



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:06 PM GMT

PDB ID : 1WCM
Title : COMPLETE 12-SUBUNIT RNA POLYMERASE II AT 3.8 Å
Authors : Armache, K.-J.; Mitterweger, S.; Meinhart, A.; Cramer, P.
Deposited on : 2004-11-17
Resolution : 3.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

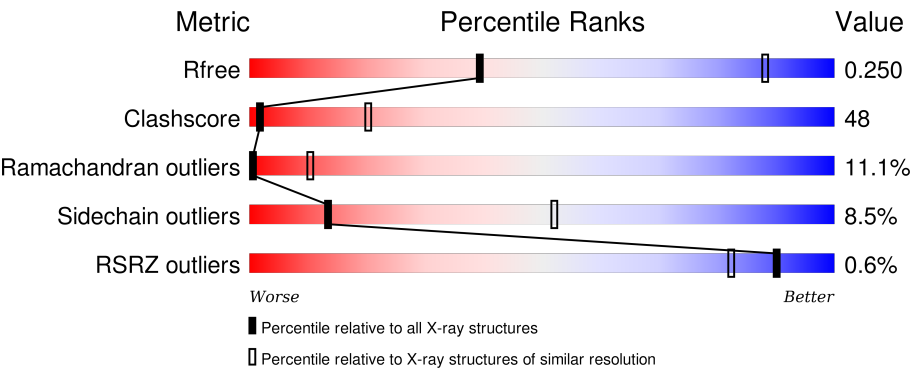
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	91344	1317 (4.10-3.50)
Clashscore	102246	1458 (4.10-3.50)
Ramachandran outliers	100387	1397 (4.10-3.50)
Sidechain outliers	100360	1392 (4.10-3.50)
RSRZ outliers	91569	1325 (4.10-3.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1733	<div><div></div><div><div>27%</div><div>43%</div><div>10%</div><div>•</div><div>18%</div></div></div>
2	B	1224	<div><div></div><div><div>29%</div><div>48%</div><div>12%</div><div>10%</div></div></div>
3	C	318	<div><div></div><div><div>23%</div><div>48%</div><div>12%</div><div>•</div><div>16%</div></div></div>
4	D	177	<div><div></div><div><div>42%</div><div>46%</div><div>11%</div><div>•</div></div></div>
5	E	215	<div><div></div><div><div>40%</div><div>54%</div><div>6%</div></div></div>

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Mol	Chain	Length	Quality of chain
6	F	155	<div><div></div><div>18%30%6%46%</div></div>
7	G	171	<div><div></div><div>39%51%9%</div></div>
8	H	146	<div><div>%</div><div></div><div>32%49%10%9%</div></div>
9	I	122	<div><div>2%</div><div></div><div>40%43%12%.</div></div>
10	J	70	<div><div></div><div>17%53%23%7%</div></div>
11	K	120	<div><div></div><div>41%47%8%.</div></div>
12	L	70	<div><div>%</div><div></div><div>16%31%19%34%</div></div>

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 30945 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1416	Total	C	N	O	S	0	0	0
			11140	7021	1946	2111	62			

- Molecule 2 is a protein called DNA-DIRECTED RNA POLYMERASE II SECOND LARGEST SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1097	Total	C	N	O	S	0	0	0
			8720	5526	1523	1617	54			

- Molecule 3 is a protein called DNA-DIRECTED RNA POLYMERASE II 45 KDA POLYPEPTIDE.

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

- Molecule 4 is a protein called DNA-DIRECTED RNA POLYMERASE II 32 KDA POLYPEPTIDE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	177	Total	C	N	O	S	0	0	0
			1356	840	241	273	2			

- Molecule 5 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III 27 KDA POLYPEPTIDE.

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

- Molecule 6 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III 23

KDA POLYPEPTIDE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	84	Total	C	N	O	S	0	0	0
			679	434	115	127	3			

- Molecule 7 is a protein called DNA-DIRECTED RNA POLYMERASE II 19 KD POLYPEPTIDE.

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

- Molecule 8 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III 14.5 KDA POLYPEPTIDE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	133	Total	C	N	O	S	0	0	0
			1068	673	180	211	4			

- Molecule 9 is a protein called DNA-DIRECTED RNA POLYMERASE II 14.2 KDA POLYPEPTIDE.

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

- Molecule 10 is a protein called DNA-DIRECTED RNA POLYMERASES I, II AND III 8.3 KDA POLYPEPTIDE.

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

- Molecule 11 is a protein called DNA-DIRECTED RNA POLYMERASE II 13.6 KDA POLYPEPTIDE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	115	Total	C	N	O	S	0	0	1
			920	590	157	171	2			

- Molecule 12 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III 7.7 KDA POLYPEPTIDE.

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

- Molecule 13 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

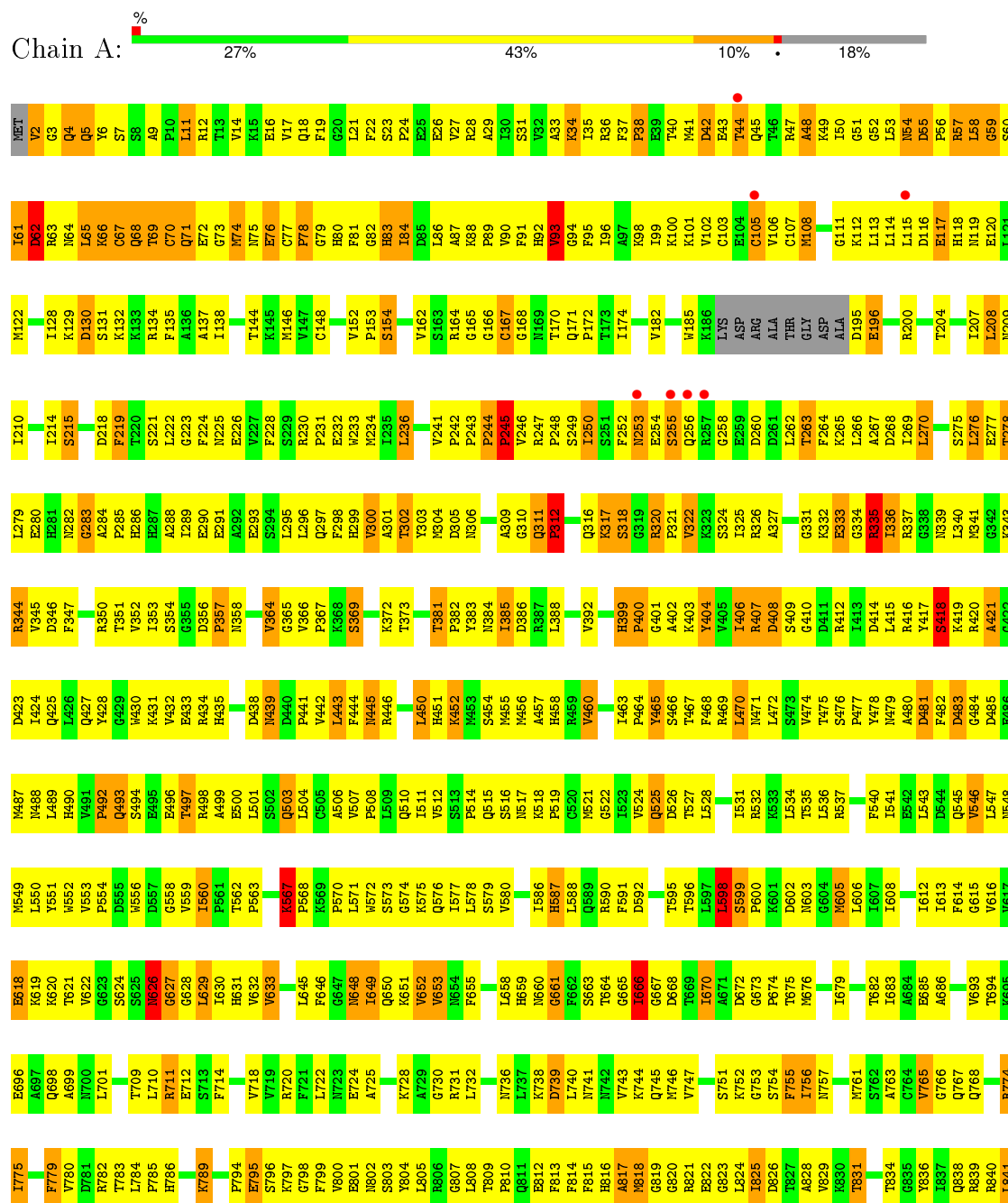
- Molecule 14 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

3 Residue-property plots

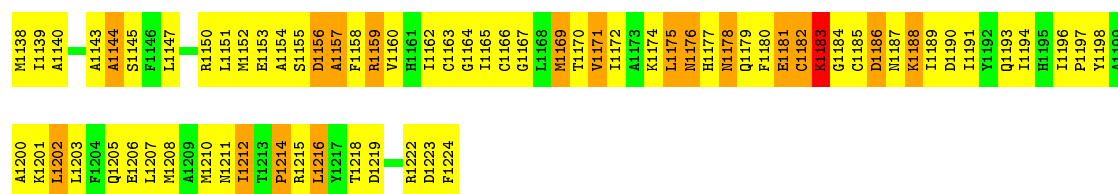
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($\text{RSRZ} > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT

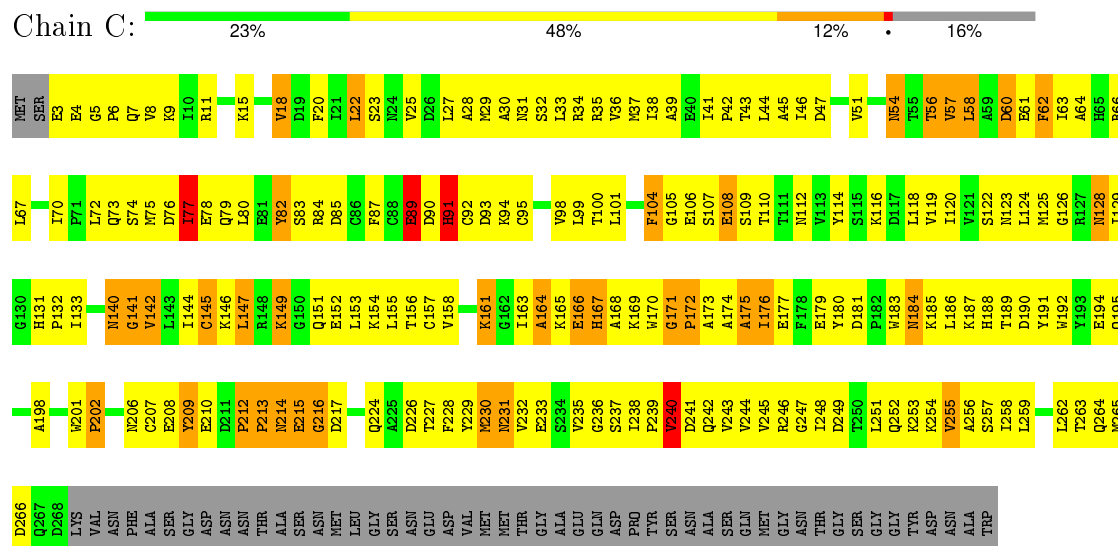


● Molecule 2: DNA-DIRECTED RNA POLYMERASE II SECOND LARGEST SUBUNIT

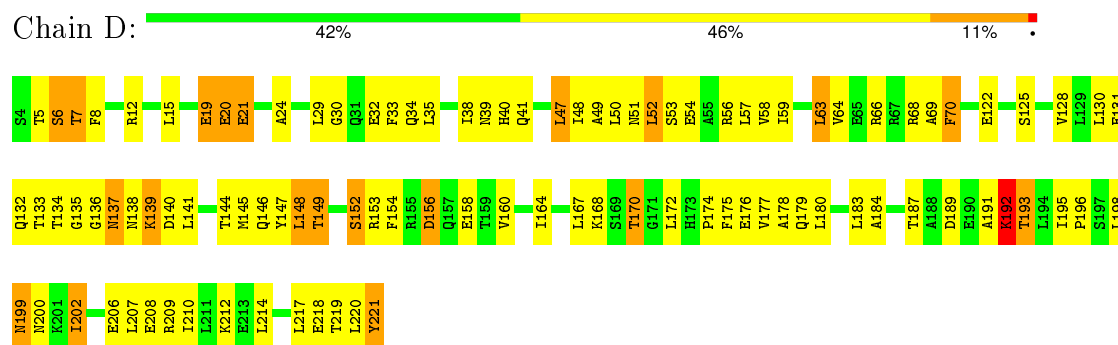
G1068	E997	H1S	G867	L803	E741	E678	V613	G548	G478	A409	LEU	K270	K193	F129	E85
F1069	D998	S933	R668	T806	E742	T679	S614	T649	V479	G410	GLY	K270	E194	V130	D66
M1072	P999	R935	S869	T807	E743	T680	M615	D550	S480	P411	ILE	L273	E195	D131	S67
N1073	F1000	D936	T871	A808	T745	G682	I616	P551	L483	L412	LVS	L273	P196	V132	T68
N1074	T1002	A937	E872	M809	P745	S633	R617	N552	N484	L413	K345	I276	F197	K133	L69
T1077	A1003	S938	T873	E810	S746	L684	R620	T554	R485	A414	K347	K277	D198	K134	I70
		T939		Y811	T747	L685	E621	T555	T486	Q415		Q278	M199	ARG	LEU
		P940	P877		I748	R686	K622	T556	T487	R418	Y351	T280	G201	THR	GLU
K1080	V1007	R878	Q878	R815	L749	G687	E623	F557	Y488	T419		T281	G202	TYR	GLN
L1081	P1008	R879	E688	R816	G750	G688	R623	L558	Y489	L420		T282	F203	GLU	LEU
M1082	D1009	S943	T880	L817	W751	L689	K625	S559	S490	F421	L355	V283	I204	ALA	ALA
A1083	L1010	R881	R881	P813	A752	V690	K626	E560	T491		L356	I205	I204	ILE	GLN
Q1084	I1011	R882	T882	A819	A753	E691	F627	N561	L492	L424	K358	T285	I205	ASP	HIS
I1085	T1012	L883	L883	G820		T692	T628	G562	S493		E359	R286	N206	VAL	THR
F1086	N1013	Q821	R884	Q821	I756	T693	D629	N563	H494	D427	F360	R287	G207	PRO	THR
F1087	P940	G888		N822	F757	D694	A630	L566	L495	F428	L361	A288	K210	GLY	GLU
T1089	A1016	A823	G888	A823	F758	A695	G631	L566	L496	F429	P362	I212	F211	ASP	ASP
P1089	I1017	T889	T889	T824	P759	E696	R632	L569	R497		H363	I281	V211	ASN	GLU
T1090	P1018	R890	T890	V625	D760	E697	V633	P569	T498	T435	I364	T282	I212	LEU	LEU
Y1091	S1019	A826	R891	R825	H761	E698	V634	P570	N498	V436	T365	T283	I213	LYS	ILE
R1094	R1020	V954	K892	L827	N762	E699	R635	P571	T500	E437	K366	D284	A214	TYR	SER
L1095	M1021	T955	L893		Q763	S700	P636	H572	P501	GLU	L367	G285	R217	LEU	ARG
R1096	T1022	T956	D894	Y830	Q764	T707	L637	D573	I502	ALA	E368	E296		LYS	LYS
R1097	H1031	Q957		S831	P765	E708	F638	S574	GLY	HIS	G369	I297	V223	TYR	GLU
H1098	L1026	Q958	G897	G832	R766	I703	I639	P575	ARG	ASP	F370	L288	Q224	GLU	I90
M1099	L1027	D959	L898	Y833	N767	A704	V640	D676	ASP	PHE	E371	E299	V225	GLU	S91
D1100	E1028	F963	A900	R835	T768	N705	E641	A577	GLY	ASN	L372	H300	F226	SER	F92
D1101	C1029	V964	P901	E836	Q770	Q706	D642	T578	LVS	NET	R373		K227	GLU	
K1102	L1030	K965	G902	D837	Q771	E708	D643	H579	LEU	LVS	K374	V305	K228	ASP	I95
I1103	L1031	V966	V903	D837	A772	D709	E644	V580	A509	L446	A375	N306	A229	ASP	Y96
H1104	S1032	Q904	R904	M839	M773		H648	V582	K510	A447	F376	D307	A230	SER	Y97
R1105	R1033	R969	V905	T840	G774	E711	K649	V585	Q513	A450	F377	N308	P231	GLU	T98
R1106	T1034	T970	M841	N841	K775	P712	E650	H586	L514	L453	G379	N310	P232	GLY	P100
A1107	A1035	T971	G907	N842	Q776		L651	H587	H515	T454	M381	L311	P233	SER	M101
R1108	A1036	K972	E908	Q843	A777	A715	K652	H588	H516	T455	I382	E312	I234	V165	V102
G1109	G1039	I973	D909	S844	M778	ASN	V653	G589		S455	N383	N313	S235	F166	H103
P1110	N1040	P974	V910	S845	G779	GLU	R654	H589	T517	G456	N384	L314	V237	E104	
T1115	E1041	Q976	I911	R846	V780	GLU	K655	H590	H518	L457	R384	K315	E238	G168	
Q1117	A1044	G977	G913	R848	L782	ASN	G656	N591	W519	K458	L386	F316	E239		
P1118	S1045	I976	T912	L850	F781	ASP	H657	N592	G520	V459	L387	C317	I240	V108	
V1119	P1046	A981	T916	F851	Y785	LEU	I658	A594	V522	L461	C388	I240	I240	T109	
R1122	F1047	S982	P917	R852	M786	D722	L661	H596	C523	K462	A389	C317	I240	P171	
S1123	I1050	R983	S919	S853	V787	P725	T664	L600	A525	L463	C388	I240	I240	M172	
R1124	T1051	H984	P90	F855	R788	T726	E663	E526	A526	T463	A389	I240	I240	M173	
D1125	G1054	Q985	ASP	F856		K727	E665	T527	T527	G464	D391	I251	I251	M174	
G1126	G1054	Q986	GLU	R857	M792	R728	D668	P601	P628	V466	K393	I254	I254	M178	
G1127	S1056	T989	GLU	S858	A793	I729	I603	T602	E529	G467	D394	A330	K357	R118	
G1131	S1056	T989	GLU	S859	N794	R730	I604	L603	G530	GLU	D396	L331	L258	L119	
L1059	L1059	I990	LEU	Y859	I795	V731	GLU	H605	R638	LYS	D396	D332	Y259	T185	
M1132	L1059	G991	GLY	M860	L796	H733	GLY	K606	N638	LYS	H400	I334	R261	N121	
R1060	R1060	I992	GLN	Q862	Y797	H734	PHE	G607	L639	ALA	F401	ARG	S265	T123	
E1134	E1134	T993	ARG	E863	F799	A735	GLU	T609	M642	SER	K404	ARG	A266	Y124	
R1135	S1065	R994	THR	K864	Q800	T736	ASP	T609	M642	SER	K405	GLY	A267	S125	
C1137	R1067	R996	ALA	K865	T737	F738	VAL	P611	S546	ARG	R405	THR	T268	G127	
			TYR	Y866	P802		GLU	E612	V547	A477	L408	ALA	I269	L192	



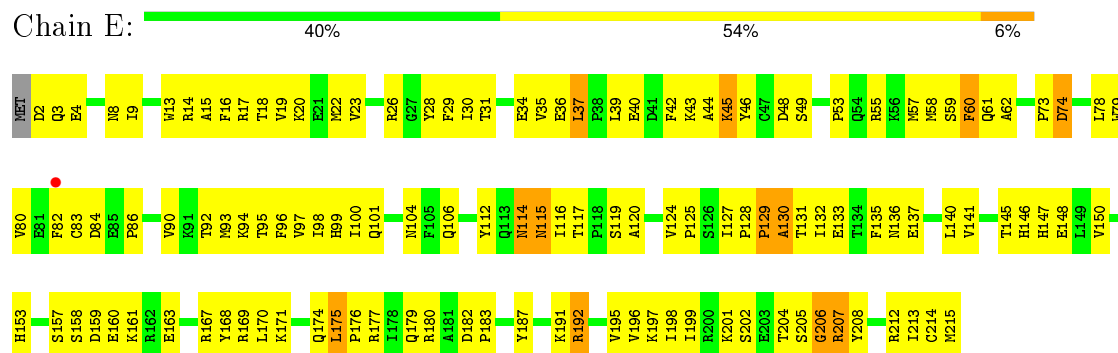
• Molecule 3: DNA-DIRECTED RNA POLYMERASE II 45 KDA POLYPEPTIDE



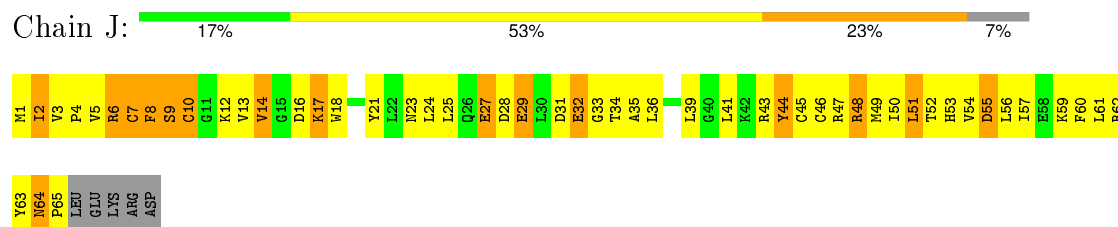
• Molecule 4: DNA-DIRECTED RNA POLYMERASE II 32 KDA POLYPEPTIDE



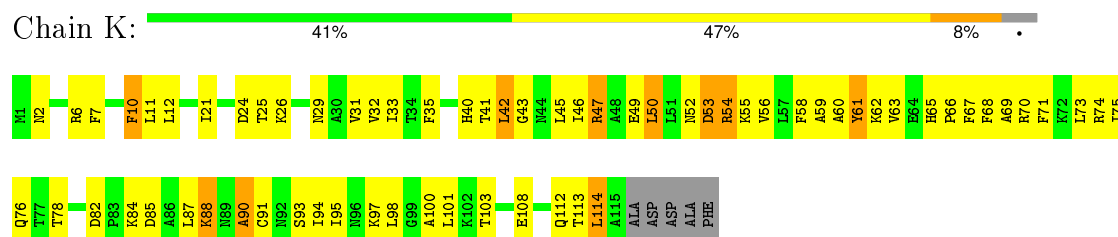
• Molecule 5: DNA-DIRECTED RNA POLYMERASES I, II, AND III 27 KDA POLYPEPTIDE



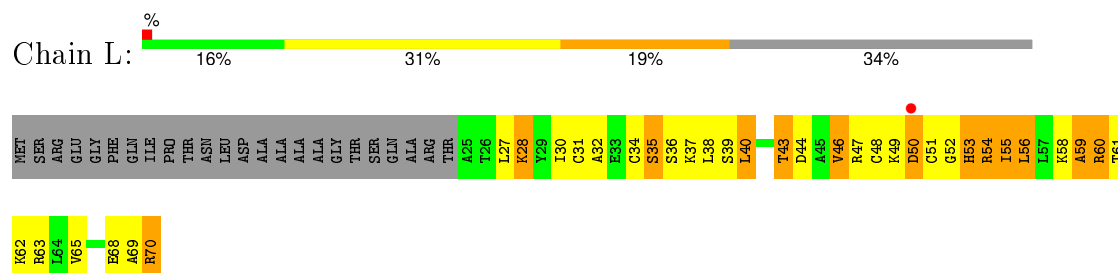
- Molecule 10: DNA-DIRECTED RNA POLYMERASES I, II AND III 8.3 KDA POLYPEPTIDE



- Molecule 11: DNA-DIRECTED RNA POLYMERASE II 13.6 KDA POLYPEPTIDE



- Molecule 12: DNA-DIRECTED RNA POLYMERASES I, II, AND III 7.7 KDA POLYPEPTIDE



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	222.72Å 395.13Å 284.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.80 47.39 – 3.80	Depositor EDS
% Data completeness (in resolution range)	99.1 (50.00-3.80) 99.2 (47.39-3.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.21 (at 3.77Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.257 , 0.285 0.222 , 0.250	Depositor DCC
R_{free} test set	2439 reflections (2.04%)	DCC
Wilson B-factor (Å ²)	116.1	Xtriage
Anisotropy	0.510	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 70.8	EDS
Estimated twinning fraction	0.015 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.021 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 121835 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	30945	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.81% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.48	0/11339	0.73	4/15334 (0.0%)
2	B	0.47	0/8890	0.70	1/11990 (0.0%)
3	C	0.52	0/2133	0.76	0/2891
4	D	0.45	0/1365	0.71	1/1837 (0.1%)
5	E	0.43	0/1788	0.64	0/2406
6	F	0.53	0/691	0.78	0/933
7	G	0.53	0/1368	0.74	0/1844
8	H	0.40	0/1086	0.66	0/1470
9	I	0.48	0/989	0.77	0/1331
10	J	0.54	0/541	0.89	1/727 (0.1%)
11	K	0.50	0/938	0.68	0/1267
12	L	0.55	0/365	0.79	0/485
All	All	0.48	0/31493	0.72	7/42515 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
3	C	0	1
All	All	0	2

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	J	10	CYS	CA-CB-SG	8.66	129.59	114.00
1	A	1403	GLU	N-CA-C	5.38	125.53	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	567	LYS	C-N-CD	5.34	139.62	128.40
2	B	1185	CYS	N-CA-C	-5.30	96.69	111.00
1	A	452	LYS	N-CA-C	-5.21	96.94	111.00
4	D	7	THR	N-CA-C	5.15	124.90	111.00
1	A	344	ARG	N-CA-C	-5.05	97.37	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	303	TYR	Sidechain
3	C	82	TYR	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	11140	0	11217	1180	0
2	B	8720	0	8745	919	0
3	C	2095	0	2051	244	0
4	D	1356	0	1319	114	0
5	E	1752	0	1776	154	0
6	F	679	0	701	84	0
7	G	1340	0	1357	150	0
8	H	1068	0	1040	104	0
9	I	971	0	927	94	0
10	J	532	0	542	93	0
11	K	920	0	929	83	0
12	L	363	0	386	45	0
13	A	2	0	0	0	0
13	B	1	0	0	0	0
13	C	1	0	0	0	0
13	I	2	0	0	0	0
13	J	1	0	0	0	0
13	L	1	0	0	0	0
14	A	1	0	0	0	0
All	All	30945	0	30990	2984	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 48.

All (2984) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:CYS:O	1:A:78:PRO:O	1.65	1.14
10:J:5:VAL:HG12	10:J:6:ARG:HG3	1.30	1.11
7:G:138:THR:HG22	7:G:139:ILE:H	1.12	1.09
1:A:53:LEU:HD23	1:A:54:ASN:N	1.69	1.06
4:D:40:HIS:HB3	7:G:73:LYS:NZ	1.69	1.06
2:B:273:LEU:HB2	2:B:276:ILE:HD12	1.37	1.04
8:H:100:THR:HG23	8:H:138:GLU:HA	1.37	1.03
2:B:217:ARG:HE	2:B:405:ARG:HB2	1.21	1.03
4:D:48:ILE:HG21	7:G:4:ILE:HB	1.40	1.03
1:A:855:THR:HG21	1:A:857:ARG:HE	1.22	1.02
1:A:1161:THR:HG22	1:A:1163:ILE:H	1.23	1.02
7:G:15:PRO:HA	7:G:18:PHE:CD1	1.96	1.00
2:B:549:THR:HG22	2:B:550:ASP:H	1.24	0.99
2:B:65:GLU:HG3	2:B:66:ASP:H	1.27	0.98
2:B:806:THR:HG22	2:B:808:ALA:H	1.27	0.98
9:I:85:PHE:HD2	9:I:85:PHE:H	1.06	0.98
1:A:1017:LEU:HB2	5:E:206:GLY:H	1.26	0.98
2:B:800:GLN:HB3	10:J:52:THR:HG21	1.46	0.97
7:G:7:LEU:HB2	7:G:74:TYR:CE2	2.00	0.97
6:F:93:ILE:HD11	6:F:134:ILE:HD11	1.42	0.97
1:A:779:PHE:HE1	1:A:785:PRO:HD3	1.28	0.97
2:B:23:ALA:HB1	2:B:24:PRO:HD2	1.45	0.97
1:A:563:PRO:HG3	1:A:572:TRP:CZ2	2.00	0.97
1:A:1329:THR:HG22	1:A:1331:SER:H	1.30	0.95
1:A:754:SER:H	1:A:757:ASN:HD22	1.11	0.95
1:A:77:CYS:SG	1:A:77:CYS:O	2.24	0.95
2:B:46:GLN:HG3	2:B:47:GLN:H	1.28	0.95
2:B:189:LEU:HA	2:B:192:LEU:HD12	1.45	0.95
3:C:166:GLU:HG3	11:K:10:PHE:HZ	1.31	0.95
3:C:142:VAL:H	10:J:16:ASP:HB3	1.31	0.95
3:C:39:ALA:HA	3:C:164:ALA:HB3	1.47	0.95
2:B:806:THR:N	2:B:809:MET:HE3	1.81	0.94
11:K:47:ARG:HH11	11:K:47:ARG:HB3	1.32	0.94
4:D:47:LEU:HD13	4:D:48:ILE:H	1.31	0.94
1:A:84:ILE:HD11	1:A:270:LEU:HD13	1.50	0.94
1:A:709:THR:HG22	1:A:711:ARG:H	1.32	0.93
1:A:768:GLN:HG2	1:A:816:HIS:HA	1.50	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:LEU:HD23	1:A:54:ASN:H	1.26	0.93
8:H:4:THR:HA	8:H:60:ALA:HB2	1.52	0.92
9:I:34:TYR:HD2	9:I:35:VAL:N	1.67	0.92
2:B:1072:MET:HE3	2:B:1085:ILE:HB	1.50	0.92
1:A:901:LEU:H	1:A:926:GLN:NE2	1.67	0.92
1:A:963:ILE:HD11	1:A:1048:ASN:HB3	1.50	0.92
1:A:40:THR:HG22	1:A:41:MET:HG3	1.52	0.92
3:C:47:ASP:HA	12:L:69:ALA:HB3	1.50	0.92
6:F:81:THR:HG21	6:F:136:ARG:HD3	1.52	0.91
1:A:399:HIS:HB3	1:A:400:PRO:HD3	1.51	0.91
2:B:824:ILE:HG22	2:B:1087:PHE:HE2	1.31	0.91
4:D:134:THR:HG22	4:D:136:GLY:H	1.36	0.90
9:I:7:CYS:HB3	9:I:14:LEU:HD21	1.53	0.90
2:B:1201:LYS:HE2	2:B:1205:GLN:OE1	1.72	0.89
5:E:180:ARG:HH21	5:E:192:ARG:HB2	1.38	0.89
10:J:3:VAL:HG21	10:J:18:TRP:HB2	1.54	0.89
1:A:524:VAL:HG12	1:A:525:GLN:H	1.37	0.89
2:B:1072:MET:CE	2:B:1085:ILE:HB	2.03	0.89
11:K:65:HIS:HD2	11:K:67:PHE:H	1.21	0.88
2:B:212:LEU:HD23	2:B:480:SER:HB2	1.55	0.88
2:B:800:GLN:HB3	10:J:52:THR:CG2	2.04	0.88
2:B:98:THR:O	2:B:126:SER:HB2	1.73	0.88
1:A:353:ILE:HG21	1:A:487:MET:HE3	1.55	0.87
1:A:55:ASP:C	1:A:57:ARG:H	1.72	0.87
1:A:567:LYS:CG	1:A:568:PRO:HD2	2.04	0.87
9:I:34:TYR:CD2	9:I:35:VAL:N	2.42	0.87
8:H:81:PRO:HB2	8:H:82:PRO:HD2	1.56	0.87
5:E:22:MET:HE3	5:E:26:ARG:HE	1.40	0.87
10:J:16:ASP:OD1	10:J:17:LYS:HD2	1.75	0.87
3:C:44:LEU:HB2	3:C:77:ILE:HD11	1.53	0.86
1:A:1445:ILE:H	1:A:1445:ILE:HD12	1.39	0.86
9:I:75:CYS:SG	9:I:79:HIS:N	2.49	0.86
1:A:903:ASN:HD22	1:A:904:THR:N	1.73	0.86
4:D:40:HIS:HB3	7:G:73:LYS:HZ1	1.38	0.86
4:D:144:THR:O	4:D:148:LEU:HB2	1.75	0.86
5:E:94:LYS:HE2	5:E:98:ILE:HD11	1.57	0.86
2:B:589:VAL:HG12	2:B:590:HIS:H	1.40	0.86
7:G:1:MET:SD	7:G:79:PHE:CD1	2.69	0.86
10:J:57:ILE:HA	10:J:60:PHE:HD2	1.41	0.86
1:A:56:PRO:O	1:A:57:ARG:HG3	1.76	0.86
3:C:232:VAL:HG21	3:C:244:VAL:HG22	1.58	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1242:VAL:HG12	1:A:1243:VAL:H	1.38	0.86
1:A:1189:SER:O	1:A:1241:ARG:HD3	1.75	0.85
2:B:168:GLY:H	2:B:450:ALA:HB1	1.38	0.85
3:C:164:ALA:HA	3:C:167:HIS:O	1.76	0.85
3:C:20:PHE:HE1	3:C:22:LEU:HD12	1.42	0.85
2:B:1224:PHE:HE2	5:E:171:LYS:HG3	1.40	0.85
1:A:351:THR:HB	2:B:1103:ILE:HD12	1.58	0.85
3:C:57:VAL:HG11	10:J:60:PHE:HB3	1.57	0.85
3:C:47:ASP:HA	12:L:69:ALA:CB	2.06	0.85
2:B:515:HIS:H	2:B:518:HIS:HD2	1.19	0.85
2:B:705:MET:H	2:B:710:LEU:HD12	1.42	0.85
7:G:1:MET:SD	7:G:79:PHE:HD1	2.00	0.84
7:G:138:THR:HG22	7:G:139:ILE:N	1.92	0.84
2:B:955:THR:HG23	12:L:54:ARG:O	1.77	0.84
2:B:483:LEU:HD11	2:B:491:THR:HG23	1.58	0.84
2:B:37:PHE:CE1	2:B:41:LYS:HG3	2.13	0.84
3:C:43:THR:HG22	3:C:44:LEU:N	1.93	0.84
1:A:1094:VAL:HG13	1:A:1113:THR:HG21	1.58	0.84
5:E:19:VAL:O	5:E:23:VAL:HG23	1.78	0.84
2:B:806:THR:H	2:B:809:MET:HE3	1.41	0.83
2:B:882:THR:HG22	2:B:884:ARG:H	1.44	0.83
3:C:213:PRO:O	3:C:214:ASN:HB2	1.76	0.83
2:B:282:ILE:HD12	2:B:382:ILE:HD13	1.60	0.83
1:A:70:CYS:O	1:A:72:GLU:HG2	1.76	0.83
2:B:233:PRO:HG2	2:B:234:ILE:HD12	1.58	0.83
2:B:1007:VAL:HG22	2:B:1008:PRO:HD2	1.61	0.83
10:J:64:ASN:HB3	10:J:65:PRO:CD	2.08	0.83
2:B:363:HIS:O	2:B:364:ILE:HB	1.77	0.83
2:B:842:ASN:ND2	2:B:845:SER:H	1.77	0.83
1:A:1329:THR:HG22	1:A:1331:SER:N	1.93	0.83
1:A:79:GLY:HA3	1:A:243:PRO:CG	2.08	0.83
1:A:598:LEU:HA	8:H:122:LEU:HD13	1.61	0.83
8:H:23:VAL:HG22	8:H:43:ASN:HA	1.61	0.83
7:G:34:VAL:HG12	7:G:45:ILE:HG21	1.61	0.82
3:C:66:ARG:NH2	10:J:5:VAL:HG23	1.94	0.82
2:B:847:ASP:HB3	3:C:167:HIS:HE2	1.45	0.82
1:A:868:TYR:CE1	1:A:1064:VAL:HG11	2.15	0.82
8:H:40:LEU:HD13	8:H:123:MET:HB2	1.61	0.82
1:A:335:ARG:NH1	2:B:1202:LEU:HD13	1.94	0.82
5:E:135:PHE:HD2	5:E:140:LEU:HD21	1.45	0.81
7:G:128:PRO:O	7:G:138:THR:HG23	1.78	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:847:ASP:HB3	3:C:167:HIS:NE2	1.95	0.81
2:B:35:SER:HA	2:B:811:TYR:HE2	1.45	0.81
1:A:503:GLN:HE21	6:F:90:ARG:HH21	1.25	0.81
7:G:13:LEU:HD21	7:G:17:PHE:HB2	1.60	0.81
1:A:438:ASP:O	1:A:439:ASN:HB2	1.78	0.81
2:B:1096:ARG:O	2:B:1097:HIS:HB2	1.79	0.81
1:A:779:PHE:CE1	1:A:785:PRO:HD3	2.13	0.81
1:A:567:LYS:HG3	1:A:568:PRO:HD2	1.60	0.81
1:A:1118:VAL:HG12	1:A:1327:ILE:HG13	1.63	0.81
1:A:709:THR:HG23	9:I:94:ASP:HA	1.63	0.81
1:A:534:LEU:O	1:A:574:GLY:HA3	1.81	0.81
1:A:340:LEU:HD13	1:A:1429:ILE:HG23	1.61	0.81
3:C:56:THR:HG22	3:C:57:VAL:H	1.46	0.81
1:A:335:ARG:HA	1:A:339:ASN:HB2	1.64	0.80
1:A:567:LYS:NZ	8:H:46:LEU:HB2	1.96	0.80
1:A:1332:PHE:H	1:A:1332:PHE:HD2	1.27	0.80
2:B:577:ALA:HB1	2:B:589:VAL:HG11	1.62	0.80
2:B:1163:CYS:SG	2:B:1165:ILE:HB	2.21	0.80
4:D:170:THR:CG2	4:D:172:LEU:HG	2.11	0.80
1:A:670:ILE:HG23	1:A:805:LEU:HD21	1.63	0.80
1:A:249:SER:O	1:A:250:ILE:HG13	1.81	0.80
1:A:344:ARG:HD2	2:B:1118:PRO:O	1.82	0.80
1:A:1155:ASP:OD2	1:A:1161:THR:HG23	1.80	0.80
1:A:76:GLU:O	1:A:76:GLU:HG3	1.81	0.80
7:G:23:LYS:HG3	7:G:56:ILE:HD11	1.63	0.80
2:B:401:PHE:HA	2:B:404:LYS:HG3	1.61	0.80
1:A:741:ASN:HD22	1:A:744:LYS:H	1.26	0.80
3:C:32:SER:O	3:C:36:VAL:HG23	1.82	0.80
2:B:918:ILE:HB	2:B:935:ARG:HD2	1.62	0.80
10:J:14:VAL:CG1	10:J:50:ILE:HD11	2.12	0.80
2:B:1162:ILE:HG22	2:B:1163:CYS:H	1.47	0.80
2:B:102:VAL:HG23	2:B:112:LEU:HB2	1.62	0.79
2:B:515:HIS:HD2	2:B:517:THR:H	1.27	0.79
3:C:212:PRO:HB3	3:C:213:PRO:HD2	1.63	0.79
5:E:29:PHE:O	5:E:30:ILE:HG13	1.82	0.79
1:A:886:ILE:HD11	1:A:943:LEU:HB3	1.62	0.79
1:A:67:CYS:O	1:A:70:CYS:HB3	1.82	0.79
2:B:25:ILE:HD11	2:B:653:VAL:O	1.82	0.79
2:B:1159:ARG:HD3	2:B:1193:GLN:HG3	1.64	0.79
11:K:113:THR:O	11:K:114:LEU:HB2	1.81	0.79
3:C:262:LEU:HD11	11:K:87:LEU:HD23	1.62	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:43:THR:HG22	3:C:44:LEU:H	1.48	0.79
1:A:356:ASP:HB2	1:A:469:ARG:NH1	1.97	0.79
1:A:93:VAL:HG13	1:A:301:ALA:HB1	1.62	0.78
10:J:64:ASN:HB3	10:J:65:PRO:HD3	1.64	0.78
2:B:465:ASN:HD22	2:B:465:ASN:N	1.78	0.78
1:A:855:THR:HG21	1:A:857:ARG:NE	1.97	0.78
4:D:153:ARG:NH2	4:D:184:ALA:HA	1.98	0.78
1:A:858:ASN:ND2	1:A:860:LEU:H	1.81	0.78
2:B:200:GLY:HA2	2:B:202:TYR:CE2	2.18	0.78
2:B:611:PRO:HB3	2:B:685:LEU:HD11	1.64	0.78
2:B:1065:GLN:HE21	2:B:1066:SER:N	1.82	0.78
2:B:1065:GLN:HE21	2:B:1067:ARG:H	1.30	0.78
8:H:102:TYR:OH	8:H:122:LEU:HD22	1.82	0.78
1:A:340:LEU:HD21	2:B:1200:ALA:N	1.99	0.78
4:D:40:HIS:HB3	7:G:73:LYS:HZ3	1.48	0.77
8:H:42:ILE:HG23	8:H:95:TYR:HE1	1.47	0.77
4:D:130:LEU:C	4:D:132:GLN:H	1.86	0.77
5:E:175:LEU:HD23	5:E:176:PRO:HD2	1.66	0.77
2:B:120:ARG:HG2	2:B:955:THR:HG21	1.65	0.77
2:B:613:VAL:HG13	2:B:627:PHE:O	1.85	0.77
1:A:1329:THR:H	1:A:1335:ILE:HD11	1.49	0.77
1:A:1341:ILE:HG23	1:A:1342:GLU:N	1.98	0.77
1:A:285:PRO:HG2	1:A:288:ALA:HB3	1.64	0.77
1:A:567:LYS:HB3	8:H:95:TYR:HA	1.65	0.77
2:B:1034:VAL:HG12	2:B:1035:ALA:N	1.98	0.77
1:A:388:LEU:O	1:A:392:VAL:HG23	1.85	0.77
1:A:1424:VAL:HG11	2:B:1139:ILE:HD13	1.67	0.77
7:G:81:PRO:HG3	7:G:106:MET:SD	2.25	0.77
2:B:955:THR:HG22	2:B:956:THR:N	2.00	0.77
3:C:98:VAL:C	3:C:99:LEU:HD23	2.05	0.77
3:C:77:ILE:HG23	3:C:161:LYS:HE3	1.67	0.77
2:B:53:GLN:HG2	2:B:547:VAL:HG22	1.67	0.77
1:A:1116:LEU:N	1:A:1308:THR:HG22	2.00	0.77
1:A:855:THR:HG23	1:A:857:ARG:HG3	1.67	0.76
11:K:45:LEU:HG	11:K:94:ILE:HD13	1.65	0.76
2:B:763:GLN:HG2	2:B:765:PRO:HD2	1.66	0.76
2:B:863:GLU:OE2	2:B:873:THR:HA	1.85	0.76
1:A:356:ASP:HB2	1:A:469:ARG:HH11	1.50	0.76
1:A:445:ASN:HB2	1:A:455:MET:HG2	1.67	0.76
1:A:1409:LEU:HD13	2:B:1207:LEU:HD21	1.67	0.76
1:A:590:ARG:NH1	1:A:590:ARG:HG3	2.00	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:117:THR:HG22	5:E:119:SER:H	1.50	0.76
1:A:598:LEU:HD22	8:H:25:ARG:NH1	2.01	0.76
2:B:361:LEU:HD21	2:B:377:PHE:CD2	2.19	0.76
2:B:37:PHE:CD1	2:B:41:LYS:HG3	2.20	0.76
2:B:778:MET:HE1	2:B:1094:ARG:HD3	1.66	0.76
1:A:1341:ILE:HD12	1:A:1379:GLY:O	1.85	0.76
11:K:21:ILE:HG12	11:K:33:ILE:HG12	1.67	0.76
2:B:579:ARG:HB2	2:B:586:TRP:NE1	2.00	0.76
1:A:528:LEU:O	1:A:531:ILE:HG22	1.86	0.76
1:A:265:LYS:HZ3	1:A:322:VAL:HG13	1.49	0.76
1:A:588:LEU:O	1:A:606:LEU:HA	1.85	0.76
9:I:34:TYR:HE2	9:I:36:GLU:HB3	1.49	0.76
2:B:172:ILE:HD13	2:B:178:ASN:HB3	1.68	0.76
1:A:590:ARG:HH11	1:A:590:ARG:HG3	1.51	0.75
1:A:23:SER:HB3	1:A:233:TRP:CZ2	2.21	0.75
1:A:1422:ARG:HH22	2:B:1224:PHE:C	1.90	0.75
1:A:560:ILE:HG13	8:H:78:SER:HB2	1.68	0.75
2:B:1069:PHE:HD1	2:B:1069:PHE:H	1.34	0.75
2:B:521:LEU:HD22	2:B:633:VAL:HG12	1.68	0.75
5:E:90:VAL:HG23	5:E:120:ALA:HA	1.69	0.75
1:A:91:PHE:HB2	1:A:297:GLN:NE2	2.02	0.75
11:K:46:ILE:O	11:K:50:LEU:HB2	1.85	0.75
2:B:879:ARG:HH11	2:B:883:LEU:HD22	1.50	0.75
2:B:37:PHE:HE2	2:B:542:MET:HA	1.52	0.75
2:B:999:MET:HG3	2:B:1000:PRO:HD2	1.68	0.75
1:A:23:SER:HB3	1:A:233:TRP:CE2	2.21	0.75
7:G:43:GLY:HA3	7:G:80:LYS:HB3	1.68	0.74
7:G:15:PRO:HA	7:G:18:PHE:CE1	2.22	0.74
2:B:580:VAL:HG22	2:B:624:LEU:HB3	1.69	0.74
5:E:198:ILE:HD11	5:E:212:ARG:HG3	1.69	0.74
1:A:230:ARG:H	1:A:233:TRP:HE3	1.34	0.74
1:A:87:ALA:HB3	1:A:276:LEU:HD23	1.67	0.74
6:F:111:LEU:C	6:F:113:GLY:H	1.90	0.74
2:B:642:ASP:HB3	2:B:649:LYS:CD	2.17	0.74
2:B:1065:GLN:NE2	2:B:1067:ARG:H	1.84	0.74
1:A:244:PRO:HB2	1:A:245:PRO:HD3	1.69	0.74
1:A:836:TYR:CE2	1:A:840:ARG:HD2	2.21	0.74
1:A:87:ALA:CB	1:A:276:LEU:HD23	2.18	0.74
1:A:1323:ASP:OD1	1:A:1325:THR:HB	1.88	0.74
2:B:801:LYS:O	10:J:52:THR:HG23	1.86	0.74
12:L:48:CYS:HB3	12:L:51:CYS:O	1.88	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:899:ILE:HD11	2:B:911:ILE:HA	1.68	0.74
2:B:859:TYR:OH	2:B:941:LEU:HD12	1.86	0.74
1:A:1312:ASN:O	1:A:1316:VAL:HG23	1.88	0.74
5:E:2:ASP:O	5:E:3:GLN:HG2	1.87	0.74
4:D:66:ARG:HD2	4:D:133:THR:HB	1.68	0.74
2:B:978:ASP:OD2	2:B:1098:MET:HG2	1.88	0.74
1:A:590:ARG:NH2	1:A:620:LYS:HB3	2.01	0.74
1:A:55:ASP:C	1:A:57:ARG:N	2.41	0.74
1:A:1450:LEU:HG	1:A:1450:LEU:O	1.88	0.74
2:B:953:LEU:HD21	2:B:965:LYS:HB2	1.68	0.74
1:A:1402:PHE:CE1	1:A:1403:GLU:HG3	2.23	0.74
2:B:806:THR:HG22	2:B:808:ALA:N	2.03	0.73
1:A:768:GLN:CG	1:A:816:HIS:HA	2.18	0.73
2:B:955:THR:HG22	2:B:956:THR:H	1.53	0.73
2:B:1183:LYS:HE3	2:B:1183:LYS:N	2.03	0.73
1:A:535:THR:HG21	1:A:616:VAL:HA	1.70	0.73
2:B:847:ASP:HB3	3:C:167:HIS:CD2	2.24	0.73
1:A:253:ASN:HB3	2:B:935:ARG:NH2	2.03	0.73
1:A:254:GLU:HB2	2:B:935:ARG:HH12	1.52	0.73
5:E:22:MET:HE3	5:E:26:ARG:NE	2.03	0.73
5:E:202:SER:OG	5:E:204:THR:HG22	1.89	0.73
1:A:1332:PHE:HD2	1:A:1332:PHE:N	1.86	0.73
1:A:351:THR:HB	2:B:1103:ILE:CD1	2.18	0.73
5:E:192:ARG:HH11	5:E:192:ARG:HG3	1.51	0.73
1:A:321:PRO:O	1:A:322:VAL:HB	1.88	0.73
8:H:59:ILE:HG22	8:H:60:ALA:N	2.02	0.73
5:E:213:ILE:HG12	5:E:214:CYS:H	1.54	0.73
8:H:36:CYS:HA	8:H:126:GLU:O	1.89	0.73
2:B:408:LEU:HG	2:B:409:ALA:H	1.52	0.73
7:G:138:THR:CG2	7:G:139:ILE:H	1.95	0.73
1:A:754:SER:H	1:A:757:ASN:ND2	1.86	0.73
1:A:164:ARG:HG3	1:A:165:GLY:H	1.52	0.73
1:A:853:ASP:OD1	1:A:855:THR:HB	1.89	0.73
12:L:30:ILE:O	12:L:56:LEU:HA	1.88	0.73
7:G:115:MET:HB3	7:G:116:PRO:HD2	1.69	0.73
1:A:567:LYS:HD3	8:H:95:TYR:CD2	2.24	0.73
5:E:16:PHE:CZ	5:E:20:LYS:HE2	2.24	0.73
1:A:335:ARG:HH12	2:B:1202:LEU:HD13	1.54	0.72
2:B:871:THR:HG22	2:B:872:GLU:O	1.88	0.72
4:D:5:THR:O	4:D:6:SER:O	2.07	0.72
1:A:1445:ILE:N	1:A:1445:ILE:HD12	2.04	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:73:GLN:HB3	3:C:131:HIS:H	1.55	0.72
2:B:766:ARG:HH22	2:B:1020:ARG:HH11	1.37	0.72
10:J:36:LEU:HD12	10:J:47:ARG:NH1	2.04	0.72
8:H:81:PRO:CB	8:H:82:PRO:HD2	2.18	0.72
2:B:378:LEU:HD12	2:B:378:LEU:O	1.88	0.72
2:B:516:ASN:N	2:B:516:ASN:HD22	1.87	0.72
2:B:616:ILE:HG13	2:B:697:GLU:HG3	1.70	0.72
2:B:411:PRO:O	2:B:414:ALA:HB3	1.88	0.72
1:A:567:LYS:CD	1:A:568:PRO:HD2	2.20	0.72
2:B:594:ALA:HA	2:B:617:ARG:NH1	2.05	0.72
1:A:475:THR:HG23	1:A:476:SER:N	2.05	0.72
2:B:217:ARG:NE	2:B:405:ARG:HB2	2.03	0.72
1:A:1420:ASP:HB3	1:A:1422:ARG:HG3	1.71	0.72
2:B:701:ILE:HD11	2:B:703:ILE:HD11	1.72	0.72
2:B:603:LEU:HD13	2:B:608:ASP:HB2	1.72	0.72
4:D:130:LEU:O	4:D:132:GLN:N	2.22	0.72
1:A:741:ASN:HD21	1:A:743:VAL:HB	1.54	0.72
2:B:1182:CYS:SG	2:B:1182:CYS:O	2.48	0.72
2:B:1115:THR:HG22	2:B:1117:GLN:HG3	1.71	0.72
2:B:745:PRO:O	2:B:748:ILE:HG12	1.89	0.71
1:A:783:THR:HG21	1:A:815:PHE:CZ	2.25	0.71
2:B:364:ILE:HG12	2:B:585:VAL:HG13	1.70	0.71
2:B:39:ARG:NH2	2:B:665:GLU:HG2	2.05	0.71
12:L:32:ALA:HB3	12:L:55:ILE:HD12	1.71	0.71
1:A:1114:PRO:O	1:A:1115:SER:O	2.06	0.71
1:A:808:LEU:HD23	1:A:813:PHE:HA	1.71	0.71
10:J:5:VAL:HG12	10:J:6:ARG:CG	2.15	0.71
7:G:80:LYS:HD3	7:G:80:LYS:N	2.06	0.71
6:F:138:LEU:HB3	6:F:139:PRO:HD2	1.72	0.71
1:A:1437:GLY:O	1:A:1439:GLY:N	2.23	0.71
1:A:1121:GLU:HG2	1:A:1122:PRO:HD2	1.72	0.71
3:C:175:ALA:O	3:C:176:ILE:HG13	1.90	0.71
1:A:1239:ARG:HH22	1:A:1241:ARG:NH2	1.88	0.71
7:G:18:PHE:HA	7:G:22:MET:HE3	1.73	0.71
2:B:1099:VAL:O	2:B:1101:ASP:N	2.24	0.71
1:A:1152:ILE:HG13	9:I:44:TYR:HB3	1.71	0.71
8:H:113:ALA:HB2	8:H:126:GLU:HG3	1.72	0.71
2:B:1169:MET:HE1	2:B:1201:LYS:HA	1.71	0.70
8:H:59:ILE:HG22	8:H:60:ALA:H	1.54	0.70
4:D:47:LEU:HD13	4:D:48:ILE:N	2.03	0.70
2:B:708:GLU:O	2:B:710:LEU:N	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:75:ASN:O	1:A:76:GLU:HB3	1.91	0.70
2:B:365:THR:HG23	2:B:367:LEU:H	1.54	0.70
1:A:164:ARG:HG3	1:A:165:GLY:N	2.04	0.70
1:A:384:ASN:OD1	1:A:388:LEU:HD12	1.91	0.70
1:A:91:PHE:HB2	1:A:297:GLN:HE22	1.54	0.70
5:E:179:GLN:HB2	5:E:182:ASP:HB2	1.73	0.70
1:A:899:VAL:HB	1:A:929:LEU:CD1	2.21	0.70
2:B:227:LYS:HB2	2:B:395:GLN:OE1	1.90	0.70
2:B:1159:ARG:NH1	2:B:1159:ARG:HB3	2.06	0.70
1:A:816:HIS:CD2	2:B:764:SER:HB2	2.26	0.70
2:B:830:TYR:CE2	2:B:1000:PRO:HD3	2.27	0.70
2:B:579:ARG:HB2	2:B:586:TRP:HE1	1.57	0.70
1:A:794:PRO:HG2	1:A:795:GLU:OE2	1.92	0.70
3:C:167:HIS:CE1	12:L:70:ARG:HB3	2.27	0.70
2:B:211:VAL:O	2:B:480:SER:HA	1.91	0.70
2:B:1197:PRO:HG2	2:B:1200:ALA:CB	2.22	0.70
1:A:441:PRO:HD2	1:A:498:ARG:NH2	2.06	0.70
2:B:1006:ILE:HD13	10:J:44:TYR:CE2	2.26	0.70
1:A:901:LEU:HD22	1:A:919:ILE:CG2	2.22	0.70
1:A:1438:THR:HB	2:B:1144:ALA:HB3	1.74	0.70
11:K:47:ARG:HB3	11:K:47:ARG:NH1	2.05	0.70
2:B:593:PRO:HG2	2:B:617:ARG:NH2	2.06	0.70
1:A:1308:THR:HG23	1:A:1309:ASP:N	2.06	0.70
1:A:92:HIS:O	1:A:94:GLY:N	2.24	0.70
2:B:642:ASP:HB3	2:B:649:LYS:CG	2.21	0.70
1:A:302:THR:HA	1:A:305:ASP:O	1.92	0.70
7:G:14:HIS:CD2	7:G:16:SER:HB2	2.27	0.70
7:G:18:PHE:HA	7:G:22:MET:CE	2.22	0.70
1:A:466:SER:O	2:B:1103:ILE:HD11	1.92	0.70
1:A:68:GLN:C	1:A:70:CYS:H	1.95	0.70
1:A:1424:VAL:HG13	1:A:1436:ILE:HD11	1.74	0.70
1:A:913:LEU:HD12	1:A:914:GLU:N	2.05	0.69
11:K:65:HIS:CD2	11:K:67:PHE:H	2.05	0.69
1:A:14:VAL:HG21	2:B:1216:LEU:HD13	1.75	0.69
2:B:393:LYS:HA	2:B:393:LYS:HE3	1.74	0.69
4:D:33:PHE:CE1	7:G:80:LYS:HE3	2.27	0.69
1:A:901:LEU:HG	1:A:926:GLN:HE21	1.57	0.69
1:A:1445:ILE:HG12	7:G:18:PHE:CE2	2.27	0.69
2:B:1065:GLN:HE21	2:B:1067:ARG:N	1.91	0.69
4:D:48:ILE:CG2	7:G:4:ILE:HB	2.19	0.69
2:B:642:ASP:O	2:B:644:GLU:N	2.22	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:225:ASN:HD22	1:A:228:PHE:H	1.39	0.69
2:B:1087:PHE:HD2	2:B:1088:GLY:N	1.90	0.69
2:B:737:THR:HG21	9:I:66:PRO:HA	1.74	0.69
3:C:184:ASN:ND2	3:C:187:LYS:HA	2.07	0.69
2:B:975:GLN:HG2	2:B:976:ILE:H	1.56	0.69
2:B:351:TYR:CE1	2:B:355:ILE:HD11	2.28	0.69
1:A:1004:ASN:ND2	5:E:167:ARG:HD2	2.07	0.69
3:C:45:ALA:HA	3:C:72:LEU:HD12	1.74	0.69
2:B:778:MET:CE	2:B:1094:ARG:HD3	2.22	0.69
5:E:135:PHE:HB3	5:E:140:LEU:HD11	1.75	0.69
2:B:766:ARG:NH2	2:B:1020:ARG:HH11	1.90	0.69
9:I:71:SER:OG	9:I:83:ASN:HB2	1.92	0.69
8:H:4:THR:HA	8:H:60:ALA:CB	2.22	0.69
6:F:86:THR:OG1	6:F:89:GLU:HG3	1.93	0.69
3:C:20:PHE:CE1	3:C:22:LEU:HD12	2.25	0.69
4:D:170:THR:HG21	4:D:172:LEU:HG	1.74	0.69
11:K:50:LEU:HD11	11:K:75:ILE:HD13	1.73	0.69
2:B:953:LEU:O	2:B:953:LEU:HD23	1.92	0.69
2:B:728:ARG:HH12	2:B:1047:PHE:HB3	1.57	0.69
6:F:82:THR:HG22	6:F:84:TYR:H	1.58	0.69
1:A:1343:ALA:HB2	5:E:150:VAL:HG22	1.75	0.69
2:B:654:ARG:H	2:B:657:HIS:HD2	1.39	0.69
2:B:642:ASP:HB3	2:B:649:LYS:HG3	1.74	0.69
1:A:1120:LEU:O	1:A:1323:ASP:HB2	1.93	0.69
2:B:770:GLN:OE1	2:B:983:ARG:HA	1.92	0.69
1:A:78:PRO:HA	2:B:1201:LYS:NZ	2.08	0.69
1:A:1329:THR:CG2	1:A:1331:SER:H	2.03	0.69
3:C:166:GLU:HG3	11:K:10:PHE:CZ	2.21	0.69
1:A:858:ASN:HD22	1:A:858:ASN:C	1.94	0.69
2:B:1017:ILE:HB	2:B:1018:PRO:HD3	1.74	0.69
1:A:463:ILE:HD12	1:A:469:ARG:HD2	1.74	0.68
1:A:106:VAL:HG13	1:A:112:LYS:O	1.93	0.68
2:B:333:PHE:O	2:B:334:ILE:HG13	1.92	0.68
1:A:1239:ARG:HH22	1:A:1241:ARG:HH22	1.40	0.68
1:A:1424:VAL:HG13	1:A:1436:ILE:CD1	2.24	0.68
1:A:107:CYS:H	1:A:114:LEU:HD21	1.57	0.68
3:C:172:PRO:O	3:C:235:VAL:HG23	1.93	0.68
1:A:666:ILE:HD12	1:A:667:GLY:H	1.57	0.68
9:I:111:THR:HG22	9:I:112:SER:N	2.09	0.68
1:A:248:PRO:O	1:A:260:ASP:HB2	1.93	0.68
5:E:124:VAL:HG13	5:E:132:ILE:HB	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1291:VAL:HG13	1:A:1292:PRO:HD2	1.74	0.68
2:B:65:GLU:HG3	2:B:66:ASP:N	2.05	0.68
6:F:97:ARG:O	6:F:101:ILE:HG13	1.93	0.68
1:A:1002:GLY:HA3	1:A:1007:ILE:HG21	1.75	0.68
1:A:152:VAL:CG1	1:A:153:PRO:HD2	2.24	0.68
2:B:95:ILE:HG13	2:B:130:VAL:HG22	1.75	0.68
1:A:35:ILE:HG22	1:A:35:ILE:O	1.93	0.68
2:B:521:LEU:HB3	2:B:633:VAL:HG11	1.75	0.68
1:A:450:LEU:N	1:A:450:LEU:HD12	2.09	0.68
2:B:1197:PRO:HG2	2:B:1200:ALA:HB2	1.76	0.68
12:L:38:LEU:O	12:L:39:SER:HB3	1.93	0.68
3:C:263:THR:C	3:C:265:MET:H	1.97	0.68
3:C:179:GLU:HG2	3:C:180:TYR:N	2.09	0.68
1:A:856:THR:HB	1:A:865:GLN:HB2	1.75	0.68
2:B:112:LEU:HD12	2:B:113:TYR:H	1.58	0.68
9:I:13:MET:HG3	9:I:14:LEU:N	2.09	0.68
2:B:1099:VAL:CG1	2:B:1100:ASP:N	2.56	0.68
1:A:107:CYS:N	1:A:114:LEU:HD21	2.08	0.68
1:A:19:PHE:O	1:A:1416:ALA:HA	1.93	0.68
1:A:675:THR:O	1:A:679:ILE:HG13	1.93	0.68
1:A:809:THR:OG1	1:A:812:GLU:HG3	1.94	0.68
4:D:34:GLN:O	4:D:47:LEU:HD23	1.94	0.68
2:B:707:PRO:O	2:B:711:GLU:HG3	1.93	0.68
11:K:31:VAL:HG12	11:K:32:VAL:N	2.08	0.68
2:B:549:THR:HG22	2:B:550:ASP:N	2.05	0.67
1:A:351:THR:HG22	2:B:1103:ILE:HA	1.75	0.67
2:B:1162:ILE:HG22	2:B:1163:CYS:N	2.09	0.67
2:B:1073:TYR:CE2	2:B:1080:LYS:HG2	2.29	0.67
1:A:427:GLN:HG3	1:A:430:TRP:CZ2	2.28	0.67
1:A:63:ARG:HA	1:A:74:MET:SD	2.35	0.67
1:A:54:ASN:HB3	1:A:247:ARG:HH12	1.59	0.67
4:D:40:HIS:CB	7:G:73:LYS:HZ3	2.07	0.67
1:A:798:GLY:HA2	1:A:815:PHE:CD1	2.29	0.67
2:B:39:ARG:HH21	2:B:665:GLU:HG2	1.59	0.67
4:D:29:LEU:HD22	7:G:82:PHE:CE2	2.28	0.67
7:G:14:HIS:ND1	7:G:15:PRO:HD2	2.09	0.67
9:I:50:THR:HG22	9:I:52:ILE:H	1.60	0.67
3:C:114:TYR:HB3	3:C:140:ASN:O	1.94	0.67
2:B:1002:THR:HG23	2:B:1006:ILE:HG13	1.77	0.67
2:B:839:MET:HG3	2:B:1010:LEU:HD11	1.77	0.67
5:E:15:ALA:O	5:E:19:VAL:HG23	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:93:TYR:HB3	8:H:144:ILE:O	1.93	0.67
9:I:101:PHE:N	9:I:101:PHE:CD1	2.61	0.67
3:C:67:LEU:HD11	3:C:155:LEU:CD1	2.25	0.67
2:B:995:ARG:HH12	3:C:165:LYS:HG2	1.59	0.67
1:A:903:ASN:C	1:A:903:ASN:HD22	1.97	0.67
2:B:569:TYR:CE1	2:B:589:VAL:HG21	2.30	0.67
2:B:515:HIS:CD2	2:B:517:THR:H	2.11	0.67
1:A:388:LEU:HD22	1:A:432:VAL:HG21	1.76	0.67
1:A:23:SER:HA	1:A:233:TRP:CD1	2.30	0.67
1:A:567:LYS:HE3	8:H:46:LEU:HB2	1.77	0.67
6:F:97:ARG:HD3	6:F:130:ILE:HG23	1.77	0.67
8:H:81:PRO:CB	8:H:82:PRO:CD	2.72	0.67
3:C:186:LEU:HD21	3:C:224:GLN:O	1.95	0.67
1:A:567:LYS:CE	8:H:46:LEU:HB2	2.24	0.67
2:B:999:MET:HA	2:B:999:MET:CE	2.25	0.67
2:B:563:MET:HE3	2:B:580:VAL:HB	1.76	0.67
4:D:176:GLU:O	4:D:178:ALA:N	2.26	0.67
7:G:143:ILE:HG22	7:G:144:ARG:N	2.08	0.67
1:A:842:VAL:HG11	2:B:1136:ASP:OD2	1.95	0.67
3:C:123:ASN:HD22	3:C:125:MET:HG2	1.59	0.67
1:A:79:GLY:HA3	1:A:243:PRO:HG2	1.74	0.67
4:D:53:SER:HB3	4:D:152:SER:CB	2.25	0.67
2:B:831:SER:HB3	2:B:994:TYR:OH	1.95	0.67
6:F:125:LEU:O	6:F:125:LEU:HG	1.94	0.67
1:A:567:LYS:HB3	8:H:96:VAL:H	1.60	0.66
2:B:192:LEU:O	2:B:193:LYS:HB2	1.94	0.66
6:F:90:ARG:HD3	6:F:155:LEU:CD1	2.24	0.66
2:B:615:MET:HB3	2:B:626:ILE:HG12	1.76	0.66
1:A:311:GLN:HB3	1:A:312:PRO:HD3	1.76	0.66
7:G:91:VAL:HB	7:G:139:ILE:O	1.95	0.66
9:I:34:TYR:CE2	9:I:36:GLU:HB3	2.30	0.66
2:B:980:PHE:CE2	2:B:1094:ARG:HG3	2.30	0.66
2:B:36:ALA:HA	2:B:39:ARG:HD2	1.76	0.66
9:I:51:ASN:O	9:I:54:GLU:HG3	1.95	0.66
9:I:52:ILE:HG13	9:I:52:ILE:O	1.95	0.66
1:A:979:SER:OG	1:A:981:LEU:HG	1.94	0.66
1:A:1107:VAL:O	1:A:1107:VAL:HG12	1.96	0.66
2:B:1159:ARG:HB3	2:B:1159:ARG:HH11	1.60	0.66
2:B:635:ARG:NH2	2:B:742:GLU:OE2	2.26	0.66
2:B:1051:THR:HB	2:B:1054:GLY:H	1.61	0.66
1:A:75:ASN:O	1:A:76:GLU:CB	2.43	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:179:GLU:HG2	3:C:180:TYR:H	1.61	0.66
1:A:18:GLN:HB2	2:B:1215:ARG:HB2	1.77	0.66
2:B:902:GLY:O	12:L:65:VAL:HG11	1.96	0.66
1:A:1332:PHE:N	1:A:1332:PHE:CD2	2.58	0.66
3:C:18:VAL:HG12	3:C:18:VAL:O	1.94	0.66
2:B:1223:ASP:O	2:B:1224:PHE:HB2	1.94	0.66
1:A:843:LYS:HD3	1:A:846:GLU:OE2	1.95	0.66
5:E:48:ASP:CG	5:E:49:SER:H	1.99	0.66
1:A:2:VAL:HG21	2:B:1158:PHE:N	2.11	0.66
1:A:541:ILE:HD13	1:A:549:MET:CE	2.26	0.66
2:B:996:ARG:NH1	3:C:38:ILE:HG23	2.10	0.66
2:B:370:PHE:HE2	2:B:373:ARG:HH11	1.42	0.66
1:A:902:LEU:HG	1:A:926:GLN:HG3	1.76	0.66
1:A:69:THR:C	1:A:71:GLN:H	1.98	0.66
2:B:1202:LEU:O	2:B:1206:GLU:HG3	1.96	0.66
6:F:90:ARG:HG3	6:F:91:ALA:N	2.11	0.66
2:B:1056:SER:HB3	2:B:1066:SER:HB2	1.78	0.66
2:B:952:VAL:HG12	2:B:953:LEU:H	1.61	0.66
2:B:557:PHE:CD2	2:B:557:PHE:C	2.68	0.66
1:A:84:ILE:HG23	1:A:84:ILE:O	1.95	0.66
1:A:55:ASP:CG	1:A:55:ASP:O	2.32	0.66
1:A:385:ILE:HG22	1:A:386:ASP:N	2.10	0.66
2:B:1045:SER:O	2:B:1046:PRO:O	2.14	0.66
1:A:866:PHE:O	1:A:867:ILE:HG13	1.94	0.66
2:B:999:MET:HE3	2:B:999:MET:HA	1.76	0.66
3:C:238:ILE:CG2	3:C:242:GLN:HB2	2.25	0.66
2:B:378:LEU:O	2:B:382:ILE:HG13	1.96	0.66
1:A:399:HIS:O	1:A:401:GLY:N	2.28	0.66
3:C:147:LEU:HB2	3:C:151:GLN:HB2	1.78	0.66
3:C:152:GLU:OE2	3:C:154:LYS:HE3	1.95	0.66
1:A:1227:ILE:HG22	1:A:1228:TRP:N	2.10	0.66
1:A:1161:THR:HG22	1:A:1163:ILE:N	2.04	0.66
5:E:176:PRO:O	5:E:212:ARG:HA	1.96	0.66
12:L:40:LEU:HD13	12:L:44:ASP:HB3	1.77	0.66
3:C:189:THR:HG22	3:C:190:ASP:H	1.60	0.65
2:B:710:LEU:HA	2:B:733:HIS:HB3	1.78	0.65
7:G:30:LEU:HD13	7:G:72:VAL:HG11	1.77	0.65
2:B:1001:PHE:CE1	2:B:1073:TYR:HB2	2.31	0.65
1:A:332:LYS:HG3	1:A:333:GLU:HG2	1.79	0.65
1:A:986:ILE:HG22	1:A:987:VAL:N	2.10	0.65
4:D:122:GLU:HA	4:D:125:SER:OG	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:604:ARG:NH2	2:B:613:VAL:O	2.29	0.65
2:B:642:ASP:HA	2:B:649:LYS:HA	1.77	0.65
4:D:176:GLU:C	4:D:178:ALA:H	1.98	0.65
2:B:857:ARG:HD2	2:B:945:GLU:OE1	1.95	0.65
1:A:867:ILE:HD12	5:E:208:TYR:HE1	1.58	0.65
3:C:43:THR:CG2	3:C:44:LEU:H	2.08	0.65
3:C:177:GLU:HB2	3:C:231:ASN:HB3	1.78	0.65
12:L:58:LYS:O	12:L:58:LYS:HG2	1.96	0.65
8:H:56:THR:HB	8:H:145:ARG:HG2	1.79	0.65
1:A:372:LYS:HA	1:A:435:HIS:ND1	2.11	0.65
1:A:384:ASN:CG	1:A:388:LEU:HD12	2.17	0.65
2:B:1182:CYS:C	2:B:1183:LYS:HE3	2.17	0.65
2:B:758:PHE:CE2	2:B:1044:ALA:HA	2.31	0.65
1:A:547:LEU:HD22	11:K:58:PHE:CD1	2.32	0.65
1:A:69:THR:O	1:A:71:GLN:N	2.29	0.65
5:E:46:TYR:CD2	5:E:58:MET:HG2	2.31	0.65
2:B:229:ALA:HB1	2:B:231:PRO:HD2	1.79	0.65
2:B:197:PHE:CZ	2:B:816:GLU:HG2	2.32	0.65
1:A:1394:THR:HG21	1:A:1398:MET:SD	2.37	0.65
3:C:189:THR:HG22	3:C:190:ASP:N	2.11	0.65
1:A:979:SER:OG	1:A:980:ASP:N	2.28	0.65
2:B:850:LEU:HD12	2:B:851:PHE:H	1.62	0.65
6:F:119:ARG:HG3	6:F:119:ARG:HH11	1.61	0.65
2:B:798:TYR:HE2	3:C:62:PHE:CE2	2.15	0.65
1:A:590:ARG:HH21	1:A:620:LYS:HB3	1.62	0.65
4:D:50:LEU:HD11	7:G:4:ILE:HD11	1.79	0.65
2:B:975:GLN:O	2:B:990:ILE:HD12	1.97	0.65
12:L:39:SER:O	12:L:40:LEU:HG	1.97	0.65
5:E:84:ASP:O	5:E:86:PRO:HD3	1.97	0.65
7:G:7:LEU:HD11	7:G:45:ILE:HD11	1.78	0.65
3:C:43:THR:CG2	3:C:44:LEU:N	2.59	0.65
1:A:504:LEU:HD11	6:F:91:ALA:HB1	1.77	0.65
6:F:111:LEU:N	6:F:111:LEU:HD12	2.12	0.65
12:L:32:ALA:HB3	12:L:55:ILE:CD1	2.27	0.65
9:I:102:VAL:HG12	9:I:103:CYS:N	2.12	0.65
8:H:38:LEU:HD12	8:H:124:ARG:O	1.96	0.65
2:B:847:ASP:C	2:B:849:GLY:H	1.98	0.65
3:C:168:ALA:O	3:C:170:TRP:N	2.30	0.65
1:A:818:MET:HA	2:B:514:LEU:HB3	1.79	0.65
2:B:357:GLN:O	2:B:366:GLN:HA	1.97	0.65
2:B:653:VAL:CG2	2:B:689:LEU:HB3	2.27	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:541:ILE:HG22	1:A:546:VAL:HG23	1.79	0.65
2:B:798:TYR:HE2	3:C:62:PHE:CZ	2.14	0.65
1:A:1017:LEU:HB3	5:E:205:SER:HA	1.79	0.65
2:B:704:ALA:HB3	2:B:741:CYS:SG	2.37	0.65
2:B:770:GLN:CD	2:B:983:ARG:HA	2.16	0.65
7:G:110:VAL:HG22	7:G:161:GLY:O	1.97	0.65
1:A:869:GLY:O	5:E:204:THR:HG21	1.97	0.64
2:B:824:ILE:HG22	2:B:1087:PHE:CE2	2.23	0.64
1:A:1341:ILE:HG23	1:A:1342:GLU:H	1.61	0.64
12:L:31:CYS:HB3	12:L:35:SER:N	2.13	0.64
1:A:1348:LEU:HG	1:A:1372:VAL:HG23	1.78	0.64
2:B:1172:ILE:O	2:B:1172:ILE:HG22	1.96	0.64
1:A:844:ALA:C	1:A:845:LEU:HD23	2.18	0.64
3:C:165:LYS:O	11:K:6:ARG:NH1	2.30	0.64
11:K:53:ASP:HB3	11:K:56:VAL:HG23	1.79	0.64
6:F:135:ARG:HD3	6:F:143:PHE:CD2	2.32	0.64
2:B:899:ILE:CD1	2:B:911:ILE:HA	2.27	0.64
2:B:1180:PHE:HB3	2:B:1191:ILE:HD12	1.80	0.64
1:A:535:THR:HG23	1:A:575:LYS:HE2	1.79	0.64
3:C:183:TRP:CZ2	3:C:207:CYS:HB3	2.32	0.64
1:A:1017:LEU:HB2	5:E:206:GLY:N	2.07	0.64
2:B:23:ALA:HB1	2:B:24:PRO:CD	2.26	0.64
1:A:1115:SER:O	1:A:1116:LEU:HB3	1.96	0.64
1:A:50:ILE:O	1:A:52:GLY:N	2.28	0.64
1:A:442:VAL:HB	1:A:489:LEU:HD11	1.77	0.64
1:A:154:SER:HB3	1:A:162:VAL:HG21	1.79	0.64
1:A:1293:SER:OG	1:A:1294:PRO:HD2	1.97	0.64
2:B:880:THR:O	2:B:881:ASN:HB2	1.96	0.64
2:B:1007:VAL:CG2	2:B:1008:PRO:HD2	2.26	0.64
1:A:665:GLY:HA2	2:B:1026:LEU:HD21	1.78	0.64
1:A:23:SER:HA	1:A:233:TRP:NE1	2.12	0.64
1:A:1039:LYS:HG3	1:A:1043:ASP:OD2	1.98	0.64
2:B:601:ARG:O	2:B:605:ARG:HG3	1.97	0.64
1:A:672:ASP:HB2	1:A:736:ASN:OD1	1.98	0.64
7:G:34:VAL:CG1	7:G:45:ILE:HG21	2.26	0.64
1:A:743:VAL:O	1:A:747:VAL:HG23	1.96	0.64
1:A:1191:TRP:CD1	1:A:1256:GLU:HB2	2.33	0.64
7:G:59:GLY:HA3	7:G:70:PHE:CD2	2.33	0.64
3:C:66:ARG:NH1	10:J:2:ILE:HG21	2.13	0.64
4:D:56:ARG:HB2	4:D:148:LEU:HD22	1.80	0.64
2:B:580:VAL:HG22	2:B:624:LEU:CB	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1348:LEU:HG	1:A:1372:VAL:CG2	2.27	0.64
7:G:9:LEU:HD12	7:G:10:ASN:H	1.63	0.64
4:D:56:ARG:HA	4:D:148:LEU:HD13	1.79	0.64
1:A:503:GLN:HE21	6:F:90:ARG:NH2	1.95	0.64
1:A:670:ILE:HG23	1:A:805:LEU:CD2	2.28	0.64
1:A:720:ARG:O	1:A:724:GLU:HB2	1.97	0.64
5:E:157:SER:OG	5:E:160:GLU:HG3	1.97	0.64
1:A:88:LYS:HE3	1:A:280:GLU:OE2	1.98	0.64
2:B:604:ARG:NH1	2:B:691:GLU:OE2	2.31	0.64
12:L:31:CYS:SG	12:L:34:CYS:N	2.69	0.64
8:H:89:LEU:C	8:H:91:ASP:H	2.02	0.64
1:A:47:ARG:HH12	1:A:254:GLU:HG2	1.63	0.64
2:B:1085:ILE:HD12	2:B:1085:ILE:N	2.12	0.64
2:B:1165:ILE:HG22	2:B:1166:CYS:N	2.13	0.64
1:A:1193:LEU:HD12	1:A:1194:ARG:N	2.13	0.64
2:B:842:ASN:HD22	2:B:845:SER:CB	2.11	0.63
10:J:47:ARG:HH11	10:J:47:ARG:HG2	1.63	0.63
5:E:22:MET:CE	5:E:26:ARG:HH21	2.11	0.63
1:A:1063:MET:HG3	1:A:1436:ILE:HG23	1.80	0.63
2:B:862:GLN:HG2	2:B:963:PHE:HD1	1.63	0.63
1:A:899:VAL:HB	1:A:929:LEU:HD11	1.80	0.63
4:D:54:GLU:O	4:D:58:VAL:HG23	1.99	0.63
1:A:404:TYR:HB2	1:A:433:GLU:HB2	1.81	0.63
3:C:99:LEU:HA	3:C:119:VAL:O	1.98	0.63
5:E:213:ILE:HG12	5:E:214:CYS:N	2.12	0.63
1:A:500:GLU:OE2	2:B:1145:SER:HB2	1.99	0.63
2:B:731:VAL:HG12	2:B:732:SER:H	1.62	0.63
3:C:66:ARG:HH21	10:J:5:VAL:HG23	1.60	0.63
11:K:49:GLU:HG3	11:K:94:ILE:HG12	1.80	0.63
1:A:897:TYR:HD2	1:A:936:LEU:HD13	1.62	0.63
2:B:309:GLN:HG3	9:I:52:ILE:CD1	2.29	0.63
2:B:622:LYS:HE2	9:I:59:VAL:HG22	1.79	0.63
7:G:1:MET:HE3	7:G:80:LYS:C	2.19	0.63
3:C:212:PRO:CB	3:C:213:PRO:HD2	2.29	0.63
1:A:1341:ILE:CG2	1:A:1342:GLU:N	2.62	0.63
1:A:4:GLN:O	1:A:5:GLN:O	2.17	0.63
7:G:74:TYR:HD2	7:G:74:TYR:H	1.46	0.63
1:A:591:PHE:HA	1:A:595:THR:HG21	1.80	0.63
2:B:879:ARG:NH1	2:B:883:LEU:HD22	2.13	0.63
1:A:981:LEU:HD21	1:A:1038:THR:C	2.19	0.63
4:D:191:ALA:O	4:D:193:THR:N	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1224:LEU:HD12	1:A:1241:ARG:O	1.99	0.63
1:A:1057:VAL:HG12	1:A:1058:VAL:H	1.63	0.63
6:F:86:THR:HG23	6:F:89:GLU:OE1	1.98	0.63
9:I:8:ARG:CG	9:I:34:TYR:HE1	2.12	0.63
1:A:886:ILE:HG22	1:A:887:GLY:N	2.13	0.63
1:A:295:LEU:O	1:A:298:PHE:HB3	1.97	0.63
5:E:124:VAL:HG13	5:E:132:ILE:HD12	1.79	0.63
1:A:567:LYS:CB	8:H:95:TYR:HA	2.28	0.62
5:E:23:VAL:HG13	5:E:78:LEU:HD13	1.80	0.62
8:H:99:GLY:N	8:H:118:PHE:HD2	1.97	0.62
2:B:121:ASN:HA	2:B:207:GLY:HA2	1.81	0.62
2:B:217:ARG:C	2:B:217:ARG:HD2	2.19	0.62
1:A:114:LEU:HD13	1:A:171:GLN:OE1	1.99	0.62
2:B:63:ILE:O	2:B:67:SER:HB3	1.98	0.62
4:D:40:HIS:CB	7:G:73:LYS:NZ	2.55	0.62
2:B:212:LEU:CD2	2:B:480:SER:HB2	2.29	0.62
11:K:49:GLU:HG3	11:K:94:ILE:CG1	2.29	0.62
2:B:906:SER:O	2:B:941:LEU:HD23	1.99	0.62
9:I:101:PHE:HD1	9:I:101:PHE:H	1.46	0.62
2:B:205:ILE:O	2:B:207:GLY:N	2.32	0.62
1:A:1261:LYS:O	1:A:1264:GLU:HB3	1.99	0.62
2:B:953:LEU:CD2	2:B:965:LYS:HB2	2.28	0.62
1:A:1206:ASP:HB3	1:A:1274:ARG:HH12	1.64	0.62
1:A:1445:ILE:HG12	7:G:18:PHE:HE2	1.62	0.62
6:F:89:GLU:OE2	6:F:134:ILE:HG21	1.98	0.62
1:A:1454:MET:O	1:A:1454:MET:HG3	1.98	0.62
1:A:129:LYS:O	1:A:130:ASP:HB2	1.99	0.62
9:I:6:PHE:HB3	9:I:12:ASN:O	1.98	0.62
1:A:90:VAL:HG13	1:A:297:GLN:HA	1.82	0.62
2:B:1152:MET:CE	2:B:1157:ALA:HA	2.29	0.62
1:A:366:VAL:HG21	1:A:460:VAL:HG22	1.81	0.62
1:A:1021:LEU:O	1:A:1024:SER:HB3	1.99	0.62
7:G:1:MET:C	7:G:1:MET:SD	2.78	0.62
1:A:475:THR:CG2	1:A:476:SER:N	2.63	0.62
1:A:646:PHE:O	1:A:650:GLN:HG3	1.99	0.62
3:C:238:ILE:HG23	3:C:242:GLN:HB2	1.81	0.62
10:J:12:LYS:O	10:J:14:VAL:HG23	2.00	0.62
2:B:97:VAL:HG12	2:B:178:ASN:HD21	1.64	0.62
1:A:134:ARG:HG2	1:A:134:ARG:O	1.99	0.62
2:B:171:PRO:HD2	2:B:457:LEU:HD13	1.82	0.62
1:A:1121:GLU:CG	1:A:1122:PRO:HD2	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:481:ASP:OD1	1:A:485:ASP:OD2	2.18	0.62
2:B:121:ASN:HA	2:B:207:GLY:CA	2.29	0.62
1:A:590:ARG:HD2	1:A:605:MET:HB3	1.82	0.62
2:B:1065:GLN:NE2	2:B:1066:SER:N	2.47	0.62
1:A:1120:LEU:HD12	1:A:1120:LEU:N	2.14	0.62
1:A:412:ARG:NH2	2:B:1108:ARG:NH1	2.48	0.62
2:B:549:THR:H	2:B:628:THR:HG23	1.65	0.61
2:B:365:THR:HG23	2:B:367:LEU:HG	1.82	0.61
6:F:111:LEU:H	6:F:111:LEU:HD12	1.65	0.61
1:A:722:LEU:O	1:A:725:ALA:HB3	1.99	0.61
4:D:202:ILE:HG21	4:D:207:LEU:HB2	1.82	0.61
3:C:244:VAL:O	3:C:248:ILE:HG13	2.00	0.61
2:B:43:LEU:HD11	2:B:811:TYR:O	1.99	0.61
1:A:1027:ALA:O	1:A:1031:VAL:HG23	2.00	0.61
1:A:1444:MET:CE	6:F:135:ARG:HB2	2.30	0.61
1:A:467:THR:O	1:A:469:ARG:HG3	2.00	0.61
2:B:999:MET:HE2	2:B:1000:PRO:HD2	1.80	0.61
1:A:49:LYS:HE2	1:A:61:ILE:HD12	1.81	0.61
5:E:157:SER:C	5:E:159:ASP:H	2.04	0.61
2:B:731:VAL:HG12	2:B:732:SER:N	2.16	0.61
9:I:85:PHE:N	9:I:85:PHE:HD2	1.88	0.61
2:B:852:ARG:HH22	12:L:70:ARG:C	2.04	0.61
2:B:1001:PHE:CE2	3:C:34:ARG:CZ	2.84	0.61
1:A:382:PRO:HB3	1:A:428:TYR:HE2	1.65	0.61
8:H:100:THR:OG1	8:H:138:GLU:HG3	2.00	0.61
8:H:126:GLU:C	8:H:130:ARG:HH22	2.03	0.61
7:G:122:ASN:ND2	7:G:125:SER:HB3	2.16	0.61
2:B:882:THR:HG22	2:B:884:ARG:N	2.13	0.61
2:B:465:ASN:ND2	2:B:465:ASN:N	2.49	0.61
1:A:1299:VAL:HG12	1:A:1300:LYS:N	2.15	0.61
10:J:53:HIS:C	10:J:53:HIS:CD2	2.73	0.61
1:A:1116:LEU:HG	1:A:1308:THR:HB	1.83	0.61
7:G:23:LYS:HG3	7:G:56:ILE:CD1	2.29	0.61
1:A:407:ARG:HG2	1:A:430:TRP:CH2	2.35	0.61
2:B:860:MET:HG2	2:B:861:ASP:N	2.14	0.61
1:A:1444:MET:HG2	7:G:60:ARG:HA	1.83	0.61
1:A:907:THR:CG2	1:A:908:LEU:N	2.63	0.61
2:B:642:ASP:HB3	2:B:649:LYS:HD2	1.82	0.61
2:B:314:LEU:O	2:B:317:CYS:HB3	2.00	0.61
1:A:1436:ILE:O	1:A:1437:GLY:C	2.39	0.61
1:A:1007:ILE:C	1:A:1009:ASN:H	2.02	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:ASN:O	1:A:122:MET:HB3	2.01	0.61
1:A:144:THR:O	1:A:146:MET:HG3	2.01	0.61
1:A:590:ARG:O	1:A:591:PHE:HB2	2.01	0.61
2:B:824:ILE:CG2	2:B:1087:PHE:HE2	2.08	0.61
2:B:287:ARG:NH1	2:B:324:ILE:O	2.34	0.61
2:B:949:VAL:HG12	2:B:950:ASP:N	2.15	0.61
1:A:1151:GLU:OE2	9:I:45:ARG:HD2	2.01	0.61
1:A:1074:GLU:HB3	1:A:1075:PRO:CD	2.30	0.61
1:A:1097:GLY:O	1:A:1100:ARG:HB3	2.01	0.61
5:E:78:LEU:HD23	5:E:79:TRP:N	2.16	0.60
9:I:111:THR:HG22	9:I:112:SER:H	1.65	0.60
3:C:238:ILE:HG22	3:C:243:VAL:HG23	1.83	0.60
1:A:265:LYS:NZ	1:A:322:VAL:HG22	2.15	0.60
2:B:758:PHE:CE1	2:B:1027:ILE:HG22	2.37	0.60
2:B:197:PHE:HZ	2:B:816:GLU:HG2	1.65	0.60
1:A:518:LYS:HE2	1:A:624:SER:O	2.02	0.60
1:A:738:LYS:HB2	1:A:740:LEU:HG	1.83	0.60
5:E:207:ARG:HH11	5:E:207:ARG:CB	2.13	0.60
9:I:2:THR:O	9:I:3:THR:C	2.39	0.60
6:F:93:ILE:HD11	6:F:134:ILE:CD1	2.26	0.60
3:C:45:ALA:HA	3:C:72:LEU:CD1	2.31	0.60
2:B:980:PHE:HE2	2:B:1094:ARG:CG	2.14	0.60
2:B:859:TYR:CZ	2:B:941:LEU:HD12	2.37	0.60
1:A:146:MET:HA	1:A:171:GLN:HB2	1.83	0.60
1:A:728:LYS:O	1:A:732:LEU:HG	2.01	0.60
4:D:198:LEU:O	4:D:200:ASN:N	2.33	0.60
9:I:62:ILE:O	9:I:62:ILE:HG12	2.01	0.60
1:A:590:ARG:HB3	1:A:605:MET:N	2.15	0.60
2:B:778:MET:HE1	2:B:1094:ARG:CD	2.31	0.60
3:C:22:LEU:HD13	3:C:230:MET:CE	2.32	0.60
1:A:108:MET:SD	1:A:210:ILE:HD13	2.41	0.60
2:B:745:PRO:O	2:B:747:MET:N	2.33	0.60
2:B:46:GLN:HG3	2:B:47:GLN:N	2.07	0.60
1:A:524:VAL:HG12	1:A:525:GLN:N	2.12	0.60
1:A:224:PHE:CE2	1:A:231:PRO:HG3	2.36	0.60
1:A:472:LEU:HD11	2:B:835:GLN:NE2	2.17	0.60
1:A:1343:ALA:HB2	5:E:150:VAL:CG2	2.31	0.60
2:B:1152:MET:HE3	2:B:1157:ALA:HA	1.84	0.60
2:B:118:ARG:HH22	2:B:194:GLU:CD	2.04	0.60
2:B:446:LEU:O	2:B:447:ALA:HB3	2.02	0.60
7:G:51:TYR:C	7:G:51:TYR:CD2	2.75	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:822:ASN:O	10:J:48:ARG:NH1	2.34	0.60
1:A:337:ARG:HD3	2:B:1132:GLU:OE1	2.02	0.60
1:A:666:ILE:HD11	2:B:1067:ARG:O	2.02	0.60
2:B:606:LYS:HD2	2:B:608:ASP:OD2	2.01	0.60
1:A:185:TRP:CZ3	1:A:200:ARG:HG2	2.37	0.60
7:G:119:LEU:HD12	7:G:131:GLN:O	2.02	0.60
1:A:503:GLN:NE2	6:F:90:ARG:HH21	1.97	0.60
11:K:21:ILE:HG23	11:K:31:VAL:HG11	1.82	0.60
3:C:208:GLU:O	3:C:210:GLU:N	2.34	0.60
10:J:1:MET:H2	10:J:56:LEU:N	1.98	0.60
1:A:399:HIS:CB	1:A:400:PRO:HD3	2.28	0.60
4:D:144:THR:HG21	7:G:46:LEU:HD13	1.83	0.60
2:B:1099:VAL:HG12	2:B:1100:ASP:H	1.67	0.60
3:C:124:LEU:O	3:C:125:MET:HB2	2.01	0.60
2:B:840:ILE:HB	2:B:1011:ILE:HB	1.84	0.60
2:B:310:MET:O	2:B:313:MET:HB2	2.02	0.60
3:C:56:THR:HG22	3:C:57:VAL:N	2.16	0.60
2:B:189:LEU:O	2:B:192:LEU:N	2.28	0.60
1:A:254:GLU:HB2	2:B:935:ARG:NH1	2.17	0.60
1:A:255:SER:OG	2:B:918:ILE:HG23	2.02	0.60
8:H:81:PRO:HB2	8:H:82:PRO:CD	2.29	0.60
4:D:56:ARG:HD3	4:D:149:THR:HA	1.82	0.60
1:A:384:ASN:O	1:A:386:ASP:N	2.34	0.60
11:K:60:ALA:O	11:K:73:LEU:HD12	2.01	0.60
1:A:854:ASN:HB3	1:A:1000:LEU:HD21	1.83	0.60
1:A:1059:HIS:ND1	6:F:86:THR:HA	2.17	0.60
2:B:955:THR:CG2	2:B:956:THR:H	2.15	0.60
1:A:613:ILE:O	1:A:614:PHE:HB3	2.01	0.60
1:A:1291:VAL:HG13	1:A:1292:PRO:CD	2.31	0.60
2:B:29:ASP:HB3	2:B:658:ILE:HD13	1.83	0.60
12:L:60:ARG:HG2	12:L:61:THR:H	1.67	0.60
1:A:401:GLY:C	1:A:435:HIS:HD2	2.06	0.59
2:B:1115:THR:O	2:B:1116:ARG:HB2	2.01	0.59
9:I:105:SER:O	9:I:106:CYS:HB3	2.01	0.59
8:H:91:ASP:C	8:H:93:TYR:H	2.05	0.59
2:B:1224:PHE:CE2	5:E:171:LYS:HG3	2.30	0.59
2:B:705:MET:N	2:B:710:LEU:HD12	2.16	0.59
1:A:69:THR:C	1:A:71:GLN:N	2.55	0.59
1:A:12:ARG:HD2	2:B:1218:THR:HB	1.83	0.59
3:C:35:ARG:NH1	11:K:41:THR:OG1	2.35	0.59
2:B:834:ASN:HB3	2:B:840:ILE:HG13	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1015:VAL:HG12	1:A:1019:CYS:SG	2.42	0.59
3:C:66:ARG:NH1	3:C:144:ILE:O	2.35	0.59
1:A:768:GLN:HG2	1:A:816:HIS:CA	2.30	0.59
1:A:152:VAL:HG12	1:A:153:PRO:HD2	1.83	0.59
10:J:57:ILE:HA	10:J:60:PHE:CD2	2.30	0.59
2:B:744:HIS:CG	2:B:745:PRO:HD2	2.37	0.59
9:I:85:PHE:HD1	9:I:99:LEU:HD13	1.67	0.59
11:K:10:PHE:CD2	11:K:10:PHE:N	2.71	0.59
1:A:469:ARG:NH2	2:B:991:GLY:O	2.36	0.59
2:B:172:ILE:HD13	2:B:178:ASN:CB	2.32	0.59
1:A:115:LEU:O	1:A:122:MET:HE2	2.02	0.59
2:B:622:LYS:CE	9:I:59:VAL:HG22	2.32	0.59
4:D:220:LEU:O	4:D:221:TYR:HD1	1.85	0.59
3:C:254:LYS:O	3:C:256:ALA:N	2.35	0.59
2:B:1099:VAL:HG12	2:B:1100:ASP:N	2.17	0.59
2:B:515:HIS:H	2:B:518:HIS:CD2	2.10	0.59
2:B:616:ILE:CG1	2:B:697:GLU:HA	2.33	0.59
1:A:1313:LEU:O	1:A:1315:GLU:N	2.35	0.59
1:A:866:PHE:C	1:A:867:ILE:HG13	2.22	0.59
4:D:128:VAL:O	4:D:132:GLN:HG3	2.03	0.59
10:J:14:VAL:HG12	10:J:14:VAL:O	2.03	0.59
1:A:1341:ILE:CG2	1:A:1342:GLU:H	2.15	0.59
1:A:384:ASN:O	1:A:385:ILE:C	2.41	0.59
9:I:26:LEU:HD23	9:I:37:GLU:HA	1.83	0.59
2:B:787:VAL:O	2:B:787:VAL:HG12	2.02	0.59
1:A:310:GLY:O	1:A:312:PRO:HD2	2.03	0.59
2:B:118:ARG:HH11	2:B:204:ILE:HD11	1.68	0.59
9:I:55:THR:HG21	9:I:109:ILE:HD13	1.84	0.59
4:D:156:ASP:C	4:D:158:GLU:H	2.03	0.59
1:A:913:LEU:HD12	1:A:914:GLU:H	1.66	0.59
2:B:980:PHE:HD2	2:B:1094:ARG:HA	1.67	0.59
2:B:1180:PHE:O	2:B:1181:GLU:O	2.20	0.59
1:A:774:ARG:NH2	1:A:797:LYS:HB2	2.17	0.59
11:K:58:PHE:HB3	11:K:76:GLN:HB3	1.85	0.59
5:E:90:VAL:HA	5:E:120:ALA:HB2	1.85	0.59
1:A:472:LEU:O	1:A:475:THR:HB	2.03	0.59
1:A:1430:LEU:HB2	1:A:1432:GLN:HG3	1.85	0.59
8:H:44:VAL:HG12	8:H:44:VAL:O	2.03	0.59
1:A:1017:LEU:CB	5:E:205:SER:HA	2.33	0.59
1:A:407:ARG:HB3	1:A:430:TRP:CE2	2.38	0.59
1:A:1345:ARG:HG3	1:A:1376:THR:HG21	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:782:ARG:NH2	2:B:699:GLU:O	2.34	0.59
1:A:1385:THR:HG22	1:A:1386:ARG:N	2.18	0.59
1:A:855:THR:CG2	1:A:857:ARG:HE	2.07	0.58
6:F:103:MET:O	6:F:104:ASN:HB2	2.03	0.58
1:A:107:CYS:SG	1:A:171:GLN:HG2	2.42	0.58
2:B:196:PRO:HG2	2:B:197:PHE:H	1.68	0.58
2:B:205:ILE:HD12	2:B:205:ILE:N	2.17	0.58
5:E:131:THR:HG21	5:E:191:LYS:NZ	2.18	0.58
1:A:1105:LEU:HD22	1:A:1384:VAL:HG21	1.83	0.58
1:A:971:PHE:CE2	1:A:1040:GLN:HG2	2.37	0.58
2:B:838:SER:HB2	2:B:989:THR:O	2.03	0.58
3:C:254:LYS:O	3:C:258:ILE:HD13	2.04	0.58
2:B:180:TYR:HD1	2:B:180:TYR:H	1.51	0.58
11:K:63:VAL:HG23	11:K:63:VAL:O	2.03	0.58
1:A:853:ASP:OD1	1:A:855:THR:CB	2.51	0.58
7:G:14:HIS:HD2	7:G:16:SER:HB2	1.66	0.58
4:D:130:LEU:HD22	4:D:134:THR:OG1	2.03	0.58
1:A:532:ARG:HH22	1:A:745:GLN:HG2	1.67	0.58
1:A:1444:MET:HE2	6:F:135:ARG:HB2	1.86	0.58
2:B:359:GLU:O	2:B:362:PRO:HD3	2.04	0.58
12:L:53:HIS:O	12:L:55:ILE:HG12	2.04	0.58
1:A:800:VAL:HG22	1:A:812:GLU:HB3	1.85	0.58
1:A:658:LEU:HD23	1:A:659:HIS:CE1	2.38	0.58
4:D:51:ASN:O	4:D:54:GLU:HB3	2.04	0.58
2:B:265:SER:O	2:B:266:ALA:HB3	2.02	0.58
4:D:33:PHE:CZ	7:G:80:LYS:HE3	2.38	0.58
2:B:825:VAL:CG1	2:B:826:ALA:N	2.67	0.58
2:B:705:MET:H	2:B:710:LEU:CD1	2.14	0.58
2:B:616:ILE:N	2:B:616:ILE:HD12	2.18	0.58
9:I:102:VAL:CG1	9:I:103:CYS:N	2.65	0.58
3:C:241:ASP:O	3:C:245:VAL:HG23	2.03	0.58
1:A:567:LYS:CG	1:A:568:PRO:CD	2.79	0.58
6:F:99:LEU:HD12	6:F:99:LEU:O	2.04	0.58
2:B:811:TYR:N	2:B:811:TYR:CD1	2.71	0.58
1:A:325:ILE:HG21	2:B:1210:MET:HG3	1.84	0.58
5:E:39:LEU:O	5:E:42:PHE:HB3	2.02	0.58
1:A:262:LEU:O	1:A:264:PHE:N	2.37	0.58
10:J:23:ASN:C	10:J:25:LEU:H	2.05	0.58
2:B:283:VAL:O	2:B:286:PHE:N	2.37	0.58
8:H:143:LEU:N	8:H:143:LEU:HD12	2.19	0.58
1:A:254:GLU:HG3	2:B:935:ARG:HH22	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:957:ASN:O	2:B:959:ASP:N	2.37	0.58
1:A:828:ALA:CB	2:B:530:GLY:HA2	2.33	0.58
12:L:43:THR:O	12:L:43:THR:HG22	2.02	0.58
1:A:135:PHE:C	1:A:137:ALA:H	2.06	0.58
1:A:1155:ASP:OD1	1:A:1161:THR:HA	2.03	0.58
9:I:8:ARG:HG3	9:I:34:TYR:CE1	2.38	0.58
4:D:134:THR:CG2	4:D:135:GLY:N	2.66	0.58
11:K:65:HIS:CD2	11:K:67:PHE:HB2	2.38	0.58
1:A:67:CYS:O	1:A:68:GLN:HB2	2.04	0.58
1:A:1057:VAL:HG12	1:A:1058:VAL:N	2.18	0.58
1:A:665:GLY:O	1:A:667:GLY:N	2.37	0.58
1:A:63:ARG:HA	1:A:74:MET:CE	2.34	0.58
1:A:1030:ARG:NH1	1:A:1035:TYR:OH	2.37	0.58
11:K:12:LEU:H	11:K:12:LEU:HD12	1.68	0.58
1:A:1166:ASP:OD2	1:A:1239:ARG:HD2	2.03	0.58
9:I:14:LEU:HA	9:I:28:GLU:O	2.04	0.58
3:C:235:VAL:HG13	10:J:13:VAL:CG2	2.34	0.58
1:A:471:ASN:OD1	1:A:472:LEU:N	2.36	0.58
1:A:2:VAL:HG21	2:B:1158:PHE:CA	2.34	0.58
1:A:549:MET:SD	1:A:577:ILE:HD11	2.43	0.58
1:A:1116:LEU:HD11	1:A:1118:VAL:HG13	1.86	0.58
2:B:102:VAL:CG2	2:B:112:LEU:HD22	2.34	0.58
11:K:47:ARG:HH11	11:K:47:ARG:CB	2.11	0.58
2:B:1103:ILE:O	2:B:1122:ARG:NH1	2.37	0.58
1:A:1400:CYS:SG	1:A:1409:LEU:HG	2.44	0.58
1:A:1418:LEU:HD23	2:B:1222:ARG:HD2	1.86	0.58
5:E:114:ASN:O	5:E:115:ASN:HB3	2.03	0.58
1:A:278:THR:O	1:A:282:ASN:HB2	2.04	0.58
5:E:14:ARG:HH21	5:E:141:VAL:CG1	2.17	0.58
1:A:965:GLN:O	1:A:968:GLN:HB2	2.04	0.58
2:B:117:ALA:HA	2:B:122:LEU:HD12	1.85	0.57
1:A:35:ILE:HA	1:A:52:GLY:O	2.04	0.57
2:B:589:VAL:HG12	2:B:590:HIS:N	2.17	0.57
4:D:153:ARG:HH22	4:D:184:ALA:HA	1.68	0.57
1:A:265:LYS:NZ	1:A:322:VAL:HG13	2.17	0.57
2:B:1031:LEU:HD23	2:B:1044:ALA:HB2	1.85	0.57
12:L:27:LEU:O	12:L:28:LYS:HG2	2.03	0.57
8:H:18:GLY:O	8:H:19:ARG:HB2	2.04	0.57
1:A:77:CYS:O	1:A:78:PRO:C	2.40	0.57
1:A:853:ASP:O	1:A:854:ASN:HB2	2.04	0.57
1:A:35:ILE:HG22	1:A:84:ILE:HD12	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:868:TYR:HD2	1:A:1058:VAL:HG21	1.68	0.57
9:I:55:THR:CG2	9:I:58:VAL:HG21	2.34	0.57
1:A:446:ARG:HD3	1:A:480:ALA:HB2	1.86	0.57
8:H:17:PRO:HB3	8:H:24:CYS:SG	2.43	0.57
2:B:460:ALA:HB1	2:B:466:TRP:CZ3	2.38	0.57
1:A:79:GLY:HA3	1:A:243:PRO:HG3	1.86	0.57
7:G:7:LEU:CD1	7:G:45:ILE:HD11	2.33	0.57
7:G:106:MET:CG	7:G:107:LYS:N	2.66	0.57
7:G:3:PHE:CD1	7:G:80:LYS:NZ	2.70	0.57
2:B:65:GLU:CG	2:B:66:ASP:H	2.11	0.57
10:J:44:TYR:HA	10:J:47:ARG:HB2	1.85	0.57
1:A:50:ILE:C	1:A:52:GLY:H	2.06	0.57
1:A:666:ILE:CD1	1:A:667:GLY:H	2.18	0.57
2:B:737:THR:CG2	9:I:66:PRO:HA	2.33	0.57
1:A:49:LYS:HZ1	1:A:61:ILE:N	2.03	0.57
1:A:61:ILE:O	1:A:63:ARG:N	2.38	0.57
4:D:189:ASP:O	4:D:193:THR:HB	2.05	0.57
1:A:1051:ALA:O	1:A:1055:ARG:HG3	2.04	0.57
7:G:1:MET:O	7:G:3:PHE:CE1	2.58	0.57
1:A:1164:PRO:HG2	1:A:1165:GLU:H	1.69	0.57
2:B:604:ARG:HH22	2:B:614:SER:HA	1.69	0.57
1:A:47:ARG:HH12	1:A:254:GLU:CG	2.17	0.57
1:A:698:GLN:HA	9:I:97:MET:O	2.04	0.57
5:E:198:ILE:CD1	5:E:212:ARG:HG3	2.32	0.57
1:A:1209:MET:HE1	1:A:1236:LEU:HB3	1.85	0.57
1:A:289:ILE:C	1:A:291:GLU:H	2.07	0.57
6:F:109:VAL:HG12	6:F:110:ASP:N	2.20	0.57
2:B:244:LEU:HD21	2:B:366:GLN:NE2	2.20	0.57
2:B:952:VAL:HG12	2:B:953:LEU:N	2.20	0.57
3:C:239:PRO:HB2	3:C:241:ASP:OD1	2.05	0.57
1:A:195:ASP:O	1:A:196:GLU:HB3	2.02	0.57
2:B:1196:ILE:HB	2:B:1197:PRO:HD2	1.86	0.57
1:A:11:LEU:HB2	2:B:1193:GLN:OE1	2.04	0.57
1:A:321:PRO:O	1:A:322:VAL:CB	2.53	0.57
2:B:615:MET:C	2:B:616:ILE:HD12	2.25	0.57
5:E:197:LYS:HE2	5:E:199:ILE:HD11	1.86	0.57
1:A:1029:ARG:HG3	1:A:1029:ARG:HH11	1.70	0.57
7:G:7:LEU:O	7:G:73:LYS:HD2	2.05	0.57
3:C:36:VAL:HG21	3:C:251:LEU:HD22	1.86	0.57
1:A:658:LEU:HD13	2:B:831:SER:HA	1.86	0.57
2:B:850:LEU:HD12	2:B:851:PHE:N	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1349:TYR:CE1	1:A:1368:MET:HE3	2.40	0.57
8:H:99:GLY:N	8:H:118:PHE:CD2	2.72	0.57
7:G:99:PHE:HZ	7:G:163:ILE:HD13	1.70	0.57
1:A:1362:TYR:CD1	1:A:1363:VAL:N	2.73	0.57
10:J:1:MET:N	10:J:56:LEU:N	2.53	0.57
1:A:244:PRO:CB	1:A:245:PRO:HD3	2.34	0.57
1:A:863:VAL:HG11	1:A:866:PHE:CD2	2.39	0.57
5:E:78:LEU:C	5:E:78:LEU:HD23	2.24	0.57
2:B:1001:PHE:CE2	3:C:34:ARG:NE	2.73	0.57
1:A:2:VAL:HG21	2:B:1157:ALA:C	2.25	0.57
1:A:875:ALA:HA	1:A:878:ILE:HD12	1.87	0.57
8:H:83:GLN:C	8:H:85:GLY:H	2.08	0.57
1:A:490:HIS:HB3	2:B:1150:ARG:NH1	2.20	0.57
1:A:1198:ASP:O	1:A:1202:MET:HG2	2.05	0.57
7:G:3:PHE:CE1	7:G:80:LYS:HE2	2.40	0.57
2:B:980:PHE:CD2	2:B:1094:ARG:HA	2.40	0.57
2:B:579:ARG:HG2	2:B:579:ARG:HH11	1.70	0.57
1:A:836:TYR:CD2	1:A:840:ARG:HD2	2.40	0.57
1:A:231:PRO:HA	1:A:234:MET:HE2	1.86	0.57
1:A:1396:ALA:O	1:A:1398:MET:N	2.38	0.57
2:B:949:VAL:HG12	2:B:950:ASP:H	1.70	0.57
11:K:61:TYR:C	11:K:61:TYR:CD2	2.78	0.57
7:G:1:MET:HG3	7:G:85:GLU:OE2	2.05	0.56
3:C:31:ASN:O	3:C:32:SER:C	2.42	0.56
2:B:899:ILE:HD11	2:B:910:VAL:O	2.04	0.56
2:B:911:ILE:HD11	2:B:941:LEU:HD13	1.86	0.56
2:B:309:GLN:HG3	9:I:52:ILE:HD11	1.87	0.56
1:A:897:TYR:CD2	1:A:936:LEU:HD13	2.40	0.56
1:A:1364:ASN:HD22	1:A:1365:TYR:N	2.02	0.56
4:D:59:ILE:HG21	4:D:145:MET:SD	2.45	0.56
2:B:1099:VAL:C	2:B:1101:ASP:H	2.07	0.56
2:B:955:THR:CG2	2:B:956:THR:N	2.67	0.56
1:A:844:ALA:O	1:A:845:LEU:HD23	2.05	0.56
1:A:21:LEU:HG	1:A:1413:GLY:O	2.05	0.56
1:A:541:ILE:HD13	1:A:549:MET:HE1	1.88	0.56
4:D:52:LEU:HD21	4:D:147:TYR:HE2	1.70	0.56
1:A:998:LEU:H	1:A:998:LEU:HD12	1.69	0.56
1:A:958:VAL:O	1:A:958:VAL:HG12	2.05	0.56
1:A:663:SER:OG	1:A:664:THR:N	2.36	0.56
10:J:3:VAL:HA	10:J:53:HIS:CE1	2.39	0.56
7:G:35:GLU:OE2	7:G:48:VAL:HG23	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:130:ILE:O	6:F:148:VAL:HG21	2.06	0.56
6:F:109:VAL:HG11	6:F:123:LYS:HG2	1.85	0.56
2:B:114:PRO:O	2:B:116:GLU:N	2.38	0.56
1:A:252:PHE:O	1:A:256:GLN:NE2	2.39	0.56
5:E:180:ARG:HH21	5:E:192:ARG:CB	2.15	0.56
2:B:376:PHE:CE2	2:B:569:TYR:HD2	2.23	0.56
3:C:252:GLN:HG3	11:K:95:ILE:HG23	1.87	0.56
2:B:1001:PHE:HE2	3:C:34:ARG:CZ	2.17	0.56
10:J:14:VAL:HG12	10:J:50:ILE:HD11	1.87	0.56
1:A:886:ILE:HD11	1:A:943:LEU:CB	2.35	0.56
2:B:1034:VAL:CG1	2:B:1035:ALA:N	2.67	0.56
1:A:311:GLN:HB3	1:A:312:PRO:CD	2.33	0.56
2:B:54:PHE:HA	2:B:58:THR:HB	1.86	0.56
2:B:224:GLN:O	2:B:238:ALA:HA	2.05	0.56
2:B:527:THR:OG1	2:B:528:PRO:HD2	2.06	0.56
1:A:1283:VAL:HG12	1:A:1284:MET:N	2.21	0.56
8:H:116:TYR:HB2	8:H:123:MET:HB3	1.86	0.56
1:A:1063:MET:CG	1:A:1436:ILE:HG23	2.34	0.56
1:A:265:LYS:HE2	1:A:322:VAL:CG1	2.35	0.56
4:D:68:ARG:C	4:D:70:PHE:H	2.09	0.56
3:C:146:LYS:C	3:C:147:LEU:HD23	2.26	0.56
8:H:98:TYR:C	8:H:118:PHE:HD2	2.08	0.56
1:A:714:PHE:O	1:A:718:VAL:HG23	2.05	0.56
1:A:907:THR:HG22	1:A:908:LEU:N	2.20	0.56
1:A:1409:LEU:HD13	2:B:1207:LEU:CD2	2.36	0.56
11:K:21:ILE:HG23	11:K:31:VAL:CG1	2.36	0.56
1:A:382:PRO:HD3	1:A:428:TYR:CD2	2.40	0.56
1:A:427:GLN:HB2	1:A:430:TRP:CD1	2.41	0.56
1:A:185:TRP:HZ3	1:A:200:ARG:HG2	1.71	0.56
3:C:60:ASP:OD2	12:L:60:ARG:NH2	2.39	0.56
2:B:984:HIS:CG	2:B:1025:HIS:HB2	2.41	0.56
8:H:40:LEU:CD1	8:H:123:MET:HB2	2.34	0.56
1:A:547:LEU:HD22	11:K:58:PHE:CE1	2.41	0.56
2:B:637:LEU:HD12	2:B:693:ILE:HD12	1.88	0.56
2:B:351:TYR:O	2:B:355:ILE:HG13	2.05	0.56
1:A:1035:TYR:O	1:A:1037:LEU:N	2.37	0.56
2:B:190:TYR:CE2	10:J:62:ARG:HB3	2.40	0.56
7:G:111:THR:HB	7:G:114:LEU:HB2	1.88	0.56
1:A:940:ARG:HG2	1:A:940:ARG:HH11	1.71	0.56
3:C:5:GLY:O	3:C:7:GLN:HG3	2.06	0.56
1:A:1441:PHE:CZ	6:F:89:GLU:HA	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:963:ILE:HD13	1:A:1049:ILE:HG12	1.87	0.56
5:E:94:LYS:CE	5:E:98:ILE:HD11	2.31	0.56
6:F:90:ARG:HD3	6:F:155:LEU:HD11	1.88	0.56
2:B:1162:ILE:HD11	2:B:1194:ILE:HD13	1.87	0.56
2:B:465:ASN:HD22	2:B:465:ASN:H	1.53	0.56
11:K:90:ALA:O	11:K:94:ILE:HG13	2.04	0.56
3:C:51:VAL:HG22	3:C:155:LEU:HD22	1.88	0.56
2:B:295:GLY:H	2:B:298:LEU:HD23	1.70	0.56
4:D:192:LYS:HZ3	4:D:199:ASN:HA	1.71	0.56
1:A:416:ARG:C	1:A:417:TYR:HD2	2.09	0.56
1:A:852:TYR:CE2	1:A:1060:PRO:HB2	2.40	0.56
11:K:82:ASP:OD1	11:K:84:LYS:N	2.38	0.56
6:F:75:PRO:O	6:F:77:ASP:O	2.23	0.56
5:E:93:MET:SD	5:E:97:VAL:HG23	2.46	0.56
1:A:586:ILE:HG22	1:A:587:HIS:N	2.21	0.56
10:J:53:HIS:CD2	10:J:54:VAL:N	2.74	0.56
7:G:1:MET:O	7:G:1:MET:SD	2.64	0.56
1:A:356:ASP:OD2	11:K:65:HIS:HE1	1.88	0.56
2:B:361:LEU:HD21	2:B:377:PHE:HD2	1.66	0.56
1:A:492:PRO:O	1:A:493:GLN:NE2	2.38	0.56
1:A:774:ARG:O	1:A:775:ILE:C	2.43	0.56
2:B:526:GLU:OE2	2:B:752:ALA:HB2	2.06	0.56
9:I:25:LEU:HB3	9:I:38:ALA:HB2	1.88	0.56
1:A:1074:GLU:HB3	1:A:1075:PRO:HD3	1.87	0.56
2:B:833:TYR:N	2:B:833:TYR:CD1	2.73	0.56
12:L:47:ARG:HG3	12:L:47:ARG:HH11	1.70	0.56
1:A:1127:ASP:HB3	1:A:1130:GLN:CB	2.35	0.56
2:B:604:ARG:NH2	2:B:614:SER:HA	2.20	0.56
7:G:88:ASP:HB3	7:G:144:ARG:HA	1.88	0.56
1:A:722:LEU:HD22	1:A:799:PHE:CD1	2.41	0.56
4:D:156:ASP:C	4:D:158:GLU:N	2.60	0.56
4:D:192:LYS:HZ3	4:D:192:LYS:HB3	1.70	0.56
2:B:745:PRO:C	2:B:747:MET:H	2.09	0.55
2:B:114:PRO:HG2	2:B:115:GLN:H	1.71	0.55
1:A:265:LYS:HD2	1:A:265:LYS:N	2.20	0.55
2:B:893:LEU:HD11	2:B:910:VAL:HG11	1.88	0.55
5:E:35:VAL:C	5:E:37:LEU:H	2.10	0.55
1:A:798:GLY:HA2	1:A:815:PHE:HD1	1.68	0.55
1:A:1279:ILE:HD11	1:A:1316:VAL:HG21	1.88	0.55
2:B:603:LEU:HB3	2:B:609:ILE:CD1	2.37	0.55
1:A:899:VAL:HB	1:A:929:LEU:HD12	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1336:MET:HE3	1:A:1381:LEU:HG	1.88	0.55
1:A:1010:ALA:HA	1:A:1013:ASP:OD2	2.06	0.55
2:B:376:PHE:HB3	2:B:586:TRP:CZ3	2.42	0.55
2:B:53:GLN:HG2	2:B:547:VAL:CG2	2.36	0.55
1:A:98:LYS:O	1:A:99:ILE:C	2.45	0.55
7:G:145:VAL:HG12	7:G:146:LYS:N	2.21	0.55
2:B:258:LEU:O	2:B:258:LEU:HG	2.05	0.55
1:A:567:LYS:HE3	8:H:46:LEU:HD12	1.89	0.55
5:E:23:VAL:O	5:E:28:TYR:HB2	2.07	0.55
1:A:504:LEU:HD12	1:A:504:LEU:N	2.21	0.55
5:E:29:PHE:C	5:E:30:ILE:HG13	2.26	0.55
1:A:268:ASP:HB3	1:A:299:HIS:CE1	2.41	0.55
1:A:265:LYS:HD2	1:A:265:LYS:H	1.72	0.55
5:E:3:GLN:HG3	5:E:4:GLU:N	2.20	0.55
3:C:174:ALA:O	3:C:175:ALA:HB2	2.05	0.55
2:B:29:ASP:HB3	2:B:658:ILE:CD1	2.36	0.55
12:L:36:SER:O	12:L:37:LYS:C	2.44	0.55
1:A:1197:LEU:HD12	1:A:1209:MET:HE1	1.87	0.55
9:I:68:LEU:HB3	9:I:84:VAL:HG23	1.87	0.55
1:A:1214:GLU:O	1:A:1218:GLN:HG2	2.05	0.55
1:A:350:ARG:HB2	1:A:488:ASN:OD1	2.07	0.55
2:B:129:PHE:HA	2:B:165:VAL:O	2.06	0.55
1:A:857:ARG:HD3	1:A:861:GLY:O	2.06	0.55
1:A:268:ASP:HB3	1:A:299:HIS:ND1	2.21	0.55
1:A:90:VAL:HG12	1:A:91:PHE:N	2.22	0.55
2:B:324:ILE:HD13	2:B:330:ALA:HA	1.88	0.55
1:A:548:ASN:HA	11:K:60:ALA:HB1	1.89	0.55
9:I:74:GLU:HA	9:I:80:SER:O	2.06	0.55
1:A:1242:VAL:O	1:A:1243:VAL:HB	2.07	0.55
7:G:17:PHE:C	7:G:19:GLY:H	2.10	0.55
3:C:31:ASN:OD1	3:C:34:ARG:NH1	2.40	0.55
2:B:1159:ARG:HD3	2:B:1193:GLN:CG	2.37	0.55
1:A:666:ILE:N	1:A:666:ILE:HD12	2.21	0.55
2:B:1034:VAL:C	2:B:1036:ALA:H	2.09	0.55
11:K:50:LEU:HD11	11:K:75:ILE:CD1	2.37	0.55
6:F:111:LEU:C	6:F:113:GLY:N	2.56	0.55
1:A:730:GLY:O	1:A:732:LEU:N	2.40	0.55
2:B:557:PHE:HD2	2:B:557:PHE:C	2.09	0.55
3:C:258:ILE:N	3:C:258:ILE:HD12	2.22	0.55
6:F:77:ASP:C	6:F:79:ARG:H	2.10	0.55
2:B:843:GLN:O	2:B:846:ILE:HB	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:882:THR:HB	2:B:934:LYS:O	2.06	0.55
1:A:71:GLN:C	1:A:73:GLY:H	2.09	0.55
4:D:51:ASN:O	4:D:52:LEU:O	2.25	0.55
2:B:696:GLU:O	2:B:699:GLU:HB2	2.07	0.55
1:A:458:HIS:CE1	1:A:507:VAL:HG21	2.41	0.55
10:J:3:VAL:HG21	10:J:18:TRP:CB	2.31	0.55
3:C:76:ASP:O	3:C:79:GLN:HG2	2.06	0.55
1:A:56:PRO:O	1:A:57:ARG:CG	2.51	0.55
7:G:27:LYS:O	7:G:30:LEU:HB3	2.07	0.55
2:B:97:VAL:HG12	2:B:178:ASN:ND2	2.22	0.55
1:A:658:LEU:HD23	1:A:659:HIS:HE1	1.72	0.55
1:A:1227:ILE:HG22	1:A:1228:TRP:H	1.71	0.55
1:A:567:LYS:HD3	8:H:95:TYR:CG	2.42	0.55
2:B:1082:MET:O	3:C:189:THR:HG23	2.07	0.55
1:A:1342:GLU:CG	5:E:198:ILE:HD13	2.37	0.55
1:A:896:ARG:NH2	1:A:1030:ARG:NH2	2.55	0.55
2:B:205:ILE:CD1	2:B:205:ILE:N	2.68	0.55
7:G:51:TYR:O	7:G:54:ILE:HG13	2.06	0.55
3:C:3:GLU:HG2	3:C:4:GLU:N	2.22	0.55
7:G:125:SER:OG	7:G:128:PRO:HA	2.07	0.55
2:B:579:ARG:N	2:B:589:VAL:HG13	2.22	0.55
2:B:35:SER:O	2:B:39:ARG:HG3	2.05	0.55
2:B:39:ARG:HG2	2:B:39:ARG:HH11	1.72	0.55
3:C:235:VAL:HG13	10:J:13:VAL:HG23	1.89	0.55
1:A:1435:PRO:HA	1:A:1439:GLY:O	2.06	0.55
1:A:92:HIS:HB3	1:A:95:PHE:HB2	1.89	0.55
1:A:114:LEU:O	1:A:115:LEU:HG	2.07	0.55
1:A:49:LYS:NZ	1:A:61:ILE:HG13	2.22	0.55
1:A:1032:LEU:O	1:A:1036:ARG:HD3	2.07	0.55
10:J:43:ARG:HG3	10:J:45:CYS:SG	2.47	0.54
2:B:710:LEU:O	2:B:711:GLU:HG2	2.06	0.54
1:A:269:ILE:HG12	1:A:299:HIS:HB3	1.88	0.54
2:B:95:ILE:CG1	2:B:130:VAL:HG22	2.37	0.54
1:A:166:GLY:O	1:A:167:CYS:SG	2.64	0.54
1:A:816:HIS:HE2	2:B:764:SER:H	1.55	0.54
3:C:18:VAL:CG2	3:C:240:VAL:HB	2.37	0.54
2:B:582:VAL:HG23	2:B:626:ILE:HB	1.89	0.54
2:B:654:ARG:H	2:B:657:HIS:CD2	2.23	0.54
3:C:263:THR:C	3:C:265:MET:N	2.61	0.54
2:B:195:CYS:SG	2:B:197:PHE:HB2	2.47	0.54
1:A:3:GLY:O	1:A:4:GLN:HB2	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:226:ASP:O	3:C:227:THR:HB	2.07	0.54
6:F:73:ALA:HA	6:F:143:PHE:CE1	2.43	0.54
6:F:90:ARG:HD3	6:F:155:LEU:HD12	1.88	0.54
1:A:939:ASP:O	1:A:943:LEU:HG	2.07	0.54
3:C:98:VAL:O	3:C:99:LEU:HD23	2.08	0.54
5:E:157:SER:C	5:E:159:ASP:N	2.60	0.54
1:A:1299:VAL:HG12	1:A:1300:LYS:H	1.72	0.54
2:B:223:VAL:HG11	2:B:381:MET:HG2	1.88	0.54
8:H:95:TYR:HB3	8:H:144:ILE:HB	1.89	0.54
2:B:746:SER:HB2	2:B:1046:PRO:HG2	1.89	0.54
1:A:1115:SER:C	1:A:1308:THR:HG22	2.28	0.54
1:A:845:LEU:HB3	1:A:848:ILE:HD12	1.88	0.54
2:B:38:PHE:HD1	2:B:811:TYR:CD2	2.24	0.54
1:A:265:LYS:CE	1:A:322:VAL:HG13	2.37	0.54
1:A:546:VAL:O	1:A:550:LEU:HG	2.08	0.54
1:A:1118:VAL:O	1:A:1305:VAL:HG13	2.08	0.54
1:A:299:HIS:C	1:A:301:ALA:H	2.11	0.54
2:B:516:ASN:ND2	2:B:516:ASN:N	2.51	0.54
2:B:1115:THR:CG2	2:B:1117:GLN:HG3	2.36	0.54
1:A:1373:ASP:HA	1:A:1376:THR:HG22	1.89	0.54
11:K:12:LEU:N	11:K:12:LEU:HD12	2.22	0.54
2:B:971:THR:OG1	3:C:61:GLU:HG3	2.07	0.54
1:A:381:THR:HG23	1:A:383:TYR:H	1.73	0.54
8:H:100:THR:HG22	8:H:101:ALA:N	2.21	0.54
8:H:89:LEU:HB3	8:H:91:ASP:OD1	2.06	0.54
1:A:814:PHE:O	1:A:817:ALA:HB3	2.08	0.54
2:B:980:PHE:HE1	2:B:990:ILE:HD11	1.73	0.54
2:B:483:LEU:HD11	2:B:491:THR:CG2	2.34	0.54
2:B:872:GLU:HA	2:B:915:THR:O	2.08	0.54
5:E:207:ARG:HH11	5:E:207:ARG:HB3	1.73	0.54
1:A:108:MET:SD	1:A:108:MET:N	2.79	0.54
8:H:139:ASN:O	8:H:140:ALA:HB2	2.08	0.54
10:J:44:TYR:HA	10:J:47:ARG:CB	2.37	0.54
2:B:847:ASP:C	2:B:849:GLY:N	2.61	0.54
1:A:847:ASP:OD1	1:A:848:ILE:HG13	2.07	0.54
1:A:534:LEU:HG	1:A:534:LEU:O	2.07	0.54
9:I:50:THR:CG2	9:I:52:ILE:HG12	2.38	0.54
1:A:244:PRO:O	1:A:247:ARG:N	2.41	0.54
1:A:353:ILE:HD13	1:A:487:MET:HE2	1.90	0.54
5:E:78:LEU:HD21	5:E:80:VAL:HG23	1.89	0.54
1:A:71:GLN:O	1:A:73:GLY:N	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:234:ILE:N	2:B:234:ILE:HD12	2.23	0.54
1:A:666:ILE:H	2:B:1026:LEU:HD22	1.72	0.54
2:B:315:LYS:N	2:B:316:PRO:HD2	2.23	0.54
1:A:567:LYS:HB3	8:H:95:TYR:CA	2.37	0.54
11:K:47:ARG:O	11:K:47:ARG:HD2	2.08	0.54
4:D:56:ARG:HD2	4:D:149:THR:OG1	2.08	0.54
3:C:181:ASP:OD2	3:C:185:LYS:N	2.41	0.54
1:A:545:GLN:O	1:A:546:VAL:C	2.46	0.54
2:B:833:TYR:N	2:B:833:TYR:HD1	2.06	0.54
1:A:1149:ALA:HB2	9:I:47:GLU:HA	1.90	0.54
5:E:55:ARG:HD2	5:E:83:CYS:O	2.08	0.54
2:B:640:VAL:O	2:B:641:GLU:C	2.46	0.54
2:B:57:TYR:CD1	2:B:57:TYR:N	2.74	0.54
1:A:1220:PHE:O	1:A:1221:LYS:HB2	2.08	0.54
6:F:96:THR:O	6:F:100:GLN:HG3	2.07	0.54
1:A:1116:LEU:HB2	1:A:1329:THR:OG1	2.08	0.54
1:A:817:ALA:O	1:A:819:GLY:N	2.41	0.54
1:A:963:ILE:HD11	1:A:1048:ASN:CB	2.33	0.54
1:A:1377:THR:O	1:A:1379:GLY:N	2.41	0.54
2:B:125:SER:HA	2:B:171:PRO:HA	1.89	0.54
2:B:1180:PHE:HB3	2:B:1191:ILE:CD1	2.38	0.54
5:E:46:TYR:CE2	5:E:58:MET:HA	2.43	0.54
3:C:8:VAL:HG12	3:C:9:LYS:N	2.23	0.54
9:I:82:GLU:HB3	9:I:104:LEU:HD12	1.90	0.54
2:B:806:THR:HA	2:B:1045:SER:OG	2.07	0.53
10:J:44:TYR:N	10:J:44:TYR:CD2	2.76	0.53
1:A:694:THR:O	1:A:698:GLN:HG3	2.08	0.53
2:B:1074:ASN:HB2	2:B:1081:LEU:HD21	1.90	0.53
1:A:353:ILE:HG21	1:A:487:MET:HG3	1.90	0.53
2:B:39:ARG:HG2	2:B:39:ARG:NH1	2.23	0.53
2:B:803:LEU:CD1	2:B:1032:SER:HB3	2.38	0.53
2:B:1068:GLY:O	2:B:1069:PHE:O	2.27	0.53
4:D:202:ILE:CG2	4:D:207:LEU:HB2	2.38	0.53
4:D:24:ALA:HA	7:G:83:LYS:O	2.08	0.53
9:I:32:CYS:SG	9:I:33:SER:N	2.81	0.53
6:F:118:LEU:O	6:F:118:LEU:HD12	2.07	0.53
1:A:1279:ILE:HD11	1:A:1316:VAL:CG2	2.37	0.53
11:K:65:HIS:HD2	11:K:67:PHE:N	1.98	0.53
5:E:22:MET:HE1	5:E:26:ARG:HH21	1.74	0.53
3:C:18:VAL:HG23	3:C:240:VAL:HB	1.90	0.53
7:G:56:ILE:O	7:G:57:GLN:HB2	2.06	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1372:VAL:O	1:A:1376:THR:HG22	2.08	0.53
1:A:262:LEU:C	1:A:264:PHE:H	2.11	0.53
1:A:567:LYS:CB	1:A:568:PRO:CD	2.85	0.53
3:C:39:ALA:CA	3:C:164:ALA:HB3	2.28	0.53
1:A:47:ARG:O	1:A:48:ALA:HB2	2.08	0.53
9:I:13:MET:O	9:I:14:LEU:HD23	2.08	0.53
2:B:763:GLN:HG2	2:B:765:PRO:CD	2.35	0.53
2:B:865:LYS:NZ	2:B:869:SER:HA	2.22	0.53
1:A:475:THR:CG2	1:A:476:SER:H	2.19	0.53
1:A:417:TYR:CD2	1:A:417:TYR:N	2.75	0.53
9:I:61:ASP:C	9:I:63:GLY:H	2.12	0.53
5:E:9:ILE:HD11	5:E:53:PRO:HD3	1.91	0.53
1:A:567:LYS:HB2	1:A:568:PRO:CD	2.39	0.53
4:D:29:LEU:HD22	7:G:82:PHE:CD2	2.44	0.53
10:J:44:TYR:HD2	10:J:44:TYR:H	1.55	0.53
1:A:528:LEU:HD23	1:A:751:SER:HA	1.91	0.53
1:A:427:GLN:HG3	1:A:430:TRP:CE2	2.43	0.53
1:A:366:VAL:CG2	1:A:460:VAL:HG22	2.39	0.53
2:B:235:SER:OG	2:B:236:HIS:CD2	2.61	0.53
10:J:3:VAL:HA	10:J:53:HIS:ND1	2.24	0.53
5:E:192:ARG:NH1	5:E:192:ARG:HG3	2.21	0.53
3:C:27:LEU:O	3:C:28:ALA:C	2.47	0.53
1:A:858:ASN:ND2	1:A:858:ASN:C	2.59	0.53
2:B:213:ILE:HD12	2:B:497:ARG:HB3	1.90	0.53
2:B:181:LEU:HD22	2:B:189:LEU:HD22	1.91	0.53
2:B:841:MET:SD	2:B:846:ILE:HD11	2.49	0.53
11:K:47:ARG:HD3	11:K:59:ALA:O	2.08	0.53
1:A:356:ASP:O	1:A:358:ASN:N	2.42	0.53
2:B:999:MET:HE2	2:B:1000:PRO:CD	2.38	0.53
1:A:503:GLN:C	1:A:504:LEU:HD12	2.29	0.53
5:E:90:VAL:HG22	5:E:90:VAL:O	2.08	0.53
1:A:306:ASN:HD21	1:A:322:VAL:HB	1.74	0.53
4:D:63:LEU:HD13	4:D:133:THR:OG1	2.08	0.53
4:D:130:LEU:C	4:D:132:GLN:N	2.54	0.53
1:A:464:PRO:HG2	1:A:465:TYR:HD1	1.73	0.53
4:D:53:SER:HB3	4:D:152:SER:CA	2.38	0.53
5:E:116:ILE:HG22	5:E:117:THR:N	2.23	0.53
2:B:1050:ILE:HG22	2:B:1051:THR:N	2.24	0.53
1:A:852:TYR:CD2	1:A:1060:PRO:HB2	2.44	0.53
1:A:567:LYS:HZ1	8:H:46:LEU:HB2	1.69	0.53
1:A:43:GLU:O	1:A:44:THR:HB	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:880:THR:HB	2:B:934:LYS:HD2	1.90	0.53
1:A:90:VAL:CG1	1:A:297:GLN:HA	2.39	0.53
7:G:62:LEU:HB3	7:G:63:PRO:CD	2.39	0.53
1:A:590:ARG:HB2	1:A:605:MET:HB3	1.90	0.53
8:H:4:THR:CA	8:H:60:ALA:HB2	2.34	0.53
3:C:166:GLU:O	3:C:167:HIS:HB2	2.08	0.53
1:A:81:PHE:CZ	2:B:1208:MET:HE2	2.44	0.53
1:A:1438:THR:HB	2:B:1144:ALA:CB	2.37	0.53
4:D:191:ALA:C	4:D:193:THR:H	2.12	0.53
1:A:767:GLN:NE2	1:A:774:ARG:HB3	2.24	0.53
2:B:281:PRO:O	2:B:283:VAL:N	2.41	0.53
1:A:1336:MET:CE	1:A:1381:LEU:HG	2.38	0.53
1:A:673:GLY:O	1:A:676:MET:HB2	2.09	0.53
2:B:493:SER:HA	2:B:751:VAL:HG21	1.89	0.53
1:A:618:GLU:O	1:A:620:LYS:N	2.41	0.53
8:H:113:ALA:HB1	8:H:125:LEU:O	2.09	0.53
1:A:867:ILE:HD12	5:E:208:TYR:CE1	2.41	0.53
10:J:44:TYR:HD2	10:J:44:TYR:N	2.07	0.53
2:B:785:TYR:CD1	2:B:785:TYR:C	2.82	0.53
1:A:1094:VAL:HG12	1:A:1095:THR:N	2.24	0.53
1:A:868:TYR:CE1	1:A:1064:VAL:CG1	2.91	0.53
2:B:555:ILE:HD11	2:B:587:HIS:CE1	2.44	0.53
1:A:548:ASN:OD1	11:K:60:ALA:HB1	2.09	0.53
1:A:577:ILE:HA	1:A:580:VAL:HG23	1.91	0.53
1:A:877:HIS:C	1:A:878:ILE:HG13	2.29	0.53
1:A:1208:THR:HG22	1:A:1210:GLY:H	1.74	0.53
1:A:1164:PRO:O	1:A:1166:ASP:N	2.43	0.52
1:A:818:MET:N	2:B:514:LEU:HD23	2.24	0.52
1:A:55:ASP:N	1:A:56:PRO:HD3	2.24	0.52
3:C:147:LEU:HD12	3:C:151:GLN:O	2.09	0.52
2:B:1107:ALA:O	2:B:1108:ARG:HG2	2.09	0.52
1:A:1322:ILE:O	1:A:1324:PRO:HD3	2.10	0.52
1:A:34:LYS:HB3	1:A:36:ARG:HE	1.73	0.52
2:B:777:ALA:HA	2:B:1095:LEU:HA	1.90	0.52
10:J:27:GLU:C	10:J:29:GLU:H	2.13	0.52
1:A:567:LYS:HB3	8:H:96:VAL:N	2.23	0.52
7:G:1:MET:SD	7:G:79:PHE:CE1	3.02	0.52
2:B:843:GLN:HB2	2:B:993:THR:HB	1.91	0.52
9:I:8:ARG:HG2	9:I:34:TYR:HE1	1.73	0.52
1:A:399:HIS:HB3	1:A:400:PRO:CD	2.30	0.52
1:A:1323:ASP:C	1:A:1325:THR:H	2.12	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:73:GLN:NE2	3:C:74:SER:H	2.07	0.52
1:A:311:GLN:O	1:A:312:PRO:C	2.47	0.52
1:A:1030:ARG:HG3	1:A:1034:GLU:OE2	2.09	0.52
2:B:496:ARG:HB3	2:B:496:ARG:HH11	1.73	0.52
2:B:810:GLU:HB2	2:B:815:ARG:HH22	1.74	0.52
1:A:207:ILE:O	1:A:208:LEU:C	2.48	0.52
1:A:364:VAL:O	1:A:364:VAL:HG13	2.08	0.52
1:A:598:LEU:O	1:A:599:SER:C	2.47	0.52
8:H:41:ASP:OD2	8:H:122:LEU:N	2.41	0.52
11:K:7:PHE:HA	11:K:10:PHE:CE2	2.45	0.52
1:A:1004:ASN:OD1	1:A:1005:GLU:N	2.42	0.52
1:A:1007:ILE:C	1:A:1009:ASN:N	2.62	0.52
2:B:526:GLU:HG2	2:B:538:ASN:HD22	1.74	0.52
4:D:33:PHE:CZ	7:G:80:LYS:CE	2.92	0.52
1:A:901:LEU:HD22	1:A:919:ILE:HG22	1.91	0.52
1:A:874:ASP:N	1:A:1058:VAL:HG22	2.24	0.52
2:B:1208:MET:O	2:B:1211:ASN:N	2.40	0.52
1:A:1120:LEU:HD13	1:A:1304:TRP:O	2.09	0.52
1:A:578:LEU:HD23	1:A:612:ILE:CD1	2.39	0.52
2:B:370:PHE:HE2	2:B:373:ARG:NH1	2.08	0.52
1:A:1365:TYR:O	1:A:1367:HIS:N	2.42	0.52
2:B:240:ILE:O	2:B:240:ILE:HG23	2.09	0.52
2:B:798:TYR:CE2	3:C:62:PHE:CE2	2.97	0.52
2:B:35:SER:HA	2:B:811:TYR:CE2	2.35	0.52
1:A:306:ASN:ND2	1:A:322:VAL:HB	2.24	0.52
2:B:615:MET:CB	2:B:626:ILE:HG12	2.39	0.52
1:A:18:GLN:CB	2:B:1215:ARG:HB2	2.40	0.52
5:E:168:TYR:HB2	5:E:170:LEU:HG	1.90	0.52
8:H:31:THR:O	8:H:31:THR:HG22	2.10	0.52
8:H:127:GLY:O	8:H:128:ASN:HB2	2.10	0.52
4:D:47:LEU:HD11	7:G:3:PHE:CD2	2.45	0.52
7:G:80:LYS:HG2	7:G:80:LYS:O	2.09	0.52
6:F:109:VAL:HG13	6:F:127:GLU:OE1	2.09	0.52
1:A:401:GLY:C	1:A:435:HIS:CD2	2.82	0.52
2:B:862:GLN:HG2	2:B:963:PHE:CD1	2.44	0.52
2:B:616:ILE:HG13	2:B:697:GLU:HA	1.92	0.52
1:A:1007:ILE:O	1:A:1009:ASN:N	2.41	0.52
1:A:346:ASP:HB3	2:B:1108:ARG:H	1.75	0.52
2:B:57:TYR:HD1	2:B:57:TYR:N	2.08	0.52
5:E:161:LYS:HD2	5:E:195:VAL:HG23	1.92	0.52
7:G:79:PHE:CZ	7:G:106:MET:HE2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:101:ILE:HD11	6:F:124:GLU:OE1	2.09	0.52
1:A:757:ASN:HA	2:B:1021:MET:SD	2.50	0.52
1:A:42:ASP:HB3	1:A:45:GLN:H	1.73	0.52
11:K:31:VAL:CG1	11:K:32:VAL:N	2.72	0.52
7:G:111:THR:HG22	7:G:113:HIS:H	1.74	0.52
1:A:1289:ARG:HD2	1:A:1303:GLU:OE2	2.10	0.52
1:A:1305:VAL:HG12	1:A:1306:LEU:N	2.25	0.52
4:D:167:LEU:O	4:D:170:THR:OG1	2.23	0.52
1:A:382:PRO:HD3	1:A:428:TYR:CE2	2.45	0.52
2:B:1107:ALA:O	2:B:1108:ARG:O	2.28	0.52
2:B:948:ILE:HG22	2:B:949:VAL:O	2.09	0.52
6:F:79:ARG:HG3	6:F:144:GLU:OE1	2.10	0.52
11:K:85:ASP:O	11:K:88:LYS:HB2	2.10	0.52
1:A:78:PRO:HA	2:B:1201:LYS:HZ1	1.74	0.52
8:H:59:ILE:O	8:H:60:ALA:HB3	2.10	0.52
1:A:871:ASP:HB3	5:E:204:THR:HG23	1.91	0.52
1:A:901:LEU:H	1:A:926:GLN:HE21	1.56	0.52
1:A:901:LEU:HD22	1:A:919:ILE:HG21	1.92	0.52
1:A:463:ILE:HB	1:A:464:PRO:HD2	1.91	0.52
1:A:93:VAL:HG22	1:A:301:ALA:HA	1.92	0.52
1:A:1141:THR:OG1	1:A:1205:LYS:HD3	2.10	0.52
5:E:14:ARG:HH21	5:E:141:VAL:HG12	1.73	0.52
1:A:628:GLY:O	1:A:632:VAL:HG23	2.10	0.52
1:A:853:ASP:OD1	1:A:855:THR:N	2.43	0.52
10:J:45:CYS:O	10:J:48:ARG:HG3	2.10	0.52
2:B:1102:LYS:O	2:B:1103:ILE:C	2.47	0.52
2:B:377:PHE:C	2:B:379:GLY:N	2.62	0.52
1:A:1325:THR:O	5:E:148:GLU:HB2	2.10	0.52
1:A:64:ASN:O	1:A:65:LEU:C	2.48	0.52
1:A:18:GLN:HB3	2:B:1215:ARG:HG3	1.91	0.52
2:B:460:ALA:HB1	2:B:466:TRP:CE3	2.45	0.52
10:J:53:HIS:HD2	10:J:54:VAL:N	2.08	0.51
10:J:1:MET:HE2	10:J:60:PHE:CE2	2.45	0.51
9:I:100:PHE:N	9:I:100:PHE:CD1	2.78	0.51
6:F:81:THR:HB	6:F:136:ARG:HH11	1.75	0.51
2:B:1132:GLU:O	2:B:1135:ARG:HB3	2.09	0.51
3:C:263:THR:O	3:C:265:MET:N	2.43	0.51
1:A:996:ASN:O	1:A:998:LEU:HD12	2.10	0.51
2:B:984:HIS:CD2	2:B:1025:HIS:HB2	2.45	0.51
4:D:210:ILE:O	4:D:214:LEU:HG	2.10	0.51
11:K:69:ALA:O	11:K:70:ARG:HB3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:482:PHE:C	1:A:484:GLY:H	2.13	0.51
1:A:58:LEU:HD22	1:A:80:HIS:O	2.11	0.51
6:F:81:THR:HG21	6:F:136:ARG:CD	2.33	0.51
3:C:215:GLU:O	3:C:217:ASP:N	2.43	0.51
7:G:26:LEU:O	7:G:27:LYS:C	2.48	0.51
9:I:102:VAL:CG1	9:I:103:CYS:H	2.24	0.51
1:A:630:ILE:HD13	1:A:646:PHE:CZ	2.45	0.51
1:A:365:GLY:O	1:A:468:PHE:HA	2.11	0.51
3:C:54:ASN:HB2	3:C:153:LEU:HD12	1.93	0.51
9:I:69:PRO:HG2	9:I:85:PHE:CD2	2.46	0.51
2:B:1007:VAL:HG22	2:B:1008:PRO:CD	2.38	0.51
1:A:1342:GLU:OE2	5:E:212:ARG:NH1	2.43	0.51
2:B:1183:LYS:CE	2:B:1183:LYS:N	2.71	0.51
2:B:637:LEU:O	2:B:690:VAL:HG13	2.10	0.51
1:A:483:ASP:O	2:B:979:LYS:HE3	2.11	0.51
1:A:18:GLN:O	2:B:1215:ARG:HG2	2.09	0.51
3:C:239:PRO:O	3:C:241:ASP:N	2.43	0.51
2:B:108:VAL:HG12	2:B:109:THR:H	1.74	0.51
1:A:89:PRO:HB2	1:A:204:THR:HG22	1.92	0.51
6:F:130:ILE:O	6:F:148:VAL:CG2	2.58	0.51
3:C:6:PRO:HB3	3:C:25:VAL:HG12	1.92	0.51
12:L:34:CYS:SG	12:L:51:CYS:SG	3.08	0.51
1:A:746:MET:CE	2:B:1018:PRO:HG2	2.40	0.51
9:I:50:THR:HG22	9:I:51:ASN:N	2.26	0.51
2:B:230:ALA:N	2:B:231:PRO:HD2	2.25	0.51
1:A:1161:THR:OG1	1:A:1239:ARG:NH2	2.44	0.51
1:A:901:LEU:CG	1:A:926:GLN:HE21	2.22	0.51
1:A:840:ARG:O	1:A:841:LEU:C	2.47	0.51
1:A:608:ILE:HB	1:A:613:ILE:HD11	1.92	0.51
7:G:117:GLN:O	7:G:119:LEU:N	2.43	0.51
2:B:900:ALA:HB3	12:L:61:THR:OG1	2.10	0.51
2:B:1110:PRO:O	2:B:1119:VAL:HG13	2.11	0.51
2:B:877:PRO:C	2:B:878:GLN:HG3	2.31	0.51
2:B:327:ARG:O	2:B:331:LEU:HD13	2.11	0.51
8:H:27:GLU:HA	8:H:38:LEU:O	2.11	0.51
3:C:168:ALA:C	3:C:170:TRP:N	2.64	0.51
1:A:50:ILE:C	1:A:52:GLY:N	2.64	0.51
2:B:879:ARG:HH11	2:B:883:LEU:CD2	2.20	0.51
1:A:817:ALA:O	1:A:818:MET:C	2.48	0.51
1:A:399:HIS:CG	1:A:400:PRO:N	2.78	0.51
2:B:1166:CYS:O	2:B:1166:CYS:SG	2.69	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:953:LEU:HD23	2:B:965:LYS:H	1.76	0.51
1:A:809:THR:H	1:A:812:GLU:HB2	1.76	0.51
2:B:492:LEU:O	2:B:495:LEU:N	2.40	0.51
7:G:150:CYS:C	7:G:151:ILE:HG13	2.31	0.51
3:C:191:TYR:HD2	3:C:201:TRP:CD1	2.28	0.51
9:I:4:PHE:HE1	9:I:6:PHE:HE2	1.58	0.51
2:B:999:MET:HB3	2:B:1007:VAL:HG21	1.92	0.51
1:A:1242:VAL:HG12	1:A:1243:VAL:N	2.17	0.51
7:G:17:PHE:CD2	7:G:17:PHE:N	2.78	0.51
1:A:535:THR:CG2	1:A:616:VAL:HA	2.40	0.51
1:A:746:MET:HE3	2:B:1018:PRO:HG2	1.92	0.51
1:A:49:LYS:HZ3	1:A:61:ILE:HG13	1.75	0.51
1:A:1334:ASP:O	1:A:1336:MET:N	2.43	0.51
1:A:418:SER:O	1:A:420:ARG:N	2.43	0.51
1:A:241:VAL:HG13	1:A:266:LEU:HD13	1.91	0.51
5:E:92:THR:O	5:E:95:THR:HB	2.11	0.51
3:C:46:ILE:HG13	3:C:72:LEU:HD11	1.93	0.51
3:C:76:ASP:O	3:C:77:ILE:C	2.48	0.51
2:B:1065:GLN:NE2	2:B:1067:ARG:N	2.53	0.51
1:A:265:LYS:HE2	1:A:322:VAL:HG13	1.93	0.51
4:D:66:ARG:O	4:D:70:PHE:HB2	2.10	0.51
1:A:134:ARG:O	1:A:138:ILE:HG13	2.11	0.51
1:A:632:VAL:O	1:A:633:VAL:C	2.48	0.51
7:G:49:LEU:HG	7:G:76:ALA:HA	1.93	0.51
1:A:263:THR:HG22	1:A:263:THR:O	2.09	0.51
1:A:37:PHE:N	1:A:37:PHE:CD1	2.79	0.51
3:C:142:VAL:N	10:J:16:ASP:HB3	2.14	0.51
1:A:244:PRO:CB	1:A:245:PRO:CD	2.89	0.51
4:D:175:PHE:HZ	7:G:85:GLU:HG3	1.75	0.51
2:B:1087:PHE:HD2	2:B:1088:GLY:H	1.58	0.51
3:C:39:ALA:HA	3:C:164:ALA:CB	2.31	0.51
2:B:1084:GLN:OE1	3:C:189:THR:CG2	2.59	0.51
3:C:22:LEU:HD13	3:C:230:MET:HE1	1.93	0.51
1:A:388:LEU:HD22	1:A:432:VAL:CG2	2.41	0.51
1:A:23:SER:O	1:A:24:PRO:C	2.47	0.51
2:B:594:ALA:HA	2:B:617:ARG:HH12	1.76	0.51
1:A:60:SER:C	1:A:61:ILE:HG13	2.30	0.51
4:D:176:GLU:C	4:D:178:ALA:N	2.63	0.51
2:B:240:ILE:CG2	2:B:254:LEU:HB3	2.41	0.51
2:B:780:VAL:HG12	2:B:782:LEU:O	2.10	0.51
7:G:1:MET:O	7:G:3:PHE:CD1	2.64	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1153:TYR:CE1	9:I:42:LEU:HD13	2.46	0.51
1:A:783:THR:HG21	1:A:815:PHE:CE2	2.46	0.51
2:B:102:VAL:HG22	2:B:112:LEU:HD22	1.93	0.51
3:C:47:ASP:CA	12:L:69:ALA:CB	2.87	0.51
8:H:82:PRO:O	8:H:84:ALA:N	2.35	0.51
12:L:40:LEU:HD22	12:L:44:ASP:CG	2.31	0.51
1:A:1157:ASP:C	1:A:1159:ARG:H	2.14	0.51
1:A:763:ALA:O	1:A:803:SER:HB3	2.11	0.51
5:E:128:PRO:HA	5:E:129:PRO:C	2.32	0.51
2:B:44:VAL:O	2:B:45:SER:C	2.48	0.51
1:A:68:GLN:O	1:A:70:CYS:N	2.43	0.50
1:A:1342:GLU:HG3	5:E:198:ILE:HD13	1.93	0.50
1:A:1063:MET:SD	1:A:1436:ILE:HG12	2.52	0.50
1:A:24:PRO:HD2	1:A:233:TRP:CD1	2.45	0.50
3:C:258:ILE:CD1	3:C:258:ILE:N	2.74	0.50
1:A:1364:ASN:O	1:A:1365:TYR:C	2.50	0.50
3:C:215:GLU:O	3:C:216:GLY:C	2.50	0.50
1:A:76:GLU:CG	1:A:76:GLU:O	2.57	0.50
2:B:364:ILE:HG22	2:B:365:THR:N	2.26	0.50
1:A:14:VAL:CG2	2:B:1216:LEU:HD13	2.40	0.50
6:F:119:ARG:NH1	6:F:119:ARG:HG3	2.26	0.50
2:B:235:SER:C	2:B:236:HIS:HD2	2.14	0.50
5:E:168:TYR:CB	5:E:170:LEU:HG	2.40	0.50
3:C:91:HIS:HD2	3:C:91:HIS:O	1.94	0.50
2:B:1174:LYS:O	2:B:1176:ASN:N	2.44	0.50
2:B:997:GLU:H	2:B:997:GLU:CD	2.13	0.50
7:G:53:ASN:HD22	7:G:53:ASN:N	2.09	0.50
2:B:973:ILE:HG23	2:B:974:PRO:HD2	1.93	0.50
4:D:134:THR:HG22	4:D:135:GLY:N	2.27	0.50
5:E:96:PHE:CZ	5:E:100:ILE:HD11	2.46	0.50
2:B:282:ILE:CD1	2:B:382:ILE:HD13	2.37	0.50
1:A:1447:GLU:OE2	7:G:23:LYS:HB2	2.12	0.50
1:A:269:ILE:CG1	1:A:299:HIS:HB3	2.42	0.50
3:C:98:VAL:HG23	3:C:122:SER:HB3	1.93	0.50
1:A:442:VAL:O	1:A:457:ALA:HA	2.12	0.50
2:B:309:GLN:OE1	9:I:52:ILE:HD11	2.11	0.50
1:A:577:ILE:O	1:A:580:VAL:HG23	2.11	0.50
1:A:218:ASP:HA	1:A:221:SER:OG	2.11	0.50
1:A:1028:THR:O	1:A:1032:LEU:HD12	2.12	0.50
7:G:117:GLN:C	7:G:119:LEU:H	2.15	0.50
1:A:885:THR:O	1:A:940:ARG:HD2	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1039:GLY:HA2	10:J:51:LEU:HD21	1.91	0.50
1:A:909:ASP:O	1:A:911:SER:N	2.45	0.50
1:A:823:GLY:O	1:A:825:ILE:N	2.44	0.50
1:A:829:VAL:C	1:A:831:THR:H	2.14	0.50
2:B:1022:THR:HG23	2:B:1022:THR:O	2.10	0.50
3:C:145:CYS:HA	10:J:2:ILE:HD11	1.92	0.50
2:B:179:CYS:SG	2:B:181:LEU:HB2	2.52	0.50
2:B:300:HIS:CE1	2:B:376:PHE:CE1	2.99	0.50
7:G:26:LEU:O	7:G:29:LYS:N	2.43	0.50
2:B:360:PHE:CD2	2:B:360:PHE:C	2.85	0.50
2:B:758:PHE:CE1	2:B:1027:ILE:CG2	2.95	0.50
1:A:881:GLN:NE2	1:A:958:VAL:O	2.38	0.50
1:A:406:ILE:HG13	1:A:431:LYS:HB2	1.93	0.50
1:A:784:LEU:HB3	1:A:785:PRO:HD2	1.94	0.50
1:A:367:PRO:HA	1:A:463:ILE:O	2.10	0.50
4:D:56:ARG:NH2	4:D:57:LEU:HD21	2.26	0.50
1:A:283:GLY:O	1:A:285:PRO:HD3	2.10	0.50
2:B:1034:VAL:HG12	2:B:1035:ALA:H	1.74	0.50
2:B:765:PRO:O	2:B:768:THR:N	2.44	0.50
1:A:1120:LEU:CD1	1:A:1120:LEU:H	2.24	0.50
2:B:311:LEU:O	2:B:312:GLU:C	2.48	0.50
2:B:63:ILE:HD12	2:B:421:PHE:CE2	2.46	0.50
2:B:435:THR:CG2	2:B:437:GLU:HB2	2.41	0.50
7:G:80:LYS:O	7:G:82:PHE:CE1	2.65	0.50
2:B:882:THR:O	2:B:883:LEU:HB2	2.11	0.50
1:A:399:HIS:CB	1:A:400:PRO:CD	2.88	0.50
4:D:64:VAL:C	4:D:66:ARG:H	2.14	0.50
9:I:55:THR:HG22	9:I:58:VAL:HG21	1.92	0.50
10:J:23:ASN:C	10:J:25:LEU:N	2.64	0.50
1:A:1209:MET:CE	1:A:1236:LEU:HB3	2.42	0.50
1:A:244:PRO:HB2	1:A:245:PRO:CD	2.41	0.50
1:A:857:ARG:NH1	6:F:139:PRO:HB2	2.27	0.50
3:C:22:LEU:HD13	3:C:230:MET:HE3	1.93	0.50
1:A:874:ASP:CA	1:A:1058:VAL:HG22	2.42	0.50
1:A:443:LEU:O	1:A:489:LEU:HD12	2.12	0.50
2:B:552:MET:C	2:B:554:ILE:H	2.15	0.50
1:A:1005:GLU:O	1:A:1009:ASN:HB2	2.12	0.50
1:A:738:LYS:C	1:A:740:LEU:H	2.15	0.50
2:B:806:THR:CG2	2:B:808:ALA:HB3	2.41	0.50
9:I:100:PHE:N	9:I:100:PHE:HD1	2.09	0.50
2:B:642:ASP:CB	2:B:649:LYS:HA	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:111:THR:HG22	9:I:113:ASP:N	2.27	0.50
1:A:215:SER:HB3	1:A:218:ASP:OD2	2.12	0.50
12:L:27:LEU:HD13	12:L:37:LYS:HE2	1.94	0.50
1:A:416:ARG:C	1:A:417:TYR:CD2	2.85	0.50
2:B:1039:GLY:HA2	10:J:51:LEU:CD2	2.42	0.50
2:B:890:TYR:O	2:B:892:LYS:N	2.45	0.50
2:B:558:LEU:C	2:B:560:GLU:H	2.15	0.50
7:G:81:PRO:HA	7:G:85:GLU:OE1	2.12	0.50
1:A:466:SER:HB3	2:B:1103:ILE:HG12	1.93	0.50
2:B:642:ASP:CA	2:B:649:LYS:HA	2.41	0.50
1:A:1319:VAL:HG13	1:A:1320:PRO:HD2	1.94	0.50
2:B:806:THR:HG22	2:B:808:ALA:HB3	1.94	0.49
3:C:168:ALA:C	3:C:170:TRP:H	2.16	0.49
3:C:18:VAL:O	3:C:20:PHE:HD2	1.95	0.49
2:B:521:LEU:HD13	2:B:633:VAL:HB	1.93	0.49
12:L:48:CYS:SG	12:L:49:LYS:N	2.85	0.49
1:A:794:PRO:C	1:A:796:SER:H	2.15	0.49
2:B:284:ILE:HG12	2:B:324:ILE:HD12	1.92	0.49
2:B:1006:ILE:HD13	10:J:44:TYR:HE2	1.72	0.49
2:B:579:ARG:CB	2:B:586:TRP:HE1	2.24	0.49
1:A:1410:PHE:HA	2:B:1212:ILE:CD1	2.41	0.49
2:B:603:LEU:HB3	2:B:609:ILE:HG13	1.92	0.49
2:B:995:ARG:NH1	3:C:165:LYS:HG2	2.27	0.49
1:A:1130:GLN:O	1:A:1134:ILE:HG13	2.12	0.49
1:A:512:VAL:HA	1:A:519:PRO:HA	1.93	0.49
10:J:32:GLU:O	10:J:34:THR:N	2.44	0.49
1:A:58:LEU:O	1:A:59:GLY:O	2.30	0.49
8:H:102:TYR:N	8:H:102:TYR:CD2	2.80	0.49
8:H:27:GLU:HG2	8:H:39:THR:HG23	1.93	0.49
8:H:84:ALA:C	8:H:86:ASP:H	2.15	0.49
5:E:22:MET:CE	5:E:26:ARG:NH2	2.74	0.49
3:C:243:VAL:HG12	3:C:243:VAL:O	2.11	0.49
1:A:1420:ASP:O	1:A:1421:CYS:HB2	2.12	0.49
1:A:504:LEU:HD11	6:F:91:ALA:CB	2.41	0.49
3:C:140:ASN:O	3:C:141:GLY:O	2.30	0.49
1:A:982:THR:HB	1:A:985:ASP:H	1.76	0.49
2:B:299:GLU:HB3	2:B:571:PRO:HG3	1.94	0.49
1:A:316:GLN:O	1:A:317:LYS:C	2.50	0.49
2:B:550:ASP:OD1	2:B:551:PRO:HD2	2.13	0.49
2:B:1002:THR:HG21	2:B:1006:ILE:HD12	1.93	0.49
10:J:7:CYS:SG	10:J:49:MET:HE3	2.52	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:783:THR:HG22	1:A:784:LEU:HG	1.93	0.49
2:B:980:PHE:HE2	2:B:1094:ARG:CB	2.24	0.49
1:A:873:MET:C	1:A:1058:VAL:CG2	2.80	0.49
1:A:873:MET:HG2	1:A:957:PRO:HB3	1.95	0.49
4:D:153:ARG:C	4:D:154:PHE:CD1	2.86	0.49
1:A:402:ALA:CB	1:A:434:ARG:HA	2.43	0.49
1:A:1004:ASN:O	1:A:1008:GLN:HB2	2.12	0.49
1:A:541:ILE:HD13	1:A:549:MET:HE3	1.94	0.49
1:A:852:TYR:HA	1:A:1060:PRO:HB3	1.94	0.49
2:B:496:ARG:NH1	2:B:539:LEU:HB2	2.27	0.49
3:C:90:ASP:O	3:C:91:HIS:CB	2.60	0.49
2:B:773:MET:C	2:B:775:LYS:H	2.13	0.49
1:A:84:ILE:HD11	1:A:270:LEU:CD1	2.34	0.49
3:C:99:LEU:HD23	3:C:99:LEU:N	2.26	0.49
1:A:311:GLN:CB	1:A:312:PRO:HD3	2.42	0.49
1:A:1349:TYR:HB2	1:A:1372:VAL:HG21	1.95	0.49
1:A:877:HIS:O	1:A:878:ILE:CG1	2.60	0.49
2:B:1174:LYS:O	2:B:1176:ASN:HB2	2.11	0.49
1:A:317:LYS:O	1:A:318:SER:CB	2.60	0.49
1:A:573:SER:O	1:A:576:GLN:HB2	2.12	0.49
1:A:116:ASP:O	1:A:118:HIS:N	2.45	0.49
1:A:765:VAL:HG12	1:A:766:GLY:N	2.26	0.49
2:B:199:MET:N	2:B:199:MET:SD	2.79	0.49
3:C:66:ARG:NH2	10:J:3:VAL:O	2.45	0.49
8:H:41:ASP:O	8:H:42:ILE:HG13	2.13	0.49
9:I:99:LEU:C	9:I:100:PHE:HD1	2.16	0.49
2:B:916:THR:O	2:B:935:ARG:HG3	2.12	0.49
1:A:903:ASN:C	1:A:903:ASN:ND2	2.64	0.49
1:A:903:ASN:ND2	1:A:905:ASP:H	2.09	0.49
1:A:1094:VAL:HG13	1:A:1113:THR:CG2	2.37	0.49
3:C:30:ALA:O	3:C:33:LEU:HB3	2.11	0.49
2:B:728:ARG:NH1	2:B:1047:PHE:HB3	2.26	0.49
1:A:61:ILE:HG22	1:A:62:ASP:H	1.78	0.49
3:C:254:LYS:C	3:C:256:ALA:H	2.15	0.49
1:A:1127:ASP:HB3	1:A:1130:GLN:HB3	1.92	0.49
7:G:80:LYS:HD3	7:G:80:LYS:H	1.77	0.49
1:A:845:LEU:O	1:A:846:GLU:C	2.49	0.49
1:A:340:LEU:HD21	2:B:1200:ALA:CA	2.43	0.49
1:A:1120:LEU:CD1	1:A:1120:LEU:N	2.76	0.49
12:L:49:LYS:O	12:L:50:ASP:CB	2.60	0.49
1:A:311:GLN:CB	1:A:312:PRO:CD	2.91	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:545:GLN:O	1:A:548:ASN:N	2.45	0.49
1:A:414:ASP:OD1	1:A:416:ARG:HG3	2.11	0.49
1:A:540:PHE:HB3	1:A:571:LEU:HD23	1.95	0.49
5:E:153:HIS:HB3	5:E:196:VAL:HG11	1.94	0.49
1:A:622:VAL:HG22	1:A:622:VAL:O	2.13	0.49
2:B:1197:PRO:HG2	2:B:1200:ALA:HB3	1.92	0.49
1:A:299:HIS:O	1:A:301:ALA:N	2.46	0.49
2:B:360:PHE:O	2:B:361:LEU:C	2.51	0.49
1:A:262:LEU:C	1:A:264:PHE:N	2.66	0.49
1:A:1053:PHE:C	1:A:1055:ARG:H	2.15	0.49
2:B:773:MET:C	2:B:775:LYS:N	2.65	0.49
1:A:1280:GLU:O	1:A:1281:ARG:O	2.30	0.49
2:B:210:LYS:HG3	2:B:461:LEU:O	2.13	0.49
1:A:244:PRO:HG2	1:A:245:PRO:CD	2.43	0.49
1:A:244:PRO:O	1:A:246:VAL:N	2.46	0.49
1:A:854:ASN:CB	1:A:1000:LEU:HD21	2.43	0.49
2:B:287:ARG:HG2	2:B:292:ILE:HA	1.93	0.49
1:A:21:LEU:HD11	1:A:1414:ALA:HA	1.95	0.49
2:B:831:SER:CB	2:B:994:TYR:OH	2.60	0.49
1:A:981:LEU:CD2	1:A:1039:LYS:HA	2.43	0.49
10:J:27:GLU:O	10:J:29:GLU:N	2.45	0.49
1:A:1076:ALA:HA	1:A:1079:MET:CE	2.41	0.49
1:A:1195:LEU:HD11	1:A:1267:MET:HE3	1.95	0.49
1:A:1388:GLY:O	1:A:1390:ASN:N	2.46	0.49
2:B:734:HIS:O	2:B:735:ALA:HB2	2.12	0.49
1:A:1327:ILE:HG22	5:E:147:HIS:CE1	2.48	0.49
2:B:189:LEU:O	2:B:192:LEU:HB2	2.13	0.49
12:L:34:CYS:O	12:L:35:SER:C	2.52	0.49
1:A:450:LEU:H	1:A:450:LEU:HD12	1.78	0.49
3:C:163:ILE:O	3:C:165:LYS:N	2.45	0.49
7:G:9:LEU:HG	7:G:10:ASN:N	2.27	0.49
8:H:99:GLY:HA3	8:H:118:PHE:HA	1.95	0.49
5:E:169:ARG:HH12	6:F:74:ILE:HD11	1.78	0.49
1:A:629:LEU:O	1:A:633:VAL:HG23	2.12	0.49
5:E:202:SER:HB3	5:E:205:SER:O	2.12	0.48
2:B:563:MET:HA	2:B:589:VAL:O	2.13	0.48
2:B:1034:VAL:O	2:B:1036:ALA:N	2.46	0.48
2:B:872:GLU:CD	2:B:914:LYS:HE2	2.33	0.48
11:K:108:GLU:O	11:K:112:GLN:HG2	2.12	0.48
2:B:251:ILE:HG22	2:B:251:ILE:O	2.13	0.48
1:A:1045:VAL:O	1:A:1049:ILE:HG13	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:335:ARG:CA	1:A:339:ASN:HB2	2.40	0.48
2:B:653:VAL:HG23	2:B:689:LEU:HB3	1.94	0.48
2:B:361:LEU:N	2:B:362:PRO:CD	2.75	0.48
12:L:46:VAL:CG1	12:L:56:LEU:HD12	2.43	0.48
3:C:147:LEU:HD23	3:C:147:LEU:N	2.28	0.48
2:B:950:ASP:O	2:B:951:GLN:HB2	2.14	0.48
1:A:82:GLY:O	1:A:241:VAL:N	2.42	0.48
1:A:552:TRP:O	1:A:554:PRO:HD3	2.13	0.48
3:C:167:HIS:CD2	3:C:168:ALA:H	2.31	0.48
2:B:515:HIS:CD2	2:B:517:THR:HG23	2.48	0.48
2:B:38:PHE:CD1	2:B:811:TYR:CD2	3.01	0.48
3:C:99:LEU:HD12	3:C:118:LEU:HD13	1.94	0.48
2:B:642:ASP:CB	2:B:649:LYS:HG3	2.42	0.48
1:A:1120:LEU:HD12	1:A:1120:LEU:H	1.78	0.48
4:D:192:LYS:HB3	4:D:192:LYS:NZ	2.28	0.48
10:J:32:GLU:O	10:J:35:ALA:N	2.47	0.48
2:B:1040:ASN:O	2:B:1041:GLU:C	2.50	0.48
1:A:369:SER:CB	11:K:2:ASN:OD1	2.60	0.48
2:B:744:HIS:HD2	2:B:746:SER:OG	1.95	0.48
9:I:85:PHE:CD1	9:I:99:LEU:HD13	2.45	0.48
9:I:13:MET:HG3	9:I:14:LEU:H	1.74	0.48
1:A:300:VAL:O	1:A:300:VAL:HG12	2.12	0.48
1:A:1369:ALA:O	1:A:1373:ASP:OD2	2.31	0.48
7:G:96:GLN:HA	7:G:121:PHE:CE2	2.48	0.48
7:G:43:GLY:CA	7:G:80:LYS:HB3	2.42	0.48
1:A:785:PRO:HG2	1:A:786:HIS:HD2	1.78	0.48
1:A:40:THR:HG22	1:A:41:MET:CG	2.32	0.48
1:A:41:MET:HB3	1:A:48:ALA:O	2.13	0.48
1:A:353:ILE:HG21	1:A:487:MET:CE	2.37	0.48
3:C:25:VAL:HG23	3:C:228:PHE:CE1	2.48	0.48
1:A:341:MET:CE	2:B:1135:ARG:NH1	2.76	0.48
1:A:340:LEU:HD13	1:A:1429:ILE:CG2	2.38	0.48
12:L:52:GLY:O	12:L:53:HIS:C	2.52	0.48
5:E:124:VAL:HA	5:E:132:ILE:HD12	1.95	0.48
1:A:683:ILE:HD13	1:A:801:GLU:HG3	1.95	0.48
1:A:16:GLU:HB3	1:A:1418:LEU:HD11	1.95	0.48
1:A:977:LYS:HB3	1:A:978:PRO:HD2	1.95	0.48
1:A:174:ILE:HG23	1:A:182:VAL:O	2.13	0.48
3:C:255:VAL:O	3:C:255:VAL:HG12	2.14	0.48
6:F:124:GLU:HB3	6:F:130:ILE:HG12	1.94	0.48
6:F:89:GLU:HB3	6:F:134:ILE:HD13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:24:ASP:OD1	11:K:26:LYS:HB2	2.14	0.48
5:E:22:MET:HE3	5:E:26:ARG:HH21	1.77	0.48
1:A:351:THR:HG21	2:B:1103:ILE:HG13	1.95	0.48
2:B:842:ASN:ND2	2:B:845:SER:OG	2.44	0.48
12:L:46:VAL:O	12:L:46:VAL:HG12	2.14	0.48
5:E:13:TRP:O	5:E:16:PHE:HB3	2.14	0.48
1:A:1340:GLY:O	1:A:1343:ALA:N	2.43	0.48
2:B:180:TYR:CD1	2:B:180:TYR:N	2.82	0.48
1:A:277:GLU:C	1:A:279:LEU:H	2.17	0.48
1:A:357:PRO:HD2	2:B:833:TYR:CE1	2.48	0.48
2:B:223:VAL:CG1	2:B:381:MET:HG2	2.42	0.48
1:A:626:ASN:O	1:A:628:GLY:N	2.44	0.48
4:D:20:GLU:O	4:D:21:GLU:O	2.32	0.48
1:A:551:TYR:CE2	11:K:62:LYS:HE2	2.49	0.48
4:D:35:LEU:N	4:D:35:LEU:HD12	2.29	0.48
10:J:16:ASP:O	10:J:18:TRP:N	2.47	0.48
7:G:1:MET:CE	7:G:1:MET:O	2.61	0.48
2:B:542:MET:HG2	2:B:747:MET:HB3	1.96	0.48
2:B:520:GLY:HA2	2:B:748:ILE:HG22	1.95	0.48
2:B:847:ASP:O	2:B:849:GLY:N	2.47	0.48
1:A:38:PRO:HA	1:A:270:LEU:HD23	1.95	0.48
2:B:125:SER:HA	2:B:172:ILE:H	1.78	0.48
2:B:333:PHE:C	2:B:334:ILE:HG13	2.34	0.48
3:C:91:HIS:CD2	3:C:91:HIS:O	2.67	0.48
3:C:105:GLY:O	3:C:149:LYS:O	2.32	0.48
3:C:11:ARG:HD3	3:C:209:TYR:CE2	2.48	0.48
1:A:960:ILE:O	1:A:961:ARG:C	2.50	0.48
1:A:78:PRO:HA	2:B:1201:LYS:HZ2	1.77	0.48
1:A:1220:PHE:CD1	1:A:1224:LEU:HD23	2.49	0.48
1:A:901:LEU:HG	1:A:926:GLN:NE2	2.25	0.48
8:H:84:ALA:C	8:H:86:ASP:N	2.67	0.48
1:A:68:GLN:C	1:A:70:CYS:N	2.65	0.48
2:B:803:LEU:HD12	2:B:1032:SER:HB3	1.95	0.48
2:B:893:LEU:HD11	2:B:910:VAL:CG1	2.44	0.48
2:B:616:ILE:HG12	2:B:697:GLU:HA	1.94	0.48
2:B:593:PRO:HG2	2:B:617:ARG:CZ	2.43	0.48
1:A:541:ILE:HG21	1:A:549:MET:HE3	1.94	0.48
2:B:205:ILE:O	2:B:206:ASN:C	2.52	0.48
3:C:254:LYS:C	3:C:256:ALA:N	2.67	0.48
1:A:166:GLY:O	1:A:167:CYS:CB	2.62	0.48
1:A:1073:GLY:O	1:A:1076:ALA:HB3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:387:LEU:O	2:B:392:ARG:HB2	2.13	0.48
2:B:459:TYR:CD2	2:B:459:TYR:C	2.86	0.48
1:A:53:LEU:CD2	1:A:54:ASN:N	2.61	0.48
1:A:567:LYS:HD2	1:A:568:PRO:HD2	1.93	0.48
1:A:1327:ILE:HG22	5:E:147:HIS:HE1	1.77	0.48
3:C:77:ILE:CG2	3:C:161:LYS:HE3	2.39	0.48
7:G:13:LEU:CD2	7:G:17:PHE:HB2	2.38	0.48
2:B:954:VAL:O	12:L:55:ILE:O	2.31	0.48
6:F:77:ASP:C	6:F:79:ARG:N	2.67	0.48
1:A:381:THR:CG2	1:A:383:TYR:H	2.27	0.48
2:B:461:LEU:HD12	2:B:461:LEU:N	2.29	0.48
3:C:209:TYR:H	3:C:209:TYR:HD1	1.60	0.48
2:B:1187:ASN:HD21	2:B:1190:ASP:HB3	1.79	0.48
4:D:138:ASN:OD1	4:D:141:LEU:HB2	2.13	0.48
1:A:929:LEU:HD23	1:A:983:ILE:HG21	1.96	0.48
1:A:1001:ARG:O	1:A:1002:GLY:O	2.31	0.48
1:A:62:ASP:HB3	1:A:64:ASN:ND2	2.28	0.48
1:A:332:LYS:O	1:A:334:GLY:N	2.46	0.48
1:A:1451:VAL:C	1:A:1453:TYR:H	2.15	0.48
1:A:420:ARG:O	1:A:421:ALA:C	2.51	0.48
3:C:194:GLU:O	3:C:195:GLN:HG3	2.14	0.48
7:G:91:VAL:HG12	7:G:92:VAL:N	2.28	0.47
6:F:99:LEU:HD21	7:G:64:THR:O	2.14	0.47
2:B:844:SER:O	2:B:847:ASP:HB2	2.14	0.47
4:D:137:ASN:HD22	4:D:137:ASN:C	2.17	0.47
2:B:234:ILE:H	2:B:234:ILE:HD12	1.79	0.47
7:G:26:LEU:HD12	7:G:56:ILE:HD13	1.95	0.47
3:C:35:ARG:NH1	11:K:41:THR:H	2.12	0.47
1:A:730:GLY:C	1:A:732:LEU:H	2.17	0.47
11:K:93:SER:O	11:K:97:LYS:HG3	2.14	0.47
7:G:77:VAL:O	7:G:77:VAL:HG12	2.14	0.47
10:J:2:ILE:HG12	10:J:57:ILE:HD12	1.95	0.47
8:H:58:THR:HG22	8:H:59:ILE:H	1.79	0.47
2:B:806:THR:HG22	2:B:808:ALA:CB	2.44	0.47
1:A:863:VAL:HG11	1:A:866:PHE:CE2	2.49	0.47
6:F:132:LEU:N	6:F:132:LEU:HD23	2.28	0.47
3:C:214:ASN:HB3	3:C:217:ASP:OD2	2.15	0.47
10:J:64:ASN:CB	10:J:65:PRO:CD	2.88	0.47
2:B:864:LYS:N	2:B:872:GLU:OE1	2.46	0.47
1:A:326:ARG:HH22	1:A:1407:GLU:HG3	1.77	0.47
1:A:236:LEU:HD23	1:A:236:LEU:N	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:143:ILE:CG2	7:G:144:ARG:N	2.75	0.47
3:C:107:SER:C	3:C:109:SER:H	2.17	0.47
7:G:44:TYR:O	7:G:78:VAL:HA	2.14	0.47
1:A:1101:LEU:O	1:A:1101:LEU:HD12	2.14	0.47
1:A:1446:ASP:HB2	6:F:133:VAL:CG2	2.44	0.47
8:H:91:ASP:O	8:H:93:TYR:N	2.46	0.47
6:F:127:GLU:O	6:F:129:LYS:HG3	2.14	0.47
1:A:35:ILE:CG2	1:A:84:ILE:HD12	2.44	0.47
1:A:768:GLN:NE2	1:A:816:HIS:ND1	2.62	0.47
1:A:741:ASN:ND2	1:A:743:VAL:HB	2.24	0.47
1:A:1291:VAL:HG13	1:A:1292:PRO:N	2.29	0.47
2:B:27:ALA:O	2:B:29:ASP:N	2.47	0.47
2:B:903:VAL:HG12	2:B:904:ARG:N	2.28	0.47
1:A:1333:ILE:HG22	1:A:1334:ASP:N	2.29	0.47
2:B:750:GLY:O	2:B:751:VAL:C	2.53	0.47
5:E:161:LYS:C	5:E:163:GLU:H	2.17	0.47
5:E:161:LYS:C	5:E:163:GLU:N	2.68	0.47
2:B:523:CYS:SG	2:B:524:PRO:HD2	2.54	0.47
1:A:1162:VAL:HG12	1:A:1162:VAL:O	2.14	0.47
3:C:70:ILE:HD11	3:C:144:ILE:HG12	1.97	0.47
8:H:58:THR:HB	8:H:143:LEU:HD13	1.97	0.47
1:A:563:PRO:HG3	1:A:572:TRP:CE2	2.49	0.47
3:C:46:ILE:HG23	3:C:157:CYS:HB3	1.96	0.47
1:A:921:GLY:O	1:A:922:ASP:C	2.53	0.47
1:A:93:VAL:CG1	1:A:301:ALA:HB1	2.37	0.47
1:A:1431:GLY:HA3	2:B:1152:MET:SD	2.55	0.47
1:A:444:PHE:HB2	1:A:458:HIS:HD2	1.80	0.47
1:A:1006:ILE:HD12	5:E:163:GLU:HG3	1.95	0.47
2:B:882:THR:HG21	2:B:935:ARG:HA	1.95	0.47
3:C:238:ILE:HD11	3:C:246:ARG:NH1	2.30	0.47
1:A:341:MET:HE1	1:A:843:LYS:HZ3	1.79	0.47
1:A:92:HIS:HB2	1:A:236:LEU:HD21	1.96	0.47
1:A:95:PHE:O	1:A:96:ILE:C	2.53	0.47
2:B:373:ARG:CG	2:B:566:LEU:HD23	2.45	0.47
5:E:157:SER:HG	5:E:160:GLU:HG3	1.78	0.47
1:A:167:CYS:O	1:A:167:CYS:SG	2.72	0.47
6:F:140:ASP:C	6:F:140:ASP:OD1	2.52	0.47
4:D:40:HIS:CE1	4:D:41:GLN:HG3	2.49	0.47
2:B:745:PRO:C	2:B:747:MET:N	2.68	0.47
1:A:1441:PHE:HB2	6:F:135:ARG:O	2.15	0.47
2:B:918:ILE:HD12	2:B:935:ARG:HD3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:242:GLN:C	3:C:244:VAL:N	2.68	0.47
10:J:13:VAL:C	10:J:14:VAL:HG23	2.34	0.47
1:A:299:HIS:C	1:A:301:ALA:N	2.67	0.47
1:A:730:GLY:C	1:A:732:LEU:N	2.67	0.47
1:A:1227:ILE:CG2	1:A:1228:TRP:N	2.78	0.47
1:A:1127:ASP:HB3	1:A:1130:GLN:HB2	1.96	0.47
1:A:1265:ASN:O	1:A:1268:LEU:N	2.41	0.47
8:H:33:GLN:C	8:H:35:GLN:H	2.18	0.47
2:B:1160:VAL:HG11	2:B:1169:MET:SD	2.55	0.47
10:J:16:ASP:OD1	10:J:17:LYS:N	2.42	0.47
8:H:89:LEU:C	8:H:91:ASP:N	2.68	0.47
8:H:138:GLU:O	8:H:139:ASN:C	2.52	0.47
10:J:47:ARG:HG2	10:J:47:ARG:NH1	2.29	0.47
10:J:48:ARG:HD2	10:J:49:MET:N	2.29	0.47
1:A:547:LEU:HD22	11:K:58:PHE:HD1	1.78	0.47
2:B:1084:GLN:C	2:B:1085:ILE:HD12	2.34	0.47
3:C:6:PRO:HB3	3:C:25:VAL:CG1	2.45	0.47
1:A:872:GLY:O	1:A:1058:VAL:HG23	2.13	0.47
1:A:496:GLU:O	1:A:499:ALA:HB3	2.15	0.47
2:B:653:VAL:HG22	2:B:689:LEU:HB3	1.95	0.47
9:I:111:THR:CG2	9:I:112:SER:N	2.77	0.47
3:C:183:TRP:O	3:C:185:LYS:N	2.48	0.47
2:B:205:ILE:HG22	2:B:206:ASN:N	2.30	0.47
1:A:1451:VAL:O	1:A:1454:MET:HG2	2.15	0.47
2:B:225:VAL:HA	2:B:237:VAL:O	2.14	0.47
9:I:61:ASP:O	9:I:63:GLY:N	2.47	0.47
1:A:898:ARG:HB2	1:A:933:TYR:CE1	2.49	0.47
2:B:383:ASN:O	2:B:384:ARG:C	2.53	0.47
2:B:1214:PRO:HG2	2:B:1214:PRO:O	2.14	0.47
2:B:305:VAL:O	2:B:305:VAL:HG12	2.15	0.47
1:A:648:ASN:O	1:A:649:ILE:C	2.53	0.47
10:J:1:MET:HE2	10:J:60:PHE:HE2	1.80	0.47
1:A:567:LYS:HD2	1:A:568:PRO:CD	2.45	0.47
1:A:590:ARG:CG	1:A:590:ARG:HH11	2.18	0.47
5:E:22:MET:HE3	5:E:26:ARG:NH2	2.30	0.47
9:I:75:CYS:SG	9:I:80:SER:N	2.85	0.47
4:D:64:VAL:C	4:D:66:ARG:N	2.67	0.47
2:B:333:PHE:O	2:B:334:ILE:CG1	2.61	0.47
7:G:143:ILE:HG22	7:G:144:ARG:H	1.76	0.47
2:B:230:ALA:N	2:B:231:PRO:CD	2.77	0.47
1:A:1261:LYS:HA	1:A:1264:GLU:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:195:ILE:HG22	4:D:198:LEU:HG	1.95	0.47
1:A:279:LEU:O	1:A:284:ALA:HB2	2.15	0.47
3:C:89:GLU:O	3:C:90:ASP:HB3	2.15	0.47
1:A:699:ALA:HB3	1:A:701:LEU:HG	1.95	0.47
5:E:145:THR:HG21	5:E:187:TYR:CE2	2.50	0.47
4:D:206:GLU:C	4:D:208:GLU:N	2.68	0.47
2:B:455:SER:O	2:B:456:GLY:C	2.51	0.47
8:H:111:LEU:HD23	8:H:127:GLY:O	2.15	0.47
11:K:59:ALA:HA	11:K:74:ARG:O	2.15	0.47
1:A:402:ALA:HB1	1:A:433:GLU:O	2.15	0.47
2:B:552:MET:HA	2:B:555:ILE:HB	1.96	0.47
5:E:157:SER:O	5:E:159:ASP:N	2.48	0.47
5:E:55:ARG:C	5:E:57:MET:H	2.17	0.47
3:C:90:ASP:OD1	3:C:90:ASP:O	2.33	0.47
2:B:1187:ASN:OD1	2:B:1188:LYS:N	2.40	0.47
1:A:553:VAL:HG22	1:A:652:VAL:CG2	2.44	0.47
11:K:52:ASN:O	11:K:54:ARG:N	2.48	0.47
3:C:133:ILE:HD12	3:C:237:SER:HA	1.96	0.47
10:J:56:LEU:O	10:J:59:LYS:N	2.45	0.47
3:C:77:ILE:O	3:C:79:GLN:N	2.46	0.47
5:E:135:PHE:CD2	5:E:140:LEU:HD21	2.37	0.47
7:G:13:LEU:O	7:G:67:SER:HA	2.15	0.47
2:B:865:LYS:HE2	2:B:871:THR:OG1	2.15	0.47
1:A:326:ARG:HG2	1:A:327:ALA:N	2.29	0.47
2:B:1050:ILE:CG2	2:B:1051:THR:N	2.78	0.47
1:A:2:VAL:CG2	2:B:1158:PHE:HA	2.45	0.47
1:A:347:PHE:H	2:B:1107:ALA:HA	1.80	0.47
2:B:298:LEU:HD13	2:B:314:LEU:HD13	1.97	0.47
3:C:253:LYS:O	3:C:256:ALA:HB3	2.15	0.47
5:E:55:ARG:C	5:E:57:MET:N	2.69	0.47
2:B:558:LEU:O	2:B:560:GLU:N	2.47	0.47
1:A:984:LYS:O	1:A:985:ASP:C	2.54	0.47
5:E:153:HIS:HB3	5:E:196:VAL:CG1	2.44	0.47
7:G:121:PHE:HB2	7:G:130:TYR:CE2	2.50	0.47
8:H:15:VAL:HG22	8:H:26:ILE:HD11	1.96	0.47
6:F:128:LYS:HD3	6:F:149:GLU:O	2.15	0.47
9:I:85:PHE:N	9:I:85:PHE:CD2	2.60	0.46
6:F:132:LEU:O	6:F:148:VAL:HG22	2.15	0.46
6:F:99:LEU:C	6:F:99:LEU:HD12	2.36	0.46
2:B:582:VAL:HG12	2:B:587:HIS:NE2	2.30	0.46
1:A:500:GLU:OE2	1:A:1438:THR:HG21	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1017:ILE:CB	2:B:1018:PRO:HD3	2.44	0.46
1:A:510:GLN:HA	1:A:510:GLN:OE1	2.14	0.46
4:D:38:ILE:HG22	4:D:39:ASN:O	2.14	0.46
9:I:56:ALA:O	9:I:57:GLY:O	2.34	0.46
7:G:14:HIS:HD2	7:G:16:SER:CB	2.28	0.46
10:J:8:PHE:H	10:J:49:MET:CE	2.28	0.46
2:B:376:PHE:HE2	2:B:569:TYR:HD2	1.62	0.46
4:D:154:PHE:HB2	4:D:160:VAL:HG22	1.97	0.46
1:A:1435:PRO:O	1:A:1436:ILE:HG13	2.15	0.46
1:A:105:CYS:O	1:A:114:LEU:HG	2.14	0.46
1:A:1147:THR:HG22	9:I:48:LEU:HD12	1.97	0.46
3:C:133:ILE:CD1	3:C:237:SER:HA	2.45	0.46
2:B:681:TRP:O	2:B:683:SER:N	2.49	0.46
1:A:1222:ASN:O	1:A:1223:ASP:HB3	2.14	0.46
4:D:47:LEU:CD1	4:D:48:ILE:N	2.77	0.46
1:A:1444:MET:HE1	6:F:135:ARG:HB2	1.97	0.46
1:A:761:MET:HA	1:A:804:TYR:HB2	1.97	0.46
1:A:335:ARG:O	1:A:336:ILE:C	2.52	0.46
2:B:39:ARG:HH21	2:B:665:GLU:CG	2.26	0.46
5:E:124:VAL:CG1	5:E:132:ILE:HB	2.43	0.46
3:C:179:GLU:O	3:C:180:TYR:HB3	2.14	0.46
2:B:758:PHE:HE1	2:B:1027:ILE:HG22	1.77	0.46
2:B:756:ILE:O	2:B:759:PRO:HD3	2.14	0.46
1:A:1369:ALA:O	1:A:1370:LEU:C	2.52	0.46
1:A:89:PRO:C	1:A:204:THR:HG21	2.36	0.46
1:A:1237:ILE:HG22	1:A:1238:ILE:N	2.29	0.46
8:H:142:LEU:C	8:H:143:LEU:HD12	2.36	0.46
1:A:853:ASP:O	1:A:854:ASN:CB	2.64	0.46
6:F:109:VAL:HG21	6:F:124:GLU:HA	1.97	0.46
6:F:131:PRO:C	6:F:132:LEU:HD23	2.35	0.46
1:A:254:GLU:O	1:A:256:GLN:N	2.47	0.46
2:B:1001:PHE:C	2:B:1001:PHE:CD1	2.89	0.46
2:B:653:VAL:HG22	2:B:689:LEU:HD13	1.97	0.46
6:F:111:LEU:O	6:F:113:GLY:N	2.48	0.46
7:G:115:MET:HB3	7:G:116:PRO:CD	2.42	0.46
2:B:766:ARG:HD3	2:B:766:ARG:HA	1.70	0.46
2:B:638:PHE:HB2	2:B:741:CYS:O	2.16	0.46
2:B:654:ARG:O	2:B:656:GLY:N	2.48	0.46
3:C:112:ASN:HB2	3:C:114:TYR:CE1	2.50	0.46
1:A:979:SER:HG	1:A:981:LEU:HG	1.80	0.46
2:B:726:ALA:HB1	2:B:1051:THR:HG21	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:577:ILE:C	1:A:579:SER:N	2.65	0.46
1:A:896:ARG:NH2	1:A:1030:ARG:HH21	2.13	0.46
1:A:1019:CYS:O	1:A:1022:LEU:N	2.48	0.46
1:A:369:SER:HB3	11:K:2:ASN:HD21	1.80	0.46
2:B:613:VAL:HG22	2:B:628:THR:HA	1.96	0.46
6:F:143:PHE:C	6:F:143:PHE:CD1	2.89	0.46
2:B:400:HIS:ND1	2:B:517:THR:HG21	2.31	0.46
2:B:104:GLU:OE1	12:L:54:ARG:NH2	2.49	0.46
2:B:401:PHE:HD2	2:B:521:LEU:HD12	1.79	0.46
2:B:603:LEU:HD13	2:B:608:ASP:CB	2.43	0.46
1:A:498:ARG:O	1:A:501:LEU:N	2.47	0.46
9:I:106:CYS:O	9:I:107:SER:HB2	2.16	0.46
2:B:834:ASN:HA	2:B:838:SER:O	2.15	0.46
1:A:1150:SER:O	1:A:1151:GLU:HG3	2.15	0.46
12:L:27:LEU:HD23	12:L:27:LEU:N	2.29	0.46
4:D:19:GLU:O	4:D:21:GLU:N	2.49	0.46
3:C:82:TYR:O	3:C:83:SER:C	2.54	0.46
2:B:999:MET:HG2	2:B:1007:VAL:HG22	1.97	0.46
2:B:1197:PRO:O	2:B:1200:ALA:N	2.48	0.46
2:B:865:LYS:HZ2	2:B:869:SER:HA	1.81	0.46
1:A:500:GLU:OE2	2:B:1145:SER:CB	2.63	0.46
1:A:17:VAL:HA	2:B:1215:ARG:O	2.15	0.46
1:A:1369:ALA:O	1:A:1372:VAL:HG12	2.14	0.46
2:B:981:ALA:HB3	2:B:1095:LEU:HD21	1.97	0.46
1:A:626:ASN:O	1:A:631:HIS:CD2	2.69	0.46
2:B:1060:ARG:HD2	2:B:1060:ARG:HA	1.53	0.46
3:C:66:ARG:CZ	10:J:2:ILE:HG21	2.46	0.46
8:H:123:MET:HG2	8:H:124:ARG:N	2.31	0.46
8:H:25:ARG:HA	8:H:41:ASP:HA	1.98	0.46
8:H:58:THR:HG22	8:H:59:ILE:N	2.31	0.46
2:B:1084:GLN:HG2	3:C:201:TRP:CZ2	2.51	0.46
2:B:990:ILE:HG22	2:B:991:GLY:N	2.31	0.46
2:B:465:ASN:ND2	2:B:465:ASN:H	2.12	0.46
2:B:1034:VAL:HG23	2:B:1059:LEU:HD13	1.98	0.46
1:A:614:PHE:C	1:A:614:PHE:CD1	2.89	0.46
2:B:284:ILE:HG23	2:B:324:ILE:CD1	2.45	0.46
2:B:1152:MET:O	2:B:1154:ALA:N	2.49	0.46
1:A:1283:VAL:HG12	1:A:1284:MET:H	1.81	0.46
1:A:1132:LYS:O	1:A:1134:ILE:N	2.49	0.46
1:A:34:LYS:HD3	1:A:34:LYS:N	2.31	0.46
1:A:7:SER:CB	2:B:1175:LEU:HD22	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1265:ASN:C	1:A:1267:MET:N	2.67	0.46
3:C:100:THR:HG22	3:C:101:LEU:N	2.31	0.46
3:C:259:LEU:CD1	11:K:91:CYS:HB2	2.45	0.46
1:A:1116:LEU:C	1:A:1116:LEU:HD12	2.36	0.46
2:B:563:MET:CE	2:B:580:VAL:HB	2.43	0.46
3:C:33:LEU:O	3:C:34:ARG:C	2.54	0.46
3:C:181:ASP:OD1	3:C:186:LEU:HD13	2.16	0.46
1:A:655:PHE:O	1:A:658:LEU:HB3	2.16	0.46
1:A:1100:ARG:NH2	1:A:1351:GLU:HG2	2.31	0.46
4:D:192:LYS:NZ	4:D:199:ASN:HA	2.30	0.46
5:E:35:VAL:O	5:E:37:LEU:N	2.48	0.46
2:B:1174:LYS:O	2:B:1175:LEU:C	2.53	0.46
3:C:104:PHE:HD2	3:C:105:GLY:N	2.14	0.46
2:B:1189:ILE:HG22	2:B:1190:ASP:N	2.31	0.46
1:A:553:VAL:HG13	1:A:648:ASN:HB3	1.97	0.46
2:B:843:GLN:O	2:B:844:SER:C	2.54	0.46
11:K:58:PHE:HB3	11:K:76:GLN:HE21	1.81	0.46
1:A:524:VAL:HG12	1:A:525:GLN:HE21	1.81	0.46
1:A:525:GLN:CD	2:B:836:GLU:HG2	2.36	0.46
5:E:22:MET:HE3	5:E:26:ARG:CZ	2.46	0.46
2:B:711:GLU:H	2:B:712:PRO:HD2	1.80	0.46
1:A:344:ARG:HG2	1:A:344:ARG:HH11	1.80	0.46
2:B:893:LEU:HD22	2:B:897:GLY:C	2.36	0.46
2:B:118:ARG:HG2	2:B:204:ILE:HD13	1.97	0.46
1:A:134:ARG:HD3	1:A:221:SER:O	2.16	0.46
1:A:971:PHE:HE2	1:A:1040:GLN:HG2	1.80	0.46
2:B:560:GLU:O	2:B:561:TRP:CD1	2.69	0.46
1:A:600:PRO:C	1:A:602:ASP:H	2.19	0.46
2:B:185:THR:H	2:B:188:ASP:HB2	1.80	0.46
7:G:108:VAL:HG13	7:G:159:ALA:O	2.15	0.46
2:B:405:ARG:HA	2:B:631:GLY:O	2.16	0.46
7:G:14:HIS:CD2	7:G:16:SER:CB	2.98	0.46
1:A:779:PHE:CE1	1:A:785:PRO:CD	2.93	0.46
1:A:253:ASN:HB3	2:B:935:ARG:CZ	2.45	0.46
2:B:882:THR:CG2	2:B:884:ARG:HB2	2.46	0.46
6:F:81:THR:HB	6:F:136:ARG:NH1	2.30	0.46
3:C:242:GLN:C	3:C:244:VAL:H	2.18	0.46
1:A:28:ARG:O	1:A:29:ALA:C	2.55	0.46
10:J:23:ASN:O	10:J:25:LEU:N	2.49	0.46
10:J:21:TYR:HB2	10:J:39:LEU:CD1	2.46	0.46
2:B:345:LYS:O	2:B:347:LYS:HG2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:7:ASP:O	8:H:8:ASP:HB2	2.15	0.46
2:B:729:ILE:O	2:B:729:ILE:HG22	2.15	0.46
8:H:110:ASP:O	8:H:128:ASN:ND2	2.48	0.45
8:H:128:ASN:CG	8:H:128:ASN:O	2.54	0.45
1:A:43:GLU:O	1:A:44:THR:CB	2.64	0.45
9:I:4:PHE:HE1	9:I:6:PHE:CE2	2.34	0.45
3:C:75:MET:O	3:C:246:ARG:NH2	2.49	0.45
2:B:168:GLY:HA2	2:B:454:THR:OG1	2.15	0.45
1:A:71:GLN:C	1:A:73:GLY:N	2.69	0.45
1:A:608:ILE:HG13	1:A:613:ILE:HD12	1.97	0.45
7:G:115:MET:CB	7:G:116:PRO:HD2	2.41	0.45
1:A:1053:PHE:C	1:A:1055:ARG:N	2.70	0.45
5:E:161:LYS:O	5:E:163:GLU:N	2.49	0.45
2:B:1186:ASP:C	2:B:1186:ASP:OD1	2.54	0.45
1:A:1297:GLU:HG3	1:A:1297:GLU:H	1.51	0.45
3:C:70:ILE:HG12	3:C:142:VAL:HG11	1.98	0.45
8:H:93:TYR:CD1	8:H:93:TYR:N	2.84	0.45
1:A:871:ASP:OD1	1:A:1366:ARG:NH2	2.50	0.45
2:B:800:GLN:HB3	10:J:52:THR:HG22	1.92	0.45
1:A:1444:MET:CG	7:G:60:ARG:HA	2.46	0.45
2:B:114:PRO:O	2:B:117:ALA:N	2.48	0.45
2:B:1162:ILE:CG2	2:B:1163:CYS:H	2.25	0.45
1:A:1377:THR:O	1:A:1378:GLN:C	2.54	0.45
11:K:31:VAL:HG12	11:K:32:VAL:H	1.79	0.45
1:A:231:PRO:C	1:A:233:TRP:H	2.18	0.45
2:B:1182:CYS:O	2:B:1183:LYS:C	2.54	0.45
3:C:67:LEU:HD11	3:C:155:LEU:HD12	1.97	0.45
1:A:1018:PHE:O	1:A:1021:LEU:HB3	2.17	0.45
3:C:256:ALA:C	3:C:258:ILE:H	2.19	0.45
1:A:408:ASP:C	1:A:410:GLY:H	2.18	0.45
3:C:63:ILE:O	3:C:64:ALA:C	2.55	0.45
2:B:511:PRO:O	2:B:512:ARG:C	2.54	0.45
1:A:1098:VAL:N	1:A:1099:PRO:HD2	2.31	0.45
7:G:139:ILE:HG22	7:G:140:LYS:N	2.31	0.45
7:G:106:MET:HG2	7:G:107:LYS:N	2.31	0.45
7:G:1:MET:HE1	7:G:80:LYS:H	1.80	0.45
2:B:115:GLN:HG2	2:B:193:LYS:HB2	1.97	0.45
2:B:785:TYR:C	2:B:787:VAL:H	2.19	0.45
2:B:879:ARG:O	2:B:880:THR:HB	2.15	0.45
1:A:874:ASP:O	1:A:876:ALA:N	2.50	0.45
1:A:250:ILE:O	1:A:258:GLY:HA3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:298:PHE:O	1:A:301:ALA:HB3	2.15	0.45
4:D:53:SER:HB3	4:D:152:SER:HA	1.98	0.45
1:A:95:PHE:CD1	1:A:234:MET:HG2	2.51	0.45
1:A:492:PRO:HB2	1:A:497:THR:HG22	1.98	0.45
2:B:284:ILE:HD13	2:B:333:PHE:HD2	1.81	0.45
1:A:120:GLU:C	1:A:122:MET:N	2.70	0.45
3:C:112:ASN:N	3:C:112:ASN:HD22	2.12	0.45
1:A:673:GLY:N	1:A:674:PRO:HD2	2.30	0.45
3:C:90:ASP:O	3:C:91:HIS:HB3	2.16	0.45
2:B:570:VAL:HA	2:B:571:PRO:HD2	1.74	0.45
1:A:755:PHE:O	1:A:756:ILE:C	2.55	0.45
7:G:73:LYS:HE3	7:G:74:TYR:O	2.17	0.45
1:A:41:MET:HB2	1:A:42:ASP:H	1.46	0.45
1:A:33:ALA:O	1:A:83:HIS:HD2	1.99	0.45
12:L:30:ILE:HG22	12:L:31:CYS:N	2.32	0.45
2:B:899:ILE:O	2:B:952:VAL:HG21	2.16	0.45
5:E:17:ARG:O	5:E:20:LYS:HB2	2.16	0.45
2:B:130:VAL:HG23	2:B:167:ILE:HD12	1.98	0.45
1:A:1348:LEU:O	1:A:1352:VAL:HG23	2.16	0.45
4:D:54:GLU:OE1	4:D:164:ILE:HD11	2.16	0.45
1:A:1156:PRO:HA	1:A:1190:PRO:CB	2.46	0.45
1:A:474:VAL:HG22	1:A:474:VAL:O	2.16	0.45
2:B:293:PRO:HG2	2:B:296:GLU:HB3	1.98	0.45
6:F:147:SER:OG	6:F:150:GLU:HG3	2.15	0.45
2:B:46:GLN:CG	2:B:47:GLN:H	2.10	0.45
2:B:826:ALA:HB2	2:B:1008:PRO:HB3	1.98	0.45
8:H:82:PRO:C	8:H:84:ALA:H	2.17	0.45
2:B:521:LEU:HB3	2:B:633:VAL:CG1	2.46	0.45
1:A:1001:ARG:HG2	1:A:1001:ARG:HH11	1.82	0.45
1:A:2:VAL:HG21	2:B:1158:PHE:HA	1.98	0.45
4:D:51:ASN:ND2	4:D:54:GLU:OE2	2.50	0.45
7:G:117:GLN:C	7:G:119:LEU:N	2.69	0.45
1:A:135:PHE:C	1:A:137:ALA:N	2.70	0.45
1:A:289:ILE:O	1:A:291:GLU:N	2.50	0.45
2:B:237:VAL:HG12	2:B:238:ALA:N	2.31	0.45
2:B:969:ARG:NH1	3:C:61:GLU:OE1	2.49	0.45
10:J:51:LEU:O	10:J:51:LEU:HD12	2.17	0.45
1:A:1195:LEU:HD11	1:A:1267:MET:CE	2.46	0.45
1:A:701:LEU:HD21	9:I:114:GLN:HB2	1.98	0.45
2:B:936:ASP:OD1	2:B:938:SER:N	2.43	0.45
2:B:784:ASN:O	2:B:788:ARG:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:410:GLY:O	2:B:412:LEU:N	2.50	0.45
8:H:62:SER:O	8:H:63:LEU:C	2.54	0.45
5:E:136:ASN:OD1	5:E:137:GLU:N	2.50	0.45
1:A:84:ILE:O	1:A:84:ILE:CG2	2.63	0.45
4:D:153:ARG:HB3	4:D:154:PHE:CE1	2.52	0.45
2:B:1065:GLN:HE21	2:B:1066:SER:CA	2.30	0.45
2:B:873:THR:O	2:B:914:LYS:HA	2.16	0.45
5:E:167:ARG:HD3	5:E:167:ARG:HA	1.78	0.45
1:A:1343:ALA:O	1:A:1346:ALA:HB3	2.16	0.45
2:B:840:ILE:CG2	2:B:994:TYR:HD1	2.30	0.45
3:C:146:LYS:HB2	10:J:61:LEU:HD11	1.97	0.45
1:A:332:LYS:HG3	1:A:333:GLU:N	2.30	0.45
12:L:58:LYS:O	12:L:59:ALA:O	2.34	0.45
1:A:767:GLN:HB2	1:A:799:PHE:HD1	1.82	0.45
3:C:105:GLY:HA3	3:C:149:LYS:O	2.17	0.45
2:B:854:LEU:HB3	2:B:856:PHE:HE1	1.81	0.45
8:H:4:THR:O	8:H:5:LEU:HD23	2.17	0.45
1:A:1161:THR:CG2	1:A:1163:ILE:HG13	2.46	0.45
7:G:15:PRO:O	7:G:16:SER:C	2.55	0.45
2:B:115:GLN:HG2	2:B:193:LYS:CB	2.46	0.45
3:C:76:ASP:OD2	3:C:128:ASN:N	2.49	0.45
1:A:44:THR:O	1:A:45:GLN:HB2	2.17	0.45
1:A:253:ASN:CB	2:B:935:ARG:CZ	2.94	0.45
1:A:709:THR:HG22	1:A:710:LEU:N	2.32	0.45
1:A:524:VAL:CG1	1:A:525:GLN:H	2.18	0.45
1:A:353:ILE:CD1	1:A:487:MET:HE2	2.46	0.45
1:A:353:ILE:CG2	1:A:487:MET:HE3	2.38	0.45
1:A:499:ALA:O	1:A:503:GLN:HB2	2.16	0.45
5:E:212:ARG:HH11	5:E:212:ARG:HG3	1.82	0.45
2:B:603:LEU:HA	2:B:603:LEU:HD22	1.86	0.45
2:B:979:LYS:HG3	2:B:989:THR:HG22	1.98	0.45
1:A:1053:PHE:O	1:A:1055:ARG:N	2.50	0.45
5:E:129:PRO:O	5:E:130:ALA:O	2.34	0.45
1:A:982:THR:O	1:A:985:ASP:HB2	2.16	0.45
2:B:294:ASP:N	2:B:294:ASP:OD2	2.50	0.45
1:A:415:LEU:HD23	1:A:415:LEU:HA	1.75	0.45
9:I:15:TYR:N	9:I:15:TYR:CD1	2.84	0.45
1:A:244:PRO:HG2	1:A:245:PRO:HD2	1.99	0.45
8:H:143:LEU:C	8:H:144:ILE:HG13	2.38	0.45
3:C:77:ILE:C	3:C:79:GLN:H	2.20	0.45
1:A:353:ILE:HB	1:A:470:LEU:CD2	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1001:PHE:CD2	3:C:34:ARG:NH2	2.84	0.45
1:A:666:ILE:CD1	1:A:667:GLY:N	2.80	0.45
9:I:110:PHE:CD2	9:I:110:PHE:N	2.85	0.45
2:B:204:ILE:C	2:B:205:ILE:HD12	2.36	0.45
2:B:769:TYR:O	2:B:772:ALA:N	2.50	0.45
1:A:1445:ILE:HD11	7:G:61:ILE:HG12	1.99	0.45
1:A:341:MET:HE1	1:A:843:LYS:NZ	2.31	0.45
1:A:841:LEU:O	1:A:845:LEU:HG	2.16	0.45
1:A:608:ILE:HD12	1:A:613:ILE:CD1	2.47	0.45
11:K:46:ILE:O	11:K:46:ILE:HG22	2.16	0.45
2:B:603:LEU:HB3	2:B:609:ILE:HD11	1.99	0.45
2:B:307:ASP:O	2:B:309:GLN:N	2.50	0.45
11:K:53:ASP:O	11:K:55:LYS:N	2.50	0.45
1:A:108:MET:HB3	1:A:210:ILE:CD1	2.46	0.45
1:A:947:PHE:CD2	1:A:954:TRP:CZ2	3.04	0.45
1:A:1215:ARG:HA	1:A:1215:ARG:HD2	1.72	0.45
1:A:590:ARG:HH21	1:A:620:LYS:CB	2.28	0.45
2:B:113:TYR:CD2	2:B:192:LEU:HD22	2.51	0.45
2:B:1081:LEU:O	2:B:1082:MET:C	2.55	0.45
2:B:1008:PRO:HB2	2:B:1010:LEU:O	2.17	0.45
1:A:668:ASP:HA	1:A:741:ASN:OD1	2.17	0.45
1:A:1409:LEU:O	1:A:1412:ALA:HB3	2.17	0.45
2:B:1177:HIS:O	2:B:1179:GLN:N	2.50	0.45
2:B:758:PHE:N	2:B:759:PRO:CD	2.80	0.45
1:A:1349:TYR:CA	1:A:1372:VAL:HG21	2.47	0.45
5:E:43:LYS:O	5:E:45:LYS:N	2.48	0.45
2:B:329:THR:O	2:B:332:ASP:HB3	2.16	0.45
3:C:144:ILE:O	3:C:145:CYS:HB3	2.17	0.44
7:G:31:LEU:HD22	7:G:48:VAL:HG21	1.99	0.44
1:A:325:ILE:O	1:A:326:ARG:C	2.55	0.44
1:A:1401:SER:O	1:A:1402:PHE:HB2	2.18	0.44
3:C:38:ILE:HA	3:C:173:ALA:HB2	1.98	0.44
2:B:730:ARG:O	2:B:731:VAL:O	2.36	0.44
2:B:294:ASP:O	2:B:296:GLU:N	2.48	0.44
7:G:48:VAL:HG13	7:G:74:TYR:HD1	1.82	0.44
3:C:44:LEU:HD23	3:C:45:ALA:N	2.32	0.44
2:B:562:GLY:HA3	2:B:590:HIS:CE1	2.53	0.44
3:C:262:LEU:HA	3:C:262:LEU:HD23	1.75	0.44
1:A:929:LEU:CD2	1:A:983:ILE:HG21	2.47	0.44
5:E:124:VAL:HB	5:E:125:PRO:HD3	2.00	0.44
1:A:407:ARG:HG2	1:A:430:TRP:CZ3	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:123:ASN:ND2	3:C:125:MET:SD	2.90	0.44
1:A:1451:VAL:C	1:A:1453:TYR:N	2.70	0.44
2:B:640:VAL:O	2:B:640:VAL:HG12	2.16	0.44
2:B:570:VAL:HG23	2:B:573:GLN:HB3	1.99	0.44
1:A:1265:ASN:O	1:A:1267:MET:N	2.50	0.44
2:B:661:LEU:C	2:B:663:ALA:H	2.19	0.44
2:B:546:SER:OG	2:B:631:GLY:N	2.39	0.44
1:A:41:MET:O	1:A:42:ASP:C	2.56	0.44
1:A:709:THR:HB	1:A:712:GLU:HG3	1.99	0.44
9:I:8:ARG:CG	9:I:34:TYR:CE1	2.94	0.44
2:B:1072:MET:HE3	2:B:1085:ILE:HD13	2.00	0.44
1:A:352:VAL:HG12	1:A:353:ILE:N	2.32	0.44
3:C:27:LEU:O	3:C:30:ALA:N	2.50	0.44
2:B:1001:PHE:HD2	3:C:34:ARG:HH21	1.66	0.44
11:K:42:LEU:O	11:K:46:ILE:HG13	2.17	0.44
2:B:1178:ASN:O	2:B:1179:GLN:C	2.56	0.44
7:G:9:LEU:CD1	7:G:10:ASN:H	2.30	0.44
1:A:1011:GLN:NE2	1:A:1015:VAL:HG21	2.31	0.44
1:A:215:SER:O	1:A:218:ASP:HB2	2.17	0.44
1:A:1280:GLU:O	1:A:1281:ARG:C	2.55	0.44
1:A:1101:LEU:HB2	1:A:1355:VAL:HG11	1.99	0.44
2:B:293:PRO:HG2	2:B:296:GLU:CB	2.47	0.44
7:G:127:PRO:HG2	7:G:138:THR:HG21	1.98	0.44
1:A:595:THR:O	1:A:596:THR:HG23	2.18	0.44
10:J:48:ARG:HE	10:J:49:MET:HE2	1.82	0.44
6:F:89:GLU:HB3	6:F:134:ILE:CD1	2.48	0.44
1:A:901:LEU:O	1:A:921:GLY:N	2.48	0.44
11:K:95:ILE:O	11:K:98:LEU:HB2	2.17	0.44
4:D:170:THR:HB	4:D:172:LEU:H	1.83	0.44
1:A:93:VAL:CG2	1:A:301:ALA:HA	2.48	0.44
1:A:666:ILE:HD12	1:A:667:GLY:N	2.30	0.44
1:A:92:HIS:O	1:A:95:PHE:N	2.34	0.44
2:B:324:ILE:CG2	2:B:325:GLN:N	2.79	0.44
5:E:48:ASP:CG	5:E:49:SER:N	2.69	0.44
2:B:753:ALA:HA	2:B:756:ILE:HD12	2.00	0.44
2:B:108:VAL:HG12	2:B:109:THR:N	2.33	0.44
11:K:35:PHE:CD1	11:K:71:PHE:CE1	3.05	0.44
7:G:34:VAL:HG12	7:G:45:ILE:CG2	2.41	0.44
2:B:744:HIS:CD2	2:B:745:PRO:HD2	2.53	0.44
11:K:24:ASP:OD2	11:K:74:ARG:NH1	2.49	0.44
1:A:33:ALA:HB1	1:A:35:ILE:HG13	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:34:TYR:C	9:I:34:TYR:CD2	2.90	0.44
2:B:1084:GLN:NE2	2:B:1084:GLN:N	2.66	0.44
1:A:401:GLY:O	1:A:435:HIS:CD2	2.71	0.44
3:C:248:ILE:HG23	11:K:98:LEU:HD22	2.00	0.44
3:C:246:ARG:HA	3:C:249:ASP:HB3	1.99	0.44
2:B:581:PHE:HA	2:B:585:VAL:O	2.17	0.44
3:C:36:VAL:HG21	3:C:251:LEU:HB2	1.98	0.44
2:B:862:GLN:O	2:B:914:LYS:HE3	2.18	0.44
2:B:1181:GLU:O	2:B:1182:CYS:HB2	2.18	0.44
1:A:103:CYS:O	1:A:106:VAL:O	2.35	0.44
2:B:308:TRP:HA	2:B:311:LEU:HD12	1.99	0.44
2:B:258:LEU:O	2:B:259:TYR:O	2.36	0.44
3:C:83:SER:O	3:C:85:ASP:N	2.51	0.44
8:H:11:GLN:HA	8:H:53:ASP:O	2.18	0.44
1:A:1426:GLU:H	1:A:1426:GLU:HG2	1.57	0.44
2:B:436:VAL:HG12	2:B:436:VAL:O	2.18	0.44
6:F:116:ASP:C	6:F:116:ASP:OD1	2.55	0.44
10:J:53:HIS:NE2	10:J:55:ASP:HA	2.33	0.44
1:A:243:PRO:O	1:A:244:PRO:C	2.55	0.44
1:A:1153:TYR:CD2	1:A:1163:ILE:HD11	2.52	0.44
1:A:1335:ILE:CG2	1:A:1335:ILE:O	2.65	0.44
2:B:846:ILE:HG23	2:B:974:PRO:HG2	1.99	0.44
1:A:336:ILE:HG22	1:A:337:ARG:N	2.32	0.44
1:A:93:VAL:HG23	1:A:304:MET:HE3	1.99	0.44
2:B:172:ILE:CG2	2:B:173:MET:N	2.81	0.44
9:I:111:THR:HG21	9:I:113:ASP:HB2	1.99	0.44
2:B:312:GLU:O	2:B:315:LYS:N	2.50	0.44
1:A:18:GLN:H	2:B:1215:ARG:HB2	1.83	0.44
1:A:883:LEU:CD2	1:A:1021:LEU:HB2	2.48	0.44
1:A:218:ASP:O	1:A:219:PHE:C	2.56	0.44
5:E:114:ASN:O	5:E:115:ASN:CB	2.65	0.44
1:A:278:THR:HG22	1:A:278:THR:O	2.17	0.44
1:A:282:ASN:O	1:A:284:ALA:N	2.51	0.44
1:A:652:VAL:O	1:A:653:VAL:C	2.56	0.44
4:D:49:ALA:HB2	4:D:174:PRO:HB3	1.99	0.44
2:B:680:THR:O	2:B:684:LEU:HD12	2.18	0.44
8:H:10:PHE:N	8:H:10:PHE:CD1	2.85	0.44
8:H:116:TYR:HE2	8:H:140:ALA:CB	2.30	0.44
1:A:1116:LEU:CD1	1:A:1118:VAL:HG13	2.48	0.44
3:C:161:LYS:O	3:C:170:TRP:NE1	2.51	0.44
1:A:51:GLY:HA2	1:A:56:PRO:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:291:ILE:HD13	2:B:300:HIS:CD2	2.53	0.44
1:A:335:ARG:HB3	1:A:336:ILE:H	1.65	0.44
10:J:13:VAL:O	10:J:14:VAL:CG2	2.66	0.44
1:A:494:SER:H	1:A:497:THR:HB	1.82	0.44
1:A:1438:THR:HG22	1:A:1438:THR:O	2.17	0.44
2:B:1031:LEU:CD2	2:B:1044:ALA:HB2	2.48	0.44
1:A:1370:LEU:O	1:A:1374:VAL:HG23	2.17	0.44
7:G:9:LEU:CG	7:G:10:ASN:N	2.81	0.44
12:L:61:THR:CG2	12:L:63:ARG:HG2	2.48	0.44
2:B:265:SER:O	2:B:266:ALA:CB	2.65	0.44
2:B:286:PHE:CD1	2:B:297:ILE:HG23	2.53	0.44
8:H:11:GLN:O	8:H:28:ALA:HB1	2.17	0.44
2:B:424:LEU:O	2:B:428:ILE:HG13	2.18	0.44
1:A:26:GLU:O	1:A:27:VAL:C	2.54	0.44
2:B:203:PHE:N	2:B:203:PHE:CD1	2.86	0.44
1:A:966:ASN:O	1:A:967:ALA:C	2.56	0.44
7:G:3:PHE:CD1	7:G:80:LYS:HE2	2.53	0.44
2:B:181:LEU:CD2	2:B:189:LEU:HD22	2.47	0.44
1:A:47:ARG:HH22	1:A:254:GLU:HA	1.83	0.44
2:B:882:THR:O	2:B:883:LEU:CB	2.65	0.44
3:C:22:LEU:HD23	3:C:25:VAL:HG21	2.00	0.44
1:A:427:GLN:HB2	1:A:430:TRP:NE1	2.32	0.44
1:A:350:ARG:HH11	1:A:350:ARG:HG3	1.83	0.44
2:B:1110:PRO:HG3	2:B:1124:ARG:O	2.18	0.44
3:C:90:ASP:CG	3:C:90:ASP:O	2.57	0.44
2:B:661:LEU:C	2:B:663:ALA:N	2.71	0.44
10:J:1:MET:HB2	10:J:1:MET:HE2	1.86	0.44
8:H:91:ASP:C	8:H:93:TYR:N	2.72	0.44
1:A:853:ASP:OD1	1:A:855:THR:CG2	2.66	0.44
7:G:18:PHE:HZ	7:G:68:ALA:HB2	1.83	0.44
3:C:170:TRP:O	3:C:171:GLY:C	2.57	0.44
11:K:47:ARG:C	11:K:47:ARG:HD2	2.38	0.44
1:A:963:ILE:HD13	1:A:1049:ILE:CG1	2.47	0.44
5:E:94:LYS:HE2	5:E:98:ILE:CD1	2.38	0.44
2:B:1099:VAL:C	2:B:1101:ASP:N	2.70	0.44
5:E:135:PHE:CB	5:E:140:LEU:HD11	2.47	0.44
2:B:906:SER:O	2:B:907:GLY:O	2.34	0.44
1:A:1015:VAL:O	1:A:1018:PHE:N	2.49	0.44
1:A:1132:LYS:O	1:A:1135:ARG:N	2.51	0.44
1:A:89:PRO:HB2	1:A:204:THR:CG2	2.48	0.44
3:C:259:LEU:HD11	11:K:91:CYS:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:794:ASN:O	2:B:795:ILE:HD12	2.17	0.44
2:B:794:ASN:C	2:B:795:ILE:HD12	2.37	0.44
1:A:556:TRP:CZ2	1:A:558:GLY:HA2	2.53	0.44
1:A:373:THR:HG21	2:B:1105:ALA:HB3	1.98	0.44
10:J:53:HIS:CD2	10:J:54:VAL:C	2.92	0.43
4:D:138:ASN:C	4:D:140:ASP:N	2.70	0.43
8:H:10:PHE:HE2	8:H:36:CYS:HG	1.65	0.43
1:A:40:THR:CG2	1:A:41:MET:HG3	2.36	0.43
2:B:839:MET:HG3	2:B:1010:LEU:CD1	2.44	0.43
2:B:763:GLN:HG2	2:B:765:PRO:CG	2.48	0.43
3:C:73:GLN:HE21	3:C:74:SER:H	1.65	0.43
2:B:693:ILE:HD13	2:B:701:ILE:HD13	2.00	0.43
1:A:500:GLU:OE1	2:B:1143:ALA:C	2.57	0.43
1:A:526:ASP:OD1	2:B:1013:ASN:ND2	2.49	0.43
2:B:838:SER:CB	2:B:989:THR:O	2.64	0.43
1:A:18:GLN:O	2:B:1215:ARG:CG	2.66	0.43
1:A:1373:ASP:HA	1:A:1376:THR:CG2	2.47	0.43
1:A:1453:TYR:O	1:A:1454:MET:HB3	2.18	0.43
1:A:626:ASN:C	1:A:628:GLY:H	2.21	0.43
1:A:456:MET:HB2	1:A:478:TYR:OH	2.18	0.43
1:A:1226:VAL:HG22	1:A:1240:CYS:HB3	2.00	0.43
1:A:42:ASP:HB3	1:A:45:GLN:HA	2.00	0.43
2:B:579:ARG:HA	2:B:589:VAL:HG13	1.99	0.43
1:A:846:GLU:HB2	1:A:847:ASP:H	1.66	0.43
2:B:1207:LEU:HB3	2:B:1212:ILE:HG22	1.99	0.43
2:B:51:PHE:HB2	2:B:173:MET:CE	2.48	0.43
2:B:414:ALA:O	2:B:415:GLN:C	2.57	0.43
1:A:152:VAL:HG12	1:A:153:PRO:CD	2.47	0.43
1:A:932:GLU:O	1:A:936:LEU:HG	2.18	0.43
5:E:129:PRO:O	5:E:130:ALA:C	2.57	0.43
1:A:559:VAL:O	1:A:559:VAL:HG12	2.17	0.43
1:A:942:PHE:C	1:A:942:PHE:CD2	2.91	0.43
4:D:33:PHE:CE2	7:G:80:LYS:NZ	2.72	0.43
2:B:113:TYR:HB3	2:B:114:PRO:HD2	2.00	0.43
11:K:58:PHE:CB	11:K:76:GLN:HE21	2.31	0.43
11:K:58:PHE:HE2	11:K:74:ARG:HE	1.57	0.43
4:D:135:GLY:C	4:D:137:ASN:H	2.21	0.43
2:B:825:VAL:HG12	2:B:826:ALA:N	2.32	0.43
1:A:12:ARG:O	2:B:1194:ILE:HG22	2.18	0.43
2:B:765:PRO:O	2:B:767:ASN:N	2.51	0.43
1:A:224:PHE:CZ	1:A:231:PRO:HG3	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1177:HIS:C	2:B:1179:GLN:H	2.21	0.43
1:A:575:LYS:NZ	1:A:615:GLY:H	2.16	0.43
7:G:115:MET:CB	7:G:116:PRO:CD	2.96	0.43
2:B:60:GLN:O	2:B:63:ILE:HG22	2.18	0.43
1:A:522:GLY:O	1:A:646:PHE:HE2	2.01	0.43
2:B:62:ILE:HG23	2:B:418:LYS:HG2	1.99	0.43
1:A:1148:ILE:HB	1:A:1196:GLU:O	2.18	0.43
3:C:238:ILE:HD11	3:C:246:ARG:HH11	1.83	0.43
7:G:66:GLY:O	7:G:67:SER:C	2.56	0.43
10:J:41:LEU:HD11	10:J:50:ILE:HG13	2.00	0.43
1:A:269:ILE:HD11	1:A:300:VAL:HA	2.01	0.43
1:A:65:LEU:O	1:A:66:LYS:C	2.57	0.43
4:D:51:ASN:OD1	4:D:52:LEU:O	2.37	0.43
2:B:58:THR:O	2:B:62:ILE:HG13	2.18	0.43
1:A:508:PRO:O	1:A:511:ILE:HG13	2.18	0.43
2:B:1137:CYS:O	2:B:1140:ALA:HB3	2.17	0.43
3:C:41:ILE:HA	3:C:42:PRO:HD3	1.84	0.43
1:A:752:LYS:HA	1:A:752:LYS:HD3	1.83	0.43
4:D:138:ASN:O	4:D:140:ASP:N	2.52	0.43
8:H:40:LEU:HD21	8:H:142:LEU:HD21	2.00	0.43
7:G:14:HIS:CE1	7:G:15:PRO:HD2	2.52	0.43
1:A:341:MET:HE3	2:B:1135:ARG:NH1	2.33	0.43
2:B:32:ALA:O	2:B:35:SER:HB2	2.19	0.43
3:C:31:ASN:O	3:C:35:ARG:HG3	2.18	0.43
1:A:578:LEU:HD23	1:A:612:ILE:HD11	1.99	0.43
2:B:591:ARG:O	2:B:592:ASN:C	2.56	0.43
1:A:247:ARG:HG3	1:A:247:ARG:O	2.18	0.43
8:H:123:MET:HE3	8:H:142:LEU:CD2	2.48	0.43
5:E:29:PHE:O	5:E:30:ILE:CG1	2.59	0.43
11:K:31:VAL:CG1	11:K:32:VAL:H	2.31	0.43
2:B:859:TYR:CE1	2:B:941:LEU:HD12	2.53	0.43
4:D:68:ARG:C	4:D:70:PHE:N	2.70	0.43
2:B:519:TRP:C	2:B:519:TRP:CD1	2.91	0.43
7:G:88:ASP:OD2	7:G:88:ASP:N	2.49	0.43
1:A:1344:GLY:O	1:A:1345:ARG:C	2.56	0.43
4:D:51:ASN:O	4:D:52:LEU:C	2.57	0.43
1:A:896:ARG:HD3	1:A:897:TYR:HE1	1.84	0.43
7:G:119:LEU:HD13	7:G:132:SER:HB2	2.00	0.43
12:L:61:THR:HG22	12:L:63:ARG:HG2	2.01	0.43
2:B:418:LYS:O	2:B:420:LEU:N	2.51	0.43
1:A:1124:HIS:HB3	1:A:1130:GLN:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:226:ASP:O	3:C:227:THR:CB	2.66	0.43
3:C:80:LEU:HD22	3:C:129:ILE:HD13	2.01	0.43
11:K:100:ALA:O	11:K:103:THR:HB	2.18	0.43
1:A:1111:MET:H	1:A:1111:MET:HG2	1.56	0.43
3:C:70:ILE:HD11	3:C:144:ILE:CG1	2.49	0.43
10:J:2:ILE:HG22	10:J:3:VAL:O	2.18	0.43
2:B:824:ILE:CD1	10:J:48:ARG:NH1	2.81	0.43
9:I:8:ARG:HG3	9:I:34:TYR:CD1	2.54	0.43
5:E:18:THR:O	5:E:19:VAL:C	2.55	0.43
1:A:886:ILE:CD1	1:A:943:LEU:HB3	2.41	0.43
1:A:427:GLN:O	1:A:428:TYR:C	2.56	0.43
7:G:10:ASN:OD1	7:G:71:ASN:HA	2.19	0.43
1:A:1015:VAL:O	1:A:1016:THR:C	2.57	0.43
2:B:26:THR:O	2:B:29:ASP:HB2	2.17	0.43
2:B:900:ALA:O	2:B:903:VAL:HG23	2.19	0.43
8:H:103:LYS:HG2	8:H:104:PHE:N	2.34	0.43
1:A:58:LEU:HD13	1:A:243:PRO:HA	2.00	0.43
8:H:38:LEU:HD13	8:H:125:LEU:CD1	2.49	0.43
1:A:817:ALA:HA	2:B:764:SER:OG	2.17	0.43
2:B:1034:VAL:C	2:B:1036:ALA:N	2.72	0.43
3:C:99:LEU:HD22	3:C:120:ILE:HG12	2.01	0.43
1:A:23:SER:CB	1:A:233:TRP:NE1	2.82	0.43
5:E:124:VAL:HG13	5:E:132:ILE:CB	2.45	0.43
1:A:679:ILE:O	1:A:682:THR:N	2.52	0.43
1:A:682:THR:HG23	1:A:728:LYS:HE3	2.00	0.43
1:A:382:PRO:CB	1:A:428:TYR:HE2	2.30	0.43
4:D:52:LEU:CD2	4:D:147:TYR:HE2	2.31	0.43
1:A:552:TRP:HE3	1:A:651:LYS:HB3	1.83	0.43
3:C:92:CYS:C	3:C:94:LYS:N	2.72	0.43
1:A:86:LEU:HD13	1:A:90:VAL:HG23	2.00	0.43
2:B:911:ILE:HG22	2:B:912:ILE:HG13	2.00	0.43
2:B:351:TYR:CD1	2:B:355:ILE:HD11	2.53	0.43
3:C:183:TRP:CE2	3:C:207:CYS:HB3	2.54	0.43
2:B:1106:ARG:NH2	2:B:1109:GLY:H	2.17	0.43
2:B:237:VAL:HG22	2:B:257:LYS:HA	2.00	0.43
2:B:129:PHE:CD2	2:B:166:PHE:HA	2.53	0.43
8:H:15:VAL:HG22	8:H:26:ILE:CG1	2.49	0.43
1:A:477:PRO:HG2	1:A:521:MET:HG2	2.00	0.43
7:G:126:ASN:HA	7:G:126:ASN:HD22	1.56	0.43
11:K:101:LEU:HD23	11:K:101:LEU:O	2.19	0.43
8:H:40:LEU:HD22	8:H:123:MET:CE	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:3:ASN:HB3	8:H:4:THR:H	1.63	0.43
2:B:192:LEU:O	2:B:193:LYS:CB	2.62	0.43
1:A:73:GLY:O	1:A:75:ASN:N	2.52	0.43
1:A:320:ARG:HA	1:A:321:PRO:HD3	1.89	0.43
2:B:593:PRO:O	2:B:596:LEU:N	2.52	0.43
9:I:103:CYS:HB3	9:I:107:SER:H	1.83	0.43
12:L:47:ARG:HG3	12:L:47:ARG:NH1	2.33	0.43
3:C:91:HIS:ND1	3:C:158:VAL:HG11	2.33	0.43
1:A:693:VAL:HA	1:A:696:GLU:HB3	2.01	0.43
1:A:148:CYS:O	1:A:168:GLY:HA2	2.19	0.43
2:B:1029:CYS:HA	2:B:1089:PRO:O	2.19	0.43
5:E:205:SER:O	5:E:206:GLY:C	2.58	0.42
1:A:1279:ILE:HG23	1:A:1308:THR:OG1	2.19	0.42
2:B:1085:ILE:CD1	2:B:1085:ILE:N	2.81	0.42
2:B:200:GLY:HA2	2:B:202:TYR:HE2	1.81	0.42
1:A:685:GLU:HG3	1:A:686:ALA:N	2.34	0.42
1:A:309:ALA:C	1:A:311:GLN:H	2.21	0.42
2:B:758:PHE:HB3	2:B:761:HIS:CD2	2.54	0.42
9:I:84:VAL:HG13	9:I:84:VAL:O	2.19	0.42
2:B:235:SER:C	2:B:236:HIS:CD2	2.93	0.42
2:B:792:MET:HA	2:B:856:PHE:O	2.19	0.42
2:B:694:ASP:O	2:B:698:GLU:HB2	2.18	0.42
1:A:100:LYS:O	1:A:102:VAL:N	2.52	0.42
2:B:855:PHE:C	2:B:855:PHE:CD1	2.90	0.42
3:C:58:LEU:CD2	3:C:58:LEU:N	2.81	0.42
1:A:861:GLY:HA3	5:E:174:GLN:NE2	2.34	0.42
2:B:785:TYR:C	2:B:787:VAL:N	2.71	0.42
1:A:41:MET:O	1:A:50:ILE:HG13	2.20	0.42
9:I:75:CYS:SG	9:I:79:HIS:CA	3.07	0.42
2:B:710:LEU:C	2:B:711:GLU:HG2	2.40	0.42
6:F:154:ASP:HB3	6:F:155:LEU:H	1.64	0.42
3:C:33:LEU:HG	3:C:37:MET:CE	2.50	0.42
11:K:49:GLU:HG3	11:K:94:ILE:HG13	2.00	0.42
5:E:117:THR:O	5:E:120:ALA:N	2.44	0.42
2:B:123:THR:O	2:B:125:SER:N	2.47	0.42
1:A:535:THR:O	1:A:575:LYS:HG3	2.19	0.42
1:A:475:THR:HG23	1:A:476:SER:H	1.76	0.42
1:A:682:THR:HA	1:A:685:GLU:HG2	2.00	0.42
1:A:1036:ARG:HH11	1:A:1036:ARG:HG2	1.83	0.42
5:E:131:THR:HG21	5:E:191:LYS:HZ1	1.84	0.42
1:A:1209:MET:SD	1:A:1236:LEU:HD22	2.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:762:ASN:OD1	2:B:1022:THR:HA	2.19	0.42
1:A:537:ARG:NH1	8:H:120:GLY:O	2.49	0.42
5:E:31:THR:OG1	5:E:34:GLU:N	2.50	0.42
1:A:1168:GLU:O	1:A:1172:LEU:HG	2.19	0.42
1:A:1115:SER:O	1:A:1116:LEU:CB	2.67	0.42
1:A:711:ARG:HA	9:I:97:MET:HE1	1.99	0.42
5:E:22:MET:O	5:E:26:ARG:HG3	2.19	0.42
2:B:708:GLU:O	2:B:709:ASP:C	2.58	0.42
1:A:339:ASN:O	1:A:343:LYS:HG2	2.19	0.42
1:A:298:PHE:HD2	1:A:299:HIS:CD2	2.37	0.42
1:A:1409:LEU:CD1	2:B:1207:LEU:HD21	2.42	0.42
2:B:552:MET:C	2:B:554:ILE:N	2.72	0.42
2:B:654:ARG:C	2:B:656:GLY:H	2.23	0.42
12:L:40:LEU:HD13	12:L:44:ASP:CB	2.49	0.42
2:B:63:ILE:HA	2:B:421:PHE:CE2	2.54	0.42
1:A:277:GLU:O	1:A:279:LEU:N	2.52	0.42
2:B:466:TRP:CE3	2:B:466:TRP:HA	2.53	0.42
2:B:257:LYS:N	2:B:270:LYS:O	2.52	0.42
5:E:35:VAL:C	5:E:37:LEU:N	2.72	0.42
2:B:258:LEU:CG	2:B:258:LEU:O	2.66	0.42
1:A:570:PRO:C	1:A:571:LEU:HD12	2.40	0.42
5:E:112:TYR:CZ	5:E:136:ASN:HB2	2.54	0.42
3:C:92:CYS:O	3:C:94:LYS:N	2.52	0.42
7:G:1:MET:HE3	7:G:80:LYS:O	2.19	0.42
7:G:81:PRO:C	7:G:82:PHE:CD1	2.93	0.42
1:A:901:LEU:N	1:A:926:GLN:NE2	2.50	0.42
5:E:22:MET:HE1	5:E:26:ARG:NH2	2.34	0.42
2:B:651:LEU:HD11	2:B:707:PRO:CB	2.49	0.42
1:A:741:ASN:HD22	1:A:744:LYS:N	2.07	0.42
2:B:1032:SER:O	2:B:1036:ALA:HB2	2.19	0.42
1:A:29:ALA:HB1	2:B:1184:GLY:HA2	2.00	0.42
2:B:1115:THR:CG2	2:B:1117:GLN:CG	2.97	0.42
2:B:834:ASN:ND2	2:B:1013:ASN:HB2	2.34	0.42
1:A:1039:LYS:HE3	1:A:1043:ASP:OD2	2.19	0.42
4:D:146:GLN:O	4:D:147:TYR:C	2.57	0.42
2:B:298:LEU:CD2	2:B:298:LEU:N	2.83	0.42
9:I:58:VAL:O	9:I:58:VAL:HG12	2.19	0.42
5:E:114:ASN:HD22	5:E:114:ASN:HA	1.62	0.42
1:A:1147:THR:HA	1:A:1197:LEU:HD23	2.00	0.42
7:G:99:PHE:CD1	7:G:99:PHE:C	2.93	0.42
1:A:1149:ALA:CB	9:I:47:GLU:HA	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:101:GLN:NE2	5:E:127:ILE:HG21	2.34	0.42
1:A:823:GLY:C	1:A:825:ILE:N	2.72	0.42
1:A:1265:ASN:C	1:A:1267:MET:H	2.23	0.42
1:A:660:ASN:O	1:A:661:GLY:O	2.37	0.42
4:D:180:LEU:HA	4:D:180:LEU:HD23	1.75	0.42
2:B:1006:ILE:HG22	10:J:45:CYS:HB3	2.02	0.42
1:A:804:TYR:OH	1:A:816:HIS:NE2	2.53	0.42
2:B:1084:GLN:NE2	2:B:1084:GLN:H	2.17	0.42
1:A:367:PRO:HB3	1:A:465:TYR:O	2.19	0.42
3:C:236:GLY:C	3:C:238:ILE:N	2.72	0.42
1:A:324:SER:O	1:A:325:ILE:C	2.56	0.42
1:A:224:PHE:CD2	1:A:231:PRO:HG3	2.54	0.42
2:B:582:VAL:HA	2:B:626:ILE:O	2.19	0.42
1:A:19:PHE:HB3	1:A:1413:GLY:HA2	2.02	0.42
9:I:101:PHE:HD1	9:I:110:PHE:O	2.02	0.42
3:C:67:LEU:HD11	3:C:155:LEU:HD13	2.01	0.42
2:B:753:ALA:HA	2:B:756:ILE:CD1	2.48	0.42
7:G:145:VAL:CG1	7:G:146:LYS:N	2.81	0.42
1:A:1289:ARG:NH1	1:A:1326:ARG:NH1	2.67	0.42
5:E:127:ILE:O	5:E:130:ALA:HB3	2.20	0.42
1:A:1170:ILE:H	1:A:1170:ILE:HG13	1.62	0.42
1:A:53:LEU:HD22	1:A:54:ASN:HD22	1.85	0.42
1:A:853:ASP:OD1	1:A:855:THR:HG22	2.17	0.42
1:A:1161:THR:HG22	1:A:1163:ILE:HG13	2.02	0.42
1:A:1115:SER:OG	1:A:1116:LEU:N	2.53	0.42
2:B:992:ILE:HD11	11:K:66:PRO:HB2	2.01	0.42
10:J:41:LEU:CD1	10:J:50:ILE:HG13	2.49	0.42
3:C:131:HIS:HA	3:C:132:PRO:HD3	1.92	0.42
3:C:123:ASN:HD22	3:C:125:MET:CG	2.29	0.42
1:A:807:GLY:HA2	2:B:760:ASP:O	2.19	0.42
2:B:1106:ARG:HD3	2:B:1127:GLY:CA	2.49	0.42
1:A:1031:VAL:HG12	1:A:1031:VAL:O	2.20	0.42
1:A:210:ILE:O	1:A:214:ILE:HG13	2.19	0.42
1:A:264:PHE:O	1:A:267:ALA:HB3	2.20	0.42
1:A:1029:ARG:HG3	1:A:1029:ARG:NH1	2.34	0.42
1:A:31:SER:OG	1:A:82:GLY:HA2	2.19	0.42
10:J:31:ASP:O	10:J:32:GLU:C	2.58	0.42
1:A:765:VAL:HG23	1:A:802:ASN:O	2.20	0.42
3:C:80:LEU:HD11	3:C:95:CYS:CA	2.49	0.42
8:H:40:LEU:CD2	8:H:142:LEU:HD21	2.50	0.42
2:B:796:LEU:HD12	2:B:852:ARG:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:67:CYS:O	1:A:68:GLN:CB	2.67	0.42
1:A:337:ARG:CZ	1:A:839:ARG:HH12	2.33	0.42
2:B:1131:GLY:O	2:B:1132:GLU:C	2.58	0.42
2:B:1162:ILE:CG2	2:B:1163:CYS:N	2.79	0.42
5:E:177:ARG:O	5:E:212:ARG:CD	2.68	0.42
1:A:1434:ALA:HA	1:A:1435:PRO:HD3	1.76	0.42
1:A:231:PRO:O	1:A:233:TRP:N	2.52	0.42
1:A:535:THR:CG2	1:A:575:LYS:HE2	2.49	0.42
2:B:654:ARG:N	2:B:657:HIS:HD2	2.13	0.42
9:I:111:THR:CG2	9:I:113:ASP:HB2	2.49	0.42
1:A:427:GLN:HB2	1:A:430:TRP:CE2	2.55	0.42
1:A:481:ASP:OD1	1:A:483:ASP:OD2	2.38	0.42
1:A:1010:ALA:O	1:A:1013:ASP:HB2	2.20	0.42
1:A:444:PHE:CB	1:A:458:HIS:HD2	2.33	0.42
3:C:229:TYR:CD1	3:C:229:TYR:N	2.88	0.42
2:B:1198:TYR:CD2	2:B:1198:TYR:C	2.93	0.42
1:A:818:MET:H	2:B:514:LEU:HD23	1.83	0.42
1:A:466:SER:HB2	2:B:1099:VAL:HG11	2.02	0.42
1:A:249:SER:HB2	1:A:250:ILE:H	1.66	0.42
1:A:306:ASN:ND2	1:A:322:VAL:CG1	2.82	0.42
1:A:497:THR:HG22	1:A:498:ARG:N	2.34	0.42
2:B:167:ILE:HG22	2:B:453:ILE:HD12	2.01	0.42
4:D:191:ALA:C	4:D:193:THR:N	2.73	0.42
1:A:1072:ILE:O	1:A:1075:PRO:HD2	2.20	0.42
3:C:257:SER:C	3:C:258:ILE:HD12	2.40	0.42
1:A:275:SER:O	1:A:279:LEU:HG	2.19	0.42
1:A:877:HIS:C	1:A:878:ILE:CG1	2.88	0.42
4:D:7:THR:CB	7:G:42:PHE:CZ	3.03	0.42
10:J:3:VAL:HG21	10:J:18:TRP:CG	2.55	0.42
1:A:817:ALA:O	1:A:820:GLY:N	2.52	0.42
3:C:15:LYS:O	3:C:240:VAL:HG22	2.20	0.42
5:E:133:GLU:HB3	5:E:135:PHE:HE1	1.84	0.42
1:A:23:SER:HB3	1:A:233:TRP:NE1	2.35	0.42
2:B:702:LEU:HD12	2:B:703:ILE:H	1.84	0.42
2:B:1216:LEU:N	2:B:1216:LEU:HD23	2.35	0.42
2:B:731:VAL:CG1	2:B:732:SER:N	2.81	0.42
1:A:1206:ASP:HB3	1:A:1274:ARG:NH1	2.34	0.42
3:C:8:VAL:HG12	3:C:9:LYS:H	1.83	0.42
2:B:213:ILE:HD13	2:B:213:ILE:HA	1.88	0.42
2:B:1219:ASP:O	2:B:1219:ASP:OD1	2.38	0.42
2:B:986:GLN:OE1	2:B:986:GLN:HA	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1335:ILE:HG23	1:A:1339:LEU:HD12	2.01	0.42
1:A:901:LEU:HA	1:A:907:THR:OG1	2.20	0.42
9:I:12:ASN:HB3	9:I:13:MET:H	1.57	0.42
2:B:624:LEU:HA	2:B:624:LEU:HD12	1.84	0.42
2:B:366:GLN:O	2:B:367:LEU:O	2.38	0.42
1:A:606:LEU:HB3	1:A:614:PHE:CE2	2.54	0.42
1:A:231:PRO:C	1:A:233:TRP:N	2.73	0.42
2:B:1069:PHE:CD1	2:B:1069:PHE:N	2.78	0.42
3:C:174:ALA:O	3:C:175:ALA:CB	2.67	0.42
1:A:441:PRO:HD2	1:A:498:ARG:CZ	2.49	0.42
6:F:82:THR:HA	6:F:83:PRO:HD3	1.80	0.42
2:B:307:ASP:O	2:B:308:TRP:C	2.58	0.42
1:A:935:GLN:C	1:A:937:VAL:N	2.72	0.42
1:A:852:TYR:CD2	1:A:1060:PRO:CB	3.03	0.42
1:A:825:ILE:HG22	1:A:826:ASP:N	2.34	0.42
2:B:1029:CYS:HB3	2:B:1086:PHE:CZ	2.55	0.42
5:E:61:GLN:HG2	5:E:62:ALA:N	2.35	0.42
8:H:48:PRO:O	8:H:49:VAL:HG23	2.20	0.42
4:D:179:GLN:O	4:D:183:LEU:HB2	2.20	0.42
1:A:77:CYS:C	1:A:78:PRO:O	2.45	0.41
1:A:1217:LYS:O	1:A:1221:LYS:N	2.52	0.41
2:B:604:ARG:HG3	2:B:611:PRO:HA	2.02	0.41
5:E:201:LYS:HA	5:E:206:GLY:O	2.19	0.41
6:F:97:ARG:NH1	6:F:100:GLN:OE1	2.53	0.41
6:F:72:LYS:O	6:F:73:ALA:HB3	2.20	0.41
1:A:1339:LEU:HD13	5:E:147:HIS:CD2	2.55	0.41
1:A:254:GLU:CG	2:B:935:ARG:HH22	2.31	0.41
2:B:515:HIS:O	2:B:518:HIS:HB2	2.20	0.41
2:B:1182:CYS:O	2:B:1183:LYS:O	2.37	0.41
2:B:593:PRO:O	2:B:595:ARG:N	2.53	0.41
2:B:596:LEU:O	2:B:600:LEU:HG	2.19	0.41
1:A:472:LEU:O	1:A:475:THR:CB	2.68	0.41
9:I:83:ASN:HA	9:I:102:VAL:O	2.19	0.41
2:B:373:ARG:HG3	2:B:566:LEU:HD23	2.01	0.41
2:B:205:ILE:CG2	2:B:206:ASN:N	2.83	0.41
2:B:1106:ARG:HG3	2:B:1107:ALA:N	2.34	0.41
3:C:208:GLU:C	3:C:210:GLU:H	2.22	0.41
1:A:116:ASP:O	1:A:117:GLU:C	2.57	0.41
4:D:206:GLU:O	4:D:208:GLU:N	2.53	0.41
1:A:1111:MET:CE	1:A:1330:ASN:OD1	2.68	0.41
4:D:209:ARG:O	4:D:212:LYS:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:217:LEU:O	4:D:219:THR:N	2.53	0.41
2:B:610:ASN:O	2:B:612:GLU:N	2.53	0.41
10:J:2:ILE:CG2	10:J:3:VAL:N	2.83	0.41
8:H:127:GLY:HA3	8:H:130:ARG:NH2	2.35	0.41
7:G:18:PHE:HA	7:G:22:MET:HE2	1.99	0.41
1:A:1444:MET:HE3	1:A:1444:MET:HB2	1.86	0.41
6:F:143:PHE:HD1	6:F:143:PHE:C	2.23	0.41
6:F:93:ILE:HD13	6:F:148:VAL:HG13	2.02	0.41
2:B:193:LYS:HD3	2:B:787:VAL:HG11	2.01	0.41
1:A:1044:TRP:O	1:A:1045:VAL:C	2.59	0.41
2:B:1099:VAL:HG13	2:B:1100:ASP:N	2.34	0.41
2:B:233:PRO:HG2	2:B:234:ILE:CD1	2.40	0.41
1:A:843:LYS:HD3	1:A:843:LYS:HA	1.82	0.41
2:B:1197:PRO:O	2:B:1200:ALA:HB3	2.20	0.41
2:B:1165:ILE:CG2	2:B:1166:CYS:N	2.83	0.41
4:D:53:SER:CB	4:D:153:ARG:H	2.32	0.41
5:E:198:ILE:HD11	5:E:212:ARG:CG	2.46	0.41
4:D:66:ARG:CD	4:D:133:THR:HB	2.43	0.41
2:B:954:VAL:HA	2:B:964:VAL:HG22	2.01	0.41
2:B:820:GLY:C	2:B:1091:TYR:CE1	2.94	0.41
1:A:277:GLU:C	1:A:279:LEU:N	2.73	0.41
1:A:1076:ALA:HA	1:A:1079:MET:HE3	2.01	0.41
2:B:1187:ASN:OD1	2:B:1189:ILE:N	2.52	0.41
2:B:854:LEU:HD23	2:B:854:LEU:HA	1.83	0.41
3:C:94:LYS:HE3	3:C:94:LYS:HB2	1.86	0.41
2:B:278:GLN:HG2	2:B:279:ASP:H	1.85	0.41
2:B:1002:THR:O	2:B:1003:ALA:C	2.59	0.41
1:A:1059:HIS:CE1	6:F:86:THR:HA	2.55	0.41
2:B:918:ILE:HG21	2:B:935:ARG:NH1	2.36	0.41
1:A:55:ASP:N	1:A:56:PRO:CD	2.83	0.41
3:C:252:GLN:CG	11:K:95:ILE:HG23	2.50	0.41
2:B:365:THR:HG23	2:B:367:LEU:N	2.27	0.41
1:A:1372:VAL:CG1	1:A:1373:ASP:N	2.82	0.41
1:A:1206:ASP:O	1:A:1274:ARG:NH1	2.51	0.41
1:A:1385:THR:HG22	1:A:1386:ARG:H	1.84	0.41
1:A:414:ASP:OD1	1:A:416:ARG:CG	2.68	0.41
6:F:74:ILE:HG23	6:F:75:PRO:HD2	2.01	0.41
2:B:235:SER:O	2:B:236:HIS:HD2	2.04	0.41
1:A:626:ASN:HB3	1:A:627:GLY:H	1.71	0.41
1:A:890:ASP:H	1:A:1296:GLY:HA3	1.84	0.41
11:K:68:PHE:CD2	11:K:68:PHE:N	2.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:82:PHE:CD1	5:E:82:PHE:N	2.88	0.41
2:B:827:ILE:O	2:B:827:ILE:HG22	2.20	0.41
4:D:138:ASN:O	4:D:141:LEU:N	2.54	0.41
1:A:870:GLU:HG2	5:E:208:TYR:CG	2.55	0.41
2:B:822:ASN:HD22	10:J:52:THR:HG21	1.85	0.41
1:A:1041:ALA:O	1:A:1044:TRP:HB3	2.20	0.41
1:A:356:ASP:C	1:A:358:ASN:H	2.24	0.41
2:B:839:MET:HE3	2:B:1010:LEU:HD21	2.02	0.41
2:B:839:MET:HE1	2:B:980:PHE:CB	2.51	0.41
1:A:70:CYS:O	1:A:70:CYS:SG	2.78	0.41
1:A:1450:LEU:HD21	7:G:19:GLY:O	2.20	0.41
1:A:93:VAL:CG2	1:A:304:MET:HE3	2.50	0.41
4:D:153:ARG:O	4:D:154:PHE:CG	2.73	0.41
1:A:443:LEU:HD11	1:A:455:MET:SD	2.59	0.41
1:A:457:ALA:HB3	1:A:506:ALA:HA	2.01	0.41
1:A:90:VAL:HG13	1:A:297:GLN:OE1	2.20	0.41
6:F:111:LEU:N	6:F:111:LEU:CD1	2.83	0.41
2:B:638:PHE:HD2	2:B:690:VAL:HG22	1.86	0.41
2:B:603:LEU:HB3	2:B:609:ILE:CG1	2.50	0.41
1:A:683:ILE:O	1:A:686:ALA:HB3	2.20	0.41
3:C:116:LYS:HD3	3:C:140:ASN:HB3	2.03	0.41
3:C:123:ASN:HD21	3:C:125:MET:HA	1.85	0.41
2:B:821:GLN:NE2	2:B:851:PHE:HA	2.35	0.41
1:A:940:ARG:NH1	1:A:940:ARG:HG2	2.35	0.41
2:B:769:TYR:C	2:B:771:SER:N	2.73	0.41
2:B:214:ALA:HB3	2:B:498:THR:HA	2.01	0.41
10:J:56:LEU:O	10:J:57:ILE:C	2.58	0.41
4:D:138:ASN:HD21	7:G:35:GLU:HB3	1.86	0.41
6:F:96:THR:O	6:F:99:LEU:HB3	2.21	0.41
11:K:10:PHE:CD1	11:K:11:LEU:CD2	3.04	0.41
9:I:34:TYR:O	9:I:35:VAL:CG2	2.69	0.41
2:B:579:ARG:CA	2:B:589:VAL:HG13	2.51	0.41
1:A:667:GLY:HA3	3:C:192:TRP:CH2	2.56	0.41
2:B:1183:LYS:HE3	2:B:1183:LYS:O	2.20	0.41
2:B:552:MET:O	2:B:554:ILE:N	2.53	0.41
3:C:116:LYS:HD3	3:C:140:ASN:HA	2.03	0.41
2:B:948:ILE:C	2:B:949:VAL:O	2.56	0.41
1:A:1127:ASP:O	1:A:1130:GLN:HB3	2.20	0.41
1:A:444:PHE:CB	1:A:458:HIS:CD2	3.03	0.41
2:B:1164:GLY:HA3	2:B:1190:ASP:OD2	2.21	0.41
7:G:149:GLY:O	7:G:159:ALA:HB1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:474:VAL:C	1:A:477:PRO:HD2	2.41	0.41
2:B:69:LEU:HD22	2:B:429:PHE:CE1	2.56	0.41
1:A:599:SER:HB2	1:A:603:ASN:H	1.84	0.41
10:J:7:CYS:CA	10:J:49:MET:HE3	2.51	0.41
2:B:918:ILE:HD12	2:B:935:ARG:CD	2.51	0.41
1:A:356:ASP:OD2	11:K:65:HIS:CE1	2.71	0.41
2:B:291:ILE:HD13	2:B:300:HIS:NE2	2.36	0.41
5:E:171:LYS:HA	5:E:171:LYS:HD3	1.89	0.41
2:B:1162:ILE:O	2:B:1171:VAL:HG21	2.20	0.41
2:B:687:GLU:O	2:B:689:LEU:HG	2.20	0.41
1:A:265:LYS:HZ1	1:A:322:VAL:HG22	1.84	0.41
2:B:952:VAL:O	2:B:953:LEU:HB3	2.21	0.41
2:B:130:VAL:CG2	2:B:167:ILE:HD12	2.50	0.41
1:A:958:VAL:HG22	1:A:1052:GLN:HB3	2.03	0.41
1:A:1334:ASP:C	1:A:1336:MET:N	2.73	0.41
9:I:61:ASP:C	9:I:63:GLY:N	2.73	0.41
1:A:621:THR:O	1:A:629:LEU:HB2	2.21	0.41
1:A:1157:ASP:O	1:A:1159:ARG:N	2.54	0.41
1:A:822:GLU:O	1:A:825:ILE:HB	2.21	0.41
2:B:558:LEU:C	2:B:560:GLU:N	2.74	0.41
5:E:145:THR:HG21	5:E:187:TYR:CD2	2.56	0.41
2:B:575:PRO:HG2	2:B:576:ASP:H	1.86	0.41
8:H:56:THR:O	8:H:144:ILE:HA	2.21	0.41
1:A:464:PRO:HG2	1:A:465:TYR:CD1	2.54	0.41
1:A:353:ILE:HD13	1:A:487:MET:CE	2.50	0.41
5:E:98:ILE:O	5:E:99:HIS:C	2.59	0.41
3:C:240:VAL:O	3:C:244:VAL:HG23	2.21	0.41
2:B:168:GLY:N	2:B:450:ALA:HB1	2.19	0.41
5:E:60:PHE:CE2	5:E:80:VAL:HB	2.56	0.41
1:A:343:LYS:HE2	2:B:1156:ASP:OD2	2.21	0.41
1:A:1425:SER:O	1:A:1429:ILE:HG13	2.21	0.41
11:K:113:THR:O	11:K:114:LEU:CB	2.63	0.41
4:D:196:PRO:C	4:D:198:LEU:H	2.23	0.41
2:B:446:LEU:O	2:B:447:ALA:CB	2.66	0.41
11:K:12:LEU:CD1	11:K:12:LEU:H	2.32	0.41
1:A:446:ARG:NH1	1:A:479:ASN:O	2.54	0.41
1:A:1334:ASP:C	1:A:1336:MET:H	2.23	0.41
2:B:496:ARG:NH1	2:B:496:ARG:HB3	2.36	0.41
1:A:789:LYS:HE3	9:I:67:THR:HB	2.03	0.41
1:A:452:LYS:HE2	1:A:452:LYS:HB3	1.74	0.41
2:B:589:VAL:CG1	2:B:590:HIS:H	2.11	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1080:LYS:HD2	3:C:188:HIS:HB2	2.03	0.41
1:A:1410:PHE:C	1:A:1412:ALA:H	2.23	0.41
5:E:116:ILE:CG2	5:E:117:THR:N	2.83	0.41
2:B:912:ILE:HD11	2:B:966:VAL:HG23	2.03	0.41
2:B:637:LEU:HD23	2:B:742:GLU:HA	2.02	0.41
1:A:809:THR:O	1:A:810:PRO:C	2.59	0.41
1:A:774:ARG:CZ	1:A:797:LYS:CB	2.98	0.41
12:L:62:LYS:O	12:L:63:ARG:C	2.59	0.41
4:D:156:ASP:O	4:D:158:GLU:N	2.54	0.41
3:C:11:ARG:NH2	3:C:206:ASN:OD1	2.54	0.41
2:B:522:VAL:HG12	2:B:523:CYS:N	2.36	0.41
2:B:487:THR:O	2:B:490:SER:HB3	2.21	0.41
2:B:20:ASP:O	2:B:22:SER:N	2.45	0.41
1:A:242:PRO:O	1:A:247:ARG:NE	2.52	0.41
1:A:596:THR:C	1:A:598:LEU:N	2.73	0.41
1:A:1444:MET:O	6:F:132:LEU:HA	2.20	0.41
1:A:1059:HIS:CE1	6:F:87:LYS:H	2.39	0.41
6:F:99:LEU:O	6:F:103:MET:CG	2.69	0.41
2:B:102:VAL:CG2	2:B:112:LEU:HB2	2.41	0.41
2:B:479:VAL:O	2:B:480:SER:HB3	2.20	0.41
5:E:98:ILE:O	5:E:100:ILE:N	2.53	0.41
5:E:23:VAL:O	5:E:28:TYR:HD1	2.03	0.41
2:B:842:ASN:HD21	2:B:845:SER:H	1.60	0.41
1:A:343:LYS:NZ	2:B:1151:LEU:O	2.46	0.41
1:A:744:LYS:O	1:A:747:VAL:N	2.54	0.41
11:K:40:HIS:O	11:K:41:THR:C	2.59	0.41
2:B:1208:MET:HA	2:B:1212:ILE:O	2.20	0.41
5:E:90:VAL:CA	5:E:120:ALA:HB2	2.49	0.41
1:A:527:THR:O	1:A:531:ILE:HB	2.21	0.41
2:B:1068:GLY:O	2:B:1069:PHE:C	2.59	0.41
3:C:73:GLN:HE21	3:C:74:SER:N	2.19	0.41
2:B:595:ARG:O	2:B:596:LEU:C	2.59	0.41
1:A:152:VAL:HG13	1:A:153:PRO:HD2	1.97	0.41
1:A:541:ILE:CG2	1:A:546:VAL:HG23	2.50	0.41
1:A:332:LYS:C	1:A:334:GLY:H	2.25	0.41
3:C:177:GLU:HG3	3:C:231:ASN:HD22	1.86	0.41
1:A:645:LEU:O	1:A:646:PHE:C	2.59	0.41
1:A:1299:VAL:CG1	1:A:1300:LYS:N	2.83	0.41
11:K:43:GLY:HA3	11:K:61:TYR:CE1	2.56	0.41
1:A:586:ILE:CG2	1:A:587:HIS:N	2.83	0.41
1:A:1213:GLY:O	1:A:1214:GLU:C	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:492:LEU:O	2:B:493:SER:C	2.60	0.41
2:B:288:ALA:HA	2:B:331:LEU:HD12	2.02	0.41
1:A:829:VAL:C	1:A:831:THR:N	2.74	0.41
1:A:116:ASP:C	1:A:118:HIS:N	2.71	0.41
4:D:206:GLU:C	4:D:208:GLU:H	2.23	0.41
7:G:101:VAL:HG12	7:G:102:GLN:N	2.35	0.41
7:G:74:TYR:N	7:G:74:TYR:CD2	2.88	0.41
1:A:567:LYS:HG3	1:A:568:PRO:CD	2.39	0.41
2:B:65:GLU:HG3	2:B:66:ASP:OD1	2.21	0.41
2:B:800:GLN:CA	10:J:52:THR:HG22	2.51	0.41
2:B:1147:LEU:CD2	2:B:1151:LEU:HD22	2.51	0.41
2:B:1200:ALA:O	2:B:1203:LEU:HB3	2.21	0.41
2:B:910:VAL:HG12	2:B:911:ILE:N	2.35	0.41
1:A:1152:ILE:CG1	9:I:44:TYR:HB3	2.46	0.41
1:A:577:ILE:O	1:A:578:LEU:C	2.56	0.41
1:A:1019:CYS:O	1:A:1023:ARG:N	2.45	0.41
2:B:54:PHE:CE2	2:B:59:LEU:HD13	2.55	0.41
1:A:7:SER:HB2	2:B:1175:LEU:HD22	2.03	0.41
2:B:435:THR:C	2:B:437:GLU:H	2.23	0.41
1:A:838:GLN:HG2	1:A:1073:GLY:HA3	2.03	0.41
1:A:373:THR:HG21	2:B:1105:ALA:CB	2.51	0.41
2:B:390:LEU:O	2:B:391:ASP:C	2.58	0.41
3:C:62:PHE:O	3:C:66:ARG:HG3	2.21	0.40
8:H:96:VAL:HA	8:H:142:LEU:O	2.21	0.40
2:B:801:LYS:N	10:J:52:THR:HG22	2.36	0.40
1:A:445:ASN:CB	1:A:455:MET:HG2	2.44	0.40
1:A:296:LEU:O	1:A:297:GLN:C	2.58	0.40
1:A:1120:LEU:CD1	1:A:1304:TRP:O	2.69	0.40
9:I:50:THR:HG22	9:I:52:ILE:N	2.32	0.40
2:B:838:SER:CA	2:B:989:THR:O	2.69	0.40
1:A:935:GLN:O	1:A:936:LEU:C	2.59	0.40
1:A:1011:GLN:O	1:A:1012:ARG:C	2.59	0.40
2:B:100:PRO:HD2	2:B:180:TYR:CE1	2.56	0.40
1:A:416:ARG:O	1:A:417:TYR:HD2	2.03	0.40
1:A:1135:ARG:C	1:A:1137:ALA:H	2.24	0.40
2:B:810:GLU:CB	2:B:815:ARG:HH22	2.33	0.40
3:C:80:LEU:CD1	3:C:95:CYS:HA	2.51	0.40
2:B:487:THR:CG2	2:B:488:TYR:N	2.84	0.40
1:A:514:PRO:C	1:A:516:SER:N	2.75	0.40
7:G:31:LEU:CD2	7:G:48:VAL:HG21	2.51	0.40
2:B:1087:PHE:CD2	2:B:1088:GLY:N	2.80	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:123:LYS:O	6:F:124:GLU:C	2.58	0.40
2:B:841:MET:O	2:B:993:THR:HA	2.21	0.40
2:B:211:VAL:HG23	2:B:483:LEU:HB2	2.03	0.40
1:A:306:ASN:HB2	1:A:324:SER:HB3	2.02	0.40
1:A:532:ARG:O	1:A:535:THR:HB	2.22	0.40
12:L:38:LEU:O	12:L:39:SER:CB	2.63	0.40
3:C:181:ASP:CG	3:C:186:LEU:HD13	2.42	0.40
7:G:50:ASP:O	7:G:51:TYR:C	2.58	0.40
1:A:877:HIS:O	1:A:878:ILE:HG12	2.21	0.40
1:A:1333:ILE:O	1:A:1337:GLU:HG3	2.21	0.40
1:A:7:SER:C	1:A:9:ALA:H	2.23	0.40
1:A:6:TYR:CD1	1:A:7:SER:N	2.89	0.40
10:J:34:THR:O	10:J:35:ALA:C	2.59	0.40
1:A:1173:HIS:C	1:A:1174:PHE:CD1	2.94	0.40
1:A:1389:PHE:CD1	1:A:1389:PHE:C	2.94	0.40
7:G:82:PHE:CD1	7:G:82:PHE:N	2.90	0.40
1:A:1163:ILE:HG22	1:A:1164:PRO:HD2	2.04	0.40
2:B:520:GLY:H	2:B:748:ILE:HG22	1.87	0.40
1:A:870:GLU:HB2	5:E:204:THR:HG21	2.03	0.40
1:A:1118:VAL:O	1:A:1118:VAL:HG23	2.20	0.40
1:A:1332:PHE:HA	1:A:1335:ILE:HB	2.03	0.40
1:A:255:SER:O	1:A:256:GLN:HG3	2.20	0.40
1:A:913:LEU:HD23	1:A:919:ILE:HD12	2.04	0.40
1:A:399:HIS:O	1:A:400:PRO:C	2.58	0.40
1:A:70:CYS:O	1:A:71:GLN:C	2.59	0.40
2:B:1135:ARG:O	2:B:1138:MET:N	2.54	0.40
1:A:344:ARG:HG2	1:A:344:ARG:NH1	2.36	0.40
1:A:432:VAL:O	1:A:433:GLU:C	2.60	0.40
1:A:1434:ALA:CB	1:A:1436:ILE:HD12	2.52	0.40
1:A:326:ARG:NH2	1:A:1407:GLU:HG3	2.36	0.40
1:A:24:PRO:O	1:A:28:ARG:HG3	2.21	0.40
2:B:1178:ASN:O	2:B:1180:PHE:CD1	2.74	0.40
2:B:519:TRP:HE1	2:B:635:ARG:NH2	2.19	0.40
2:B:983:ARG:HD2	2:B:1091:TYR:HB3	2.02	0.40
2:B:309:GLN:CG	9:I:52:ILE:HD11	2.51	0.40
1:A:331:GLY:O	1:A:332:LYS:HB3	2.20	0.40
4:D:51:ASN:C	4:D:52:LEU:O	2.59	0.40
1:A:1313:LEU:C	1:A:1315:GLU:H	2.24	0.40
2:B:286:PHE:HE2	2:B:375:ALA:HB1	1.87	0.40
5:E:127:ILE:O	5:E:127:ILE:HG13	2.21	0.40
3:C:206:ASN:OD1	3:C:229:TYR:CD2	2.74	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:500:THR:HA	2:B:501:PRO:HD2	1.87	0.40
10:J:3:VAL:HA	10:J:4:PRO:HD3	1.88	0.40
1:A:455:MET:HE1	2:B:1134:GLU:HB3	2.02	0.40
5:E:16:PHE:O	5:E:17:ARG:C	2.59	0.40
2:B:593:PRO:O	2:B:594:ALA:C	2.60	0.40
2:B:701:ILE:HG13	2:B:702:LEU:N	2.35	0.40
1:A:1227:ILE:CG2	1:A:1228:TRP:H	2.35	0.40
2:B:758:PHE:HZ	2:B:1031:LEU:HD22	1.86	0.40
2:B:758:PHE:O	2:B:760:ASP:N	2.54	0.40
1:A:1370:LEU:O	1:A:1373:ASP:HB2	2.21	0.40
1:A:130:ASP:O	1:A:132:LYS:N	2.55	0.40
1:A:1027:ALA:O	1:A:1028:THR:C	2.59	0.40
2:B:901:PRO:O	2:B:949:VAL:HB	2.21	0.40
1:A:172:PRO:HD3	1:A:185:TRP:HE1	1.86	0.40
3:C:245:VAL:C	3:C:247:GLY:N	2.74	0.40
2:B:641:GLU:C	2:B:643:ASP:H	2.25	0.40
2:B:1124:ARG:O	2:B:1125:ASP:CB	2.68	0.40
1:A:696:GLU:O	1:A:696:GLU:HG2	2.21	0.40
1:A:1067:LEU:HD12	1:A:1071:SER:OG	2.21	0.40
2:B:798:TYR:CE2	3:C:62:PHE:HE2	2.38	0.40
10:J:2:ILE:H	10:J:57:ILE:HG22	1.87	0.40
1:A:252:PHE:HB2	1:A:256:GLN:CD	2.42	0.40
11:K:65:HIS:CG	11:K:66:PRO:HD2	2.56	0.40
5:E:23:VAL:HG13	5:E:78:LEU:CD1	2.49	0.40
5:E:23:VAL:O	5:E:23:VAL:HG12	2.21	0.40
1:A:69:THR:O	1:A:71:GLN:HG2	2.21	0.40
1:A:874:ASP:HA	1:A:1058:VAL:HG22	2.03	0.40
1:A:403:LYS:O	1:A:404:TYR:CG	2.74	0.40
1:A:222:LEU:O	1:A:224:PHE:N	2.55	0.40
1:A:1205:LYS:O	1:A:1206:ASP:C	2.59	0.40
1:A:1019:CYS:O	1:A:1020:CYS:C	2.60	0.40
1:A:1381:LEU:HD23	1:A:1381:LEU:HA	1.77	0.40
1:A:418:SER:C	1:A:420:ARG:H	2.24	0.40
7:G:49:LEU:HD23	7:G:49:LEU:N	2.35	0.40
2:B:386:LEU:O	2:B:388:CYS:N	2.55	0.40
5:E:8:ASN:O	5:E:8:ASN:OD1	2.40	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1406/1733 (81%)	949 (68%)	293 (21%)	164 (12%)	0	9
2	B	1077/1224 (88%)	735 (68%)	221 (20%)	121 (11%)	0	10
3	C	264/318 (83%)	159 (60%)	66 (25%)	39 (15%)	0	5
4	D	173/177 (98%)	122 (70%)	34 (20%)	17 (10%)	1	14
5	E	212/215 (99%)	148 (70%)	49 (23%)	15 (7%)	1	23
6	F	82/155 (53%)	64 (78%)	14 (17%)	4 (5%)	3	32
7	G	169/171 (99%)	131 (78%)	26 (15%)	12 (7%)	1	23
8	H	129/146 (88%)	84 (65%)	29 (22%)	16 (12%)	0	8
9	I	117/122 (96%)	80 (68%)	29 (25%)	8 (7%)	1	24
10	J	63/70 (90%)	37 (59%)	10 (16%)	16 (25%)	0	1
11	K	113/120 (94%)	89 (79%)	18 (16%)	6 (5%)	2	30
12	L	44/70 (63%)	19 (43%)	14 (32%)	11 (25%)	0	1
All	All	3849/4521 (85%)	2617 (68%)	803 (21%)	429 (11%)	0	10

All (429) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	48	ALA
1	A	54	ASN
1	A	55	ASP
1	A	57	ARG
1	A	62	ASP
1	A	65	LEU
1	A	74	MET
1	A	76	GLU
1	A	78	PRO
1	A	93	VAL
1	A	130	ASP

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Mol	Chain	Res	Type
1	A	154	SER
1	A	167	CYS
1	A	250	ILE
1	A	255	SER
1	A	286	HIS
1	A	311	GLN
1	A	322	VAL
1	A	333	GLU
1	A	335	ARG
1	A	385	ILE
1	A	418	SER
1	A	423	ASP
1	A	424	ILE
1	A	536	LEU
1	A	567	LYS
1	A	619	LYS
1	A	626	ASN
1	A	666	ILE
1	A	775	ILE
1	A	968	GLN
1	A	1002	GLY
1	A	1036	ARG
1	A	1115	SER
1	A	1122	PRO
1	A	1223	ASP
1	A	1281	ARG
1	A	1314	SER
1	A	1341	ILE
1	A	1365	TYR
1	A	1366	ARG
1	A	1378	GLN
1	A	1397	LEU
1	A	1403	GLU
1	A	1405	THR
1	A	1438	THR
2	B	108	VAL
2	B	115	GLN
2	B	186	GLU
2	B	206	ASN
2	B	258	LEU
2	B	259	TYR
2	B	334	ILE

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Mol	Chain	Res	Type
2	B	367	LEU
2	B	629	ASP
2	B	643	ASP
2	B	709	ASP
2	B	727	LYS
2	B	731	VAL
2	B	746	SER
2	B	751	VAL
2	B	881	ASN
2	B	891	ASP
2	B	907	GLY
2	B	958	GLN
2	B	1006	ILE
2	B	1046	PRO
2	B	1069	PHE
2	B	1100	ASP
2	B	1108	ARG
2	B	1156	ASP
2	B	1171	VAL
2	B	1175	LEU
2	B	1181	GLU
2	B	1182	CYS
2	B	1183	LYS
2	B	1186	ASP
2	B	1188	LYS
3	C	56	THR
3	C	78	GLU
3	C	91	HIS
3	C	141	GLY
3	C	149	LYS
3	C	156	THR
3	C	161	LYS
3	C	184	ASN
3	C	202	PRO
3	C	209	TYR
3	C	213	PRO
3	C	214	ASN
3	C	215	GLU
3	C	231	ASN
3	C	240	VAL
4	D	6	SER
4	D	8	PHE

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Mol	Chain	Res	Type
4	D	12	ARG
4	D	19	GLU
4	D	20	GLU
4	D	21	GLU
4	D	52	LEU
4	D	131	GLU
4	D	177	VAL
4	D	192	LYS
4	D	199	ASN
5	E	106	GLN
5	E	130	ALA
7	G	62	LEU
7	G	63	PRO
7	G	139	ILE
8	H	81	PRO
8	H	128	ASN
8	H	140	ALA
9	I	3	THR
9	I	9	ASP
9	I	106	CYS
10	J	2	ILE
10	J	6	ARG
10	J	8	PHE
10	J	9	SER
10	J	17	LYS
10	J	28	ASP
10	J	32	GLU
10	J	64	ASN
11	K	114	LEU
12	L	50	ASP
12	L	53	HIS
12	L	59	ALA
1	A	4	GLN
1	A	42	ASP
1	A	44	THR
1	A	59	GLY
1	A	61	ILE
1	A	66	LYS
1	A	70	CYS
1	A	101	LYS
1	A	111	GLY
1	A	113	LEU

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Mol	Chain	Res	Type
1	A	244	PRO
1	A	263	THR
1	A	290	GLU
1	A	312	PRO
1	A	318	SER
1	A	336	ILE
1	A	364	VAL
1	A	409	SER
1	A	421	ALA
1	A	483	ASP
1	A	661	GLY
1	A	753	GLY
1	A	765	VAL
1	A	780	VAL
1	A	789	LYS
1	A	818	MET
1	A	824	LEU
1	A	846	GLU
1	A	847	ASP
1	A	875	ALA
1	A	986	ILE
1	A	1008	GLN
1	A	1016	THR
1	A	1116	LEU
1	A	1120	LEU
1	A	1133	LEU
1	A	1165	GLU
1	A	1212	VAL
1	A	1221	LYS
1	A	1233	ASP
1	A	1335	ILE
1	A	1377	THR
1	A	1386	ARG
1	A	1389	PHE
1	A	1393	ASN
2	B	21	GLU
2	B	28	GLU
2	B	45	SER
2	B	46	GLN
2	B	114	PRO
2	B	229	ALA
2	B	260	GLY

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Mol	Chain	Res	Type
2	B	266	ALA
2	B	282	ILE
2	B	308	TRP
2	B	513	GLN
2	B	559	SER
2	B	641	GLU
2	B	655	LYS
2	B	869	SER
2	B	888	GLY
2	B	1003	ALA
2	B	1035	ALA
2	B	1041	GLU
2	B	1126	GLY
2	B	1153	GLU
2	B	1155	SER
2	B	1157	ALA
2	B	1167	GLY
2	B	1176	ASN
2	B	1178	ASN
3	C	84	ARG
3	C	87	PHE
3	C	110	THR
3	C	142	VAL
3	C	164	ALA
3	C	169	LYS
3	C	175	ALA
3	C	216	GLY
3	C	255	VAL
3	C	264	GLN
4	D	15	LEU
4	D	218	GLU
5	E	36	GLU
5	E	44	ALA
5	E	59	SER
5	E	73	PRO
5	E	74	ASP
5	E	192	ARG
5	E	206	GLY
6	F	81	THR
7	G	118	ASP
7	G	154	VAL
8	H	32	THR

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Mol	Chain	Res	Type
8	H	59	ILE
8	H	82	PRO
8	H	84	ALA
8	H	92	ASP
8	H	107	VAL
9	I	57	GLY
9	I	62	ILE
10	J	14	VAL
10	J	29	GLU
10	J	33	GLY
11	K	53	ASP
12	L	35	SER
1	A	58	LEU
1	A	71	GLN
1	A	117	GLU
1	A	131	SER
1	A	170	THR
1	A	219	PHE
1	A	223	GLY
1	A	232	GLU
1	A	253	ASN
1	A	278	THR
1	A	317	LYS
1	A	357	PRO
1	A	399	HIS
1	A	419	LYS
1	A	439	ASN
1	A	465	TYR
1	A	517	ASN
1	A	543	LEU
1	A	592	ASP
1	A	605	MET
1	A	731	ARG
1	A	817	ALA
1	A	940	ARG
1	A	1164	PRO
1	A	1309	ASP
1	A	1395	GLY
1	A	1411	GLU
2	B	58	THR
2	B	383	ASN
2	B	450	ALA

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Mol	Chain	Res	Type
2	B	459	TYR
2	B	512	ARG
2	B	571	PRO
2	B	590	HIS
2	B	591	ARG
2	B	605	ARG
2	B	648	HIS
2	B	682	SER
2	B	711	GLU
2	B	738	PHE
2	B	792	MET
2	B	797	TYR
2	B	848	ARG
2	B	878	GLN
2	B	884	ARG
2	B	943	SER
2	B	1017	ILE
3	C	60	ASP
3	C	89	GLU
3	C	93	ASP
3	C	167	HIS
5	E	115	ASN
7	G	53	ASN
8	H	17	PRO
8	H	77	ARG
8	H	108	SER
8	H	135	LEU
9	I	78	CYS
10	J	24	LEU
10	J	51	LEU
10	J	55	ASP
11	K	54	ARG
11	K	88	LYS
12	L	40	LEU
12	L	54	ARG
1	A	69	THR
1	A	276	LEU
1	A	283	GLY
1	A	400	PRO
1	A	756	ILE
1	A	795	GLU
1	A	910	PRO

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Mol	Chain	Res	Type
1	A	958	VAL
1	A	1011	GLN
1	A	1028	THR
1	A	1114	PRO
1	A	1240	CYS
1	A	1242	VAL
1	A	1297	GLU
2	B	67	SER
2	B	68	THR
2	B	100	PRO
2	B	124	TYR
2	B	257	LYS
2	B	369	GLY
2	B	419	THR
2	B	594	ALA
2	B	620	ARG
2	B	735	ALA
2	B	883	LEU
2	B	951	GLN
2	B	1011	ILE
2	B	1082	MET
2	B	1097	HIS
2	B	1144	ALA
3	C	77	ILE
3	C	198	ALA
4	D	30	GLY
7	G	19	GLY
7	G	26	LEU
8	H	44	VAL
8	H	52	GLN
9	I	47	GLU
10	J	27	GLU
11	K	29	ASN
12	L	43	THR
12	L	56	LEU
12	L	60	ARG
1	A	68	GLN
1	A	128	ILE
1	A	226	GLU
1	A	598	LEU
1	A	599	SER
1	A	633	VAL

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Mol	Chain	Res	Type
1	A	648	ASN
1	A	649	ILE
1	A	739	ASP
1	A	755	PHE
1	A	841	LEU
1	A	871	ASP
1	A	969	GLN
1	A	1054	LEU
1	A	1266	THR
2	B	27	ALA
2	B	48	LEU
2	B	65	GLU
2	B	197	PHE
2	B	309	GLN
2	B	414	ALA
2	B	418	LYS
2	B	530	GLY
2	B	636	PRO
2	B	758	PHE
2	B	766	ARG
2	B	867	GLY
2	B	1016	ALA
3	C	108	GLU
4	D	168	LYS
5	E	40	GLU
5	E	45	LYS
6	F	112	GLU
6	F	150	GLU
7	G	34	VAL
7	G	115	MET
1	A	84	ILE
1	A	245	PRO
1	A	492	PRO
1	A	525	GLN
1	A	1158	PRO
1	A	1396	ALA
2	B	313	MET
2	B	364	ILE
2	B	480	SER
2	B	836	GLU
2	B	1214	PRO
3	C	18	VAL

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Mol	Chain	Res	Type
3	C	176	ILE
3	C	230	MET
4	D	69	ALA
4	D	139	LYS
5	E	158	SER
8	H	21	ASN
9	I	34	TYR
10	J	63	TYR
11	K	90	ALA
12	L	28	LYS
12	L	46	VAL
1	A	196	GLU
1	A	300	VAL
1	A	627	GLY
1	A	1057	VAL
2	B	611	PRO
2	B	712	PRO
3	C	172	PRO
3	C	212	PRO
1	A	652	VAL
1	A	653	VAL
2	B	501	PRO
2	B	551	PRO
5	E	37	LEU
1	A	546	VAL
1	A	825	ILE
1	A	1379	GLY
1	A	1454	MET
2	B	411	PRO
2	B	818	PRO
2	B	1018	PRO
3	C	171	GLY
2	B	524	PRO
3	C	126	GLY
6	F	131	PRO
7	G	20	PRO
7	G	116	PRO
2	B	592	ASN
5	E	129	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1239/1520 (82%)	1135 (92%)	104 (8%)	14	52
2	B	952/1061 (90%)	866 (91%)	86 (9%)	12	49
3	C	234/274 (85%)	212 (91%)	22 (9%)	11	47
4	D	140/159 (88%)	124 (89%)	16 (11%)	7	37
5	E	196/197 (100%)	187 (95%)	9 (5%)	33	72
6	F	74/137 (54%)	65 (88%)	9 (12%)	6	34
7	G	152/152 (100%)	142 (93%)	10 (7%)	21	62
8	H	117/128 (91%)	111 (95%)	6 (5%)	29	69
9	I	113/116 (97%)	99 (88%)	14 (12%)	6	33
10	J	60/65 (92%)	54 (90%)	6 (10%)	9	43
11	K	99/102 (97%)	92 (93%)	7 (7%)	18	59
12	L	40/57 (70%)	37 (92%)	3 (8%)	17	57
All	All	3416/3968 (86%)	3124 (92%)	292 (8%)	13	52

All (292) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	VAL
1	A	11	LEU
1	A	22	PHE
1	A	34	LYS
1	A	38	PRO
1	A	62	ASP
1	A	67	CYS
1	A	83	HIS
1	A	93	VAL
1	A	105	CYS
1	A	108	MET
1	A	208	LEU
1	A	209	ASN
1	A	215	SER

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Mol	Chain	Res	Type
1	A	236	LEU
1	A	245	PRO
1	A	270	LEU
1	A	293	GLU
1	A	302	THR
1	A	312	PRO
1	A	320	ARG
1	A	335	ARG
1	A	345	VAL
1	A	354	SER
1	A	369	SER
1	A	381	THR
1	A	404	TYR
1	A	406	ILE
1	A	407	ARG
1	A	408	ASP
1	A	418	SER
1	A	425	GLN
1	A	443	LEU
1	A	445	ASN
1	A	450	LEU
1	A	451	HIS
1	A	454	SER
1	A	460	VAL
1	A	470	LEU
1	A	481	ASP
1	A	493	GLN
1	A	497	THR
1	A	503	GLN
1	A	515	GLN
1	A	560	ILE
1	A	562	THR
1	A	587	HIS
1	A	598	LEU
1	A	618	GLU
1	A	626	ASN
1	A	629	LEU
1	A	666	ILE
1	A	670	ILE
1	A	711	ARG
1	A	739	ASP
1	A	774	ARG

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Mol	Chain	Res	Type
1	A	779	PHE
1	A	821	ARG
1	A	831	THR
1	A	834	THR
1	A	845	LEU
1	A	854	ASN
1	A	858	ASN
1	A	890	ASP
1	A	903	ASN
1	A	929	LEU
1	A	940	ARG
1	A	949	ASP
1	A	969	GLN
1	A	1006	ILE
1	A	1016	THR
1	A	1029	ARG
1	A	1032	LEU
1	A	1035	TYR
1	A	1052	GLN
1	A	1067	LEU
1	A	1110	ASN
1	A	1111	MET
1	A	1116	LEU
1	A	1122	PRO
1	A	1127	ASP
1	A	1152	ILE
1	A	1155	ASP
1	A	1170	ILE
1	A	1173	HIS
1	A	1264	GLU
1	A	1271	ILE
1	A	1291	VAL
1	A	1295	THR
1	A	1298	TYR
1	A	1309	ASP
1	A	1332	PHE
1	A	1333	ILE
1	A	1359	ASP
1	A	1364	ASN
1	A	1366	ARG
1	A	1372	VAL
1	A	1400	CYS

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Mol	Chain	Res	Type
1	A	1405	THR
1	A	1432	GLN
1	A	1442	ASP
1	A	1443	VAL
1	A	1445	ILE
1	A	1447	GLU
2	B	44	VAL
2	B	57	TYR
2	B	61	ASP
2	B	128	LEU
2	B	175	ARG
2	B	188	ASP
2	B	194	GLU
2	B	199	MET
2	B	217	ARG
2	B	223	VAL
2	B	225	VAL
2	B	261	ARG
2	B	268	THR
2	B	286	PHE
2	B	294	ASP
2	B	298	LEU
2	B	360	PHE
2	B	365	THR
2	B	371	GLU
2	B	378	LEU
2	B	393	LYS
2	B	396	ASP
2	B	401	PHE
2	B	427	ASP
2	B	429	PHE
2	B	463	THR
2	B	465	ASN
2	B	466	TRP
2	B	485	ARG
2	B	496	ARG
2	B	498	THR
2	B	516	ASN
2	B	555	ILE
2	B	557	PHE
2	B	570	VAL
2	B	582	VAL

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Mol	Chain	Res	Type
2	B	593	PRO
2	B	603	LEU
2	B	615	MET
2	B	628	THR
2	B	635	ARG
2	B	636	PRO
2	B	644	GLU
2	B	682	SER
2	B	701	ILE
2	B	724	ASP
2	B	737	THR
2	B	742	GLU
2	B	751	VAL
2	B	811	TYR
2	B	830	TYR
2	B	835	GLN
2	B	839	MET
2	B	878	GLN
2	B	894	ASP
2	B	901	PRO
2	B	909	ASP
2	B	939	THR
2	B	953	LEU
2	B	956	THR
2	B	978	ASP
2	B	986	GLN
2	B	999	MET
2	B	1002	THR
2	B	1006	ILE
2	B	1010	LEU
2	B	1022	THR
2	B	1034	VAL
2	B	1047	PHE
2	B	1051	THR
2	B	1065	GLN
2	B	1069	PHE
2	B	1077	THR
2	B	1084	GLN
2	B	1087	PHE
2	B	1095	LEU
2	B	1099	VAL
2	B	1103	ILE

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Mol	Chain	Res	Type
2	B	1122	ARG
2	B	1159	ARG
2	B	1169	MET
2	B	1170	THR
2	B	1183	LYS
2	B	1202	LEU
2	B	1212	ILE
2	B	1216	LEU
3	C	22	LEU
3	C	23	SER
3	C	29	MET
3	C	54	ASN
3	C	57	VAL
3	C	58	LEU
3	C	62	PHE
3	C	77	ILE
3	C	89	GLU
3	C	91	HIS
3	C	104	PHE
3	C	106	GLU
3	C	108	GLU
3	C	128	ASN
3	C	140	ASN
3	C	145	CYS
3	C	147	LEU
3	C	166	GLU
3	C	202	PRO
3	C	233	GLU
3	C	240	VAL
3	C	266	ASP
4	D	32	GLU
4	D	47	LEU
4	D	63	LEU
4	D	70	PHE
4	D	137	ASN
4	D	139	LYS
4	D	148	LEU
4	D	149	THR
4	D	152	SER
4	D	156	ASP
4	D	170	THR
4	D	187	THR

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Mol	Chain	Res	Type
4	D	192	LYS
4	D	193	THR
4	D	202	ILE
4	D	221	TYR
5	E	60	PHE
5	E	74	ASP
5	E	104	ASN
5	E	114	ASN
5	E	146	HIS
5	E	175	LEU
5	E	183	PRO
5	E	207	ARG
5	E	215	MET
6	F	79	ARG
6	F	81	THR
6	F	90	ARG
6	F	99	LEU
6	F	116	ASP
6	F	119	ARG
6	F	143	PHE
6	F	148	VAL
6	F	153	VAL
7	G	1	MET
7	G	13	LEU
7	G	38	CYS
7	G	39	THR
7	G	74	TYR
7	G	78	VAL
7	G	80	LYS
7	G	96	GLN
7	G	126	ASN
7	G	171	ILE
8	H	62	SER
8	H	86	ASP
8	H	91	ASP
8	H	95	TYR
8	H	102	TYR
8	H	130	ARG
9	I	8	ARG
9	I	9	ASP
9	I	13	MET
9	I	15	TYR

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Mol	Chain	Res	Type
9	I	34	TYR
9	I	75	CYS
9	I	78	CYS
9	I	85	PHE
9	I	86	PHE
9	I	94	ASP
9	I	100	PHE
9	I	101	PHE
9	I	106	CYS
9	I	110	PHE
10	J	7	CYS
10	J	9	SER
10	J	10	CYS
10	J	44	TYR
10	J	46	CYS
10	J	48	ARG
11	K	10	PHE
11	K	25	THR
11	K	42	LEU
11	K	47	ARG
11	K	50	LEU
11	K	61	TYR
11	K	78	THR
12	L	55	ILE
12	L	68	GLU
12	L	70	ARG

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

Mol	Chain	Res	Type
1	A	54	ASN
1	A	64	ASN
1	A	68	GLN
1	A	92	HIS
1	A	225	ASN
1	A	256	GLN
1	A	282	ASN
1	A	299	HIS
1	A	306	ASN
1	A	339	ASN
1	A	358	ASN
1	A	435	HIS

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Mol	Chain	Res	Type
1	A	445	ASN
1	A	479	ASN
1	A	493	GLN
1	A	503	GLN
1	A	517	ASN
1	A	525	GLN
1	A	603	ASN
1	A	611	GLN
1	A	631	HIS
1	A	654	ASN
1	A	741	ASN
1	A	757	ASN
1	A	768	GLN
1	A	786	HIS
1	A	858	ASN
1	A	903	ASN
1	A	926	GLN
1	A	1106	ASN
1	A	1265	ASN
1	A	1364	ASN
2	B	60	GLN
2	B	178	ASN
2	B	215	GLN
2	B	236	HIS
2	B	363	HIS
2	B	366	GLN
2	B	465	ASN
2	B	484	ASN
2	B	515	HIS
2	B	518	HIS
2	B	538	ASN
2	B	734	HIS
2	B	744	HIS
2	B	821	GLN
2	B	842	ASN
2	B	975	GLN
2	B	1015	HIS
2	B	1065	GLN
2	B	1076	HIS
2	B	1117	GLN
2	B	1193	GLN
3	C	73	GLN

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Mol	Chain	Res	Type
3	C	91	HIS
3	C	112	ASN
3	C	123	ASN
3	C	167	HIS
3	C	231	ASN
3	C	252	GLN
4	D	40	HIS
4	D	137	ASN
4	D	179	GLN
5	E	8	ASN
5	E	101	GLN
5	E	104	ASN
5	E	114	ASN
5	E	147	HIS
7	G	14	HIS
7	G	53	ASN
7	G	97	HIS
7	G	126	ASN
9	I	12	ASN
9	I	60	GLN
9	I	89	GLN
10	J	53	HIS
11	K	65	HIS
11	K	76	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1416/1733 (81%)	-0.34	10 (0%) 89 80	19, 87, 162, 200	0
2	B	1097/1224 (89%)	-0.30	8 (0%) 89 80	23, 97, 166, 194	0
3	C	266/318 (83%)	-0.39	0 100 100	37, 81, 139, 160	0
4	D	177/177 (100%)	-0.34	0 100 100	52, 108, 147, 165	0
5	E	214/215 (99%)	-0.31	1 (0%) 91 85	57, 142, 187, 193	0
6	F	84/155 (54%)	-0.63	0 100 100	25, 59, 105, 124	0
7	G	171/171 (100%)	-0.29	0 100 100	57, 84, 114, 138	0
8	H	133/146 (91%)	0.06	2 (1%) 76 62	101, 139, 175, 184	0
9	I	119/122 (97%)	-0.09	2 (1%) 73 58	74, 130, 159, 200	0
10	J	65/70 (92%)	-0.57	0 100 100	42, 79, 120, 127	0
11	K	115/120 (95%)	-0.32	0 100 100	42, 83, 114, 123	0
12	L	46/70 (65%)	-0.22	1 (2%) 65 50	76, 137, 168, 177	0
All	All	3903/4521 (86%)	-0.32	24 (0%) 90 82	19, 94, 166, 200	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1176	LEU	7.5
2	B	882	THR	4.3
9	I	119	THR	3.5
2	B	919	SER	3.3
2	B	92	PHE	3.3
2	B	133	LYS	3.1
1	A	253	ASN	2.8
2	B	883	LEU	2.7
1	A	115	LEU	2.6
2	B	881	ASN	2.5
5	E	82	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	1455	PRO	2.5
8	H	139	ASN	2.4
12	L	50	ASP	2.3
1	A	105	CYS	2.3
1	A	255	SER	2.2
1	A	44	THR	2.2
1	A	257	ARG	2.2
2	B	132	VAL	2.1
2	B	167	ILE	2.1
1	A	256	GLN	2.1
8	H	140	ALA	2.0
1	A	1175	SER	2.0
9	I	77	LYS	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 carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
13	ZN	I	1121	1/1	0.99	0.14	-0.09	90,90,90,90	0
13	ZN	B	2225	1/1	0.99	0.16	-0.78	44,44,44,44	0
13	ZN	C	1269	1/1	1.00	0.08	-0.88	39,39,39,39	0
13	ZN	A	2457	1/1	1.00	0.10	-1.38	44,44,44,44	0
13	ZN	A	2456	1/1	0.97	0.07	-2.37	86,86,86,86	0
13	ZN	J	1066	1/1	0.99	0.16	-2.55	65,65,65,65	0
13	ZN	I	1122	1/1	0.91	0.06	-2.88	156,156,156,156	0
14	MG	A	2458	1/1	0.98	0.20	-	56,56,56,56	0
13	ZN	L	1071	1/1	0.99	0.12	-	115,115,115,115	0

6.5 Other polymers

There are no such residues in this entry.