR:H	2.26	0.43
2:A:508:CYS:O	2:A:508:CYS:SG	2.77	0.43
2:B:114:GLU:OE1	2:B:114:GLU:HA	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:171:LYS:HD2	2:B:520:TRP:CE3	2.54	0.43
2:B:198:LEU:H	2:B:198:LEU:CD1	2.29	0.43
2:B:340:LYS:CE	2:B:341:ARG:HH12	2.32	0.43
2:B:401:TYR:OH	2:B:424:LYS:HE3	2.19	0.43
1:C:955:G:P	2:A:961:LYS:HZ3	2.40	0.43
2:A:138:ILE:HD12	2:A:138:ILE:HA	1.87	0.43
2:A:235:VAL:C	2:A:237:GLY:H	2.27	0.43
2:A:273:LEU:HD21	2:A:440:MET:HG3	2.00	0.43
2:A:703:ARG:O	2:A:707:LEU:HD12	2.18	0.43
2:A:728:TRP:O	2:A:730:LEU:N	2.51	0.43
2:A:960:LEU:N	2:A:960:LEU:CD2	2.81	0.43
2:B:45:LEU:HD11	2:B:130:MET:HG3	2.00	0.43
2:B:119:PHE:O	2:B:120:GLU:C	2.62	0.43
2:B:211:ILE:HA	2:B:227:ALA:O	2.19	0.43
2:B:546:ASN:HD22	2:B:546:ASN:HA	1.59	0.43
2:B:573:SER:HB2	2:B:576:LYS:HG2	2.00	0.43
2:B:724:ASP:C	2:B:726:ASP:N	2.75	0.43
2:B:922:ASN:ND2	2:B:923:GLU:N	2.63	0.43
2:B:923:GLU:HB2	2:B:945:ASN:HD21	1.84	0.43
1:C:986:C:O3'	2:A:510:ARG:HD2	2.19	0.43
1:D:976:C:O2'	1:D:977:G:H5'	2.18	0.43
2:A:36:PHE:O	2:A:38:ILE:HG22	2.18	0.43
2:A:128:TYR:O	2:A:128:TYR:CD1	2.71	0.43
2:A:198:LEU:HD22	2:A:202:GLU:CB	2.49	0.43
2:A:710:GLN:C	2:A:712:ALA:H	2.26	0.43
2:A:742:ASN:O	2:A:745:GLU:N	2.52	0.43
2:A:781:TYR:O	2:A:782:VAL:C	2.62	0.43
2:B:173:LYS:HD2	2:B:175:TYR:CE2	2.54	0.43
2:B:337:GLU:O	2:B:337:GLU:HG2	2.18	0.43
2:B:379:VAL:O	2:B:383:GLY:HA3	2.19	0.43
2:B:420:VAL:C	2:B:422:GLU:N	2.77	0.43
2:B:481:ALA:O	2:B:484:ARG:N	2.34	0.43
2:B:868:ASP:C	2:B:870:LYS:N	2.75	0.43
1:D:969:G:O2'	1:D:970:A:H5'	2.18	0.43
2:A:37:TYR:CE2	2:A:39:THR:CG2	3.01	0.43
2:A:182:ARG:O	2:A:183:VAL:CB	2.66	0.43
2:A:246:ASN:OD1	2:A:247:ALA:N	2.52	0.43
2:A:380:ASN:O	2:A:384:ILE:HG13	2.19	0.43
2:A:535:TYR:CD2	2:A:535:TYR:C	2.97	0.43
2:A:566:TYR:OH	2:A:572:PHE:HD1	2.01	0.43
2:A:880:LYS:O	2:A:881:ARG:C	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:25:PRO:HD2	2:B:145:ASP:OD2	2.19	0.43
2:B:33:GLU:OE2	2:B:33:GLU:N	2.39	0.43
2:B:59:ILE:HG12	2:B:678:MET:HE1	2.00	0.43
2:B:273:LEU:CB	2:B:280:ILE:HD11	2.49	0.43
2:B:343:THR:HG23	2:B:344:GLU:HG2	2.00	0.43
2:B:539:TYR:HA	2:B:542:SER:HB2	2.01	0.43
2:B:646:LEU:O	2:B:647:GLU:HB2	2.19	0.43
2:B:728:TRP:HZ3	2:B:729:MET:CE	2.32	0.43
2:B:803:GLU:CG	2:B:815:VAL:HG12	2.49	0.43
2:B:864:TYR:OH	2:B:871:TRP:HZ2	2.02	0.43
2:A:214:PHE:HA	2:A:299:PRO:CG	2.49	0.43
2:A:231:ARG:O	2:A:234:THR:OG1	2.36	0.43
2:A:277:ASP:O	2:A:277:ASP:CG	2.62	0.43
2:A:420:VAL:C	2:A:422:GLU:N	2.76	0.43
2:A:511:LYS:HE2	2:A:524:TRP:CE2	2.53	0.43
2:A:544:HIS:HE1	2:A:593:GLU:OE2	2.01	0.43
2:B:98:ASP:OD2	2:B:99:PRO:HD2	2.19	0.43
2:B:231:ARG:O	2:B:234:THR:OG1	2.37	0.43
2:B:293:GLY:O	2:B:294:LYS:C	2.61	0.43
2:B:395:GLN:C	2:B:397:THR:H	2.27	0.43
2:B:471:ASN:OD1	2:B:473:GLU:HG2	2.18	0.43
2:B:518:LEU:C	2:B:520:TRP:H	2.27	0.43
2:B:560:THR:O	2:B:563:PHE:HB3	2.19	0.43
1:C:941:A:H2'	1:C:942:U:H6	1.84	0.42
1:C:964:G:N2	1:C:975:C:C2	2.86	0.42
1:D:920:G:H5''	1:D:921:U:C5	2.48	0.42
2:A:184:ARG:HD3	2:A:198:LEU:HD21	2.01	0.42
2:A:198:LEU:HD23	2:A:448:VAL:HG13	2.01	0.42
2:A:232:PRO:O	2:A:427:ILE:HG21	2.19	0.42
2:A:311:GLU:OE2	2:A:335:ALA:HB2	2.19	0.42
2:A:384:ILE:CG2	2:A:385:LYS:H	2.19	0.42
2:A:388:LYS:HD3	2:A:388:LYS:C	2.44	0.42
2:A:475:LYS:HE3	2:A:500:ILE:O	2.19	0.42
2:A:521:ASP:N	2:A:522:PRO:HD3	2.34	0.42
2:A:718:GLY:O	2:A:719:ASN:C	2.61	0.42
2:A:884:LYS:HB2	2:A:884:LYS:HZ3	1.82	0.42
2:B:22:ILE:HD12	2:B:22:ILE:HA	1.82	0.42
2:B:223:ILE:HG23	2:B:223:ILE:O	2.19	0.42
2:B:373:PHE:HB2	2:B:374:PRO:HD3	2.02	0.42
2:B:374:PRO:HG3	2:B:379:VAL:CG2	2.49	0.42
2:B:614:ILE:HA	2:B:618:LEU:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:698:ARG:O	2:B:701:ILE:HB	2.18	0.42
2:B:737:ILE:HG22	2:B:823:PRO:HD3	2.00	0.42
2:B:781:TYR:O	2:B:782:VAL:C	2.62	0.42
2:B:840:ARG:O	2:B:844:GLU:HG3	2.18	0.42
1:C:958:U:H2'	1:C:959:U:O5'	2.19	0.42
1:D:958:U:H2'	1:D:959:U:O5'	2.19	0.42
2:A:119:PHE:O	2:A:120:GLU:C	2.62	0.42
2:A:314:ASP:HA	2:A:315:PRO:HD3	1.89	0.42
2:A:354:ARG:NE	2:A:375:ALA:C	2.76	0.42
2:A:381:LYS:HB3	2:A:381:LYS:HZ2	1.84	0.42
2:A:675:LEU:CD1	2:A:697:LEU:HD11	2.48	0.42
2:A:714:TYR:CD2	2:A:714:TYR:N	2.88	0.42
2:A:742:ASN:C	2:A:744:LEU:N	2.77	0.42
2:A:854:LYS:HG3	2:A:855:ILE:H	1.83	0.42
2:B:54:ALA:HB2	2:B:661:PHE:CD1	2.54	0.42
2:B:355:ILE:CG2	2:B:410:PHE:CE1	3.02	0.42
2:B:706:GLU:O	2:B:709:SER:HB2	2.19	0.42
2:B:872:LYS:HD3	2:B:872:LYS:HA	1.88	0.42
1:C:960:C:C2	1:C:971:A:H1'	2.54	0.42
1:D:916:C:O2'	1:D:972:U:O3'	2.36	0.42
2:A:244:ASN:ND2	2:A:313:VAL:HG23	2.34	0.42
2:A:347:GLU:C	2:A:349:TYR:N	2.75	0.42
2:A:469:TYR:CE2	2:A:620:PHE:CD1	3.07	0.42
2:A:774:ARG:HG2	2:A:775:ASP:N	2.34	0.42
2:B:159:PHE:O	2:B:162:PHE:HB3	2.19	0.42
2:B:165:TRP:HZ2	2:B:565:ASP:OD2	2.02	0.42
2:B:376:VAL:O	2:B:377:GLU:C	2.62	0.42
2:B:706:GLU:O	2:B:707:LEU:C	2.62	0.42
2:B:717:LYS:C	2:B:717:LYS:CD	2.93	0.42
2:B:827:TRP:O	2:B:827:TRP:HD1	2.02	0.42
2:B:901:LYS:HD3	2:B:901:LYS:C	2.44	0.42
2:A:373:PHE:N	2:A:374:PRO:CD	2.83	0.42
2:A:572:PHE:HE1	2:A:595:LYS:HB3	1.85	0.42
2:A:614:ILE:HA	2:A:618:LEU:HB2	2.02	0.42
2:A:687:PHE:CD2	2:A:687:PHE:C	2.96	0.42
2:A:691:ARG:CG	2:A:691:ARG:NH1	2.80	0.42
2:A:760:ILE:O	2:A:761:MET:C	2.61	0.42
2:A:860:ARG:NH2	2:A:862:TYR:CB	2.77	0.42
2:A:862:TYR:C	2:A:862:TYR:HD2	2.26	0.42
2:A:887:MET:HE2	2:A:891:MET:CG	2.41	0.42
2:A:911:ILE:C	2:A:912:LYS:HG3	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:235:VAL:C	2:B:237:GLY:H	2.26	0.42
2:B:388:LYS:H	2:B:390:LYS:HE2	1.84	0.42
2:B:569:LEU:O	2:B:570:GLU:C	2.62	0.42
2:B:720:VAL:CG1	2:B:777:GLU:HG2	2.48	0.42
2:B:728:TRP:C	2:B:730:LEU:H	2.25	0.42
2:B:959:PRO:C	2:B:961:LYS:H	2.25	0.42
1:C:985:A:O3'	1:C:986:C:C6	2.72	0.42
2:A:75:LEU:C	2:A:75:LEU:CD1	2.84	0.42
2:A:160:SER:HB3	2:A:516:THR:HG23	2.01	0.42
2:A:191:THR:HA	2:A:192:PRO:HD3	1.88	0.42
2:A:391:GLU:C	2:A:393:LEU:N	2.78	0.42
2:A:733:LEU:HD11	2:A:789:VAL:CG2	2.48	0.42
2:B:225:LEU:HD12	2:B:264:ILE:O	2.20	0.42
2:B:800:HIS:O	2:B:802:CYS:N	2.53	0.42
2:B:819:LYS:HD2	2:B:819:LYS:N	2.34	0.42
1:C:982:C:O5'	1:C:982:C:H6	2.02	0.42
1:D:922:C:H4'	1:D:923:A:C5'	2.46	0.42
2:A:37:TYR:OH	2:A:536:MET:O	2.30	0.42
2:A:161:LYS:C	2:A:564:PHE:CE2	2.98	0.42
2:A:211:ILE:HG12	2:A:438:GLU:O	2.20	0.42
2:A:219:ASN:CG	2:A:220:GLY:H	2.17	0.42
2:A:256:ARG:NH1	2:A:278:ARG:NH1	2.68	0.42
2:A:867:GLU:O	2:A:870:LYS:C	2.63	0.42
2:A:911:ILE:HG13	2:A:912:LYS:HG3	2.02	0.42
2:B:581:GLU:HG3	2:B:586:ILE:O	2.20	0.42
2:B:616:ASN:O	2:B:619:THR:N	2.52	0.42
1:D:922:C:H5''	1:D:923:A:OP1	2.20	0.42
2:A:83:THR:HA	2:A:153:THR:HG22	2.02	0.42
2:A:145:ASP:OD1	2:A:147:SER:N	2.52	0.42
2:A:276:GLN:HE21	2:A:276:GLN:HB3	1.62	0.42
2:A:379:VAL:O	2:A:383:GLY:HA3	2.19	0.42
2:A:557:GLU:C	2:A:559:LEU:N	2.77	0.42
2:A:730:LEU:HD23	2:A:730:LEU:HA	1.90	0.42
2:A:767:TYR:OH	2:A:782:VAL:HG21	2.19	0.42
2:A:891:MET:C	2:A:893:ASP:H	2.28	0.42
2:A:947:THR:CG2	2:A:948:GLU:H	2.33	0.42
2:B:176:ILE:HD13	2:B:520:TRP:CH2	2.55	0.42
2:B:469:TYR:HB2	2:B:504:ASP:O	2.20	0.42
2:B:634:TRP:O	2:B:635:PRO:C	2.63	0.42
2:B:645:THR:OG1	2:B:688:ASP:OD1	2.28	0.42
2:B:721:GLU:HA	2:B:721:GLU:OE2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:728:TRP:O	2:B:730:LEU:N	2.53	0.42
2:B:764:LEU:HD13	2:B:786:LEU:CD1	2.48	0.42
2:B:766:TRP:O	2:B:770:ARG:N	2.45	0.42
1:C:941:A:C3'	2:A:699:LYS:HZ2	2.31	0.42
2:A:376:VAL:O	2:A:377:GLU:C	2.62	0.42
2:A:560:THR:O	2:A:563:PHE:N	2.52	0.42
2:A:711:PHE:N	2:A:711:PHE:CD1	2.88	0.42
2:A:882:ASP:C	2:A:883:PHE:CD1	2.98	0.42
2:A:959:PRO:C	2:A:960:LEU:HD22	2.45	0.42
2:B:129:PHE:HA	2:B:132:ALA:HB3	2.01	0.42
2:B:468:ASP:C	2:B:470:GLY:N	2.75	0.42
2:B:478:ALA:HB2	2:B:623:PHE:CD1	2.55	0.42
2:B:661:PHE:O	2:B:665:ILE:HG13	2.20	0.42
2:B:775:ASP:OD1	2:B:775:ASP:O	2.38	0.42
2:B:921:ILE:HD12	2:B:928:ARG:HH12	1.85	0.42
1:C:927:G:C6	1:C:928:C:C4	3.08	0.42
1:C:953:A:C5'	1:C:954:G:OP1	2.68	0.42
2:A:12:LYS:HZ1	2:A:16:ARG:HH22	1.67	0.42
2:A:67:LYS:HA	2:A:70:GLN:HB2	2.01	0.42
2:A:181:HIS:ND1	2:A:182:ARG:O	2.52	0.42
2:A:519:PRO:HG2	2:A:520:TRP:CE3	2.55	0.42
2:B:147:SER:OG	2:B:543:ARG:HG3	2.20	0.42
2:B:152:THR:HG22	2:B:159:PHE:CE1	2.55	0.42
2:B:219:ASN:O	2:B:220:GLY:C	2.62	0.42
2:B:277:ASP:OD2	2:B:462:HIS:CE1	2.73	0.42
2:B:317:ASN:O	2:B:318:ALA:HB3	2.20	0.42
2:B:576:LYS:O	2:B:580:LEU:HD13	2.20	0.42
2:B:617:HIS:ND1	2:B:617:HIS:C	2.77	0.42
2:B:714:TYR:CD1	2:B:780:ARG:HD3	2.55	0.42
2:B:725:ILE:CD1	2:B:770:ARG:NE	2.82	0.42
2:B:843:MET:HE3	2:B:938:LEU:CD1	2.49	0.42
2:B:871:TRP:CD2	2:B:920:ARG:NH2	2.80	0.42
1:D:923:A:O2'	1:D:924:A:OP2	2.30	0.42
2:A:58:THR:HG22	2:A:678:MET:HE2	2.01	0.42
2:A:146:TRP:O	2:A:147:SER:C	2.62	0.42
2:A:290:LYS:HE3	2:A:290:LYS:HB3	1.95	0.42
2:A:418:LYS:HB3	2:A:422:GLU:OE2	2.20	0.42
2:A:434:LYS:HB3	2:A:436:ILE:CG1	2.46	0.42
2:A:706:GLU:O	2:A:707:LEU:C	2.63	0.42
2:A:708:ILE:HD12	2:A:791:VAL:CG2	2.49	0.42
2:A:924:GLU:HA	2:A:927:LEU:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:32:LYS:HA	2:B:600:TYR:CE1	2.55	0.42
2:B:139:ARG:HH22	2:B:666:GLU:CD	2.28	0.42
2:B:347:GLU:C	2:B:349:TYR:H	2.28	0.42
2:B:391:GLU:C	2:B:393:LEU:N	2.77	0.42
2:B:557:GLU:C	2:B:559:LEU:N	2.77	0.42
2:B:734:ASN:HD22	2:B:734:ASN:HA	1.51	0.42
1:C:923:A:O2'	1:C:924:A:OP2	2.34	0.41
1:C:926:G:O2'	1:C:927:G:H5'	2.20	0.41
1:D:903:G:H2'	1:D:904:G:O4'	2.20	0.41
1:D:953:A:N1	2:B:966:ILE:HG12	2.35	0.41
2:A:87:ILE:O	2:A:90:ILE:HB	2.20	0.41
2:A:123:ILE:HD11	2:A:155:LEU:HD11	2.02	0.41
2:A:616:ASN:CG	2:A:617:HIS:H	2.19	0.41
2:A:780:ARG:O	2:A:781:TYR:C	2.63	0.41
2:B:325:VAL:N	2:B:332:ASP:OD2	2.51	0.41
2:B:553:LYS:HE3	2:B:553:LYS:HB3	1.80	0.41
2:B:671:ASP:HB3	2:B:798:THR:HG22	2.02	0.41
1:C:976:C:C2'	1:C:977:G:H5'	2.50	0.41
2:A:711:PHE:O	2:A:784:ARG:HG2	2.20	0.41
2:B:412:VAL:O	2:B:416:GLU:OE1	2.37	0.41
2:B:414:PRO:O	2:B:415:TYR:C	2.62	0.41
2:B:676:TYR:C	2:B:679:SER:HB3	2.45	0.41
2:B:677:ILE:HD13	2:B:677:ILE:HA	1.85	0.41
2:B:728:TRP:HE3	2:B:729:MET:N	2.18	0.41
2:B:768:LEU:O	2:B:770:ARG:N	2.52	0.41
2:B:824:VAL:HG12	2:B:825:GLU:N	2.35	0.41
2:B:825:GLU:O	2:B:825:GLU:CG	2.68	0.41
2:B:867:GLU:O	2:B:870:LYS:C	2.63	0.41
1:C:970:A:O2'	1:C:971:A:O5'	2.38	0.41
1:D:988:A:N7	2:B:529:LEU:HD21	2.36	0.41
2:A:9:ILE:HD13	2:A:804:GLU:HG2	2.02	0.41
2:A:236:TYR:CE2	2:A:414:PRO:HG2	2.55	0.41
2:A:250:VAL:CG1	2:A:285:GLU:HG3	2.50	0.41
2:A:264:ILE:O	2:A:264:ILE:HG22	2.18	0.41
2:A:339:LEU:HD22	2:A:339:LEU:C	2.45	0.41
2:A:341:ARG:HD3	2:A:341:ARG:N	2.36	0.41
2:A:414:PRO:O	2:A:415:TYR:C	2.62	0.41
2:A:691:ARG:O	2:A:694:VAL:CG1	2.64	0.41
2:A:871:TRP:CE3	2:A:920:ARG:NH2	2.88	0.41
2:B:263:TRP:N	2:B:263:TRP:CD1	2.88	0.41
2:B:264:ILE:HG23	2:B:286:PHE:CE2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:289:GLU:OE2	2:B:289:GLU:N	2.53	0.41
2:B:891:MET:C	2:B:893:ASP:H	2.28	0.41
2:B:934:MET:O	2:B:938:LEU:HD13	2.21	0.41
2:A:12:LYS:NZ	2:A:16:ARG:HH22	2.18	0.41
2:A:148:ARG:HB3	2:A:542:SER:HB3	2.02	0.41
2:A:347:GLU:C	2:A:349:TYR:H	2.27	0.41
2:A:459:LYS:CG	2:A:460:ILE:N	2.83	0.41
2:A:499:ILE:HG12	2:A:615:PRO:HA	2.02	0.41
2:A:744:LEU:O	2:A:745:GLU:C	2.63	0.41
2:A:909:LYS:NZ	2:A:913:GLU:O	2.52	0.41
2:B:173:LYS:HD2	2:B:175:TYR:HE2	1.85	0.41
2:B:212:ILE:CD1	2:B:235:VAL:HG12	2.47	0.41
2:B:510:ARG:HA	2:B:510:ARG:HE	1.84	0.41
2:B:710:GLN:C	2:B:712:ALA:H	2.28	0.41
2:B:730:LEU:O	2:B:827:TRP:NE1	2.53	0.41
2:B:768:LEU:C	2:B:770:ARG:N	2.77	0.41
2:B:847:LYS:HE3	2:B:847:LYS:HB2	1.89	0.41
1:C:987:C:H5	2:A:506:LYS:NZ	2.18	0.41
2:A:16:ARG:NH1	2:A:16:ARG:HG3	2.36	0.41
2:A:45:LEU:HD13	2:A:130:MET:CB	2.51	0.41
2:A:61:ASP:O	2:A:64:ALA:N	2.53	0.41
2:A:317:ASN:O	2:A:318:ALA:HB3	2.21	0.41
2:A:395:GLN:HG3	2:A:396:ALA:N	2.34	0.41
2:A:410:PHE:CZ	2:A:412:VAL:HG21	2.54	0.41
2:A:574:GLU:HA	2:A:577:GLU:OE1	2.20	0.41
2:A:728:TRP:C	2:A:730:LEU:H	2.26	0.41
2:A:767:TYR:OH	2:A:782:VAL:HG11	2.21	0.41
2:A:768:LEU:C	2:A:770:ARG:N	2.76	0.41
2:B:182:ARG:O	2:B:183:VAL:CB	2.69	0.41
2:B:506:LYS:HE3	2:B:527:GLU:OE1	2.21	0.41
2:B:538:TYR:O	2:B:539:TYR:C	2.63	0.41
2:B:570:GLU:OE1	2:B:576:LYS:HG3	2.20	0.41
2:B:585:GLY:C	2:B:586:ILE:HD12	2.46	0.41
2:B:617:HIS:O	2:B:618:LEU:C	2.62	0.41
2:B:662:ILE:C	2:B:664:ALA:N	2.76	0.41
2:B:774:ARG:CG	2:B:775:ASP:N	2.84	0.41
1:C:960:C:H2'	1:C:971:A:H1'	2.03	0.41
1:D:902:C:H2'	1:D:903:G:C5'	2.51	0.41
2:A:91:ALA:O	2:A:92:GLU:C	2.64	0.41
2:A:184:ARG:NH1	2:A:195:ASP:CG	2.79	0.41
2:A:540:THR:HG21	2:A:598:PHE:CD1	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:544:HIS:CE1	2:A:593:GLU:OE2	2.73	0.41
2:A:711:PHE:HA	2:A:714:TYR:CE2	2.56	0.41
2:A:816:SER:C	2:A:817:LEU:HD23	2.45	0.41
2:A:822:GLU:O	2:A:823:PRO:C	2.63	0.41
2:B:196:HIS:CD2	2:B:197:ASP:N	2.89	0.41
2:B:241:MET:HG3	2:B:296:VAL:CG2	2.51	0.41
2:B:725:ILE:HD13	2:B:770:ARG:NE	2.36	0.41
2:B:908:GLN:O	2:B:909:LYS:C	2.63	0.41
1:C:920:G:OP1	1:C:920:G:C4'	2.68	0.41
2:A:7:LYS:HB2	2:A:7:LYS:HZ3	1.85	0.41
2:A:323:MET:HE2	2:A:325:VAL:CG2	2.51	0.41
2:A:395:GLN:C	2:A:397:THR:N	2.78	0.41
2:A:412:VAL:H	2:A:416:GLU:HG2	1.86	0.41
2:A:612:ASP:OD1	2:A:613:LEU:HD23	2.21	0.41
2:A:614:ILE:N	2:A:615:PRO:CD	2.83	0.41
2:A:634:TRP:O	2:A:635:PRO:C	2.64	0.41
2:A:891:MET:HE1	2:A:900:GLY:CA	2.51	0.41
2:A:950:LYS:H	2:A:953:LYS:HZ3	1.68	0.41
2:B:136:THR:HG23	2:B:662:ILE:HB	2.02	0.41
2:B:168:TRP:C	2:B:170:LEU:N	2.78	0.41
2:B:246:ASN:OD1	2:B:246:ASN:C	2.64	0.41
2:B:342:GLU:H	2:B:342:GLU:CD	2.29	0.41
2:B:395:GLN:C	2:B:397:THR:N	2.79	0.41
2:B:856:GLU:O	2:B:857:ASN:O	2.38	0.41
2:B:863:ILE:HG13	2:B:945:ASN:HA	2.03	0.41
2:B:955:LYS:C	2:B:957:ALA:H	2.27	0.41
1:D:944:C:OP1	2:B:765:ARG:HD3	2.20	0.41
2:A:181:HIS:HD2	2:A:466:PHE:CE1	2.38	0.41
2:A:626:VAL:HG12	2:A:634:TRP:CD2	2.56	0.41
2:A:676:TYR:O	2:A:679:SER:HB3	2.21	0.41
2:A:707:LEU:O	2:A:708:ILE:C	2.63	0.41
2:A:793:LEU:HD23	2:A:821:PRO:HG3	2.03	0.41
2:B:65:ARG:HA	2:B:68:ARG:HH11	1.81	0.41
2:B:276:GLN:HE21	2:B:460:ILE:HD11	1.86	0.41
2:B:623:PHE:O	2:B:626:VAL:HG22	2.21	0.41
2:B:860:ARG:HH21	2:B:860:ARG:HB2	1.86	0.41
1:C:914:A:H1'	1:C:925:A:N1	2.36	0.41
1:C:958:U:C2'	1:C:959:U:O5'	2.68	0.41
1:D:925:A:H2'	1:D:926:G:O4'	2.21	0.41
2:A:112:PRO:HD2	2:A:115:ILE:HD12	2.02	0.41
2:A:175:TYR:CE1	2:A:474:TRP:HB2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:293:GLY:O	2:A:294:LYS:C	2.61	0.41
2:A:293:GLY:O	2:A:295:TYR:CD1	2.74	0.41
2:A:381:LYS:C	2:A:381:LYS:HZ2	2.29	0.41
2:A:406:HIS:ND1	2:A:421:GLN:OE1	2.54	0.41
2:A:467:ILE:CG1	2:A:508:CYS:HB3	2.50	0.41
2:A:644:GLY:HA2	2:A:687:PHE:O	2.20	0.41
2:A:657:ASN:O	2:A:657:ASN:CG	2.63	0.41
2:A:714:TYR:CE1	2:A:780:ARG:HG2	2.56	0.41
2:A:759:SER:O	2:A:760:ILE:C	2.64	0.41
2:A:831:THR:O	2:A:834:ALA:HB3	2.21	0.41
2:A:872:LYS:O	2:A:876:VAL:CG2	2.65	0.41
2:B:33:GLU:CD	2:B:33:GLU:N	2.74	0.41
2:B:560:THR:HB	2:B:561:PRO:CD	2.51	0.41
2:B:614:ILE:C	2:B:616:ASN:H	2.29	0.41
2:B:652:SER:HG	2:B:655:LYS:HB2	1.85	0.41
2:B:725:ILE:HB	2:B:929:GLU:OE1	2.20	0.41
2:B:846:ILE:HD12	2:B:938:LEU:CD2	2.51	0.41
2:B:849:ILE:HD12	2:B:964:ILE:CD1	2.51	0.41
2:B:914:ARG:HH21	2:B:915:THR:C	2.28	0.41
2:B:944:ILE:HG22	2:B:945:ASN:N	2.36	0.41
2:B:964:ILE:HG13	2:B:965:PHE:N	2.34	0.41
2:A:135:GLU:O	2:A:139:ARG:HB2	2.21	0.41
2:A:168:TRP:CZ3	2:A:520:TRP:CE3	3.09	0.41
2:A:173:LYS:CB	2:A:175:TYR:CE2	3.04	0.41
2:A:232:PRO:O	2:A:235:VAL:HG22	2.21	0.41
2:A:252:ALA:HB1	2:A:281:GLU:O	2.21	0.41
2:B:488:LEU:HA	2:B:488:LEU:HD23	1.81	0.41
2:B:771:THR:HB	2:B:774:ARG:HD3	2.03	0.41
2:B:846:ILE:HA	2:B:849:ILE:HD12	2.03	0.41
2:B:870:LYS:HE3	2:B:905:LYS:CE	2.40	0.41
1:C:980:C:H2'	1:C:981:C:H6	1.86	0.40
1:C:986:C:C2	2:A:507:ALA:N	2.89	0.40
2:A:9:ILE:O	2:A:12:LYS:HB3	2.22	0.40
2:A:32:LYS:C	2:A:34:LYS:H	2.28	0.40
2:A:168:TRP:C	2:A:170:LEU:N	2.78	0.40
2:A:345:ILE:O	2:A:346:LEU:HB2	2.20	0.40
2:A:581:GLU:HG3	2:A:586:ILE:O	2.21	0.40
2:A:728:TRP:O	2:A:729:MET:C	2.65	0.40
2:B:152:THR:HG22	2:B:159:PHE:CZ	2.56	0.40
2:B:240:ASN:O	2:B:324:SER:HB3	2.21	0.40
2:B:334:VAL:HG13	2:B:388:LYS:O	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:704:PHE:HD1	2:B:790:TRP:CH2	2.39	0.40
2:B:759:SER:O	2:B:760:ILE:C	2.64	0.40
2:B:914:ARG:HH21	2:B:915:THR:CG2	2.27	0.40
2:B:914:ARG:CZ	2:B:915:THR:O	2.69	0.40
2:B:914:ARG:NH2	2:B:915:THR:HG23	2.29	0.40
2:B:949:ASP:HB2	2:B:954:LYS:CE	2.45	0.40
2:A:232:PRO:CG	2:A:428:ALA:HB2	2.51	0.40
2:A:339:LEU:N	2:A:339:LEU:HD13	2.36	0.40
2:A:612:ASP:OD1	2:A:612:ASP:C	2.64	0.40
2:A:631:GLU:C	2:A:633:HIS:N	2.79	0.40
2:A:646:LEU:O	2:A:647:GLU:CB	2.69	0.40
2:A:713:GLU:O	2:A:714:TYR:O	2.40	0.40
2:A:733:LEU:HD11	2:A:789:VAL:HB	2.02	0.40
2:A:803:GLU:HA	2:A:803:GLU:OE1	2.20	0.40
2:A:824:VAL:CG1	2:A:825:GLU:N	2.84	0.40
2:B:86:PRO:O	2:B:87:ILE:C	2.64	0.40
2:B:497:GLU:O	2:B:500:ILE:N	2.54	0.40
2:B:742:ASN:C	2:B:744:LEU:N	2.78	0.40
2:A:50:HIS:H	2:A:53:HIS:HD2	1.68	0.40
2:A:115:ILE:O	2:A:116:LEU:C	2.64	0.40
2:A:173:LYS:HD3	2:A:175:TYR:HE2	1.86	0.40
2:A:441:TYR:O	2:A:442:GLU:OE2	2.40	0.40
2:A:614:ILE:C	2:A:616:ASN:H	2.29	0.40
2:A:944:ILE:O	2:A:945:ASN:C	2.64	0.40
2:A:959:PRO:O	2:A:960:LEU:HB2	2.20	0.40
2:B:13:TRP:CZ2	2:B:803:GLU:HB3	2.53	0.40
2:B:186:ASP:CB	2:B:193:LEU:HD11	2.42	0.40
2:B:216:LEU:HB2	2:B:296:VAL:HG12	2.04	0.40
2:B:337:GLU:O	2:B:339:LEU:HD12	2.21	0.40
2:B:461:ILE:HB	2:B:464:GLN:HB2	2.03	0.40
2:B:528:SER:C	2:B:530:SER:H	2.29	0.40
2:B:597:GLU:O	2:B:600:TYR:N	2.53	0.40
2:B:783:LEU:CD1	2:B:783:LEU:N	2.84	0.40
2:B:871:TRP:HZ3	2:B:918:VAL:HA	1.87	0.40
2:B:915:THR:O	2:B:916:PHE:CD2	2.74	0.40
2:A:14:GLN:HG3	2:A:14:GLN:H	1.61	0.40
2:A:77:PRO:HG3	2:A:539:TYR:CD1	2.56	0.40
2:A:217:ARG:HE	2:A:217:ARG:HB3	1.62	0.40
2:A:497:GLU:O	2:A:500:ILE:N	2.54	0.40
2:A:918:VAL:HG11	2:A:920:ARG:NH1	2.37	0.40
2:B:48:HIS:NE2	2:B:132:ALA:HB1	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:70:GLN:HB3	2:B:72:TYR:CE1	2.56	0.40
2:B:349:TYR:O	2:B:349:TYR:CG	2.74	0.40
2:B:555:ASP:OD2	2:B:557:GLU:HB2	2.22	0.40
2:B:849:ILE:HD12	2:B:964:ILE:HD11	2.04	0.40
2:A:96:ASN:N	2:A:96:ASN:ND2	2.70	0.40
2:A:330:PRO:HD3	2:A:400:ILE:HG12	2.04	0.40
2:A:535:TYR:O	2:A:536:MET:C	2.65	0.40
2:A:559:LEU:HA	2:A:563:PHE:CD2	2.57	0.40
2:A:613:LEU:C	2:A:618:LEU:HD12	2.47	0.40
2:A:867:GLU:N	2:A:867:GLU:OE1	2.38	0.40
2:B:44:TYR:O	2:B:46:SER:N	2.54	0.40
2:B:494:ALA:O	2:B:495:GLN:C	2.64	0.40
2:B:525:VAL:O	2:B:525:VAL:HG13	2.22	0.40
2:B:646:LEU:O	2:B:647:GLU:CB	2.69	0.40
2:B:919:LYS:NZ	2:B:960:LEU:HD11	2.36	0.40
2:B:921:ILE:O	2:B:924:GLU:CB	2.69	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	
2	A	944/967 (98%)	630 (67%)	211 (22%)	103 (11%)	0	2
2	B	944/967 (98%)	632 (67%)	208 (22%)	104 (11%)	0	2
All	All	1888/1934 (98%)	1262 (67%)	419 (22%)	207 (11%)	0	2

All (207) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	74	VAL
2	A	110	LYS

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Mol	Chain	Res	Type
2	A	143	SER
2	A	183	VAL
2	A	188	VAL
2	A	276	GLN
2	A	333	HIS
2	A	347	GLU
2	A	377	GLU
2	A	378	GLU
2	A	552	GLY
2	A	630	ARG
2	A	714	TYR
2	A	854	LYS
2	A	867	GLU
2	A	871	TRP
2	A	883	PHE
2	A	913	GLU
2	A	914	ARG
2	A	929	GLU
2	A	953	LYS
2	B	45	LEU
2	B	74	VAL
2	B	110	LYS
2	B	183	VAL
2	B	188	VAL
2	B	276	GLN
2	B	333	HIS
2	B	347	GLU
2	B	377	GLU
2	B	378	GLU
2	B	552	GLY
2	B	630	ARG
2	B	714	TYR
2	B	854	LYS
2	B	867	GLU
2	B	871	TRP
2	B	883	PHE
2	B	913	GLU
2	B	914	ARG
2	B	929	GLU
2	B	953	LYS
2	A	45	LEU
2	A	113	GLU

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Mol	Chain	Res	Type
2	A	181	HIS
2	A	201	GLY
2	A	219	ASN
2	A	301	SER
2	A	343	THR
2	A	374	PRO
2	A	376	VAL
2	A	415	TYR
2	A	464	GLN
2	A	494	ALA
2	A	502	TRP
2	A	528	SER
2	A	529	LEU
2	A	568	PHE
2	A	616	ASN
2	A	711	PHE
2	A	782	VAL
2	A	857	ASN
2	A	868	ASP
2	A	869	TRP
2	A	885	SER
2	A	900	GLY
2	A	921	ILE
2	A	922	ASN
2	A	950	LYS
2	A	954	LYS
2	A	955	LYS
2	B	113	GLU
2	B	143	SER
2	B	181	HIS
2	B	201	GLY
2	B	219	ASN
2	B	301	SER
2	B	343	THR
2	B	374	PRO
2	B	376	VAL
2	B	415	TYR
2	B	464	GLN
2	B	502	TRP
2	B	528	SER
2	B	529	LEU
2	B	568	PHE

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Mol	Chain	Res	Type
2	B	616	ASN
2	B	782	VAL
2	B	857	ASN
2	B	868	ASP
2	B	869	TRP
2	B	885	SER
2	B	900	GLY
2	B	921	ILE
2	B	922	ASN
2	B	950	LYS
2	B	954	LYS
2	B	955	LYS
2	A	73	ASN
2	A	223	ILE
2	A	240	ASN
2	A	453	GLY
2	A	482	LEU
2	A	558	LYS
2	A	631	GLU
2	A	775	ASP
2	A	825	GLU
2	A	895	GLU
2	A	911	ILE
2	B	73	ASN
2	B	96	ASN
2	B	220	GLY
2	B	223	ILE
2	B	240	ASN
2	B	453	GLY
2	B	494	ALA
2	B	558	LYS
2	B	631	GLU
2	B	711	PHE
2	B	775	ASP
2	B	825	GLU
2	B	891	MET
2	B	895	GLU
2	B	911	ILE
2	A	85	SER
2	A	96	ASN
2	A	117	TRP
2	A	220	GLY

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Mol	Chain	Res	Type
2	A	283	ILE
2	A	421	GLN
2	A	542	SER
2	A	623	PHE
2	A	670	ALA
2	A	719	ASN
2	A	856	GLU
2	A	881	ARG
2	A	891	MET
2	A	903	VAL
2	A	907	VAL
2	B	85	SER
2	B	117	TRP
2	B	421	GLN
2	B	482	LEU
2	B	623	PHE
2	B	670	ALA
2	B	719	ASN
2	B	790	TRP
2	B	856	GLU
2	B	881	ARG
2	B	903	VAL
2	B	907	VAL
2	A	157	PRO
2	A	337	GLU
2	A	339	LEU
2	A	394	GLU
2	A	452	PHE
2	A	519	PRO
2	A	790	TRP
2	A	878	SER
2	A	898	LYS
2	B	157	PRO
2	B	283	ILE
2	B	339	LEU
2	B	403	ALA
2	B	452	PHE
2	B	519	PRO
2	B	540	THR
2	B	542	SER
2	B	743	ALA
2	B	878	SER

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Mol	Chain	Res	Type
2	A	303	ASP
2	A	403	ALA
2	A	743	ALA
2	A	813	GLY
2	B	337	GLU
2	B	394	GLU
2	B	495	GLN
2	A	945	ASN
2	A	946	PRO
2	B	945	ASN
2	B	946	PRO
2	A	88	VAL
2	A	471	ASN
2	A	522	PRO
2	A	823	PRO
2	B	471	ASN
2	B	522	PRO
2	B	789	VAL
2	A	302	GLY
2	A	353	PRO
2	A	355	ILE
2	A	384	ILE
2	B	222	VAL
2	B	302	GLY
2	B	353	PRO
2	B	355	ILE
2	B	384	ILE
2	A	115	ILE
2	A	222	VAL
2	A	329	ALA
2	A	330	PRO
2	B	88	VAL
2	B	115	ILE
2	B	329	ALA
2	B	330	PRO
2	B	813	GLY
2	B	823	PRO

5.3.2 Protein sidechains ⓘ

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

resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	841/857 (98%)	723 (86%)	118 (14%)	3	16
2	B	841/857 (98%)	753 (90%)	88 (10%)	6	27
All	All	1682/1714 (98%)	1476 (88%)	206 (12%)	5	21

All (206) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	7	LYS
2	A	16	ARG
2	A	28	ARG
2	A	29	ASP
2	A	35	LYS
2	A	38	ILE
2	A	42	PHE
2	A	70	GLN
2	A	75	LEU
2	A	77	PRO
2	A	131	LYS
2	A	135	GLU
2	A	138	ILE
2	A	139	ARG
2	A	157	PRO
2	A	163	ILE
2	A	172	GLU
2	A	183	VAL
2	A	195	ASP
2	A	213	LYS
2	A	217	ARG
2	A	230	LEU
2	A	233	GLU
2	A	234	THR
2	A	239	THR
2	A	246	ASN
2	A	276	GLN
2	A	278	ARG
2	A	289	GLU
2	A	331	PHE
2	A	339	LEU

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Mol	Chain	Res	Type
2	A	341	ARG
2	A	347	GLU
2	A	349	TYR
2	A	373	PHE
2	A	381	LYS
2	A	424	LYS
2	A	433	GLU
2	A	449	ILE
2	A	455	ARG
2	A	463	ASP
2	A	492	ARG
2	A	499	ILE
2	A	527	GLU
2	A	529	LEU
2	A	531	ASP
2	A	536	MET
2	A	540	THR
2	A	544	HIS
2	A	551	GLU
2	A	553	LYS
2	A	562	GLU
2	A	567	ILE
2	A	569	LEU
2	A	590	ILE
2	A	602	TYR
2	A	616	ASN
2	A	624	ASN
2	A	625	HIS
2	A	636	LYS
2	A	640	VAL
2	A	645	THR
2	A	649	GLN
2	A	658	VAL
2	A	659	LEU
2	A	675	LEU
2	A	678	MET
2	A	685	SER
2	A	691	ARG
2	A	700	GLN
2	A	703	ARG
2	A	707	LEU
2	A	720	VAL

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Mol	Chain	Res	Type
2	A	722	LEU
2	A	723	LYS
2	A	727	ARG
2	A	733	LEU
2	A	744	LEU
2	A	760	ILE
2	A	771	THR
2	A	776	ASP
2	A	783	LEU
2	A	786	LEU
2	A	792	ARG
2	A	809	LEU
2	A	815	VAL
2	A	817	LEU
2	A	819	LYS
2	A	820	TRP
2	A	823	PRO
2	A	825	GLU
2	A	826	GLU
2	A	828	TRP
2	A	829	ASN
2	A	837	GLU
2	A	839	ILE
2	A	850	ILE
2	A	852	VAL
2	A	860	ARG
2	A	862	TYR
2	A	869	TRP
2	A	872	LYS
2	A	879	GLU
2	A	881	ARG
2	A	884	LYS
2	A	910	LEU
2	A	916	PHE
2	A	917	ASP
2	A	919	LYS
2	A	922	ASN
2	A	923	GLU
2	A	932	GLU
2	A	933	PHE
2	A	940	ILE
2	A	942	ILE

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Mol	Chain	Res	Type
2	A	953	LYS
2	A	960	LEU
2	A	964	ILE
2	B	7	LYS
2	B	18	LEU
2	B	35	LYS
2	B	42	PHE
2	B	44	TYR
2	B	49	LEU
2	B	82	ILE
2	B	97	ARG
2	B	139	ARG
2	B	163	ILE
2	B	172	GLU
2	B	177	VAL
2	B	196	HIS
2	B	203	ASP
2	B	213	LYS
2	B	233	GLU
2	B	234	THR
2	B	276	GLN
2	B	285	GLU
2	B	331	PHE
2	B	338	ASP
2	B	339	LEU
2	B	341	ARG
2	B	347	GLU
2	B	373	PHE
2	B	388	LYS
2	B	424	LYS
2	B	429	LYS
2	B	451	ARG
2	B	479	ARG
2	B	483	GLU
2	B	505	LYS
2	B	527	GLU
2	B	528	SER
2	B	533	THR
2	B	536	MET
2	B	540	THR
2	B	545	ILE
2	B	546	ASN

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Mol	Chain	Res	Type
2	B	547	LYS
2	B	551	GLU
2	B	557	GLU
2	B	565	ASP
2	B	599	GLU
2	B	620	PHE
2	B	624	ASN
2	B	625	HIS
2	B	630	ARG
2	B	636	LYS
2	B	641	ASN
2	B	649	GLN
2	B	650	LYS
2	B	658	VAL
2	B	674	ARG
2	B	675	LEU
2	B	690	ARG
2	B	703	ARG
2	B	714	TYR
2	B	722	LEU
2	B	729	MET
2	B	732	ARG
2	B	734	ASN
2	B	735	LYS
2	B	738	LYS
2	B	744	LEU
2	B	748	ARG
2	B	750	ARG
2	B	751	THR
2	B	793	LEU
2	B	812	GLU
2	B	819	LYS
2	B	825	GLU
2	B	826	GLU
2	B	828	TRP
2	B	837	GLU
2	B	839	ILE
2	B	855	ILE
2	B	860	ARG
2	B	869	TRP
2	B	885	SER
2	B	886	SER

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Mol	Chain	Res	Type
2	B	889	GLU
2	B	919	LYS
2	B	920	ARG
2	B	940	ILE
2	B	942	ILE
2	B	953	LYS
2	B	964	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (52) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	53	HIS
2	A	70	GLN
2	A	73	ASN
2	A	81	HIS
2	A	96	ASN
2	A	166	GLN
2	A	196	HIS
2	A	219	ASN
2	A	244	ASN
2	A	276	GLN
2	A	317	ASN
2	A	421	GLN
2	A	447	ASN
2	A	464	GLN
2	A	544	HIS
2	A	616	ASN
2	A	617	HIS
2	A	624	ASN
2	A	625	HIS
2	A	641	ASN
2	A	731	HIS
2	A	742	ASN
2	A	762	ASN
2	A	800	HIS
2	A	908	GLN
2	A	922	ASN
2	B	53	HIS
2	B	70	GLN
2	B	73	ASN
2	B	96	ASN
2	B	124	ASN

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Mol	Chain	Res	Type
2	B	166	GLN
2	B	196	HIS
2	B	244	ASN
2	B	276	GLN
2	B	298	ASN
2	B	317	ASN
2	B	333	HIS
2	B	387	GLN
2	B	406	HIS
2	B	421	GLN
2	B	447	ASN
2	B	495	GLN
2	B	546	ASN
2	B	616	ASN
2	B	625	HIS
2	B	731	HIS
2	B	734	ASN
2	B	742	ASN
2	B	762	ASN
2	B	908	GLN
2	B	922	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C	87/88 (98%)	24 (27%)	7 (8%)
1	D	87/88 (98%)	22 (25%)	8 (9%)
All	All	174/176 (98%)	46 (26%)	15 (8%)

All (46) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C	907	G
1	C	908	U
1	C	910	G
1	C	916	C
1	C	917	C
1	C	918	U
1	C	919	G
1	C	920	G
1	C	921	U

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Mol	Chain	Res	Type
1	C	922	C
1	C	923	A
1	C	924	A
1	C	936	U
1	C	937	C
1	C	952	U
1	C	953	A
1	C	954	G
1	C	961	C
1	C	968	C
1	C	971	A
1	C	972	U
1	C	983	G
1	C	987	C
1	C	988	A
1	D	903	G
1	D	905	G
1	D	908	U
1	D	909	U
1	D	910	G
1	D	917	C
1	D	918	U
1	D	919	G
1	D	920	G
1	D	921	U
1	D	923	A
1	D	924	A
1	D	936	U
1	D	952	U
1	D	961	C
1	D	971	A
1	D	972	U
1	D	973	C
1	D	984	C
1	D	985	A
1	D	987	C
1	D	988	A

All (15) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C	907	G

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Mol	Chain	Res	Type
1	C	922	C
1	C	923	A
1	C	953	A
1	C	960	C
1	C	970	A
1	C	972	U
1	D	907	G
1	D	920	G
1	D	922	C
1	D	923	A
1	D	953	A
1	D	960	C
1	D	970	A
1	D	972	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	C	88/88 (100%)	-0.14	1 (1%) 78 60	53, 78, 126, 149	0
1	D	88/88 (100%)	-0.17	2 (2%) 61 41	53, 91, 146, 150	0
2	A	948/967 (98%)	-0.35	8 (0%) 82 67	8, 59, 131, 150	0
2	B	948/967 (98%)	-0.07	5 (0%) 87 76	48, 102, 149, 150	0
All	All	2072/2110 (98%)	-0.21	16 (0%) 82 67	8, 82, 143, 150	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	920	ARG	3.3
2	A	929	GLU	3.1
2	A	864	TYR	3.0
2	A	862	TYR	2.7
1	C	987	C	2.7
1	D	936	U	2.6
2	B	862	TYR	2.5
2	A	356	VAL	2.5
2	A	718	GLY	2.3
2	A	869	TRP	2.3
2	B	469	TYR	2.2
2	B	334	VAL	2.1
2	B	919	LYS	2.0
1	D	988	A	2.0
2	A	863	ILE	2.0
2	B	868	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.