



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:36 AM GMT

PDB ID : 2R92
Title : Elongation complex of RNA polymerase II with artificial RdRP scaffold
Authors : Lehmann, E.; Brueckner, F.; Cramer, P.
Deposited on : 2007-09-12
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

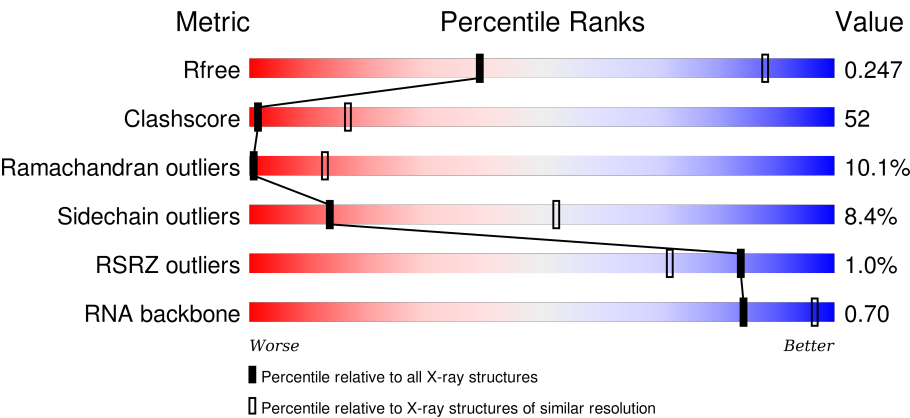
1 Overall quality at a glance i

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)
RNA backbone	2183	1070 (4.76-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	P	16	<div><div>13%</div><div>13%38%6%44%</div></div>
2	T	17	<div><div>41%</div><div>6%29%6%18%41%</div></div>
3	A	1733	<div><div>27%44%9%18%</div></div>
4	B	1224	<div><div>%27%53%10%9%</div></div>

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Mol	Chain	Length	Quality of chain
5	C	318	<div><div></div><div>24%47%13%16%</div></div>
6	D	221	<div><div></div><div>31%39%9%19%</div></div>
7	E	215	<div><div></div><div>2%36%55%8%</div></div>
8	F	155	<div><div></div><div>16%35%6%43%</div></div>
9	G	171	<div><div></div><div>33%60%7%</div></div>
10	H	146	<div><div></div><div>3%28%51%13%8%</div></div>
11	I	122	<div><div></div><div>29%52%12%5%</div></div>
12	J	70	<div><div></div><div>23%49%21%7%</div></div>
13	K	120	<div><div></div><div>36%46%11%7%</div></div>
14	L	70	<div><div></div><div>%14%30%20%34%</div></div>

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 31611 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called RNA (5'-R(*UP*GP*CP*AP*UP*AP*AP*AP*GP*AP*CP*CP*AP*GP*GP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	P	9	Total	C	N	O	P	0	0	0
			192	87	39	58	8			

- Molecule 2 is a RNA chain called RNA (5'-R(*CP*UP*UP*GP*AP*CP*GP*CP*CP*UP*GP*GP*UP*CP*AP*AP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	T	10	Total	C	N	O	P	0	0	0
			208	94	36	69	9			

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	1422	Total	C	N	O	S	0	0	0
			11194	7054	1959	2119	62			

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	1112	Total	C	N	O	S	0	0	0
			8841	5596	1550	1640	55			

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	C	267	Total	C	N	O	S	0	0	0
			2101	1320	349	419	13			

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit RPB4.

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

- Molecule 7 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

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

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	F	88	Total	C	N	O	S	0	0	0
			712	455	120	134	3			

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB7.

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

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	H	135	Total	C	N	O	S	0	0	0
			1084	683	183	214	4			

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	I	116	Total	C	N	O	S	0	0	0
			944	581	172	181	10			

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

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

- Molecule 13 is a protein called DNA-directed RNA polymerase II subunit RPB11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	K	112	Total	C	N	O	S	0	0	0
			904	580	154	168	2			

- Molecule 14 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	L	46	Total	C	N	O	S	0	0	0
			364	224	72	64	4			

- Molecule 15 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

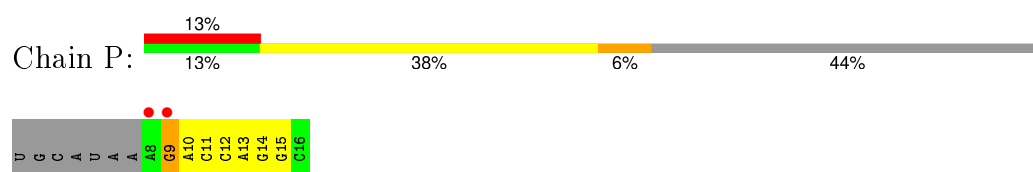
- Molecule 16 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

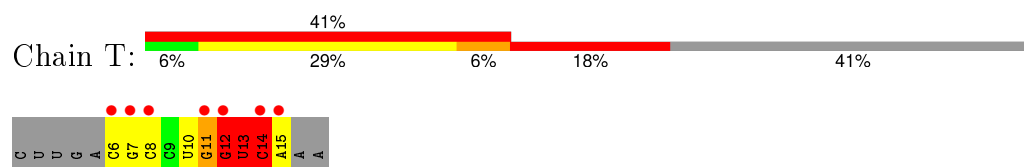
3 Residue-property plots

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 ($RSRZ > 2$). 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.

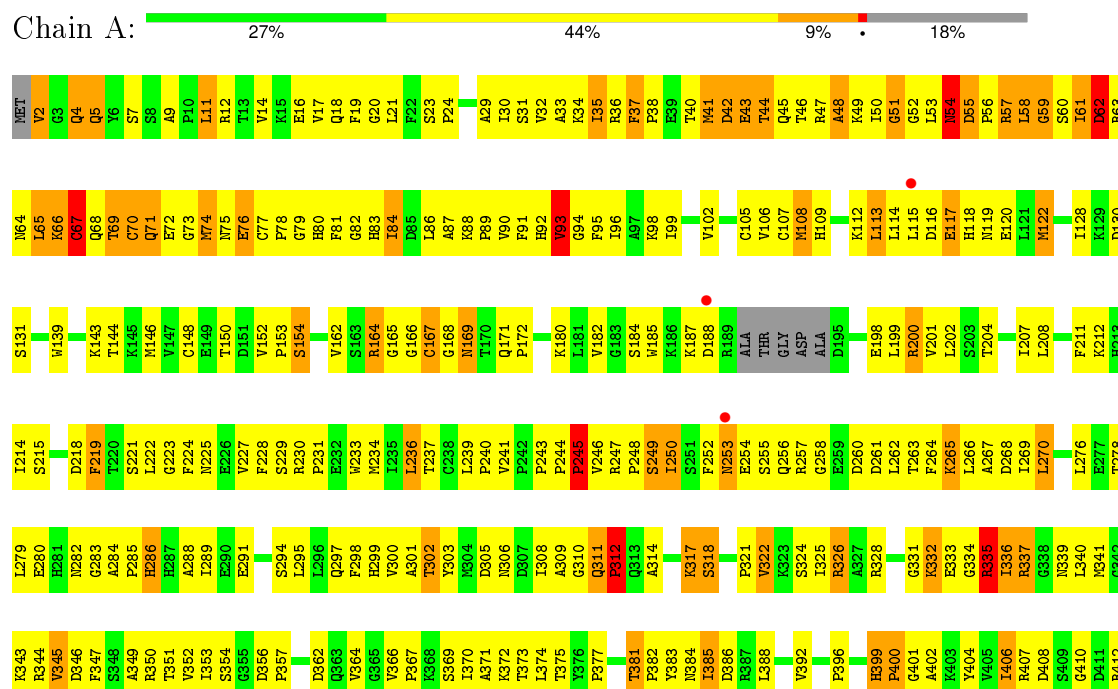
- Molecule 1: RNA (5'-R(*UP*GP*CP*AP*UP*AP*AP*AP*GP*AP*CP*CP*AP*GP*GP*C)-3')



- Molecule 2: RNA (5'-R(*CP*UP*UP*GP*AP*CP*GP*CP*CP*UP*GP*GP*UP*CP*AP*AP*A)-3')

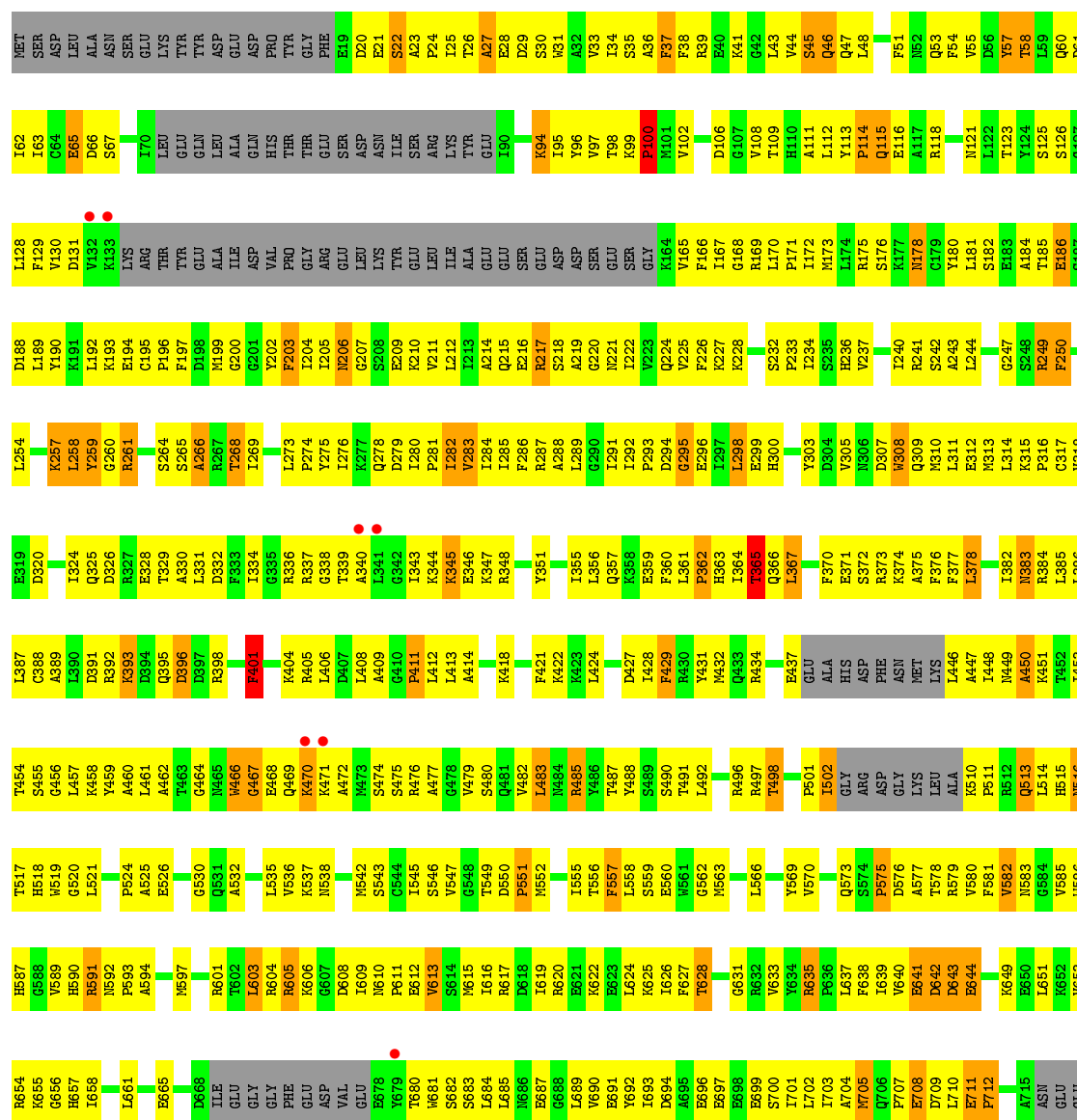


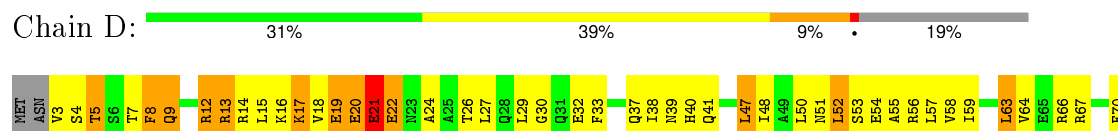
- Molecule 3: DNA-directed RNA polymerase II subunit RPB1



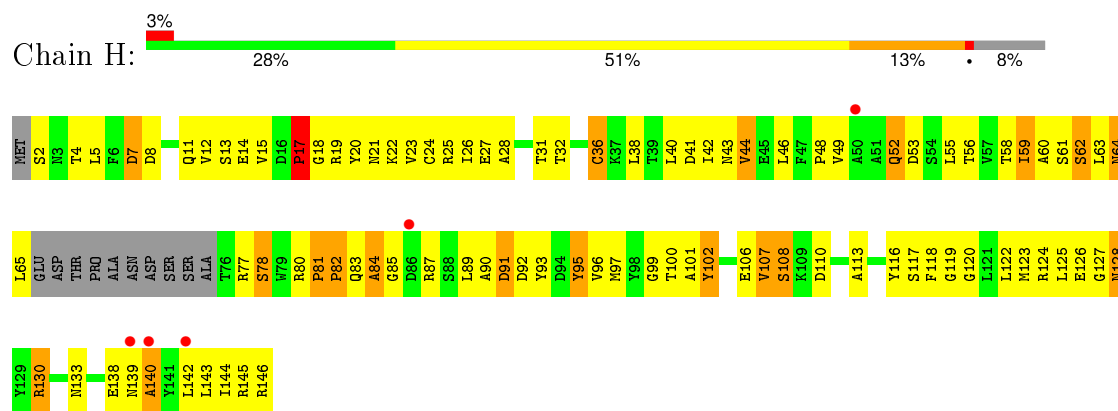
LYS	L1326	R1326	P1190	Y1119	Q1052	D985	L901	G835	C764	I687	I612	E542	S476	L413
ILE	I1327	I1327	W1191	L1120	Q1052	I986	L902	Y836	V765	I687	I613	E543	P477	D414
THR	I1328	I1328	L1192	E1121	F1053	V987	N903	I837	G766	I689	I614	L543	Y478	D415
GLU	I1329	I1329	L1193	P1122	L1054	L988	T904	Q838	Q767	T694	G615	V546	N479	L416
ILE	I1330	I1330	R1194	G1123	R1055	D992	D905	R839	Q768	K695	V616	L547	A480	Y417
ASP	I1331	E1264	H1124	H1124	V1058	L993	H906	R840	R774	K696	E618	N548	D481	S418
GLY	F1332	H1265	L1197	A1125	H1059	L993	T907	L841	I775	A697	K619	K549	P482	K419
GLY	E1333	L1266	D1198	A1126	P1060	N996	L908	V842	I775	Q698	K620	L550	D483	K420
GLN	L1335	L1268	A1201	Q1128	G1061	L997	L913	A844	F779	A699	T621	V552	M487	D423
ASP	M1336	L1268	M1202	Q1128	E1062	L998	E914	L345	V780	N700	T621	V553	N488	L424
GLY	V1406	E1129	M1063	Q1130	M1063	L998	T907	E846	D781	L701	G622	V553	K489	Q425
VAL	E1407	I1271	K1205	Q1130	M1063	L998	L908	D847	D782	H706	G623	V559	L490	Q426
THR	L1338	I1272	D1206	I1134	G1065	R1001	L920	I843	T783	I706	G624	V560	L491	Q427
PRO	G1340	R1274	L1273	R1135	V1066	G1002	G921	I849	L784	T709	G625	V561	P492	Y428
THR	L1341	L1274	L1273	L1135	L1067	R1003	L921	I849	P785	L710	G627	V562	Q493	G429
SER	E1342	I1279	M1209	A1137	Q1070	E1005	Q926	Y852	H786	R711	G628	V563	S494	W430
ASN	A1343	E1280	G1210	I1138	G1073	I1006	L929	D853	H787	E712	L629	V564	K431	K431
GLU	G1413	E1281	Q1211	I1138	S1071	I1007	L929	N854	S788	S713	L630	V565	E495	V432
SER	G1415	V1282	V1212	T1141	I1072	Q1008	L929	T855	K789	F714	H631	V566	T497	E433
GLY	A1416	V1283	G1213	K1144	G1073	N1009	Y933	T856	Y792	N717	V632	K567	R498	E434
LEU	A1347	M1284	E1214	R1144	E1074	K934	K934	R857	S793	N718	V633	V568	A499	H435
VAL	L1348	M1285	R1215	K1144	P1075	Q935	Q935	N858	P794	V719	T634	V569	E500	
ASN	Y1349	I1216	K1216	T1147	A1076	L936	L936	S859	P794	R720	R635	V570	Q503	D438
ALA	K1350	R1289	K1217	I1148	H1079	D1013	D839	L860	E795	R720	G642	V571	L504	N439
ASP	E1351	R1290	Q1218	A1149	T1080	A1014	R940	G861	S796	F721	G642	V572	L504	D440
LEU	V1352	V1291	T1219	S1150	T1081	V1015	R940	N862	K797	L722	L645	V573	C905	P441
ASP	G1423	P1292	F1220	E1151	L1081	T1016	K941	V863	G798	N723	L646	V574	A506	V442
VAL	V1355	S1293	K1221	ASN	ASN	L1017	F942	I864	F799	E724	F646	V575	V507	L443
LYS	I1356	P1294	N1222	Y1153	THR	F1018	L943	Q865	V800	A725	G647	V576	P508	F444
ASP	E1426	D1223	P1295	P1154	PHE	C1019	R866	Q866	E801	K728	N648	V577	L569	N445
GLU	D1369	L1224	F1225	D1155	HIS	G1020	W954	T867	N802	K728	L649	V578	Q510	R446
LEU	Y1362	E1297	F1225	P1156	PHE	L1021	P955	T868	S803	N736	Q650	V579	L511	
MET	G1430	Y1298	V1226	T1161	ALA	L1022	L956	G869	Y804	R731	K651	V580	S513	L450
SER	G1431	P1292	I1227	V1162	GLY	R1023	P957	E870	L805	L732	V652	V581	Q515	K451
PRO	M1433	R1364	N1228	I1163	VAL	S1024	V958	D871	R806	V735	V653	V582	Q516	K452
LEU	A1434	P1164	D1166	P1164	SER	L1026	L960	N873	L808	N736	L657	V583	S516	K453
VAL	P1435	E1165	D1166	E1165	K1092	A1027	R961	D874	T809	L737	L658	V584	S517	S454
ASP	I1436	D1166	D1166	D1166	K1093	T1028	R962	A875		K738	L659	V585	K518	N455
VAL	E1436	E1303	D1233	E1303	ALA	R1029	F963	I878	E812	D739	S663	V586	C520	N456
ASP	I1436	W1304	L1236	L1170	V1094	R1030	L964	I878	F813	L740	T664	V587	M521	A457
GLY	L1370	V1305	I1237	I1170	T1095	R1031	Q965	I878	F814	N741	T664	V588	G522	R458
SER	L1371	E1307	I1238	Q1171	S1096	L1032	N966	I883	F815	N742	G665	V589	I523	V460
ASN	V1372	T1308	R1239	Q1171	G1097	L1032	N966	I883	H816	V743	G667	V590	V524	K461
ASP	D1373	D1309	G1240	F1174	G1097	Q1033	A967	I883	H816	V743	G667	V591	G520	V462
ALA	V1374	G1310	R1241	F1174	G1097	Q1033	A967	I883	H816	V743	G667	V592	G520	V463
ALA	M1375	V1311	V1242	S1175	R1100	E1034	Q968	I883	H816	V743	G667	V593	G520	V464
MET	T1376	N1312	V1243	L1176	L1101	Y1035	Q969	I883	H816	V743	G667	V594	G520	V465
ALA	M1444	L1313	R1244	L1177	K1102	R1036	T970	I883	H816	V743	G667	V595	G520	V466
GLY	Q1378	S1314	P1245	ASP	E1103	L1037	F971	G888	R821	V747	G673	V596	G520	V467
GLY	G1379	E1315	LYS	GLU	L1104	T1038	H972	S889	E822	N748	P674	V597	G520	V468
PHE	E1447	V1316	SER	GLU	L1105	K1039	I973	D890	E822	N748	P674	V598	G520	V469
THR	T1385	M1317	LEU	GLU	L1106	Q1040	I973	A891	I825	A749	T676	V599	G520	V470
ALA	R1386	T1318	ASP	ALA	V1107	A1041	K977	E894	I825	A749	T676	V599	G520	V471
TTR	H1387	V1319	ALA	GLN	V1107	A1041	K977	E894	I825	A749	T676	V599	G520	V472
GLY	F1388	V1320	GLU	PHE	T1113	V1045	P978	E894	I825	A749	T676	V599	G520	V473
ALA	F1389	G1321	THR	PHE	T1113	V1045	P978	E894	I825	A749	T676	V599	G520	V474
ALA	M1454	I1322	GLU	ASP	S1115	L1046	D980	R896	A828	N757	T832	V600	L534	L470
ASP	P1455	L1323	A1254	Q1187	S1116	L1046	L981	R897	V829	N757	T832	V601	L536	L471
GLY	M1454	P1323	E1254	Q1187	L1116	L1046	L981	R897	V829	N757	T832	V602	L536	L472
TTR	L1393	P1324	GLU	Q1188	L1117	S1047	T982	R898	T831	N761	T833	V603	L537	L473
GLY	T1394	E1256	E1256	S1189	V1118	I1049	K984	D900	T834	A763	A686	V610	L541	L474

- Molecule 4: DNA-directed RNA polymerase II subunit RPB2

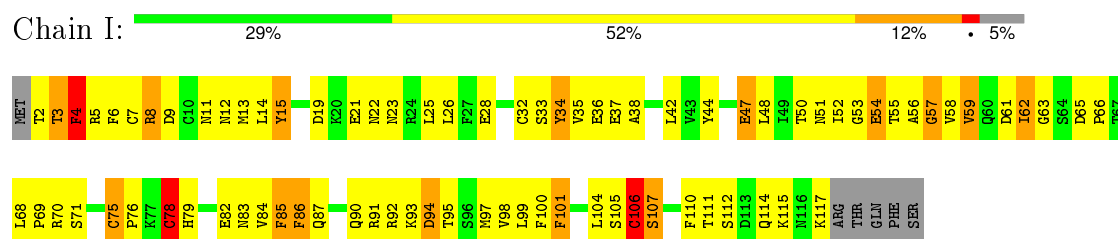




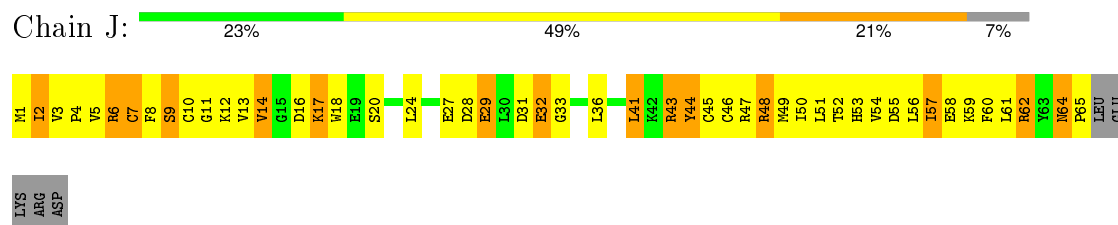
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC3



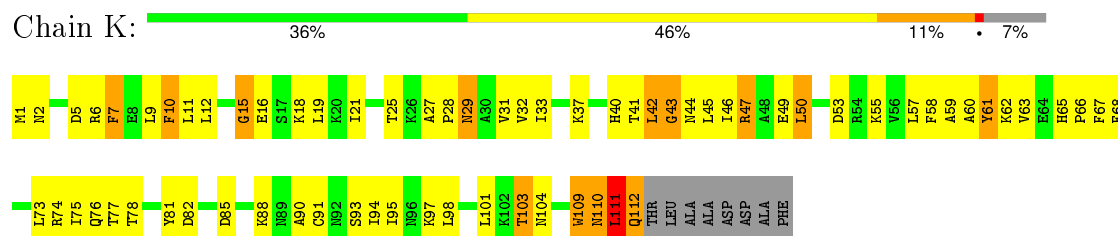
- Molecule 11: DNA-directed RNA polymerase II subunit RPB9



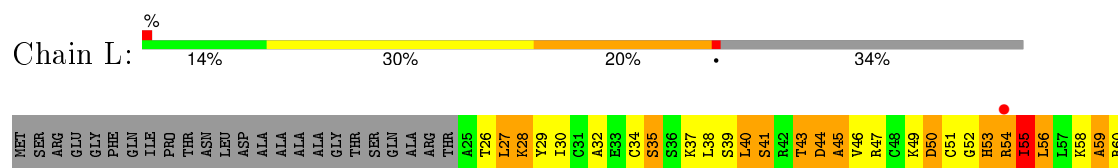
- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC5

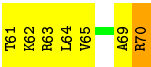


- Molecule 13: DNA-directed RNA polymerase II subunit RPB11



- Molecule 14: DNA-directed RNA polymerases I, II, and III subunit RPABC4





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	222.68Å 393.85Å 283.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.80 48.51 – 3.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-3.80) 99.9 (48.51-3.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.44 (at 3.77Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.212 , 0.246 0.217 , 0.247	Depositor DCC
R_{free} test set	2431 reflections (1.99%)	DCC
Wilson B-factor (Å ²)	114.7	Xtriage
Anisotropy	0.449	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 67.2	EDS
Estimated twinning fraction	0.038 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.037 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	0 of 122098 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	31611	wwPDB-VP
Average B, all atoms (Å ²)	128.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.79% 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	P	0.63	0/215	0.81	0/334
2	T	0.71	0/231	1.32	5/358 (1.4%)
3	A	0.42	0/11394	0.73	7/15407 (0.0%)
4	B	0.41	0/9012	0.68	1/12149 (0.0%)
5	C	0.43	0/2138	0.71	0/2896
6	D	0.39	0/1444	0.66	0/1935
7	E	0.39	0/1788	0.63	0/2406
8	F	0.45	0/724	0.76	0/977
9	G	0.45	0/1368	0.72	0/1844
10	H	0.37	0/1102	0.62	0/1492
11	I	0.38	0/962	0.65	0/1295
12	J	0.47	0/541	0.75	0/727
13	K	0.45	0/922	0.68	0/1244
14	L	0.46	0/366	0.69	0/485
All	All	0.42	0/32207	0.71	13/43549 (0.0%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1176	LEU	CA-CB-CG	13.45	146.23	115.30
2	T	12	G	N9-C1'-C2'	9.04	125.76	114.00
2	T	12	G	O4'-C1'-N9	8.14	114.72	108.20
2	T	13	U	O4'-C1'-N1	7.87	114.50	108.20
3	A	1176	LEU	CB-CA-C	-7.05	96.81	110.20
3	A	1177	LEU	N-CA-C	-6.94	92.26	111.00
2	T	14	C	O4'-C1'-N1	6.57	113.45	108.20
3	A	452	LYS	N-CA-C	-6.12	94.48	111.00
3	A	1176	LEU	CA-C-O	5.52	131.68	120.10
2	T	13	U	N1-C1'-C2'	5.32	120.91	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1176	LEU	CA-C-N	-5.30	105.53	117.20
4	B	111	ALA	N-CA-C	-5.22	96.91	111.00
3	A	567	LYS	C-N-CD	5.02	138.94	128.40

There are no chirality outliers.

There are no planarity outliers.

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	P	192	0	101	6	0
2	T	208	0	110	16	0
3	A	11194	0	11278	1259	0
4	B	8841	0	8874	1006	0
5	C	2101	0	2055	275	0
6	D	1434	0	1460	146	0
7	E	1752	0	1776	163	0
8	F	712	0	738	89	0
9	G	1340	0	1357	182	0
10	H	1084	0	1057	140	0
11	I	944	0	903	120	0
12	J	532	0	542	90	0
13	K	904	0	911	93	0
14	L	364	0	388	54	0
15	A	2	0	0	0	0
15	B	1	0	0	0	0
15	C	1	0	0	0	0
15	I	2	0	0	0	0
15	J	1	0	0	0	0
15	L	1	0	0	0	0
16	A	1	0	0	0	0
All	All	31611	0	31550	3310	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 52.

All (3310) 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)
3:A:58:LEU:HD12	3:A:59:GLY:H	0.99	1.11
4:B:343:ILE:HG23	4:B:347:LYS:HB2	1.25	1.09
4:B:510:LYS:HG2	4:B:511:PRO:HD3	1.22	1.08
3:A:53:LEU:HD23	3:A:54:ASN:N	1.68	1.08
5:C:43:THR:HG22	5:C:44:LEU:H	0.98	1.07
6:D:40:HIS:HB3	9:G:73:LYS:HZ3	1.12	1.06
3:A:63:ARG:HA	3:A:74:MET:HE1	1.32	1.05
3:A:868:TYR:CE1	3:A:1064:VAL:HG11	1.90	1.05
12:J:5:VAL:HG12	12:J:6:ARG:HG3	1.39	1.05
4:B:589:VAL:HG12	4:B:590:HIS:H	1.20	1.04
4:B:882:THR:HG22	4:B:884:ARG:H	1.18	1.04
4:B:521:LEU:HD22	4:B:633:VAL:HG12	1.38	1.03
7:E:94:LYS:HE2	7:E:98:ILE:HD11	1.35	1.03
4:B:273:LEU:HB2	4:B:276:ILE:HD12	1.37	1.02
4:B:37:PHE:HE1	4:B:41:LYS:HG3	1.25	1.02
3:A:901:LEU:H	3:A:926:GLN:NE2	1.55	1.02
3:A:254:GLU:HB2	4:B:935:ARG:HH12	1.25	1.02
10:H:100:THR:HG23	10:H:138:GLU:HA	1.40	1.02
3:A:53:LEU:HD23	3:A:54:ASN:H	0.89	1.00
11:I:115:LYS:HD3	11:I:117:LYS:HE3	1.40	0.99
3:A:1161:THR:HG22	3:A:1163:ILE:H	1.25	0.98
3:A:1329:THR:HG22	3:A:1331:SER:H	1.27	0.98
4:B:583:ASN:HD21	4:B:628:THR:HG22	1.26	0.98
9:G:15:PRO:HA	9:G:18:PHE:CD1	1.99	0.97
3:A:34:LYS:HE2	3:A:57:ARG:HH22	1.28	0.97
4:B:37:PHE:CE1	4:B:41:LYS:HG3	1.98	0.97
3:A:567:LYS:CG	3:A:568:PRO:HD2	1.96	0.96
3:A:225:ASN:HD22	3:A:228:PHE:H	1.08	0.96
5:C:43:THR:HG22	5:C:44:LEU:N	1.80	0.96
10:H:4:THR:HA	10:H:60:ALA:HB2	1.42	0.96
3:A:754:SER:H	3:A:757:ASN:HD22	1.00	0.95
4:B:287:ARG:HG2	4:B:292:ILE:HA	1.46	0.95
3:A:446:ARG:HD3	3:A:480:ALA:HB2	1.48	0.95
9:G:138:THR:HG22	9:G:139:ILE:H	1.32	0.95
12:J:64:ASN:HB3	12:J:65:PRO:CD	1.97	0.95
4:B:364:ILE:HG12	4:B:585:VAL:HG13	1.44	0.95
3:A:1063:MET:SD	3:A:1436:ILE:HG12	2.07	0.95
4:B:1072:MET:CE	4:B:1085:ILE:HB	1.97	0.94
11:I:34:TYR:HD2	11:I:35:VAL:N	1.63	0.94
3:A:58:LEU:HD12	3:A:59:GLY:N	1.82	0.94
3:A:779:PHE:HE1	3:A:785:PRO:HD3	1.29	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:49:GLU:HG3	13:K:94:ILE:HG12	1.49	0.94
3:A:855:THR:HG21	3:A:857:ARG:HE	1.32	0.93
2:T:13:U:O2'	2:T:14:C:O5'	1.84	0.93
5:C:43:THR:CG2	5:C:44:LEU:H	1.82	0.93
6:D:40:HIS:HB3	9:G:73:LYS:NZ	1.84	0.93
4:B:1002:THR:HG23	4:B:1006:ILE:HG13	1.50	0.93
3:A:767:GLN:NE2	3:A:774:ARG:HB3	1.84	0.93
6:D:56:ARG:HB2	6:D:148:LEU:HD22	1.50	0.93
14:L:32:ALA:HB3	14:L:55:ILE:HD12	1.51	0.93
3:A:535:THR:HG21	3:A:616:VAL:HA	1.49	0.92
5:C:47:ASP:HA	14:L:69:ALA:HB3	1.52	0.92
4:B:999:MET:HG3	4:B:1000:PRO:HD2	1.52	0.92
5:C:57:VAL:HG11	12:J:60:PHE:HB3	1.49	0.92
3:A:58:LEU:CD1	3:A:59:GLY:H	1.83	0.92
5:C:39:ALA:HA	5:C:164:ALA:HB3	1.48	0.92
10:H:130:ARG:H	10:H:130:ARG:HD2	1.35	0.92
4:B:746:SER:HB2	4:B:1046:PRO:HG2	1.51	0.91
4:B:806:THR:HG22	4:B:808:ALA:H	1.33	0.91
6:D:17:LYS:HE3	6:D:17:LYS:HA	1.52	0.91
3:A:1127:ASP:HB3	3:A:1130:GLN:HB3	1.52	0.91
4:B:336:ARG:HG2	4:B:348:ARG:HD3	1.50	0.91
7:E:19:VAL:O	7:E:23:VAL:HG23	1.71	0.91
4:B:637:LEU:HD12	4:B:693:ILE:HD12	1.53	0.90
4:B:172:ILE:HD13	4:B:178:ASN:HB3	1.51	0.90
3:A:1438:THR:HB	4:B:1144:ALA:HB3	1.50	0.90
3:A:903:ASN:HD22	3:A:904:THR:N	1.69	0.90
12:J:1:MET:H1	12:J:57:ILE:H	0.93	0.90
3:A:1445:ILE:H	3:A:1445:ILE:HD12	1.37	0.90
4:B:247:GLY:H	4:B:418:LYS:NZ	1.70	0.90
3:A:563:PRO:HG3	3:A:572:TRP:CZ2	2.07	0.90
4:B:510:LYS:HG2	4:B:511:PRO:CD	2.02	0.89
3:A:53:LEU:CD2	3:A:54:ASN:H	1.82	0.89
4:B:1177:HIS:HB2	4:B:1179:GLN:HE21	1.35	0.89
5:C:32:SER:O	5:C:36:VAL:HG23	1.72	0.89
4:B:1159:ARG:HD3	4:B:1193:GLN:HG3	1.54	0.89
12:J:16:ASP:OD1	12:J:17:LYS:HD2	1.72	0.89
3:A:1004:ASN:ND2	7:E:167:ARG:HD2	1.86	0.89
4:B:879:ARG:NH1	4:B:883:LEU:HD22	1.85	0.89
3:A:399:HIS:HB3	3:A:400:PRO:HD3	1.53	0.89
4:B:800:GLN:HB3	12:J:52:THR:HG21	1.54	0.89
12:J:3:VAL:HG21	12:J:18:TRP:HB2	1.51	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:39:THR:HG22	9:G:40:GLY:H	1.37	0.88
3:A:658:LEU:HD13	4:B:831:SER:H	1.37	0.88
3:A:19:PHE:O	3:A:1416:ALA:HA	1.73	0.88
4:B:549:THR:HG22	4:B:550:ASP:H	1.37	0.88
4:B:577:ALA:HB1	4:B:589:VAL:HG11	1.56	0.88
3:A:567:LYS:HB3	10:H:96:VAL:H	1.38	0.88
3:A:901:LEU:H	3:A:926:GLN:HE21	0.90	0.88
12:J:64:ASN:HB3	12:J:65:PRO:HD3	1.56	0.88
3:A:567:LYS:CD	3:A:568:PRO:HD2	2.04	0.87
4:B:515:HIS:H	4:B:518:HIS:HD2	1.22	0.87
9:G:111:THR:HG22	9:G:113:HIS:H	1.37	0.87
3:A:763:ALA:O	3:A:803:SER:HB3	1.74	0.87
11:I:26:LEU:HD23	11:I:37:GLU:HA	1.53	0.87
7:E:180:ARG:HH21	7:E:192:ARG:HB2	1.38	0.87
5:C:101:LEU:HD13	5:C:118:LEU:HD23	1.58	0.86
6:D:144:THR:O	6:D:148:LEU:HB2	1.73	0.86
3:A:93:VAL:HG13	3:A:301:ALA:HB1	1.57	0.86
3:A:356:ASP:HB2	3:A:469:ARG:NH1	1.89	0.86
4:B:467:GLY:H	4:B:475:SER:HB3	1.37	0.86
3:A:590:ARG:NH2	3:A:620:LYS:HB3	1.91	0.86
13:K:47:ARG:HB3	13:K:47:ARG:HH11	1.41	0.86
9:G:26:LEU:HD12	9:G:56:ILE:HD13	1.58	0.85
5:C:164:ALA:HA	5:C:167:HIS:O	1.75	0.85
3:A:963:ILE:HD11	3:A:1048:ASN:HB3	1.58	0.85
3:A:868:TYR:HE1	3:A:1064:VAL:HG11	1.38	0.85
5:C:166:GLU:HG3	13:K:10:PHE:HZ	1.42	0.85
3:A:1345:ARG:HG3	3:A:1376:THR:HG21	1.58	0.85
1:P:9:G:H2'	1:P:10:A:C8	2.12	0.85
13:K:65:HIS:HD2	13:K:67:PHE:H	1.24	0.85
11:I:34:TYR:CD2	11:I:35:VAL:N	2.45	0.85
11:I:85:PHE:HD2	11:I:85:PHE:H	1.25	0.85
4:B:1072:MET:HE1	4:B:1085:ILE:HB	1.59	0.84
4:B:112:LEU:HD12	4:B:113:TYR:H	1.40	0.84
5:C:6:PRO:HB3	5:C:25:VAL:HG12	1.57	0.84
9:G:7:LEU:HB2	9:G:74:TYR:CE2	2.11	0.84
3:A:560:ILE:HG13	10:H:78:SER:HB2	1.59	0.84
3:A:33:ALA:HB1	3:A:56:PRO:HB2	1.58	0.84
5:C:44:LEU:HB2	5:C:77:ILE:HD11	1.57	0.84
3:A:40:THR:HG22	3:A:41:MET:HG3	1.56	0.84
5:C:99:LEU:HD12	5:C:118:LEU:HB3	1.60	0.84
4:B:879:ARG:HH11	4:B:883:LEU:HD22	1.39	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:164:ARG:HG3	3:A:165:GLY:H	1.42	0.84
7:E:198:ILE:HD11	7:E:212:ARG:HG3	1.60	0.84
3:A:308:ILE:HG22	3:A:309:ALA:H	1.42	0.84
4:B:343:ILE:CG2	4:B:347:LYS:HB2	2.07	0.84
3:A:1017:LEU:HB2	7:E:206:GLY:H	1.41	0.84
4:B:1201:LYS:HE2	4:B:1205:GLN:OE1	1.78	0.83
12:J:1:MET:H1	12:J:57:ILE:N	1.74	0.83
3:A:901:LEU:N	3:A:926:GLN:HE21	1.75	0.83
3:A:265:LYS:HD2	3:A:265:LYS:H	1.42	0.83
9:G:143:ILE:HG22	9:G:144:ARG:N	1.93	0.83
5:C:98:VAL:O	5:C:99:LEU:HD22	1.78	0.83
4:B:212:LEU:HD23	4:B:480:SER:HB2	1.59	0.83
3:A:34:LYS:HE2	3:A:57:ARG:NH2	1.93	0.83
3:A:899:VAL:HB	3:A:929:LEU:HD11	1.61	0.83
3:A:699:ALA:HB1	11:I:114:GLN:HB2	1.58	0.83
3:A:1420:ASP:HB3	3:A:1422:ARG:HG3	1.59	0.83
5:C:77:ILE:HG23	5:C:161:LYS:HE3	1.61	0.82
9:G:1:MET:SD	9:G:79:PHE:HD1	2.03	0.82
9:G:138:THR:HG22	9:G:139:ILE:N	1.92	0.82
8:F:99:LEU:O	8:F:103:MET:HG2	1.80	0.82
6:D:40:HIS:CB	9:G:73:LYS:NZ	2.41	0.82
13:K:21:ILE:HG12	13:K:33:ILE:HG12	1.59	0.82
4:B:770:GLN:OE1	4:B:983:ARG:HA	1.78	0.82
4:B:613:VAL:HG13	4:B:627:PHE:O	1.79	0.82
3:A:265:LYS:HD2	3:A:265:LYS:N	1.94	0.82
6:D:47:LEU:HD13	6:D:48:ILE:N	1.95	0.81
8:F:93:ILE:HD11	8:F:134:ILE:HD11	1.59	0.81
3:A:1424:VAL:HG11	4:B:1139:ILE:HD13	1.61	0.81
11:I:8:ARG:HG3	11:I:34:TYR:HE1	1.44	0.81
11:I:75:CYS:HG	11:I:78:CYS:HG	1.23	0.81
3:A:913:LEU:HD12	3:A:914:GLU:H	1.46	0.81
5:C:239:PRO:HB2	5:C:241:ASP:OD1	1.81	0.81
3:A:1325:THR:O	7:E:148:GLU:HB2	1.79	0.81
3:A:779:PHE:CE1	3:A:785:PRO:HD3	2.15	0.81
4:B:121:ASN:HA	4:B:207:GLY:HA2	1.61	0.81
3:A:58:LEU:HD11	3:A:243:PRO:HB3	1.61	0.81
3:A:34:LYS:CE	3:A:57:ARG:HH12	1.92	0.81
3:A:666:ILE:HD12	3:A:667:GLY:H	1.46	0.81
4:B:115:GLN:HG2	4:B:193:LYS:HB2	1.63	0.81
6:D:134:THR:HG22	6:D:135:GLY:N	1.95	0.81
3:A:679:ILE:HG12	3:A:732:LEU:HD12	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1028:THR:O	3:A:1032:LEU:HD12	1.79	0.81
4:B:654:ARG:H	4:B:657:HIS:HD2	1.28	0.81
3:A:442:VAL:HB	3:A:489:LEU:HD11	1.61	0.81
3:A:225:ASN:ND2	3:A:228:PHE:H	1.79	0.81
3:A:451:HIS:CD2	3:A:1074:GLU:HG3	2.16	0.81
3:A:1312:ASN:O	3:A:1316:VAL:HG23	1.81	0.81
3:A:518:LYS:HE2	3:A:624:SER:O	1.80	0.80
4:B:778:MET:CE	4:B:1094:ARG:HD3	2.10	0.80
4:B:35:SER:O	4:B:39:ARG:HG3	1.82	0.80
4:B:1007:VAL:HG22	4:B:1008:PRO:HD2	1.63	0.80
7:E:16:PHE:CZ	7:E:20:LYS:HE2	2.15	0.80
9:G:1:MET:SD	9:G:79:PHE:CD1	2.75	0.80
3:A:598:LEU:HA	10:H:122:LEU:HD13	1.64	0.80
3:A:629:LEU:O	3:A:633:VAL:HG23	1.82	0.80
3:A:1189:SER:O	3:A:1241:ARG:HD3	1.82	0.80
5:C:238:ILE:HG23	5:C:242:GLN:HB2	1.63	0.80
10:H:93:TYR:HB3	10:H:144:ILE:O	1.82	0.80
11:I:8:ARG:HG3	11:I:34:TYR:CE1	2.17	0.80
3:A:1120:LEU:HD12	3:A:1120:LEU:N	1.98	0.79
4:B:902:GLY:O	14:L:65:VAL:HG11	1.82	0.79
3:A:567:LYS:HD2	3:A:568:PRO:HD2	1.63	0.79
4:B:22:SER:HA	4:B:654:ARG:CB	2.11	0.79
5:C:66:ARG:NH1	12:J:2:ILE:HG21	1.97	0.79
3:A:70:CYS:O	3:A:72:GLU:HG2	1.82	0.79
9:G:49:LEU:HD21	9:G:77:VAL:HG23	1.65	0.79
8:F:86:THR:OG1	8:F:89:GLU:HG3	1.83	0.79
4:B:370:PHE:HE2	4:B:373:ARG:HH11	1.31	0.79
4:B:882:THR:HG22	4:B:884:ARG:N	1.98	0.79
9:G:127:PRO:HG2	9:G:138:THR:HG21	1.63	0.79
3:A:868:TYR:HD2	3:A:1058:VAL:HG21	1.45	0.79
3:A:577:ILE:O	3:A:580:VAL:HG23	1.82	0.79
8:F:69:LEU:C	8:F:71:GLU:H	1.83	0.79
6:D:159:THR:O	6:D:163:VAL:HG23	1.82	0.79
3:A:58:LEU:HD11	3:A:243:PRO:CB	2.12	0.78
3:A:567:LYS:HD3	10:H:95:TYR:CD2	2.18	0.78
3:A:855:THR:HG21	3:A:857:ARG:NE	1.98	0.78
3:A:244:PRO:HG2	3:A:245:PRO:HD3	1.64	0.78
4:B:467:GLY:N	4:B:475:SER:HB3	1.97	0.78
7:E:22:MET:HE3	7:E:26:ARG:HE	1.46	0.78
9:G:13:LEU:HD21	9:G:17:PHE:HB2	1.64	0.78
4:B:23:ALA:HB1	4:B:24:PRO:HD2	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:899:ILE:HD11	4:B:911:ILE:HA	1.64	0.78
13:K:49:GLU:HG3	13:K:94:ILE:CG1	2.13	0.78
4:B:65:GLU:HG3	4:B:66:ASP:H	1.48	0.78
4:B:622:LYS:HE2	11:I:59:VAL:HG22	1.65	0.78
4:B:1183:LYS:HE3	4:B:1183:LYS:N	1.99	0.78
9:G:122:ASN:ND2	9:G:125:SER:HB3	1.99	0.77
4:B:955:THR:HG22	4:B:956:THR:N	1.97	0.77
13:K:40:HIS:HD1	13:K:61:TYR:HH	1.24	0.77
9:G:34:VAL:HG12	9:G:45:ILE:HG21	1.64	0.77
3:A:665:GLY:O	3:A:667:GLY:N	2.18	0.77
3:A:709:THR:HG22	3:A:711:ARG:H	1.49	0.77
4:B:906:SER:O	4:B:941:LEU:HD23	1.85	0.77
3:A:858:ASN:HD22	3:A:858:ASN:C	1.84	0.77
12:J:36:LEU:HD22	12:J:41:LEU:HD12	1.66	0.77
6:D:153:ARG:NH2	6:D:184:ALA:HA	2.00	0.77
4:B:1095:LEU:HD12	4:B:1095:LEU:H	1.49	0.77
4:B:579:ARG:HB2	4:B:586:TRP:NE1	1.99	0.77
4:B:860:MET:HB2	4:B:965:LYS:HG2	1.67	0.77
5:C:18:VAL:O	5:C:18:VAL:HG12	1.84	0.77
3:A:23:SER:HA	3:A:233:TRP:NE1	2.00	0.77
3:A:381:THR:HG23	3:A:383:TYR:H	1.50	0.77
4:B:232:SER:HB3	4:B:261:ARG:HH21	1.50	0.77
3:A:866:PHE:C	3:A:867:ILE:HD12	2.06	0.77
4:B:580:VAL:HG22	4:B:624:LEU:HB3	1.66	0.77
4:B:1072:MET:HE3	4:B:1085:ILE:HB	1.65	0.77
4:B:801:LYS:O	12:J:52:THR:HG23	1.84	0.77
4:B:516:ASN:N	4:B:516:ASN:HD22	1.80	0.76
7:E:124:VAL:HG13	7:E:132:ILE:HD12	1.67	0.76
3:A:1341:ILE:HD12	3:A:1379:GLY:O	1.85	0.76
3:A:1032:LEU:O	3:A:1036:ARG:HD3	1.85	0.76
6:D:39:ASN:HD21	6:D:41:GLN:NE2	1.82	0.76
3:A:61:ILE:HG22	3:A:62:ASP:H	1.49	0.76
3:A:332:LYS:HG3	3:A:333:GLU:HG2	1.67	0.76
4:B:502:ILE:H	4:B:502:ILE:HD12	1.48	0.76
12:J:43:ARG:HG3	12:J:45:CYS:SG	2.26	0.76
7:E:192:ARG:HH11	7:E:192:ARG:HG3	1.50	0.76
3:A:384:ASN:OD1	3:A:388:LEU:HD12	1.85	0.76
3:A:902:LEU:HG	3:A:926:GLN:HG3	1.67	0.76
4:B:515:HIS:HD2	4:B:517:THR:H	1.31	0.76
13:K:65:HIS:CD2	13:K:67:PHE:H	2.04	0.76
4:B:22:SER:HA	4:B:654:ARG:HB3	1.66	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:589:VAL:HG12	4:B:590:HIS:N	2.00	0.76
9:G:88:ASP:HB3	9:G:144:ARG:HA	1.68	0.76
5:C:241:ASP:O	5:C:245:VAL:HG23	1.86	0.76
4:B:216:GLU:OE1	4:B:537:LYS:HE2	1.85	0.76
4:B:882:THR:CG2	4:B:884:ARG:HB2	2.16	0.76
3:A:1002:GLY:HA3	3:A:1007:ILE:HG21	1.67	0.76
3:A:768:GLN:HG2	3:A:816:HIS:HA	1.66	0.76
3:A:738:LYS:HB2	3:A:740:LEU:HG	1.67	0.76
6:D:173:HIS:O	6:D:177:VAL:HG23	1.86	0.75
4:B:1202:LEU:O	4:B:1206:GLU:HG3	1.85	0.75
4:B:1065:GLN:HE21	4:B:1067:ARG:N	1.84	0.75
4:B:1065:GLN:HE21	4:B:1067:ARG:H	1.34	0.75
4:B:806:THR:HG22	4:B:808:ALA:N	2.00	0.75
3:A:93:VAL:HG22	3:A:301:ALA:HA	1.68	0.75
3:A:821:ARG:HB2	3:A:821:ARG:HH11	1.51	0.75
4:B:642:ASP:HB3	4:B:649:LYS:HD2	1.69	0.75
3:A:87:ALA:CB	3:A:276:LEU:HD23	2.17	0.75
4:B:798:TYR:HE2	5:C:62:PHE:CE2	2.04	0.75
4:B:114:PRO:HG2	4:B:115:GLN:H	1.51	0.75
3:A:164:ARG:HG3	3:A:165:GLY:N	2.01	0.75
7:E:202:SER:HB3	7:E:205:SER:O	1.86	0.75
3:A:1329:THR:HG22	3:A:1331:SER:N	2.01	0.75
3:A:567:LYS:HG3	3:A:568:PRO:HD2	1.67	0.75
3:A:321:PRO:O	3:A:322:VAL:HB	1.87	0.75
3:A:1332:PHE:H	3:A:1332:PHE:HD2	1.34	0.75
3:A:382:PRO:HB3	3:A:428:TYR:HE2	1.50	0.75
2:T:12:G:O2'	2:T:13:U:O5'	2.02	0.75
4:B:1163:CYS:SG	4:B:1165:ILE:HB	2.25	0.75
4:B:611:PRO:HB3	4:B:685:LEU:HD11	1.68	0.75
6:D:12:ARG:HG2	6:D:14:ARG:HG3	1.69	0.75
4:B:800:GLN:HB3	12:J:52:THR:CG2	2.17	0.74
3:A:699:ALA:HB3	3:A:701:LEU:HG	1.68	0.74
4:B:1162:ILE:HD11	4:B:1194:ILE:HD13	1.67	0.74
3:A:249:SER:O	3:A:250:ILE:HG13	1.87	0.74
3:A:34:LYS:CE	3:A:57:ARG:HH22	2.00	0.74
11:I:34:TYR:HE2	11:I:36:GLU:HB3	1.52	0.74
4:B:758:PHE:CE1	4:B:1027:ILE:HG22	2.22	0.74
3:A:69:THR:O	3:A:71:GLN:N	2.20	0.74
10:H:102:TYR:OH	10:H:122:LEU:HD22	1.88	0.74
10:H:59:ILE:HG22	10:H:60:ALA:N	2.01	0.74
4:B:642:ASP:HA	4:B:649:LYS:HA	1.67	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:351:THR:HB	4:B:1103:ILE:HD12	1.70	0.74
9:G:14:HIS:ND1	9:G:15:PRO:HD2	2.03	0.74
3:A:853:ASP:O	3:A:854:ASN:HB2	1.86	0.74
3:A:337:ARG:HD3	4:B:1132:GLU:OE1	1.88	0.74
5:C:8:VAL:HG12	5:C:9:LYS:H	1.53	0.74
4:B:53:GLN:HG2	4:B:547:VAL:HG22	1.69	0.74
3:A:67:CYS:O	3:A:70:CYS:HB3	1.87	0.74
5:C:189:THR:HG22	5:C:190:ASP:N	2.03	0.74
3:A:239:LEU:HD12	3:A:240:PRO:HD2	1.69	0.74
4:B:60:GLN:O	4:B:63:ILE:HG22	1.88	0.74
3:A:62:ASP:HB3	3:A:64:ASN:ND2	2.02	0.74
10:H:40:LEU:HD13	10:H:123:MET:HB2	1.70	0.74
3:A:541:ILE:HG21	3:A:549:MET:HE1	1.68	0.74
3:A:783:THR:HG21	3:A:815:PHE:CZ	2.22	0.74
3:A:534:LEU:O	3:A:574:GLY:HA3	1.85	0.74
3:A:774:ARG:NH2	3:A:797:LYS:HG3	2.03	0.74
10:H:38:LEU:HD12	10:H:124:ARG:O	1.87	0.73
13:K:45:LEU:HG	13:K:94:ILE:HD13	1.68	0.73
5:C:212:PRO:HB3	5:C:213:PRO:HD2	1.69	0.73
4:B:483:LEU:HD11	4:B:491:THR:HG23	1.70	0.73
3:A:836:TYR:CE2	3:A:840:ARG:HD2	2.23	0.73
4:B:336:ARG:HH22	4:B:345:LYS:HE2	1.54	0.73
4:B:745:PRO:O	4:B:748:ILE:HG12	1.87	0.73
6:D:153:ARG:HB3	6:D:154:PHE:CE1	2.22	0.73
3:A:1100:ARG:HH21	3:A:1351:GLU:HG2	1.53	0.73
10:H:4:THR:HA	10:H:60:ALA:CB	2.18	0.73
9:G:119:LEU:HD12	9:G:131:GLN:O	1.88	0.73
13:K:90:ALA:O	13:K:94:ILE:HG13	1.88	0.73
13:K:21:ILE:HG23	13:K:31:VAL:HG11	1.71	0.73
3:A:1244:ARG:HB3	3:A:1245:PRO:HD2	1.69	0.73
3:A:114:LEU:HD13	3:A:171:GLN:HE22	1.53	0.73
10:H:89:LEU:O	10:H:91:ASP:N	2.22	0.73
3:A:55:ASP:N	3:A:56:PRO:HD3	2.04	0.73
3:A:868:TYR:CD2	3:A:1058:VAL:HG21	2.23	0.73
3:A:1118:VAL:HG12	3:A:1327:ILE:HG13	1.69	0.73
3:A:152:VAL:CG1	3:A:153:PRO:HD2	2.17	0.73
4:B:579:ARG:HB2	4:B:586:TRP:HE1	1.54	0.73
3:A:1116:LEU:N	3:A:1308:THR:HG22	2.04	0.73
3:A:754:SER:N	3:A:757:ASN:HD22	1.83	0.73
6:D:47:LEU:HD13	6:D:48:ILE:H	1.53	0.73
3:A:896:ARG:HD3	3:A:897:TYR:HE1	1.54	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1198:ASP:HB3	3:A:1201:ALA:HB3	1.68	0.73
4:B:244:LEU:HD11	4:B:366:GLN:HE22	1.54	0.73
1:P:11:C:H2'	1:P:12:C:H6	1.54	0.73
6:D:189:ASP:O	6:D:193:THR:HB	1.88	0.73
3:A:34:LYS:HE2	3:A:57:ARG:HH12	1.52	0.72
12:J:48:ARG:HE	12:J:49:MET:HE2	1.54	0.72
6:D:134:THR:HG22	6:D:135:GLY:H	1.52	0.72
3:A:1174:PHE:HA	3:A:1176:LEU:HD23	1.70	0.72
4:B:1187:ASN:O	4:B:1188:LYS:HB2	1.89	0.72
4:B:359:GLU:O	4:B:362:PRO:HD3	1.89	0.72
4:B:642:ASP:HB3	4:B:649:LYS:CD	2.19	0.72
4:B:167:ILE:HG22	4:B:453:ILE:HD12	1.70	0.72
3:A:345:VAL:HG21	4:B:1150:ARG:NH1	2.04	0.72
14:L:30:ILE:O	14:L:56:LEU:HA	1.88	0.72
4:B:1172:ILE:O	4:B:1172:ILE:HG22	1.89	0.72
4:B:863:GLU:OE2	4:B:873:THR:HA	1.89	0.72
7:E:157:SER:OG	7:E:160:GLU:HG3	1.88	0.72
3:A:244:PRO:HG2	3:A:245:PRO:CD	2.19	0.72
4:B:880:THR:O	4:B:881:ASN:HB2	1.88	0.72
3:A:285:PRO:HG2	3:A:288:ALA:HB3	1.71	0.72
4:B:336:ARG:NH2	4:B:345:LYS:HE2	2.05	0.72
4:B:340:ALA:CB	4:B:343:ILE:HD12	2.18	0.72
3:A:63:ARG:HA	3:A:74:MET:CE	2.18	0.72
3:A:230:ARG:H	3:A:233:TRP:HE3	1.32	0.72
12:J:57:ILE:HA	12:J:60:PHE:HD2	1.54	0.72
10:H:100:THR:OG1	10:H:138:GLU:HG3	1.88	0.72
3:A:1242:VAL:HG12	3:A:1243:VAL:H	1.55	0.72
4:B:365:THR:HG23	4:B:367:LEU:H	1.54	0.72
10:H:41:ASP:O	10:H:42:ILE:HG13	1.89	0.72
10:H:89:LEU:C	10:H:91:ASP:H	1.92	0.72
5:C:238:ILE:HD11	5:C:246:ARG:NH1	2.04	0.72
4:B:1115:THR:HG22	4:B:1117:GLN:HG3	1.70	0.72
4:B:1159:ARG:HE	4:B:1193:GLN:HE21	1.35	0.72
3:A:1017:LEU:HB2	7:E:206:GLY:N	2.02	0.72
9:G:143:ILE:HG22	9:G:144:ARG:H	1.52	0.72
8:F:103:MET:CE	9:G:66:GLY:H	2.03	0.72
3:A:896:ARG:NH2	3:A:1030:ARG:HH21	1.88	0.72
12:J:3:VAL:HG21	12:J:18:TRP:CB	2.19	0.72
4:B:582:VAL:HG23	4:B:626:ILE:HB	1.70	0.72
3:A:885:THR:O	3:A:940:ARG:HD2	1.90	0.72
3:A:69:THR:C	3:A:71:GLN:H	1.93	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:847:ASP:HB3	5:C:167:HIS:NE2	2.05	0.71
4:B:247:GLY:H	4:B:418:LYS:HZ1	1.35	0.71
2:T:10:U:H2'	2:T:11:G:O4'	1.89	0.71
3:A:32:VAL:HG21	3:A:68:GLN:NE2	2.05	0.71
3:A:1120:LEU:CD1	3:A:1120:LEU:H	2.03	0.71
3:A:1116:LEU:HB2	3:A:1329:THR:OG1	1.90	0.71
3:A:855:THR:HG23	3:A:857:ARG:HG3	1.71	0.71
3:A:1124:HIS:HB3	3:A:1130:GLN:HG2	1.71	0.71
8:F:69:LEU:O	8:F:71:GLU:N	2.23	0.71
4:B:193:LYS:NZ	14:L:32:ALA:HB1	2.05	0.71
3:A:986:ILE:HG22	3:A:987:VAL:N	2.05	0.71
4:B:975:GLN:HG2	4:B:976:ILE:H	1.56	0.71
14:L:32:ALA:HB3	14:L:55:ILE:CD1	2.20	0.71
4:B:859:TYR:OH	4:B:941:LEU:HD12	1.91	0.71
6:D:170:THR:HB	6:D:172:LEU:HG	1.70	0.71
3:A:913:LEU:HD12	3:A:914:GLU:N	2.05	0.71
4:B:842:ASN:ND2	4:B:845:SER:H	1.88	0.71
5:C:36:VAL:HG21	5:C:251:LEU:HD22	1.72	0.71
3:A:821:ARG:HB2	3:A:821:ARG:NH1	2.05	0.71
4:B:112:LEU:HD12	4:B:113:TYR:N	2.06	0.71
5:C:35:ARG:NH1	13:K:41:THR:N	2.38	0.71
4:B:815:ARG:HD3	4:B:1041:GLU:OE2	1.91	0.71
3:A:960:ILE:O	3:A:963:ILE:HG22	1.91	0.71
3:A:1030:ARG:HG3	3:A:1034:GLU:OE2	1.91	0.71
3:A:2:VAL:HG21	4:B:1157:ALA:HB1	1.73	0.71
3:A:477:PRO:HG2	3:A:521:MET:HG2	1.72	0.71
3:A:1115:SER:O	3:A:1116:LEU:HB3	1.89	0.70
4:B:862:GLN:HG2	4:B:963:PHE:HD1	1.54	0.70
3:A:438:ASP:O	3:A:439:ASN:HB2	1.88	0.70
4:B:708:GLU:O	4:B:710:LEU:N	2.24	0.70
3:A:646:PHE:O	3:A:650:GLN:HG3	1.91	0.70
5:C:46:ILE:HD12	5:C:67:LEU:HB3	1.72	0.70
9:G:81:PRO:HG3	9:G:106:MET:SD	2.31	0.70
5:C:213:PRO:O	5:C:214:ASN:HB2	1.91	0.70
14:L:58:LYS:HG2	14:L:58:LYS:O	1.90	0.70
3:A:139:TRP:O	3:A:143:LYS:HB3	1.90	0.70
3:A:58:LEU:HD13	3:A:80:HIS:O	1.91	0.70
4:B:39:ARG:NH2	4:B:665:GLU:HG2	2.05	0.70
3:A:1343:ALA:HB2	7:E:150:VAL:HG22	1.73	0.70
3:A:1121:GLU:HG2	3:A:1122:PRO:HD2	1.72	0.70
3:A:445:ASN:HB2	3:A:455:MET:HG2	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:35:ILE:HG22	3:A:35:ILE:O	1.90	0.70
11:I:82:GLU:OE2	11:I:104:LEU:HD12	1.90	0.70
5:C:209:TYR:H	5:C:209:TYR:HD1	1.40	0.70
4:B:343:ILE:CG2	4:B:348:ARG:HG3	2.22	0.70
6:D:40:HIS:CE1	6:D:41:GLN:HG3	2.27	0.70
12:J:12:LYS:O	12:J:14:VAL:HG23	1.92	0.70
8:F:103:MET:O	8:F:104:ASN:HB2	1.90	0.70
8:F:119:ARG:HG3	8:F:119:ARG:HH11	1.56	0.70
3:A:899:VAL:HB	3:A:929:LEU:CD1	2.21	0.70
7:E:22:MET:HE3	7:E:26:ARG:NE	2.06	0.70
3:A:1208:THR:O	3:A:1212:VAL:HG23	1.92	0.70
3:A:761:MET:HA	3:A:804:TYR:HB2	1.72	0.70
4:B:205:ILE:N	4:B:205:ILE:HD12	2.07	0.70
3:A:34:LYS:NZ	3:A:57:ARG:HH12	1.90	0.70
3:A:794:PRO:HG2	3:A:795:GLU:OE2	1.91	0.70
3:A:993:LEU:HD22	3:A:1046:LEU:HD22	1.73	0.70
3:A:1161:THR:HG22	3:A:1163:ILE:N	2.05	0.70
4:B:498:THR:HG22	4:B:537:LYS:H	1.55	0.70
3:A:412:ARG:NH2	4:B:1108:ARG:NH1	2.39	0.70
4:B:971:THR:OG1	5:C:61:GLU:HG3	1.92	0.70
9:G:143:ILE:CG2	9:G:144:ARG:H	2.05	0.69
3:A:451:HIS:NE2	3:A:1074:GLU:HG3	2.07	0.69
3:A:1261:LYS:O	3:A:1264:GLU:HB3	1.92	0.69
4:B:98:THR:O	4:B:126:SER:HB2	1.91	0.69
4:B:778:MET:HE1	4:B:1094:ARG:HD3	1.73	0.69
13:K:46:ILE:O	13:K:50:LEU:HB2	1.92	0.69
12:J:36:LEU:HD12	12:J:47:ARG:NH1	2.07	0.69
6:D:175:PHE:HZ	9:G:85:GLU:HG3	1.57	0.69
5:C:232:VAL:HG21	5:C:244:VAL:HG22	1.73	0.69
3:A:79:GLY:HA3	3:A:243:PRO:HG3	1.74	0.69
5:C:66:ARG:NH2	12:J:3:VAL:O	2.24	0.69
3:A:901:LEU:N	3:A:926:GLN:NE2	2.37	0.69
4:B:168:GLY:H	4:B:450:ALA:HB1	1.57	0.69
3:A:541:ILE:HG21	3:A:549:MET:CE	2.21	0.69
11:I:50:THR:HG22	11:I:52:ILE:H	1.58	0.69
3:A:50:ILE:C	3:A:52:GLY:H	1.96	0.69
10:H:127:GLY:O	10:H:128:ASN:HB2	1.93	0.69
10:H:61:SER:O	10:H:62:SER:HB3	1.91	0.69
3:A:254:GLU:HB2	4:B:935:ARG:NH1	2.03	0.69
3:A:709:THR:HG23	11:I:94:ASP:HA	1.73	0.69
4:B:975:GLN:O	4:B:990:ILE:HD12	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:472:LEU:HD11	4:B:835:GLN:NE2	2.08	0.69
5:C:184:ASN:ND2	5:C:187:LYS:HA	2.08	0.69
4:B:830:TYR:CE2	4:B:1000:PRO:HD3	2.28	0.69
3:A:1015:VAL:HG12	3:A:1019:CYS:SG	2.33	0.69
4:B:811:TYR:N	4:B:811:TYR:CD1	2.60	0.69
3:A:84:ILE:HD11	3:A:270:LEU:HD13	1.74	0.69
7:E:117:THR:HG22	7:E:119:SER:H	1.58	0.69
3:A:567:LYS:HB3	10:H:96:VAL:N	2.07	0.69
3:A:446:ARG:CD	3:A:480:ALA:HB2	2.22	0.69
4:B:515:HIS:CD2	4:B:516:ASN:H	2.10	0.69
3:A:1030:ARG:HG3	3:A:1034:GLU:CD	2.13	0.69
3:A:443:LEU:HD21	3:A:455:MET:HB3	1.75	0.69
4:B:710:LEU:HA	4:B:733:HIS:HB3	1.75	0.69
4:B:25:ILE:HD11	4:B:653:VAL:O	1.92	0.69
3:A:353:ILE:HG21	3:A:487:MET:HE3	1.73	0.68
4:B:615:MET:C	4:B:616:ILE:HD12	2.14	0.68
9:G:79:PHE:CZ	9:G:106:MET:HE2	2.28	0.68
3:A:344:ARG:HD2	4:B:1118:PRO:O	1.92	0.68
9:G:143:ILE:CG2	9:G:144:ARG:N	2.57	0.68
3:A:1171:GLN:HA	3:A:1174:PHE:CD1	2.29	0.68
3:A:477:PRO:CG	3:A:521:MET:HG2	2.23	0.68
4:B:1006:ILE:HD13	12:J:44:TYR:HE2	1.58	0.68
4:B:1087:PHE:HD2	4:B:1088:GLY:N	1.91	0.68
3:A:567:LYS:HD3	10:H:95:TYR:CG	2.28	0.68
3:A:903:ASN:ND2	3:A:904:THR:N	2.42	0.68
4:B:65:GLU:HG3	4:B:66:ASP:N	2.08	0.68
4:B:378:LEU:O	4:B:378:LEU:HD12	1.93	0.68
11:I:111:THR:HG22	11:I:112:SER:N	2.08	0.68
4:B:526:GLU:HG2	4:B:538:ASN:HD22	1.58	0.68
4:B:295:GLY:H	4:B:298:LEU:HD23	1.57	0.68
10:H:36:CYS:HA	10:H:126:GLU:O	1.92	0.68
3:A:903:ASN:HD22	3:A:904:THR:H	1.41	0.68
5:C:191:TYR:HD2	5:C:201:TRP:CD1	2.11	0.68
9:G:128:PRO:O	9:G:138:THR:HG23	1.93	0.68
4:B:1006:ILE:HD13	12:J:44:TYR:CE2	2.29	0.68
3:A:590:ARG:HD3	3:A:604:GLY:HA2	1.74	0.68
3:A:528:LEU:O	3:A:531:ILE:HG22	1.93	0.68
3:A:886:ILE:HD11	3:A:943:LEU:HB3	1.74	0.68
6:D:17:LYS:HE3	6:D:17:LYS:CA	2.23	0.68
3:A:694:THR:O	3:A:698:GLN:HG3	1.93	0.68
4:B:351:TYR:O	4:B:355:ILE:HG13	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:109:VAL:HG11	8:F:123:LYS:HD3	1.74	0.68
8:F:90:ARG:HD3	8:F:155:LEU:CD1	2.23	0.68
10:H:84:ALA:HA	10:H:87:ARG:HB2	1.76	0.68
3:A:836:TYR:CD2	3:A:840:ARG:HD2	2.27	0.68
3:A:443:LEU:HD12	4:B:1146:PHE:CE2	2.28	0.68
4:B:661:LEU:HD11	4:B:684:LEU:HD21	1.74	0.68
10:H:58:THR:HG22	10:H:59:ILE:H	1.59	0.68
6:D:50:LEU:HD13	6:D:55:ALA:HA	1.76	0.68
3:A:535:THR:CG2	3:A:616:VAL:HA	2.24	0.68
5:C:73:GLN:HB3	5:C:131:HIS:H	1.58	0.68
10:H:59:ILE:HG22	10:H:60:ALA:H	1.58	0.68
4:B:653:VAL:HG22	4:B:689:LEU:HB3	1.76	0.68
13:K:58:PHE:HB3	13:K:76:GLN:HB3	1.76	0.68
4:B:288:ALA:HA	4:B:331:LEU:HD12	1.73	0.68
5:C:40:GLU:HA	5:C:163:ILE:HG21	1.74	0.68
3:A:1402:PHE:CE1	3:A:1403:GLU:HG3	2.28	0.67
10:H:25:ARG:HA	10:H:41:ASP:HA	1.76	0.67
5:C:189:THR:HG22	5:C:190:ASP:H	1.59	0.67
4:B:113:TYR:HB3	4:B:114:PRO:HD2	1.75	0.67
3:A:18:GLN:HB2	4:B:1215:ARG:HB2	1.77	0.67
4:B:123:THR:OG1	4:B:458:LYS:HE2	1.94	0.67
4:B:1085:ILE:HD12	4:B:1085:ILE:N	2.09	0.67
3:A:567:LYS:HB3	10:H:95:TYR:HA	1.76	0.67
5:C:244:VAL:O	5:C:248:ILE:HG13	1.94	0.67
5:C:40:GLU:HA	5:C:163:ILE:CG2	2.24	0.67
12:J:1:MET:N	12:J:57:ILE:H	1.81	0.67
6:D:56:ARG:HA	6:D:148:LEU:HD13	1.76	0.67
4:B:859:TYR:CZ	4:B:941:LEU:HD12	2.30	0.67
3:A:182:VAL:HG22	3:A:201:VAL:HA	1.75	0.67
3:A:1094:VAL:HG12	3:A:1095:THR:H	1.60	0.67
3:A:849:MET:HE1	3:A:1061:GLY:HA2	1.75	0.67
5:C:35:ARG:HH12	13:K:41:THR:H	1.41	0.67
4:B:467:GLY:H	4:B:475:SER:CB	2.07	0.67
3:A:963:ILE:HD11	3:A:1048:ASN:CB	2.25	0.67
4:B:654:ARG:H	4:B:657:HIS:CD2	2.12	0.67
4:B:1096:ARG:O	4:B:1097:HIS:HB2	1.93	0.67
8:F:118:LEU:O	8:F:122:MET:HG3	1.95	0.67
3:A:666:ILE:H	4:B:1026:LEU:HD13	1.59	0.67
6:D:47:LEU:HD11	9:G:3:PHE:CD2	2.30	0.67
3:A:388:LEU:O	3:A:392:VAL:HG23	1.95	0.67
10:H:64:ASN:O	10:H:65:LEU:HB2	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:183:TRP:CZ2	5:C:207:CYS:HB3	2.30	0.67
4:B:606:LYS:HD2	4:B:608:ASP:OD2	1.94	0.67
7:E:207:ARG:HH11	7:E:207:ARG:HB2	1.60	0.67
12:J:57:ILE:HA	12:J:60:PHE:CD2	2.30	0.67
3:A:253:ASN:HB3	4:B:935:ARG:CZ	2.24	0.67
3:A:1120:LEU:HD12	3:A:1120:LEU:H	1.59	0.67
5:C:34:ARG:O	5:C:38:ILE:HG13	1.95	0.67
6:D:134:THR:HG22	6:D:136:GLY:H	1.59	0.67
11:I:111:THR:HG22	11:I:112:SER:H	1.59	0.67
4:B:603:LEU:HD13	4:B:608:ASP:HB2	1.77	0.67
4:B:429:PHE:HA	4:B:432:MET:HE2	1.75	0.67
4:B:408:LEU:HD22	4:B:545:ILE:HD12	1.77	0.67
5:C:133:ILE:CD1	5:C:237:SER:HA	2.25	0.67
3:A:335:ARG:HA	3:A:339:ASN:HB2	1.77	0.67
3:A:92:HIS:O	3:A:94:GLY:N	2.28	0.67
2:T:8:C:H4'	3:A:447:GLN:NE2	2.09	0.67
4:B:532:ALA:HA	4:B:535:LEU:HD12	1.77	0.67
3:A:1420:ASP:O	3:A:1421:CYS:HB2	1.95	0.67
7:E:22:MET:HE1	7:E:26:ARG:HH21	1.59	0.67
3:A:152:VAL:HG12	3:A:153:PRO:HD2	1.77	0.67
4:B:604:ARG:NH1	4:B:691:GLU:OE2	2.28	0.67
3:A:34:LYS:HE2	3:A:57:ARG:NH1	2.10	0.66
10:H:81:PRO:CB	10:H:82:PRO:HD2	2.25	0.66
5:C:251:LEU:O	5:C:255:VAL:HG23	1.96	0.66
11:I:52:ILE:HG13	11:I:52:ILE:O	1.95	0.66
11:I:55:THR:HG22	11:I:58:VAL:CG2	2.26	0.66
11:I:85:PHE:CD1	11:I:99:LEU:HD13	2.30	0.66
8:F:130:ILE:HB	8:F:148:VAL:HG21	1.76	0.66
6:D:8:PHE:CE2	9:G:6:ASP:HB2	2.30	0.66
3:A:356:ASP:HB2	3:A:469:ARG:HH12	1.58	0.66
5:C:8:VAL:HG12	5:C:9:LYS:N	2.10	0.66
3:A:1100:ARG:O	3:A:1103:GLU:HB3	1.96	0.66
3:A:458:HIS:CE1	3:A:507:VAL:HG21	2.31	0.66
4:B:847:ASP:C	4:B:849:GLY:H	1.98	0.66
12:J:14:VAL:HG12	12:J:50:ILE:HD11	1.77	0.66
4:B:737:THR:HG21	11:I:66:PRO:HA	1.76	0.66
3:A:396:PRO:HG3	3:A:416:ARG:HB3	1.78	0.66
7:E:135:PHE:HB3	7:E:140:LEU:HD11	1.76	0.66
3:A:335:ARG:NH1	4:B:1202:LEU:HD13	2.10	0.66
3:A:466:SER:O	4:B:1103:ILE:HD11	1.94	0.66
3:A:1027:ALA:O	3:A:1031:VAL:HG23	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:798:GLY:HA2	3:A:815:PHE:CD1	2.30	0.66
3:A:1127:ASP:HB3	3:A:1130:GLN:CB	2.25	0.66
5:C:35:ARG:NH1	13:K:41:THR:H	1.92	0.66
4:B:60:GLN:HE22	4:B:94:LYS:HA	1.61	0.66
2:T:12:G:O2'	2:T:13:U:H3'	1.94	0.66
4:B:999:MET:HB3	4:B:1007:VAL:HG21	1.76	0.66
4:B:955:THR:CG2	4:B:956:THR:N	2.59	0.66
3:A:1100:ARG:HH21	3:A:1351:GLU:CG	2.07	0.66
6:D:40:HIS:CB	9:G:73:LYS:HZ3	1.93	0.66
4:B:361:LEU:HD21	4:B:377:PHE:CD2	2.31	0.66
3:A:698:GLN:HA	11:I:97:MET:O	1.96	0.66
7:E:157:SER:C	7:E:159:ASP:H	1.99	0.66
8:F:116:ASP:HB3	8:F:119:ARG:HB2	1.78	0.66
4:B:792:MET:HA	4:B:856:PHE:O	1.96	0.66
3:A:254:GLU:O	3:A:256:GLN:N	2.28	0.66
4:B:999:MET:CE	4:B:999:MET:HA	2.26	0.66
4:B:642:ASP:O	4:B:644:GLU:N	2.28	0.66
3:A:856:THR:HB	3:A:865:GLN:HB2	1.77	0.66
4:B:857:ARG:HD2	4:B:945:GLU:OE1	1.94	0.66
3:A:541:ILE:HG22	3:A:546:VAL:HG23	1.76	0.66
4:B:121:ASN:HA	4:B:207:GLY:CA	2.26	0.66
9:G:96:GLN:HG3	9:G:97:HIS:HD2	1.60	0.66
3:A:63:ARG:HD3	3:A:74:MET:CE	2.26	0.66
4:B:1023:VAL:O	4:B:1026:LEU:HB2	1.95	0.66
4:B:114:PRO:HG3	4:B:181:LEU:HD11	1.77	0.66
13:K:65:HIS:CD2	13:K:67:PHE:HB2	2.31	0.66
3:A:1372:VAL:O	3:A:1376:THR:HG22	1.95	0.66
6:D:58:VAL:HG11	9:G:4:ILE:HD11	1.78	0.66
8:F:103:MET:HE2	9:G:66:GLY:H	1.61	0.66
4:B:35:SER:HA	4:B:811:TYR:HE2	1.61	0.66
4:B:525:ALA:O	4:B:768:THR:HA	1.96	0.66
5:C:161:LYS:O	5:C:170:TRP:NE1	2.28	0.65
10:H:126:GLU:C	10:H:130:ARG:HH22	2.00	0.65
4:B:830:TYR:O	4:B:832:GLY:N	2.29	0.65
3:A:1373:ASP:HA	3:A:1376:THR:CG2	2.26	0.65
3:A:475:THR:HG23	3:A:476:SER:N	2.10	0.65
5:C:11:ARG:HD3	5:C:209:TYR:CE2	2.31	0.65
3:A:1094:VAL:HG13	3:A:1113:THR:HG21	1.77	0.65
3:A:590:ARG:NH2	3:A:620:LYS:CB	2.59	0.65
6:D:47:LEU:HD11	9:G:3:PHE:CE2	2.31	0.65
3:A:87:ALA:HB3	3:A:276:LEU:HD23	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:76:PRO:CG	11:I:110:PHE:HB3	2.27	0.65
3:A:842:VAL:HG11	4:B:1136:ASP:OD2	1.95	0.65
5:C:146:LYS:HB2	12:J:61:LEU:HD11	1.78	0.65
10:H:81:PRO:HB2	10:H:82:PRO:HD2	1.78	0.65
10:H:42:ILE:HG23	10:H:95:TYR:HE1	1.61	0.65
4:B:364:ILE:HG12	4:B:585:VAL:CG1	2.25	0.65
4:B:39:ARG:HG2	4:B:39:ARG:HH11	1.61	0.65
7:E:114:ASN:O	7:E:115:ASN:HB3	1.97	0.65
6:D:130:LEU:O	6:D:132:GLN:N	2.29	0.65
3:A:35:ILE:HA	3:A:52:GLY:O	1.97	0.65
3:A:254:GLU:HG3	4:B:935:ARG:HH22	1.60	0.65
3:A:1164:PRO:HG2	3:A:1165:GLU:H	1.59	0.65
3:A:1130:GLN:HE21	3:A:1134:ILE:HD11	1.61	0.65
11:I:58:VAL:HG13	11:I:62:ILE:HD13	1.78	0.65
4:B:799:PRO:HB3	4:B:818:PRO:HG2	1.77	0.65
4:B:1162:ILE:HD11	4:B:1194:ILE:CD1	2.27	0.65
6:D:130:LEU:C	6:D:132:GLN:H	2.00	0.65
7:E:176:PRO:O	7:E:212:ARG:HA	1.96	0.65
9:G:1:MET:HG3	9:G:85:GLU:OE2	1.96	0.65
4:B:763:GLN:HG2	4:B:765:PRO:HD2	1.79	0.65
4:B:351:TYR:CE1	4:B:355:ILE:HD11	2.32	0.65
3:A:356:ASP:OD2	13:K:65:HIS:HE1	1.78	0.65
13:K:31:VAL:HG12	13:K:32:VAL:N	2.12	0.65
4:B:601:ARG:O	4:B:605:ARG:HG3	1.97	0.65
3:A:450:LEU:HB3	3:A:838:GLN:HE21	1.61	0.65
8:F:111:LEU:H	8:F:111:LEU:HD12	1.60	0.65
14:L:70:ARG:HG2	14:L:70:ARG:HH11	1.62	0.65
4:B:807:ARG:HG2	4:B:1045:SER:OG	1.97	0.65
3:A:896:ARG:HD3	3:A:897:TYR:CE1	2.31	0.65
10:H:62:SER:HB2	10:H:64:ASN:HD22	1.61	0.65
3:A:1038:THR:H	3:A:1041:ALA:HB3	1.62	0.65
3:A:211:PHE:HA	3:A:214:ILE:HG13	1.78	0.65
4:B:549:THR:HB	4:B:628:THR:OG1	1.97	0.65
9:G:122:ASN:HD22	9:G:125:SER:HB3	1.61	0.65
3:A:809:THR:H	3:A:812:GLU:HB2	1.62	0.65
4:B:294:ASP:O	4:B:296:GLU:N	2.29	0.65
4:B:515:HIS:CD2	4:B:517:THR:H	2.15	0.65
3:A:698:GLN:NE2	11:I:99:LEU:HD21	2.12	0.65
4:B:953:LEU:HD21	4:B:965:LYS:HB2	1.78	0.65
3:A:743:VAL:O	3:A:747:VAL:HG23	1.97	0.65
4:B:842:ASN:O	4:B:846:ILE:HG13	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:18:PHE:HA	9:G:22:MET:CE	2.27	0.65
2:T:13:U:O2'	2:T:14:C:H6	1.80	0.65
6:D:29:LEU:HB3	9:G:82:PHE:HE2	1.60	0.65
4:B:38:PHE:HD1	4:B:811:TYR:CD2	2.15	0.65
4:B:1180:PHE:HB3	4:B:1191:ILE:HD12	1.77	0.65
4:B:782:LEU:HD12	4:B:788:ARG:HH11	1.62	0.65
7:E:48:ASP:CG	7:E:49:SER:H	2.00	0.64
5:C:39:ALA:CA	5:C:164:ALA:HB3	2.26	0.64
4:B:1069:PHE:HD1	4:B:1069:PHE:H	1.44	0.64
3:A:1118:VAL:O	3:A:1305:VAL:HG13	1.97	0.64
3:A:366:VAL:HG21	3:A:460:VAL:HG22	1.78	0.64
6:D:67:ARG:HB2	6:D:133:THR:HG21	1.78	0.64
4:B:185:THR:H	4:B:188:ASP:HB2	1.62	0.64
5:C:174:ALA:HB2	5:C:235:VAL:HG22	1.80	0.64
4:B:1159:ARG:NE	4:B:1193:GLN:HE21	1.96	0.64
3:A:547:LEU:HD22	13:K:58:PHE:CE1	2.32	0.64
3:A:628:GLY:O	3:A:632:VAL:HG23	1.97	0.64
3:A:853:ASP:OD1	3:A:855:THR:HB	1.98	0.64
6:D:29:LEU:HD22	9:G:82:PHE:CE2	2.32	0.64
8:F:68:THR:HB	8:F:71:GLU:HB2	1.80	0.64
3:A:738:LYS:HD2	3:A:740:LEU:HD21	1.80	0.64
4:B:705:MET:H	4:B:710:LEU:CD1	2.11	0.64
9:G:45:ILE:HD13	9:G:78:VAL:HG13	1.78	0.64
5:C:18:VAL:HG23	5:C:240:VAL:HB	1.80	0.64
11:I:55:THR:HG23	11:I:86:PHE:HZ	1.62	0.64
3:A:215:SER:HB3	3:A:218:ASP:HB2	1.79	0.64
3:A:88:LYS:HE3	3:A:280:GLU:OE2	1.98	0.64
5:C:67:LEU:HD11	5:C:155:LEU:CD1	2.27	0.64
7:E:198:ILE:HD11	7:E:212:ARG:CG	2.28	0.64
4:B:955:THR:HG22	4:B:956:THR:H	1.61	0.64
4:B:865:LYS:NZ	4:B:869:SER:HA	2.12	0.64
8:F:90:ARG:HD3	8:F:155:LEU:HD11	1.79	0.64
3:A:1317:MET:O	3:A:1322:ILE:HD11	1.96	0.64
4:B:46:GLN:HG3	4:B:47:GLN:H	1.62	0.64
4:B:798:TYR:HE2	5:C:62:PHE:CZ	2.16	0.64
3:A:537:ARG:HD2	10:H:20:TYR:CE1	2.33	0.64
9:G:1:MET:HE3	9:G:80:LYS:C	2.17	0.64
3:A:886:ILE:HG13	3:A:943:LEU:HD12	1.78	0.64
3:A:42:ASP:HB3	3:A:45:GLN:H	1.63	0.64
4:B:1002:THR:CG2	4:B:1006:ILE:HG13	2.27	0.64
3:A:844:ALA:O	3:A:845:LEU:HD23	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:99:LEU:HD12	8:F:99:LEU:O	1.96	0.64
4:B:955:THR:CG2	4:B:956:THR:H	2.11	0.64
9:G:119:LEU:HD13	9:G:132:SER:HB2	1.80	0.64
4:B:603:LEU:HD12	4:B:609:ILE:HG13	1.80	0.64
3:A:372:LYS:HA	3:A:435:HIS:ND1	2.13	0.64
5:C:6:PRO:CB	5:C:25:VAL:HG12	2.28	0.64
3:A:79:GLY:HA3	3:A:243:PRO:CG	2.29	0.63
3:A:68:GLN:C	3:A:70:CYS:H	2.00	0.63
3:A:616:VAL:HG12	3:A:617:VAL:H	1.64	0.63
3:A:590:ARG:HH21	3:A:620:LYS:HB3	1.62	0.63
3:A:154:SER:HB3	3:A:162:VAL:HG21	1.79	0.63
3:A:441:PRO:HD2	3:A:498:ARG:NH2	2.13	0.63
4:B:434:ARG:O	4:B:437:GLU:HB2	1.98	0.63
4:B:847:ASP:HB3	5:C:167:HIS:CD2	2.34	0.63
3:A:1329:THR:CG2	3:A:1331:SER:H	2.06	0.63
3:A:1438:THR:HB	4:B:1144:ALA:CB	2.28	0.63
3:A:728:LYS:O	3:A:732:LEU:HG	1.97	0.63
3:A:215:SER:HB3	3:A:218:ASP:OD2	1.99	0.63
3:A:1313:LEU:HD23	3:A:1338:VAL:HG21	1.80	0.63
3:A:311:GLN:O	3:A:312:PRO:C	2.36	0.63
4:B:824:ILE:CG2	4:B:1087:PHE:HE2	2.12	0.63
9:G:79:PHE:HZ	9:G:106:MET:HE2	1.62	0.63
3:A:914:GLU:HB2	3:A:979:SER:O	1.98	0.63
3:A:105:CYS:O	3:A:114:LEU:HG	1.98	0.63
5:C:253:LYS:O	5:C:256:ALA:HB3	1.98	0.63
5:C:67:LEU:HA	5:C:70:ILE:HD12	1.79	0.63
4:B:273:LEU:HD12	4:B:280:ILE:HD12	1.80	0.63
7:E:192:ARG:HG3	7:E:192:ARG:NH1	2.13	0.63
8:F:130:ILE:O	8:F:148:VAL:HG21	1.98	0.63
3:A:310:GLY:O	3:A:312:PRO:HD2	1.99	0.63
4:B:411:PRO:O	4:B:414:ALA:HB3	1.97	0.63
6:D:71:LYS:HA	6:D:74:GLN:HB2	1.79	0.63
7:E:55:ARG:C	7:E:57:MET:H	2.00	0.63
3:A:1385:THR:HG22	3:A:1386:ARG:N	2.13	0.63
12:J:3:VAL:HG21	12:J:18:TRP:CG	2.34	0.63
3:A:567:LYS:HB2	3:A:568:PRO:CD	2.29	0.63
11:I:34:TYR:CE2	11:I:36:GLU:HB3	2.33	0.63
4:B:952:VAL:HG12	4:B:953:LEU:N	2.13	0.63
4:B:305:VAL:HG12	4:B:305:VAL:O	1.99	0.63
3:A:34:LYS:O	3:A:35:ILE:HB	1.99	0.63
4:B:227:LYS:HB2	4:B:395:GLN:OE1	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:179:GLU:HG2	5:C:180:TYR:N	2.13	0.63
5:C:101:LEU:HD13	5:C:118:LEU:CD2	2.27	0.63
4:B:1001:PHE:CZ	4:B:1073:TYR:HB2	2.33	0.63
6:D:134:THR:CG2	6:D:135:GLY:H	2.10	0.63
6:D:134:THR:CG2	6:D:135:GLY:N	2.61	0.63
3:A:144:THR:O	3:A:146:MET:HG3	1.98	0.63
3:A:984:LYS:O	3:A:988:LEU:HB2	1.98	0.63
7:E:5:ASN:O	7:E:9:ILE:HG13	1.98	0.63
5:C:45:ALA:HA	5:C:72:LEU:CD1	2.28	0.63
12:J:2:ILE:H	12:J:57:ILE:CG2	2.12	0.63
3:A:871:ASP:OD2	3:A:873:MET:HB2	1.98	0.63
5:C:73:GLN:CB	5:C:131:HIS:H	2.11	0.62
2:T:13:U:HO2'	2:T:14:C:C5'	2.08	0.62
3:A:1006:ILE:HD12	7:E:163:GLU:HG3	1.80	0.62
4:B:792:MET:HG3	4:B:855:PHE:CE1	2.34	0.62
7:E:144:ILE:HG13	7:E:145:THR:N	2.14	0.62
4:B:363:HIS:O	4:B:364:ILE:HB	1.99	0.62
3:A:858:ASN:ND2	3:A:860:LEU:H	1.97	0.62
4:B:219:ALA:HB2	4:B:405:ARG:NH1	2.14	0.62
5:C:17:ASN:O	5:C:18:VAL:HG23	1.99	0.62
12:J:7:CYS:SG	12:J:49:MET:HE3	2.39	0.62
3:A:442:VAL:HG21	3:A:460:VAL:HG23	1.80	0.62
3:A:427:GLN:HB2	3:A:430:TRP:CE2	2.34	0.62
3:A:685:GLU:HG3	3:A:686:ALA:N	2.15	0.62
3:A:7:SER:HB3	4:B:1175:LEU:HD22	1.81	0.62
8:F:69:LEU:C	8:F:71:GLU:N	2.52	0.62
4:B:792:MET:HG3	4:B:855:PHE:HE1	1.64	0.62
4:B:842:ASN:HD22	4:B:845:SER:CB	2.13	0.62
4:B:1099:VAL:CG1	4:B:1100:ASP:N	2.62	0.62
10:H:139:ASN:O	10:H:140:ALA:HB2	1.99	0.62
12:J:44:TYR:HD2	12:J:44:TYR:N	1.98	0.62
9:G:165:GLU:HB2	9:G:168:LEU:HD12	1.80	0.62
4:B:516:ASN:ND2	4:B:516:ASN:N	2.46	0.62
9:G:51:TYR:O	9:G:54:ILE:HG13	1.99	0.62
3:A:252:PHE:O	3:A:253:ASN:HB2	1.99	0.62
4:B:218:SER:HB3	4:B:241:ARG:NH1	2.15	0.62
12:J:44:TYR:HA	12:J:47:ARG:CB	2.30	0.62
3:A:714:PHE:O	3:A:718:VAL:HG23	2.00	0.62
7:E:22:MET:CE	7:E:26:ARG:HH21	2.12	0.62
7:E:124:VAL:HG13	7:E:132:ILE:HB	1.81	0.62
6:D:12:ARG:NE	6:D:14:ARG:HD2	2.15	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:1180:PHE:O	4:B:1181:GLU:O	2.18	0.62
13:K:42:LEU:CD2	13:K:46:ILE:HD11	2.30	0.62
3:A:202:LEU:HB3	3:A:207:ILE:HD11	1.81	0.62
3:A:1036:ARG:HH11	3:A:1036:ARG:HG2	1.65	0.62
3:A:1174:PHE:C	3:A:1176:LEU:N	2.53	0.62
13:K:60:ALA:O	13:K:73:LEU:HD12	1.99	0.62
7:E:213:ILE:HG12	7:E:214:CYS:N	2.13	0.62
5:C:69:LEU:N	5:C:69:LEU:HD12	2.15	0.62
4:B:616:ILE:N	4:B:616:ILE:HD12	2.14	0.62
8:F:89:GLU:OE2	8:F:134:ILE:HG21	1.99	0.62
7:E:124:VAL:HA	7:E:132:ILE:HD12	1.82	0.62
4:B:224:GLN:HA	4:B:396:ASP:OD2	2.00	0.62
14:L:27:LEU:O	14:L:28:LYS:HG2	2.00	0.62
3:A:767:GLN:HE22	3:A:774:ARG:HB3	1.62	0.61
3:A:993:LEU:HD22	3:A:1046:LEU:CD2	2.30	0.61
4:B:751:VAL:HG13	4:B:812:LEU:HD22	1.81	0.61
4:B:744:HIS:HD2	4:B:746:SER:OG	1.82	0.61
4:B:373:ARG:HG3	4:B:566:LEU:HD23	1.80	0.61
6:D:4:SER:O	6:D:5:THR:HB	1.99	0.61
3:A:785:PRO:HG2	3:A:786:HIS:HD2	1.65	0.61
3:A:786:HIS:CD2	3:A:786:HIS:N	2.67	0.61
3:A:399:HIS:HB3	3:A:400:PRO:CD	2.29	0.61
3:A:1348:LEU:O	3:A:1352:VAL:HG23	2.00	0.61
3:A:870:GLU:HG2	7:E:208:TYR:CG	2.36	0.61
4:B:1183:LYS:N	4:B:1183:LYS:CE	2.62	0.61
3:A:1095:THR:O	3:A:1095:THR:HG22	2.00	0.61
3:A:1227:ILE:HG22	3:A:1228:TRP:N	2.14	0.61
5:C:20:PHE:HE1	5:C:22:LEU:HD12	1.65	0.61
9:G:131:GLN:HG2	9:G:136:VAL:HG22	1.83	0.61
4:B:1181:GLU:HG3	4:B:1188:LYS:HE3	1.80	0.61
3:A:1114:PRO:O	3:A:1115:SER:O	2.18	0.61
3:A:1436:ILE:O	3:A:1437:GLY:C	2.39	0.61
4:B:1002:THR:O	4:B:1004:GLU:N	2.32	0.61
3:A:107:CYS:N	3:A:114:LEU:HD21	2.15	0.61
3:A:746:MET:HE3	4:B:1018:PRO:HG2	1.82	0.61
4:B:58:THR:O	4:B:62:ILE:HG13	2.00	0.61
9:G:48:VAL:HG13	9:G:74:TYR:HD1	1.65	0.61
10:H:84:ALA:CB	10:H:87:ARG:HB2	2.29	0.61
4:B:515:HIS:CD2	4:B:516:ASN:N	2.69	0.61
3:A:984:LYS:HG2	3:A:988:LEU:HD12	1.81	0.61
4:B:217:ARG:HE	4:B:405:ARG:HB2	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:818:MET:HA	4:B:514:LEU:HB3	1.82	0.61
5:C:45:ALA:HA	5:C:72:LEU:HD13	1.83	0.61
3:A:567:LYS:CB	10:H:95:TYR:HA	2.30	0.61
4:B:999:MET:HE3	4:B:999:MET:HA	1.83	0.61
4:B:1177:HIS:HB2	4:B:1179:GLN:NE2	2.12	0.61
3:A:1224:LEU:HD11	3:A:1240:CYS:HB2	1.83	0.61
3:A:1121:GLU:CG	3:A:1122:PRO:HD2	2.30	0.61
6:D:13:ARG:HA	6:D:17:LYS:HZ3	1.66	0.61
3:A:1279:ILE:HD11	3:A:1316:VAL:HG21	1.83	0.61
4:B:842:ASN:HB3	4:B:845:SER:OG	2.00	0.61
9:G:39:THR:HG22	9:G:40:GLY:N	2.12	0.61
3:A:1226:VAL:HG22	3:A:1240:CYS:HB3	1.83	0.61
3:A:87:ALA:HB1	3:A:276:LEU:HD23	1.82	0.61
3:A:1313:LEU:O	3:A:1315:GLU:N	2.34	0.61
7:E:84:ASP:O	7:E:86:PRO:HD3	2.00	0.61
4:B:278:GLN:HG2	4:B:279:ASP:H	1.65	0.61
4:B:393:LYS:HA	4:B:393:LYS:HE3	1.82	0.61
4:B:39:ARG:HH21	4:B:665:GLU:HG2	1.64	0.61
4:B:900:ALA:O	4:B:903:VAL:HG23	2.01	0.61
5:C:112:ASN:HB2	5:C:114:TYR:CE1	2.36	0.61
3:A:268:ASP:HB3	3:A:299:HIS:ND1	2.16	0.61
3:A:1206:ASP:HB3	3:A:1274:ARG:HH12	1.65	0.61
5:C:98:VAL:HG23	5:C:122:SER:HB3	1.82	0.60
5:C:66:ARG:CZ	12:J:2:ILE:HG21	2.30	0.60
4:B:583:ASN:ND2	4:B:628:THR:HG22	2.09	0.60
3:A:596:THR:C	3:A:598:LEU:H	2.05	0.60
2:T:12:G:HO2'	2:T:13:U:C5'	2.11	0.60
7:E:207:ARG:CB	7:E:207:ARG:HH11	2.14	0.60
5:C:105:GLY:HA3	5:C:149:LYS:O	2.00	0.60
4:B:291:ILE:HD13	4:B:300:HIS:NE2	2.16	0.60
3:A:1451:VAL:O	3:A:1454:MET:HG2	2.00	0.60
3:A:1305:VAL:HG12	3:A:1306:LEU:N	2.16	0.60
4:B:97:VAL:HG12	4:B:178:ASN:HD21	1.65	0.60
3:A:549:MET:SD	3:A:577:ILE:HD11	2.41	0.60
9:G:39:THR:HG22	9:G:41:LYS:H	1.64	0.60
3:A:1348:LEU:HG	3:A:1372:VAL:HG23	1.82	0.60
6:D:173:HIS:ND1	6:D:174:PRO:HD2	2.16	0.60
4:B:234:ILE:HG12	4:B:257:LYS:HD3	1.83	0.60
4:B:1180:PHE:HB3	4:B:1191:ILE:CD1	2.31	0.60
4:B:803:LEU:HD13	4:B:1032:SER:HB3	1.82	0.60
3:A:552:TRP:HE3	3:A:651:LYS:HB3	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:175:ALA:HB2	12:J:10:CYS:HB2	1.82	0.60
3:A:578:LEU:HD23	3:A:612:ILE:CD1	2.31	0.60
11:I:55:THR:HG23	11:I:86:PHE:CZ	2.37	0.60
5:C:238:ILE:CG2	5:C:242:GLN:HB2	2.31	0.60
3:A:672:ASP:HB2	3:A:736:ASN:OD1	2.01	0.60
3:A:381:THR:CG2	3:A:383:TYR:H	2.14	0.60
1:P:11:C:H2'	1:P:12:C:C6	2.35	0.60
10:H:11:GLN:HA	10:H:53:ASP:O	2.01	0.60
3:A:1293:SER:OG	3:A:1294:PRO:HD2	2.01	0.60
4:B:796:LEU:HD12	4:B:852:ARG:O	2.01	0.60
4:B:364:ILE:CG1	4:B:585:VAL:HG13	2.25	0.60
2:T:13:U:C2'	2:T:14:C:O5'	2.49	0.60
4:B:378:LEU:O	4:B:382:ILE:HG13	2.01	0.60
4:B:866:TYR:HB2	4:B:870:ILE:HB	1.83	0.60
3:A:471:ASN:OD1	3:A:472:LEU:N	2.34	0.60
6:D:192:LYS:HE3	6:D:204:ASP:OD1	2.02	0.60
3:A:11:LEU:O	3:A:11:LEU:HD23	2.01	0.60
3:A:41:MET:HB3	3:A:49:LYS:HA	1.83	0.60
12:J:44:TYR:N	12:J:44:TYR:CD2	2.68	0.60
4:B:1001:PHE:CD2	5:C:34:ARG:NH2	2.69	0.60
4:B:547:VAL:HG12	4:B:612:GLU:OE2	2.01	0.60
4:B:1034:VAL:HG12	4:B:1035:ALA:N	2.16	0.60
3:A:423:ASP:O	3:A:424:ILE:HB	2.02	0.60
3:A:1073:GLY:O	3:A:1076:ALA:HB3	2.02	0.60
3:A:600:PRO:HG2	3:A:601:LYS:H	1.65	0.60
11:I:106:CYS:O	11:I:107:SER:HB2	2.02	0.60
4:B:1031:LEU:HD11	4:B:1042:GLY:HA3	1.84	0.60
4:B:1115:THR:O	4:B:1116:ARG:HB2	2.02	0.60
4:B:976:ILE:O	4:B:990:ILE:HB	2.01	0.60
3:A:416:ARG:C	3:A:417:TYR:HD2	2.05	0.60
13:K:53:ASP:OD1	13:K:55:LYS:HB2	2.02	0.60
3:A:852:TYR:CD2	3:A:1060:PRO:HB2	2.37	0.60
4:B:873:THR:O	4:B:914:LYS:HA	2.02	0.60
3:A:565:ILE:O	3:A:570:PRO:HA	2.02	0.60
11:I:25:LEU:HB3	11:I:38:ALA:HB2	1.82	0.60
4:B:269:ILE:HD11	4:B:386:LEU:HD21	1.83	0.60
3:A:34:LYS:HG2	3:A:57:ARG:HH22	1.66	0.60
3:A:1004:ASN:O	3:A:1008:GLN:HB2	2.01	0.60
3:A:709:THR:HB	3:A:712:GLU:HG3	1.83	0.60
7:E:39:LEU:O	7:E:42:PHE:HB3	2.01	0.60
4:B:232:SER:HB3	4:B:261:ARG:NH2	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:821:GLN:HE22	4:B:851:PHE:HA	1.67	0.60
5:C:144:ILE:O	5:C:145:CYS:HB3	2.01	0.60
3:A:709:THR:HG22	3:A:710:LEU:N	2.17	0.60
11:I:101:PHE:N	11:I:101:PHE:CD1	2.70	0.60
9:G:27:LYS:HE2	9:G:54:ILE:HB	1.84	0.60
10:H:48:PRO:O	10:H:49:VAL:HG23	2.02	0.60
13:K:101:LEU:HD23	13:K:101:LEU:O	2.01	0.60
3:A:56:PRO:O	3:A:57:ARG:NE	2.35	0.60
3:A:567:LYS:CB	3:A:568:PRO:CD	2.80	0.60
10:H:84:ALA:CA	10:H:87:ARG:HB2	2.32	0.60
4:B:100:PRO:HD3	4:B:172:ILE:HD12	1.84	0.60
3:A:14:VAL:N	3:A:1432:GLN:HE22	2.00	0.60
3:A:284:ALA:O	3:A:286:HIS:N	2.34	0.60
3:A:683:ILE:HD13	3:A:801:GLU:HG3	1.84	0.60
3:A:53:LEU:HD22	3:A:54:ASN:HD22	1.66	0.59
9:G:35:GLU:OE2	9:G:48:VAL:HG23	2.01	0.59
7:E:13:TRP:O	7:E:16:PHE:HB3	2.02	0.59
3:A:427:GLN:HG3	3:A:430:TRP:CZ2	2.36	0.59
3:A:12:ARG:HE	4:B:1192:TYR:HE2	1.50	0.59
4:B:483:LEU:HD11	4:B:491:THR:CG2	2.31	0.59
9:G:51:TYR:C	9:G:51:TYR:CD2	2.75	0.59
7:E:78:LEU:HD21	7:E:80:VAL:HG23	1.83	0.59
3:A:1341:ILE:HG23	3:A:1342:GLU:N	2.18	0.59
3:A:768:GLN:CG	3:A:816:HIS:HA	2.31	0.59
3:A:1076:ALA:HA	3:A:1079:MET:CE	2.31	0.59
3:A:683:ILE:HG21	3:A:801:GLU:HG3	1.84	0.59
4:B:696:GLU:O	4:B:699:GLU:HB2	2.02	0.59
4:B:431:TYR:CE2	4:B:447:ALA:HB2	2.37	0.59
6:D:119:ARG:HD3	6:D:221:TYR:CE2	2.37	0.59
3:A:1289:ARG:HD2	3:A:1303:GLU:OE2	2.02	0.59
10:H:81:PRO:CB	10:H:82:PRO:CD	2.81	0.59
10:H:95:TYR:HB3	10:H:144:ILE:HB	1.84	0.59
9:G:144:ARG:HG2	9:G:168:LEU:HD23	1.84	0.59
3:A:407:ARG:HG2	3:A:430:TRP:CZ2	2.37	0.59
8:F:90:ARG:HG3	8:F:91:ALA:N	2.17	0.59
3:A:369:SER:HB2	13:K:2:ASN:OD1	2.02	0.59
4:B:487:THR:O	4:B:490:SER:HB3	2.02	0.59
6:D:7:THR:HG21	6:D:32:GLU:OE2	2.01	0.59
9:G:1:MET:O	9:G:3:PHE:CD1	2.56	0.59
5:C:238:ILE:HG22	5:C:243:VAL:HG23	1.84	0.59
3:A:14:VAL:H	3:A:1432:GLN:HE22	1.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:115:LEU:O	3:A:122:MET:HE2	2.02	0.59
4:B:871:THR:HG22	4:B:872:GLU:O	2.01	0.59
3:A:414:ASP:OD1	3:A:416:ARG:HG2	2.02	0.59
4:B:446:LEU:O	4:B:447:ALA:HB3	2.02	0.59
4:B:265:SER:O	4:B:266:ALA:HB3	2.03	0.59
3:A:90:VAL:CG1	3:A:297:GLN:HA	2.32	0.59
3:A:34:LYS:HB3	3:A:36:ARG:HE	1.67	0.59
3:A:53:LEU:CD2	3:A:54:ASN:HD22	2.15	0.59
3:A:49:LYS:NZ	3:A:61:ILE:HG13	2.18	0.59
4:B:705:MET:N	4:B:710:LEU:HD12	2.18	0.59
3:A:630:ILE:HD13	3:A:646:PHE:CZ	2.38	0.59
3:A:224:PHE:CE2	3:A:231:PRO:HG3	2.37	0.59
3:A:682:THR:HA	3:A:685:GLU:HG2	1.85	0.59
4:B:803:LEU:CD1	4:B:1032:SER:HB3	2.32	0.59
4:B:1077:THR:HG22	13:K:44:ASN:ND2	2.17	0.59
5:C:165:LYS:O	13:K:6:ARG:NH1	2.35	0.59
12:J:48:ARG:HE	12:J:49:MET:CE	2.14	0.59
10:H:58:THR:HB	10:H:143:LEU:HD13	1.84	0.59
4:B:745:PRO:O	4:B:747:MET:N	2.35	0.59
7:E:60:PHE:CE2	7:E:80:VAL:HB	2.37	0.59
7:E:212:ARG:HH11	7:E:212:ARG:HG3	1.68	0.59
3:A:710:LEU:HD13	11:I:94:ASP:O	2.02	0.59
3:A:547:LEU:HD22	13:K:58:PHE:CD1	2.38	0.59
3:A:496:GLU:O	3:A:499:ALA:HB3	2.02	0.59
3:A:34:LYS:HE2	3:A:57:ARG:CZ	2.33	0.59
3:A:53:LEU:CD2	3:A:54:ASN:N	2.55	0.59
4:B:824:ILE:HG23	4:B:1087:PHE:HE2	1.68	0.59
3:A:1447:GLU:OE2	9:G:23:LYS:HB2	2.02	0.59
3:A:1198:ASP:O	3:A:1202:MET:HG2	2.02	0.59
3:A:1242:VAL:HG12	3:A:1243:VAL:N	2.18	0.59
3:A:981:LEU:CD2	3:A:1039:LYS:HA	2.33	0.59
3:A:90:VAL:HG13	3:A:297:GLN:HA	1.84	0.59
3:A:55:ASP:C	3:A:57:ARG:H	2.05	0.59
4:B:309:GLN:HG3	11:I:52:ILE:CD1	2.33	0.59
3:A:1171:GLN:HA	3:A:1174:PHE:HD1	1.68	0.59
4:B:1187:ASN:O	4:B:1188:LYS:CB	2.51	0.59
4:B:653:VAL:CG2	4:B:689:LEU:HB3	2.32	0.59
9:G:49:LEU:HG	9:G:76:ALA:HA	1.83	0.59
3:A:858:ASN:ND2	3:A:858:ASN:C	2.56	0.59
11:I:50:THR:HG22	11:I:51:ASN:N	2.16	0.59
9:G:80:LYS:HG2	9:G:80:LYS:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:29:LEU:HD13	9:G:82:PHE:CZ	2.37	0.59
3:A:427:GLN:HB2	3:A:430:TRP:NE1	2.18	0.59
14:L:38:LEU:O	14:L:39:SER:HB3	2.01	0.59
4:B:641:GLU:HB3	4:B:643:ASP:OD2	2.03	0.59
3:A:34:LYS:NZ	3:A:57:ARG:NH1	2.50	0.59
3:A:783:THR:HG21	3:A:815:PHE:CE2	2.38	0.59
3:A:855:THR:CG2	3:A:857:ARG:HE	2.13	0.59
12:J:14:VAL:HG12	12:J:14:VAL:O	2.03	0.59
4:B:247:GLY:H	4:B:418:LYS:HZ3	1.49	0.59
3:A:1370:LEU:O	3:A:1374:VAL:HG23	2.03	0.59
9:G:88:ASP:OD2	9:G:88:ASP:N	2.35	0.59
5:C:203:GLN:HG2	5:C:207:CYS:SG	2.41	0.59
4:B:221:ASN:N	4:B:241:ARG:O	2.30	0.58
3:A:722:LEU:HD22	3:A:799:PHE:CD1	2.37	0.58
3:A:23:SER:HB3	3:A:233:TRP:CZ2	2.38	0.58
3:A:332:LYS:H	3:A:337:ARG:HB3	1.68	0.58
3:A:1030:ARG:NH1	3:A:1035:TYR:OH	2.35	0.58
4:B:546:SER:OG	4:B:631:GLY:N	2.32	0.58
5:C:145:CYS:HA	12:J:2:ILE:HD11	1.85	0.58
6:D:53:SER:H	6:D:148:LEU:CD2	2.15	0.58
4:B:911:ILE:HD11	4:B:941:LEU:HD13	1.86	0.58
3:A:897:TYR:HD2	3:A:936:LEU:HD13	1.67	0.58
3:A:1450:LEU:HG	3:A:1450:LEU:O	2.03	0.58
3:A:901:LEU:HD22	3:A:919:ILE:CG2	2.33	0.58
10:H:23:VAL:HG22	10:H:43:ASN:HA	1.85	0.58
4:B:702:LEU:HD12	4:B:703:ILE:H	1.67	0.58
3:A:1373:ASP:HA	3:A:1376:THR:HG22	1.85	0.58
13:K:21:ILE:HG23	13:K:31:VAL:CG1	2.33	0.58
3:A:782:ARG:NH2	4:B:699:GLU:O	2.36	0.58
3:A:168:GLY:O	3:A:169:ASN:C	2.42	0.58
11:I:115:LYS:HB3	11:I:117:LYS:HG3	1.85	0.58
3:A:596:THR:O	3:A:598:LEU:N	2.35	0.58
10:H:102:TYR:N	10:H:102:TYR:CD2	2.72	0.58
12:J:44:TYR:HA	12:J:47:ARG:HB2	1.85	0.58
3:A:541:ILE:HD13	3:A:549:MET:CE	2.34	0.58
8:F:109:VAL:HG12	8:F:110:ASP:N	2.18	0.58
3:A:444:PHE:HB2	3:A:458:HIS:HD2	1.67	0.58
8:F:130:ILE:O	8:F:148:VAL:CG2	2.51	0.58
3:A:1100:ARG:NH2	3:A:1351:GLU:HG2	2.19	0.58
5:C:254:LYS:O	5:C:258:ILE:HD13	2.02	0.58
4:B:995:ARG:HH12	5:C:165:LYS:HG2	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:1065:GLN:HG3	4:B:1067:ARG:H	1.68	0.58
5:C:17:ASN:N	5:C:240:VAL:HG11	2.18	0.58
12:J:2:ILE:H	12:J:57:ILE:HG22	1.67	0.58
4:B:418:LYS:HG2	4:B:422:LYS:HE3	1.86	0.58
11:I:76:PRO:HG2	11:I:110:PHE:HB3	1.84	0.58
4:B:856:PHE:HD2	4:B:967:ARG:HD2	1.68	0.58
5:C:131:HIS:O	5:C:133:ILE:N	2.36	0.58
12:J:1:MET:N	12:J:57:ILE:HG22	2.19	0.58
3:A:1445:ILE:N	3:A:1445:ILE:HD12	2.13	0.58
3:A:399:HIS:CB	3:A:400:PRO:HD3	2.30	0.58
3:A:845:LEU:HD22	3:A:1374:VAL:HG21	1.84	0.58
11:I:85:PHE:CE1	11:I:99:LEU:HD13	2.39	0.58
4:B:1152:MET:CE	4:B:1157:ALA:HA	2.34	0.58
3:A:524:VAL:HG12	3:A:525:GLN:H	1.69	0.58
3:A:828:ALA:CB	4:B:530:GLY:HA2	2.34	0.58
3:A:901:LEU:HD22	3:A:919:ILE:HG22	1.85	0.58
10:H:12:VAL:HG13	10:H:26:ILE:HG23	1.86	0.58
10:H:40:LEU:HD22	10:H:123:MET:CE	2.33	0.58
7:E:60:PHE:HE2	7:E:80:VAL:HB	1.68	0.58
11:I:50:THR:CG2	11:I:52:ILE:HG12	2.34	0.58
7:E:22:MET:HE1	7:E:26:ARG:NH2	2.19	0.58
4:B:580:VAL:HG22	4:B:624:LEU:CB	2.33	0.58
5:C:209:TYR:N	5:C:209:TYR:CD1	2.72	0.58
4:B:557:PHE:CD2	4:B:557:PHE:C	2.76	0.58
3:A:871:ASP:OD1	3:A:1366:ARG:NH2	2.37	0.58
3:A:1147:THR:HB	11:I:48:LEU:HD12	1.84	0.58
10:H:17:PRO:HB3	10:H:24:CYS:SG	2.43	0.58
9:G:138:THR:CG2	9:G:139:ILE:H	2.02	0.58
3:A:23:SER:HA	3:A:233:TRP:CD1	2.38	0.58
3:A:940:ARG:HG2	3:A:940:ARG:HH11	1.69	0.58
3:A:1141:THR:OG1	3:A:1205:LYS:HD3	2.04	0.58
6:D:22:GLU:H	6:D:22:GLU:CD	2.07	0.58
4:B:583:ASN:HD21	4:B:628:THR:CG2	2.08	0.58
3:A:1445:ILE:H	3:A:1445:ILE:CD1	2.04	0.58
9:G:59:GLY:HA3	9:G:70:PHE:CD2	2.38	0.58
4:B:193:LYS:HZ1	14:L:32:ALA:HB1	1.68	0.58
4:B:309:GLN:HG3	11:I:52:ILE:HD11	1.85	0.58
3:A:935:GLN:HE21	3:A:1023:ARG:NH1	2.01	0.58
10:H:62:SER:C	10:H:64:ASN:H	2.06	0.58
3:A:547:LEU:HD13	13:K:58:PHE:CD1	2.38	0.58
3:A:264:PHE:O	3:A:267:ALA:HB3	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:14:HIS:CD2	9:G:16:SER:HB2	2.40	0.57
7:E:24:LYS:HB3	7:E:30:ILE:HD12	1.85	0.57
4:B:357:GLN:O	4:B:366:GLN:HA	2.03	0.57
4:B:365:THR:HG23	4:B:367:LEU:N	2.18	0.57
3:A:1343:ALA:O	3:A:1346:ALA:HB3	2.03	0.57
4:B:969:ARG:NH1	5:C:61:GLU:OE1	2.37	0.57
5:C:124:LEU:O	5:C:127:ARG:HG2	2.04	0.57
3:A:172:PRO:HD3	3:A:185:TRP:NE1	2.18	0.57
3:A:55:ASP:CG	3:A:55:ASP:O	2.41	0.57
4:B:846:ILE:HG23	4:B:974:PRO:HG2	1.85	0.57
3:A:1445:ILE:HD11	9:G:68:ALA:HB1	1.87	0.57
4:B:218:SER:HB3	4:B:241:ARG:HH11	1.70	0.57
2:T:13:U:HO2'	2:T:14:C:P	2.24	0.57
5:C:212:PRO:CB	5:C:213:PRO:HD2	2.34	0.57
4:B:185:THR:O	4:B:188:ASP:HB2	2.04	0.57
14:L:28:LYS:HB2	14:L:39:SER:HB2	1.86	0.57
3:A:1227:ILE:HG22	3:A:1228:TRP:H	1.67	0.57
4:B:997:GLU:H	4:B:997:GLU:CD	2.06	0.57
5:C:172:PRO:O	5:C:235:VAL:HG23	2.05	0.57
12:J:1:MET:N	12:J:56:LEU:N	2.53	0.57
3:A:598:LEU:HD22	10:H:25:ARG:NH1	2.19	0.57
5:C:31:ASN:OD1	5:C:34:ARG:HD3	2.04	0.57
3:A:1002:GLY:HA3	3:A:1007:ILE:CG2	2.33	0.57
3:A:979:SER:OG	3:A:980:ASP:N	2.35	0.57
4:B:214:ALA:HB3	4:B:498:THR:HA	1.86	0.57
3:A:382:PRO:CB	3:A:428:TYR:HE2	2.18	0.57
4:B:1103:ILE:O	4:B:1122:ARG:NH1	2.37	0.57
10:H:100:THR:HG22	10:H:101:ALA:N	2.19	0.57
9:G:18:PHE:HA	9:G:22:MET:HE3	1.85	0.57
12:J:64:ASN:CB	12:J:65:PRO:CD	2.79	0.57
3:A:1342:GLU:OE2	7:E:212:ARG:NH1	2.38	0.57
3:A:24:PRO:HD2	3:A:233:TRP:CD1	2.38	0.57
3:A:1097:GLY:O	3:A:1100:ARG:HB3	2.05	0.57
14:L:40:LEU:HD22	14:L:44:ASP:CB	2.34	0.57
7:E:153:HIS:HB3	7:E:196:VAL:HG11	1.86	0.57
4:B:340:ALA:HB2	4:B:343:ILE:HD12	1.86	0.57
3:A:535:THR:HG21	3:A:616:VAL:CA	2.30	0.57
3:A:675:THR:OG1	3:A:736:ASN:ND2	2.37	0.57
3:A:427:GLN:HB2	3:A:430:TRP:CD1	2.40	0.57
7:E:207:ARG:NH1	7:E:207:ARG:HB2	2.18	0.57
3:A:875:ALA:HA	3:A:878:ILE:CD1	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:4:SER:O	6:D:5:THR:CB	2.51	0.57
3:A:1454:MET:O	3:A:1454:MET:HG3	2.04	0.57
7:E:154:ILE:H	7:E:196:VAL:HG13	1.70	0.57
4:B:1222:ARG:O	4:B:1222:ARG:HG2	2.05	0.57
3:A:1222:ASN:O	3:A:1223:ASP:HB3	2.05	0.57
4:B:549:THR:HG22	4:B:550:ASP:N	2.15	0.57
3:A:567:LYS:HD2	3:A:568:PRO:CD	2.33	0.57
10:H:41:ASP:OD2	10:H:122:LEU:N	2.37	0.57
3:A:754:SER:H	3:A:757:ASN:ND2	1.86	0.57
4:B:189:LEU:O	4:B:192:LEU:N	2.34	0.57
5:C:36:VAL:HG21	5:C:251:LEU:HB2	1.85	0.57
4:B:166:PHE:C	4:B:167:ILE:HG13	2.25	0.57
4:B:872:GLU:HG2	4:B:916:THR:OG1	2.04	0.57
3:A:886:ILE:HG22	3:A:887:GLY:N	2.18	0.57
3:A:886:ILE:HG13	3:A:943:LEU:CD1	2.34	0.57
3:A:215:SER:HB3	3:A:218:ASP:CG	2.24	0.57
6:D:119:ARG:HG2	6:D:120:GLU:N	2.19	0.57
3:A:1299:VAL:HG12	3:A:1300:LYS:N	2.20	0.57
4:B:27:ALA:O	4:B:29:ASP:N	2.37	0.57
3:A:1193:LEU:HD12	3:A:1194:ARG:N	2.20	0.57
4:B:466:TRP:O	4:B:468:GLU:N	2.37	0.57
3:A:1377:THR:O	3:A:1379:GLY:N	2.38	0.57
3:A:841:LEU:O	3:A:845:LEU:HG	2.05	0.57
9:G:1:MET:O	9:G:3:PHE:CE1	2.58	0.57
8:F:68:THR:HG21	8:F:71:GLU:OE2	2.03	0.57
4:B:237:VAL:HG22	4:B:257:LYS:HA	1.87	0.57
3:A:69:THR:C	3:A:71:GLN:N	2.56	0.57
8:F:119:ARG:NH1	8:F:119:ARG:HG3	2.20	0.57
2:T:8:C:H4'	3:A:447:GLN:HE22	1.70	0.57
3:A:222:LEU:O	3:A:224:PHE:N	2.37	0.57
9:G:145:VAL:HG12	9:G:146:LYS:N	2.19	0.57
4:B:128:LEU:HD11	4:B:170:LEU:HB2	1.87	0.57
3:A:119:ASN:O	3:A:122:MET:HB3	2.05	0.57
4:B:1096:ARG:O	4:B:1097:HIS:CB	2.53	0.57
4:B:751:VAL:HG13	4:B:812:LEU:CD2	2.35	0.57
4:B:957:ASN:O	4:B:959:ASP:N	2.38	0.57
13:K:59:ALA:HA	13:K:74:ARG:O	2.05	0.57
5:C:99:LEU:HB2	5:C:157:CYS:HB2	1.87	0.57
9:G:17:PHE:CD2	9:G:17:PHE:N	2.71	0.57
3:A:341:MET:CE	3:A:843:LYS:NZ	2.68	0.57
3:A:821:ARG:HD2	3:A:825:ILE:HD11	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:351:THR:HB	4:B:1103:ILE:CD1	2.35	0.57
3:A:1244:ARG:HB3	3:A:1245:PRO:CD	2.35	0.57
4:B:1099:VAL:HG13	4:B:1100:ASP:N	2.19	0.57
4:B:203:PHE:N	4:B:203:PHE:CD1	2.73	0.57
4:B:118:ARG:HH11	4:B:204:ILE:HD11	1.69	0.57
3:A:42:ASP:C	3:A:44:THR:H	2.06	0.57
3:A:61:ILE:O	3:A:63:ARG:N	2.38	0.57
3:A:901:LEU:HB2	3:A:926:GLN:HG2	1.86	0.57
10:H:143:LEU:N	10:H:143:LEU:HD12	2.20	0.57
6:D:55:ALA:HB3	6:D:148:LEU:HD21	1.86	0.57
11:I:55:THR:HG22	11:I:58:VAL:HG21	1.87	0.57
4:B:758:PHE:CE2	4:B:1044:ALA:HA	2.40	0.57
8:F:97:ARG:O	8:F:101:ILE:HG13	2.05	0.57
3:A:666:ILE:HG23	4:B:1026:LEU:HB3	1.87	0.56
4:B:242:SER:HB2	4:B:362:PRO:HG2	1.86	0.56
4:B:1073:TYR:CE2	4:B:1080:LYS:HG2	2.39	0.56
4:B:899:ILE:CD1	4:B:911:ILE:HA	2.34	0.56
7:E:135:PHE:HD2	7:E:140:LEU:HD21	1.70	0.56
4:B:217:ARG:NE	4:B:405:ARG:HB2	2.20	0.56
3:A:268:ASP:HB3	3:A:299:HIS:CE1	2.39	0.56
9:G:20:PRO:HG2	9:G:21:ARG:H	1.69	0.56
13:K:12:LEU:H	13:K:12:LEU:HD12	1.69	0.56
5:C:2:SER:N	5:C:3:GLU:N	2.53	0.56
4:B:745:PRO:C	4:B:747:MET:H	2.08	0.56
3:A:401:GLY:C	3:A:435:HIS:HD2	2.09	0.56
9:G:1:MET:O	9:G:1:MET:SD	2.63	0.56
6:D:160:VAL:O	6:D:164:ILE:HG13	2.05	0.56
3:A:84:ILE:HG22	3:A:239:LEU:HB3	1.87	0.56
6:D:18:VAL:O	6:D:18:VAL:HG13	2.05	0.56
3:A:244:PRO:CG	3:A:245:PRO:HD3	2.35	0.56
5:C:133:ILE:HD12	5:C:237:SER:HA	1.87	0.56
3:A:63:ARG:HD3	3:A:74:MET:HE3	1.86	0.56
5:C:147:LEU:HB2	5:C:151:GLN:HB2	1.86	0.56
3:A:798:GLY:HA2	3:A:815:PHE:HD1	1.70	0.56
4:B:126:SER:OG	4:B:172:ILE:HD11	2.04	0.56
3:A:590:ARG:O	3:A:591:PHE:HB2	2.04	0.56
1:P:9:G:H2'	1:P:10:A:H8	1.67	0.56
3:A:711:ARG:HA	11:I:97:MET:HE1	1.88	0.56
6:D:33:PHE:CE2	9:G:80:LYS:NZ	2.68	0.56
7:E:46:TYR:CD2	7:E:58:MET:HG2	2.41	0.56
3:A:114:LEU:HD13	3:A:171:GLN:NE2	2.19	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1035:TYR:O	3:A:1037:LEU:N	2.38	0.56
3:A:1174:PHE:C	3:A:1176:LEU:H	2.07	0.56
4:B:865:LYS:HE2	4:B:871:THR:OG1	2.05	0.56
3:A:450:LEU:HB3	3:A:838:GLN:NE2	2.21	0.56
3:A:298:PHE:CZ	3:A:314:ALA:HB2	2.41	0.56
3:A:1289:ARG:NH1	3:A:1326:ARG:NH1	2.54	0.56
7:E:153:HIS:HB3	7:E:196:VAL:CG1	2.35	0.56
10:H:99:GLY:HA3	10:H:118:PHE:HA	1.86	0.56
5:C:107:SER:C	5:C:109:SER:H	2.09	0.56
3:A:349:ALA:C	4:B:1128:LEU:HD11	2.25	0.56
3:A:418:SER:C	3:A:420:ARG:H	2.08	0.56
3:A:1213:GLY:O	3:A:1216:ILE:N	2.39	0.56
8:F:79:ARG:HG3	8:F:144:GLU:OE1	2.05	0.56
3:A:601:LYS:HB2	3:A:603:ASN:HD21	1.70	0.56
3:A:785:PRO:HG2	3:A:786:HIS:CD2	2.41	0.56
3:A:563:PRO:HG3	3:A:572:TRP:CE2	2.40	0.56
4:B:1001:PHE:CE1	4:B:1073:TYR:HB2	2.39	0.56
3:A:1369:ALA:O	3:A:1372:VAL:HG12	2.05	0.56
4:B:811:TYR:HD1	4:B:811:TYR:H	1.53	0.56
4:B:118:ARG:HH22	4:B:194:GLU:CD	2.08	0.56
4:B:819:ALA:O	4:B:1093:GLN:HG2	2.05	0.56
4:B:847:ASP:C	4:B:849:GLY:N	2.59	0.56
6:D:8:PHE:CD1	6:D:8:PHE:O	2.58	0.56
9:G:47:CYS:O	9:G:76:ALA:HB1	2.05	0.56
5:C:66:ARG:NH2	12:J:5:VAL:HG23	2.20	0.56
9:G:1:MET:HE3	9:G:80:LYS:O	2.04	0.56
4:B:900:ALA:HB3	14:L:61:THR:OG1	2.06	0.56
3:A:345:VAL:HG21	4:B:1150:ARG:HH11	1.70	0.56
4:B:865:LYS:HZ3	4:B:869:SER:HA	1.70	0.56
3:A:288:ALA:HA	3:A:291:GLU:OE2	2.05	0.56
4:B:557:PHE:C	4:B:557:PHE:HD2	2.08	0.56
6:D:52:LEU:HD21	6:D:147:TYR:HE2	1.69	0.56
4:B:844:SER:O	4:B:847:ASP:HB2	2.05	0.56
3:A:41:MET:HB3	3:A:48:ALA:O	2.06	0.56
5:C:22:LEU:HB2	5:C:230:MET:HE3	1.88	0.56
3:A:1445:ILE:HD12	9:G:59:GLY:O	2.05	0.56
5:C:31:ASN:O	5:C:34:ARG:HB3	2.05	0.56
4:B:39:ARG:HG2	4:B:39:ARG:NH1	2.19	0.56
3:A:18:GLN:O	4:B:1215:ARG:HG2	2.06	0.56
3:A:215:SER:HB3	3:A:218:ASP:CB	2.36	0.56
11:I:61:ASP:C	11:I:63:GLY:H	2.09	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:34:LYS:CE	3:A:57:ARG:NH1	2.66	0.56
3:A:504:LEU:HD12	3:A:504:LEU:N	2.21	0.56
3:A:154:SER:CB	3:A:162:VAL:HG21	2.36	0.56
4:B:1106:ARG:NH1	4:B:1110:PRO:HG2	2.21	0.56
9:G:138:THR:HG22	9:G:139:ILE:HG13	1.88	0.56
7:E:198:ILE:CD1	7:E:212:ARG:HG3	2.35	0.56
4:B:770:GLN:CD	4:B:983:ARG:HA	2.26	0.56
3:A:106:VAL:HG13	3:A:112:LYS:O	2.06	0.56
3:A:1412:ALA:HA	3:A:1417:GLU:OE2	2.06	0.56
6:D:24:ALA:C	6:D:26:THR:H	2.09	0.56
4:B:424:LEU:O	4:B:428:ILE:HG13	2.05	0.56
13:K:109:TRP:O	13:K:111:LEU:N	2.39	0.56
5:C:168:ALA:C	5:C:170:TRP:H	2.10	0.56
5:C:22:LEU:HD13	5:C:230:MET:CE	2.36	0.56
10:H:113:ALA:HB1	10:H:125:LEU:O	2.06	0.56
5:C:187:LYS:C	5:C:189:THR:H	2.10	0.56
3:A:869:GLY:O	7:E:204:THR:HG21	2.05	0.56
4:B:810:GLU:HG3	4:B:815:ARG:HH22	1.69	0.56
4:B:295:GLY:N	4:B:298:LEU:HD23	2.20	0.56
5:C:98:VAL:C	5:C:99:LEU:HD22	2.25	0.56
4:B:280:ILE:HG21	4:B:285:ILE:HG13	1.87	0.56
2:T:12:G:O2'	2:T:13:U:C3'	2.54	0.56
4:B:582:VAL:HG12	4:B:587:HIS:CD2	2.41	0.56
3:A:963:ILE:HD13	3:A:1049:ILE:CG1	2.36	0.56
4:B:431:TYR:CZ	4:B:447:ALA:HB2	2.41	0.56
8:F:75:PRO:O	8:F:77:ASP:O	2.23	0.56
4:B:125:SER:HA	4:B:171:PRO:HA	1.88	0.56
3:A:744:LYS:HG2	3:A:748:MET:CE	2.36	0.56
13:K:15:GLY:O	13:K:16:GLU:HG3	2.06	0.56
5:C:18:VAL:O	5:C:20:PHE:HD2	1.89	0.55
4:B:589:VAL:CG1	4:B:590:HIS:H	2.03	0.55
10:H:89:LEU:C	10:H:91:ASP:N	2.59	0.55
3:A:470:LEU:HD22	3:A:487:MET:CE	2.36	0.55
3:A:265:LYS:O	3:A:269:ILE:HG13	2.06	0.55
6:D:29:LEU:HB3	9:G:82:PHE:CE2	2.41	0.55
3:A:1166:ASP:OD2	3:A:1239:ARG:HD2	2.05	0.55
4:B:282:ILE:HD12	4:B:382:ILE:HD13	1.89	0.55
7:E:124:VAL:HG13	7:E:132:ILE:CD1	2.36	0.55
3:A:744:LYS:HG2	3:A:748:MET:HE2	1.88	0.55
3:A:696:GLU:HG2	3:A:696:GLU:O	2.06	0.55
7:E:79:TRP:HE1	7:E:81:GLU:HB2	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:638:PHE:HD2	4:B:690:VAL:HG22	1.71	0.55
4:B:308:TRP:HA	4:B:311:LEU:HD12	1.88	0.55
9:G:27:LYS:O	9:G:30:LEU:HB3	2.06	0.55
12:J:27:GLU:C	12:J:29:GLU:H	2.10	0.55
4:B:336:ARG:NE	4:B:348:ARG:HH11	2.03	0.55
3:A:49:LYS:HZ1	3:A:61:ILE:HG13	1.71	0.55
3:A:907:THR:CG2	3:A:908:LEU:N	2.68	0.55
4:B:247:GLY:N	4:B:418:LYS:HZ1	2.04	0.55
3:A:543:LEU:H	3:A:572:TRP:HZ3	1.54	0.55
13:K:65:HIS:HD2	13:K:67:PHE:HB2	1.71	0.55
13:K:47:ARG:C	13:K:47:ARG:HD2	2.27	0.55
4:B:955:THR:HG23	14:L:54:ARG:O	2.07	0.55
3:A:863:VAL:HG11	3:A:866:PHE:CD2	2.41	0.55
3:A:84:ILE:HG23	3:A:84:ILE:O	2.06	0.55
4:B:1097:HIS:H	4:B:1098:MET:HE2	1.71	0.55
4:B:978:ASP:OD2	4:B:1098:MET:HG2	2.06	0.55
3:A:683:ILE:HD13	3:A:801:GLU:CG	2.36	0.55
4:B:757:PRO:HG3	4:B:1028:GLU:OE2	2.06	0.55
9:G:9:LEU:HD12	9:G:10:ASN:H	1.71	0.55
3:A:829:VAL:C	3:A:831:THR:H	2.10	0.55
3:A:58:LEU:HD21	3:A:243:PRO:HA	1.88	0.55
3:A:49:LYS:HZ1	3:A:61:ILE:N	2.04	0.55
11:I:26:LEU:CD2	11:I:37:GLU:HA	2.30	0.55
11:I:105:SER:O	11:I:106:CYS:HB3	2.06	0.55
3:A:250:ILE:O	3:A:258:GLY:HA3	2.05	0.55
3:A:450:LEU:N	3:A:450:LEU:HD12	2.22	0.55
4:B:850:LEU:HD12	4:B:851:PHE:H	1.72	0.55
4:B:997:GLU:N	4:B:997:GLU:OE2	2.29	0.55
7:E:169:ARG:HH12	8:F:74:ILE:HD11	1.72	0.55
3:A:663:SER:OG	3:A:664:THR:N	2.40	0.55
3:A:857:ARG:NH1	8:F:139:PRO:HB2	2.21	0.55
3:A:590:ARG:HH22	3:A:620:LYS:HB3	1.72	0.55
3:A:1332:PHE:N	3:A:1332:PHE:CD2	2.73	0.55
4:B:95:ILE:CG1	4:B:130:VAL:HG22	2.37	0.55
4:B:95:ILE:HG13	4:B:130:VAL:HG22	1.86	0.55
3:A:500:GLU:OE2	4:B:1145:SER:HB2	2.06	0.55
4:B:190:TYR:CE2	12:J:62:ARG:HB3	2.41	0.55
4:B:243:ALA:HA	4:B:250:PHE:O	2.07	0.55
11:I:115:LYS:HD3	11:I:117:LYS:CE	2.26	0.55
4:B:999:MET:HB3	4:B:1007:VAL:CG2	2.36	0.55
3:A:825:ILE:HG22	3:A:826:ASP:N	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:973:ILE:HD11	3:A:1041:ALA:HB2	1.87	0.55
7:E:55:ARG:C	7:E:57:MET:N	2.60	0.55
5:C:257:SER:HA	5:C:260:LEU:HB3	1.88	0.55
7:E:85:GLU:HB2	7:E:88:VAL:HG22	1.87	0.55
3:A:478:TYR:O	3:A:479:ASN:HB3	2.06	0.55
4:B:909:ASP:N	4:B:909:ASP:OD1	2.40	0.55
3:A:53:LEU:HD22	3:A:54:ASN:ND2	2.21	0.55
3:A:44:THR:O	3:A:45:GLN:HB2	2.06	0.55
3:A:1008:GLN:O	3:A:1011:GLN:HB3	2.07	0.55
3:A:469:ARG:HH11	3:A:469:ARG:HB3	1.71	0.55
4:B:129:PHE:HA	4:B:165:VAL:O	2.06	0.55
14:L:34:CYS:SG	14:L:34:CYS:O	2.64	0.55
4:B:1223:ASP:O	4:B:1224:PHE:HB2	2.07	0.55
7:E:197:LYS:HE2	7:E:199:ILE:HD11	1.89	0.55
7:E:44:ALA:O	7:E:45:LYS:HB2	2.06	0.55
4:B:336:ARG:CZ	4:B:348:ARG:HH11	2.20	0.55
5:C:145:CYS:HA	12:J:2:ILE:CD1	2.37	0.55
3:A:567:LYS:NZ	10:H:46:LEU:HB2	2.21	0.55
3:A:567:LYS:CB	3:A:568:PRO:HD2	2.36	0.55
10:H:40:LEU:HD22	10:H:123:MET:HE2	1.87	0.55
6:D:145:MET:O	6:D:149:THR:HB	2.07	0.55
7:E:23:VAL:O	7:E:28:TYR:HB2	2.06	0.55
13:K:19:LEU:HD22	13:K:33:ILE:CG2	2.37	0.55
4:B:899:ILE:CG2	4:B:949:VAL:HG21	2.37	0.55
3:A:407:ARG:HG2	3:A:430:TRP:CH2	2.41	0.55
9:G:117:GLN:C	9:G:119:LEU:H	2.09	0.55
3:A:1198:ASP:HB3	3:A:1201:ALA:CB	2.36	0.55
7:E:157:SER:C	7:E:159:ASP:N	2.60	0.55
4:B:1174:LYS:O	4:B:1176:ASN:N	2.39	0.55
3:A:266:LEU:HD21	3:A:303:TYR:CE1	2.41	0.55
3:A:1064:VAL:HG12	3:A:1064:VAL:O	2.05	0.55
12:J:1:MET:H3	12:J:56:LEU:N	2.05	0.55
4:B:287:ARG:NH1	4:B:324:ILE:O	2.40	0.55
3:A:590:ARG:NH1	3:A:590:ARG:HG3	2.21	0.55
4:B:1177:HIS:CB	4:B:1179:GLN:HE21	2.14	0.55
4:B:687:GLU:O	4:B:689:LEU:HG	2.06	0.55
3:A:49:LYS:HZ2	3:A:60:SER:HA	1.70	0.55
3:A:1116:LEU:HD11	3:A:1118:VAL:HG13	1.88	0.55
3:A:537:ARG:HH12	10:H:122:LEU:HG	1.71	0.55
3:A:537:ARG:HD2	10:H:20:TYR:HE1	1.72	0.55
10:H:38:LEU:HD13	10:H:125:LEU:HD13	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:167:LEU:O	6:D:170:THR:OG1	2.25	0.55
3:A:1076:ALA:HA	3:A:1079:MET:HE2	1.88	0.55
3:A:1409:LEU:O	3:A:1412:ALA:HB3	2.06	0.55
14:L:29:TYR:N	14:L:29:TYR:CD2	2.73	0.55
3:A:60:SER:C	3:A:61:ILE:HG13	2.26	0.54
3:A:767:GLN:HA	3:A:799:PHE:HA	1.88	0.54
9:G:13:LEU:CD2	9:G:17:PHE:HB2	2.36	0.54
4:B:63:ILE:HD12	4:B:421:PHE:CE2	2.41	0.54
4:B:557:PHE:HE1	4:B:603:LEU:HD11	1.72	0.54
8:F:111:LEU:N	8:F:111:LEU:HD12	2.22	0.54
4:B:847:ASP:O	4:B:849:GLY:N	2.40	0.54
5:C:234:SER:CB	5:C:240:VAL:HG13	2.38	0.54
10:H:15:VAL:HG22	10:H:26:ILE:HG12	1.90	0.54
3:A:472:LEU:O	3:A:475:THR:HB	2.06	0.54
3:A:222:LEU:O	3:A:224:PHE:HD1	1.90	0.54
8:F:76:LYS:O	8:F:79:ARG:HD3	2.07	0.54
5:C:186:LEU:HD21	5:C:224:GLN:O	2.08	0.54
3:A:559:VAL:O	3:A:559:VAL:HG12	2.06	0.54
3:A:356:ASP:HB2	3:A:469:ARG:HH11	1.72	0.54
5:C:166:GLU:HG3	13:K:10:PHE:CZ	2.33	0.54
3:A:1349:TYR:HB2	3:A:1372:VAL:HG21	1.90	0.54
4:B:575:PRO:HG2	4:B:576:ASP:H	1.72	0.54
11:I:50:THR:HG22	11:I:51:ASN:H	1.72	0.54
4:B:39:ARG:HH21	4:B:665:GLU:CD	2.11	0.54
4:B:1182:CYS:SG	4:B:1182:CYS:O	2.65	0.54
4:B:209:GLU:OE2	4:B:483:LEU:HD23	2.07	0.54
3:A:346:ASP:HB3	4:B:1108:ARG:H	1.71	0.54
14:L:70:ARG:HG2	14:L:70:ARG:NH1	2.21	0.54
3:A:1340:GLY:HA2	7:E:183:PRO:HD2	1.89	0.54
6:D:208:GLU:O	6:D:212:LYS:HG3	2.06	0.54
3:A:720:ARG:HB3	3:A:720:ARG:NH1	2.21	0.54
8:F:82:THR:HG22	8:F:84:TYR:H	1.70	0.54
4:B:102:VAL:HG23	4:B:112:LEU:HB2	1.88	0.54
4:B:1007:VAL:CG2	4:B:1008:PRO:HD2	2.37	0.54
4:B:615:MET:HB3	4:B:626:ILE:HG12	1.89	0.54
3:A:605:MET:HE2	3:A:607:ILE:HG13	1.88	0.54
3:A:1176:LEU:HD12	3:A:1177:LEU:O	2.07	0.54
3:A:1025:ARG:O	3:A:1026:LEU:HD23	2.07	0.54
3:A:58:LEU:CD1	3:A:243:PRO:HB3	2.32	0.54
6:D:40:HIS:CB	9:G:73:LYS:HZ2	2.18	0.54
4:B:192:LEU:O	4:B:193:LYS:HB2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:58:VAL:HG13	11:I:62:ILE:CD1	2.37	0.54
3:A:673:GLY:O	3:A:676:MET:HB2	2.07	0.54
3:A:746:MET:CE	4:B:1018:PRO:HG2	2.38	0.54
11:I:90:GLN:NE2	11:I:92:ARG:HD3	2.23	0.54
7:E:93:MET:SD	7:E:97:VAL:HG23	2.47	0.54
4:B:44:VAL:HG11	4:B:199:MET:HG2	1.89	0.54
3:A:37:PHE:CD1	3:A:37:PHE:N	2.76	0.54
3:A:666:ILE:HD11	4:B:1067:ARG:O	2.06	0.54
3:A:1062:GLU:OE2	8:F:88:TYR:OH	2.24	0.54
4:B:228:LYS:CB	4:B:261:ARG:HH22	2.21	0.54
4:B:731:VAL:HG12	4:B:732:SER:N	2.23	0.54
4:B:1065:GLN:NE2	4:B:1066:SER:N	2.56	0.54
4:B:798:TYR:CE2	5:C:62:PHE:CE2	2.92	0.54
4:B:806:THR:O	4:B:809:MET:HG3	2.08	0.54
8:F:125:LEU:HB2	8:F:130:ILE:HD11	1.88	0.54
4:B:952:VAL:HG12	4:B:953:LEU:H	1.71	0.54
3:A:345:VAL:HG23	3:A:346:ASP:O	2.07	0.54
3:A:404:TYR:HB2	3:A:433:GLU:HB2	1.89	0.54
6:D:220:LEU:O	6:D:221:TYR:HD1	1.90	0.54
3:A:89:PRO:HB2	3:A:204:THR:HG22	1.88	0.54
4:B:57:TYR:HD1	4:B:57:TYR:N	2.05	0.54
11:I:7:CYS:N	11:I:14:LEU:HD21	2.22	0.54
11:I:8:ARG:CG	11:I:34:TYR:HE1	2.17	0.54
14:L:53:HIS:HB3	14:L:55:ILE:CD1	2.38	0.54
4:B:616:ILE:HG13	4:B:697:GLU:HG3	1.90	0.54
4:B:247:GLY:N	4:B:418:LYS:NZ	2.50	0.54
4:B:39:ARG:HH21	4:B:665:GLU:CG	2.20	0.54
4:B:96:TYR:HB2	4:B:129:PHE:HB2	1.89	0.54
13:K:42:LEU:HD21	13:K:46:ILE:HD11	1.90	0.54
6:D:71:LYS:HA	6:D:74:GLN:CB	2.37	0.54
5:C:263:THR:C	5:C:265:MET:H	2.09	0.54
7:E:127:ILE:O	7:E:127:ILE:HG13	2.08	0.54
10:H:40:LEU:CD1	10:H:123:MET:HB2	2.36	0.54
3:A:1130:GLN:O	3:A:1134:ILE:HG13	2.08	0.54
4:B:126:SER:O	4:B:169:ARG:HA	2.07	0.54
3:A:19:PHE:HB3	3:A:1413:GLY:HA2	1.88	0.54
8:F:89:GLU:HB3	8:F:134:ILE:CD1	2.37	0.54
6:D:191:ALA:O	6:D:193:THR:N	2.41	0.54
3:A:207:ILE:O	3:A:211:PHE:HD1	1.91	0.54
14:L:49:LYS:O	14:L:50:ASP:CB	2.55	0.54
13:K:6:ARG:O	13:K:9:LEU:HG	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:7:GLN:HG2	13:K:104:ASN:HD22	1.72	0.54
3:A:1102:LYS:O	3:A:1106:ASN:ND2	2.40	0.54
4:B:459:TYR:CE1	4:B:469:GLN:HG2	2.43	0.54
6:D:64:VAL:C	6:D:66:ARG:H	2.10	0.53
4:B:590:HIS:HD2	4:B:593:PRO:HB3	1.73	0.53
10:H:15:VAL:HG22	10:H:26:ILE:CD1	2.38	0.53
4:B:217:ARG:C	4:B:217:ARG:HD2	2.28	0.53
3:A:1435:PRO:HA	3:A:1439:GLY:O	2.08	0.53
4:B:570:VAL:CG2	4:B:573:GLN:HB3	2.38	0.53
3:A:350:ARG:HH11	3:A:350:ARG:HG3	1.74	0.53
13:K:63:VAL:HG23	13:K:63:VAL:O	2.08	0.53
4:B:591:ARG:O	4:B:593:PRO:HD3	2.08	0.53
3:A:1004:ASN:CG	7:E:167:ARG:HD2	2.28	0.53
13:K:10:PHE:CD2	13:K:10:PHE:N	2.76	0.53
4:B:654:ARG:O	4:B:656:GLY:N	2.42	0.53
3:A:1239:ARG:HH22	3:A:1241:ARG:HH22	1.55	0.53
6:D:153:ARG:HB3	6:D:154:PHE:CD1	2.43	0.53
3:A:849:MET:CE	3:A:1061:GLY:HA2	2.37	0.53
4:B:459:TYR:CZ	4:B:469:GLN:HG2	2.42	0.53
4:B:315:LYS:N	4:B:316:PRO:HD2	2.23	0.53
4:B:704:ALA:HB2	4:B:738:PHE:CD2	2.44	0.53
5:C:23:SER:O	5:C:24:ASN:HB3	2.07	0.53
4:B:1196:ILE:HB	4:B:1197:PRO:HD2	1.89	0.53
5:C:46:ILE:HG23	5:C:157:CYS:HB3	1.89	0.53
3:A:699:ALA:CB	3:A:701:LEU:HG	2.36	0.53
3:A:399:HIS:O	3:A:401:GLY:N	2.41	0.53
3:A:442:VAL:CG2	3:A:460:VAL:HG23	2.38	0.53
3:A:341:MET:HE1	4:B:1135:ARG:NH1	2.24	0.53
3:A:341:MET:CE	3:A:843:LYS:HZ3	2.21	0.53
4:B:758:PHE:CE1	4:B:1027:ILE:CG2	2.92	0.53
4:B:705:MET:H	4:B:710:LEU:HD12	1.73	0.53
8:F:109:VAL:HG13	8:F:127:GLU:OE1	2.08	0.53
4:B:476:ARG:NH2	4:B:501:PRO:HG3	2.23	0.53
9:G:114:LEU:HG	9:G:162:SER:HB3	1.91	0.53
4:B:337:ARG:C	4:B:338:GLY:N	2.61	0.53
5:C:17:ASN:O	5:C:18:VAL:CG2	2.57	0.53
3:A:774:ARG:O	3:A:775:ILE:C	2.45	0.53
4:B:825:VAL:CG1	4:B:826:ALA:N	2.71	0.53
3:A:816:HIS:HE2	4:B:764:SER:H	1.55	0.53
4:B:758:PHE:CZ	4:B:1044:ALA:HA	2.43	0.53
4:B:1034:VAL:O	4:B:1037:LEU:N	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:57:TYR:CD1	4:B:57:TYR:N	2.74	0.53
3:A:1430:LEU:O	4:B:1196:ILE:HG22	2.09	0.53
4:B:326:ASP:OD2	4:B:328:GLU:HB2	2.07	0.53
3:A:166:GLY:O	3:A:167:CYS:SG	2.67	0.53
3:A:4:GLN:O	3:A:5:GLN:HB2	2.08	0.53
4:B:1147:LEU:C	4:B:1147:LEU:HD23	2.28	0.53
3:A:117:GLU:H	3:A:117:GLU:CD	2.12	0.53
4:B:594:ALA:HA	4:B:617:ARG:NH1	2.24	0.53
4:B:189:LEU:O	4:B:192:LEU:HB2	2.08	0.53
11:I:69:PRO:HG2	11:I:85:PHE:CE2	2.44	0.53
3:A:339:ASN:O	3:A:343:LYS:HG2	2.09	0.53
4:B:313:MET:CE	4:B:386:LEU:HD22	2.38	0.53
7:E:154:ILE:O	7:E:196:VAL:HA	2.09	0.53
4:B:240:ILE:CG2	4:B:254:LEU:HB3	2.38	0.53
4:B:785:TYR:CD1	4:B:786:ASN:N	2.76	0.53
3:A:1291:VAL:HG22	3:A:1292:PRO:HD2	1.90	0.53
3:A:666:ILE:HD12	3:A:667:GLY:N	2.20	0.53
10:H:58:THR:HG22	10:H:59:ILE:N	2.24	0.53
4:B:746:SER:CB	4:B:1046:PRO:HG2	2.32	0.53
3:A:698:GLN:HE21	11:I:99:LEU:HD21	1.73	0.53
4:B:983:ARG:HD2	4:B:1091:TYR:HB3	1.89	0.53
4:B:129:PHE:HD2	4:B:166:PHE:HA	1.72	0.53
4:B:343:ILE:HG21	4:B:348:ARG:HG3	1.90	0.53
3:A:64:ASN:O	3:A:65:LEU:C	2.46	0.53
3:A:1134:ILE:O	3:A:1138:ILE:HG13	2.08	0.53
3:A:711:ARG:NH2	11:I:87:GLN:OE1	2.41	0.53
4:B:479:VAL:O	4:B:480:SER:HB3	2.08	0.53
9:G:106:MET:HG2	9:G:107:LYS:N	2.22	0.53
4:B:233:PRO:HG2	4:B:234:ILE:CD1	2.39	0.53
3:A:115:LEU:HB2	3:A:122:MET:CE	2.38	0.53
5:C:3:GLU:O	5:C:4:GLU:HB2	2.06	0.53
3:A:73:GLY:O	3:A:75:ASN:N	2.42	0.53
3:A:862:ASN:HA	7:E:174:GLN:HB3	1.91	0.53
3:A:30:ILE:HG23	4:B:1170:THR:HG23	1.91	0.53
3:A:1394:THR:HG21	3:A:1398:MET:SD	2.48	0.53
3:A:1397:LEU:O	3:A:1400:CYS:HB3	2.09	0.53
3:A:618:GLU:O	3:A:620:LYS:N	2.42	0.53
3:A:710:LEU:H	3:A:710:LEU:HD12	1.74	0.53
9:G:1:MET:C	9:G:1:MET:SD	2.86	0.53
4:B:642:ASP:HB3	4:B:649:LYS:CG	2.38	0.53
3:A:475:THR:CG2	3:A:476:SER:N	2.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:64:ASN:O	10:H:65:LEU:CB	2.57	0.53
3:A:347:PHE:CE2	3:A:375:THR:HG23	2.43	0.53
4:B:1071:VAL:O	4:B:1072:MET:HG3	2.08	0.53
12:J:9:SER:HB2	12:J:45:CYS:HB2	1.90	0.53
3:A:1308:THR:HG23	3:A:1309:ASP:N	2.23	0.53
4:B:102:VAL:CG2	4:B:112:LEU:HD22	2.38	0.53
7:E:28:TYR:CE1	7:E:78:LEU:HD13	2.44	0.53
13:K:47:ARG:CB	13:K:47:ARG:HH11	2.17	0.53
3:A:997:LEU:HD13	3:A:1018:PHE:CE2	2.44	0.53
4:B:233:PRO:HG2	4:B:234:ILE:HD12	1.90	0.53
4:B:502:ILE:N	4:B:502:ILE:HD12	2.20	0.53
5:C:214:ASN:HB3	5:C:217:ASP:OD2	2.09	0.53
3:A:472:LEU:CD1	4:B:835:GLN:NE2	2.71	0.53
3:A:828:ALA:HB2	4:B:530:GLY:HA2	1.91	0.53
3:A:340:LEU:HD21	4:B:1200:ALA:N	2.24	0.53
3:A:1444:MET:HG3	9:G:60:ARG:HA	1.90	0.53
4:B:986:GLN:OE1	4:B:986:GLN:HA	2.09	0.53
3:A:50:ILE:O	3:A:52:GLY:N	2.42	0.53
3:A:61:ILE:HG22	3:A:62:ASP:N	2.23	0.53
4:B:1065:GLN:NE2	4:B:1066:SER:H	2.07	0.53
3:A:901:LEU:HA	3:A:907:THR:OG1	2.09	0.53
4:B:582:VAL:HA	4:B:626:ILE:O	2.09	0.53
8:F:109:VAL:HG21	8:F:124:GLU:HA	1.90	0.53
4:B:822:ASN:O	12:J:48:ARG:NH1	2.41	0.52
3:A:446:ARG:HB2	3:A:487:MET:SD	2.49	0.52
4:B:693:ILE:HD11	4:B:740:HIS:CD2	2.44	0.52
4:B:693:ILE:HD13	4:B:701:ILE:HD13	1.90	0.52
4:B:169:ARG:HB2	4:B:454:THR:HG23	1.91	0.52
4:B:1001:PHE:CE2	5:C:34:ARG:NE	2.77	0.52
3:A:1348:LEU:HG	3:A:1372:VAL:CG2	2.39	0.52
3:A:382:PRO:HB3	3:A:428:TYR:CE2	2.38	0.52
3:A:219:PHE:CE2	3:A:231:PRO:HD2	2.43	0.52
4:B:487:THR:CG2	4:B:488:TYR:N	2.73	0.52
11:I:32:CYS:SG	11:I:33:SER:N	2.81	0.52
4:B:766:ARG:NH2	4:B:1020:ARG:HH11	2.06	0.52
9:G:15:PRO:HA	9:G:18:PHE:CE1	2.43	0.52
3:A:767:GLN:HE21	3:A:774:ARG:HB3	1.71	0.52
4:B:542:MET:HG2	4:B:747:MET:HE3	1.91	0.52
3:A:300:VAL:O	3:A:300:VAL:HG12	2.08	0.52
8:F:100:GLN:O	8:F:103:MET:HB2	2.09	0.52
13:K:31:VAL:CG1	13:K:32:VAL:N	2.71	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:216:GLU:HA	4:B:406:LEU:CD2	2.40	0.52
4:B:797:TYR:HE1	4:B:854:LEU:CD2	2.23	0.52
4:B:797:TYR:HE1	4:B:854:LEU:HD23	1.72	0.52
3:A:113:LEU:HG	3:A:218:ASP:OD1	2.09	0.52
5:C:177:GLU:HB2	5:C:231:ASN:HB3	1.89	0.52
3:A:326:ARG:NH2	3:A:1407:GLU:HG3	2.24	0.52
3:A:34:LYS:HB3	3:A:36:ARG:NE	2.24	0.52
6:D:8:PHE:HE1	6:D:38:ILE:H	1.57	0.52
13:K:93:SER:O	13:K:97:LYS:HG3	2.09	0.52
6:D:56:ARG:NH2	6:D:57:LEU:HD21	2.23	0.52
4:B:515:HIS:H	4:B:518:HIS:CD2	2.14	0.52
7:E:202:SER:OG	7:E:204:THR:HG22	2.09	0.52
4:B:464:GLY:HA2	4:B:479:VAL:O	2.09	0.52
4:B:641:GLU:C	4:B:643:ASP:H	2.12	0.52
3:A:1215:ARG:HA	3:A:1218:GLN:HG2	1.90	0.52
9:G:94:CYS:HA	9:G:99:PHE:HA	1.90	0.52
12:J:20:SER:O	12:J:24:LEU:HG	2.09	0.52
4:B:843:GLN:O	4:B:844:SER:C	2.48	0.52
5:C:15:LYS:O	5:C:240:VAL:HG22	2.09	0.52
10:H:130:ARG:HB3	10:H:133:ASN:HB2	1.91	0.52
11:I:7:CYS:HB3	11:I:14:LEU:HD21	1.90	0.52
3:A:738:LYS:C	3:A:740:LEU:H	2.13	0.52
3:A:471:ASN:O	3:A:474:VAL:HG12	2.10	0.52
13:K:42:LEU:O	13:K:46:ILE:HG13	2.08	0.52
3:A:504:LEU:HD11	8:F:91:ALA:HB1	1.92	0.52
3:A:208:LEU:HD21	3:A:212:LYS:HE3	1.90	0.52
4:B:1039:GLY:HA2	12:J:51:LEU:HD21	1.91	0.52
3:A:996:ASN:C	3:A:998:LEU:HD12	2.29	0.52
4:B:1081:LEU:HD12	4:B:1085:ILE:HD11	1.91	0.52
3:A:1445:ILE:HG12	9:G:18:PHE:CE2	2.44	0.52
3:A:960:ILE:HA	3:A:963:ILE:HG22	1.90	0.52
3:A:1017:LEU:CB	7:E:206:GLY:H	2.20	0.52
3:A:335:ARG:O	3:A:339:ASN:HB2	2.08	0.52
3:A:12:ARG:O	4:B:1194:ILE:HG22	2.09	0.52
11:I:101:PHE:HB2	11:I:110:PHE:CE2	2.45	0.52
8:F:109:VAL:CG1	8:F:123:LYS:HD3	2.39	0.52
10:H:24:CYS:HB2	10:H:44:VAL:HG21	1.92	0.52
12:J:27:GLU:O	12:J:29:GLU:N	2.41	0.52
3:A:1324:PRO:HB2	7:E:142:VAL:HG11	1.91	0.52
3:A:1333:ILE:O	3:A:1337:GLU:HG3	2.09	0.52
3:A:971:PHE:CE2	3:A:1040:GLN:HG2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:898:ARG:HB2	3:A:933:TYR:HE1	1.75	0.52
10:H:4:THR:CA	10:H:60:ALA:HB2	2.28	0.52
3:A:546:VAL:HG21	3:A:572:TRP:CE3	2.44	0.52
4:B:225:VAL:HA	4:B:237:VAL:O	2.10	0.52
4:B:563:MET:CE	4:B:580:VAL:HB	2.40	0.52
3:A:68:GLN:O	3:A:70:CYS:N	2.37	0.52
3:A:567:LYS:HE3	10:H:46:LEU:HB2	1.90	0.52
4:B:281:PRO:HG2	4:B:284:ILE:HG13	1.92	0.52
3:A:353:ILE:HD13	3:A:487:MET:HE2	1.92	0.52
5:C:189:THR:CG2	5:C:190:ASP:H	2.21	0.52
9:G:119:LEU:CD1	9:G:132:SER:HB2	2.39	0.52
9:G:96:GLN:HB3	9:G:121:PHE:CE2	2.45	0.52
3:A:626:ASN:O	3:A:631:HIS:CD2	2.63	0.52
3:A:298:PHE:HZ	3:A:314:ALA:HB2	1.74	0.52
3:A:1147:THR:HB	11:I:48:LEU:CD1	2.39	0.52
4:B:171:PRO:HD2	4:B:457:LEU:HD13	1.90	0.52
3:A:1397:LEU:HB2	3:A:1426:GLU:OE1	2.10	0.52
6:D:198:LEU:O	6:D:200:ASN:N	2.43	0.52
5:C:182:PRO:HG3	5:C:206:ASN:O	2.09	0.52
5:C:69:LEU:O	12:J:6:ARG:HD2	2.09	0.52
4:B:824:ILE:HG12	12:J:48:ARG:HH12	1.75	0.52
3:A:779:PHE:O	3:A:780:VAL:C	2.48	0.52
5:C:251:LEU:HD12	5:C:251:LEU:O	2.09	0.52
13:K:18:LYS:NZ	13:K:37:LYS:O	2.43	0.52
11:I:62:ILE:O	11:I:62:ILE:HG12	2.10	0.52
3:A:265:LYS:HE2	3:A:322:VAL:HG11	1.91	0.52
4:B:1124:ARG:O	4:B:1125:ASP:HB3	2.08	0.52
4:B:834:ASN:HA	4:B:838:SER:O	2.09	0.52
9:G:73:LYS:HE2	9:G:74:TYR:O	2.10	0.52
4:B:562:GLY:C	4:B:590:HIS:HD1	2.13	0.52
3:A:253:ASN:HB3	4:B:935:ARG:NH2	2.24	0.52
5:C:34:ARG:NH1	5:C:35:ARG:HG2	2.25	0.52
4:B:228:LYS:HB2	4:B:261:ARG:HH22	1.75	0.52
8:F:111:LEU:C	8:F:113:GLY:H	2.13	0.52
6:D:5:THR:O	6:D:5:THR:HG23	2.10	0.52
13:K:55:LYS:HB3	13:K:81:TYR:CD1	2.45	0.52
4:B:995:ARG:NH1	5:C:165:LYS:HG2	2.24	0.52
3:A:512:VAL:HA	3:A:519:PRO:HA	1.92	0.52
11:I:71:SER:OG	11:I:83:ASN:HB2	2.08	0.52
12:J:2:ILE:HG12	12:J:57:ILE:HD12	1.92	0.52
4:B:363:HIS:CD2	4:B:585:VAL:HG22	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:616:ILE:CG1	4:B:697:GLU:HA	2.40	0.52
4:B:370:PHE:HE2	4:B:373:ARG:NH1	2.05	0.52
4:B:948:ILE:HG22	4:B:949:VAL:O	2.09	0.52
4:B:1166:CYS:HB2	4:B:1215:ARG:NH1	2.24	0.52
4:B:244:LEU:HD11	4:B:366:GLN:NE2	2.25	0.52
4:B:871:THR:HG22	4:B:872:GLU:N	2.24	0.52
4:B:466:TRP:CE3	4:B:466:TRP:HA	2.43	0.52
10:H:18:GLY:O	10:H:19:ARG:HB2	2.10	0.52
3:A:50:ILE:C	3:A:52:GLY:N	2.62	0.51
3:A:54:ASN:N	3:A:54:ASN:HD22	2.08	0.51
3:A:42:ASP:HA	3:A:46:THR:O	2.10	0.51
3:A:666:ILE:N	4:B:1026:LEU:HD13	2.25	0.51
4:B:1065:GLN:HB2	5:C:201:TRP:CZ3	2.44	0.51
10:H:123:MET:HE1	10:H:142:LEU:HD11	1.92	0.51
3:A:722:LEU:O	3:A:725:ALA:HB3	2.11	0.51
6:D:29:LEU:HD22	9:G:82:PHE:CD2	2.45	0.51
4:B:681:TRP:HA	4:B:684:LEU:CD1	2.40	0.51
13:K:110:ASN:O	13:K:111:LEU:CB	2.57	0.51
4:B:824:ILE:HG12	12:J:48:ARG:NH1	2.25	0.51
9:G:56:ILE:O	9:G:57:GLN:HB2	2.09	0.51
3:A:1400:CYS:O	3:A:1405:THR:HG23	2.10	0.51
4:B:1063:GLY:O	5:C:202:PRO:HG2	2.11	0.51
4:B:1087:PHE:HD2	4:B:1088:GLY:H	1.58	0.51
4:B:882:THR:HG22	4:B:884:ARG:HB2	1.93	0.51
3:A:1305:VAL:CG1	3:A:1306:LEU:N	2.73	0.51
3:A:1120:LEU:O	3:A:1323:ASP:HB2	2.10	0.51
10:H:113:ALA:HB2	10:H:126:GLU:HG3	1.92	0.51
4:B:542:MET:HG2	4:B:747:MET:HB3	1.91	0.51
3:A:846:GLU:OE1	3:A:1425:SER:OG	2.29	0.51
3:A:1018:PHE:O	3:A:1021:LEU:HB3	2.11	0.51
5:C:3:GLU:O	5:C:4:GLU:CB	2.59	0.51
4:B:1197:PRO:HG2	4:B:1200:ALA:CB	2.41	0.51
13:K:57:LEU:HD12	13:K:77:THR:O	2.10	0.51
4:B:1074:ASN:HB2	4:B:1081:LEU:HD21	1.92	0.51
3:A:666:ILE:HD11	4:B:1086:PHE:HE1	1.75	0.51
5:C:235:VAL:HG13	12:J:13:VAL:HG23	1.92	0.51
10:H:130:ARG:N	10:H:130:ARG:HD2	2.16	0.51
7:E:16:PHE:HZ	7:E:20:LYS:HE2	1.70	0.51
3:A:475:THR:HG23	3:A:476:SER:H	1.76	0.51
3:A:172:PRO:HD3	3:A:185:TRP:HE1	1.76	0.51
4:B:1106:ARG:HH21	4:B:1111:MET:CE	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:99:PHE:HZ	9:G:163:ILE:HD13	1.76	0.51
5:C:52:GLU:HA	14:L:64:LEU:HD22	1.91	0.51
3:A:806:ARG:HH12	4:B:729:ILE:CD1	2.23	0.51
4:B:340:ALA:HB1	4:B:343:ILE:HD12	1.92	0.51
6:D:63:LEU:HD23	9:G:47:CYS:SG	2.51	0.51
3:A:907:THR:HG23	3:A:908:LEU:N	2.26	0.51
10:H:127:GLY:N	10:H:130:ARG:HH22	2.07	0.51
6:D:173:HIS:CD2	6:D:175:PHE:H	2.29	0.51
4:B:862:GLN:CG	4:B:963:PHE:HD1	2.21	0.51
3:A:152:VAL:HG12	3:A:153:PRO:CD	2.40	0.51
3:A:897:TYR:CD2	3:A:936:LEU:HD13	2.45	0.51
4:B:872:GLU:CD	4:B:914:LYS:HE2	2.31	0.51
3:A:525:GLN:HG3	4:B:835:GLN:HG2	1.93	0.51
5:C:183:TRP:O	5:C:185:LYS:N	2.43	0.51
9:G:149:GLY:O	9:G:159:ALA:HB1	2.11	0.51
4:B:1050:ILE:HG22	4:B:1051:THR:N	2.26	0.51
14:L:43:THR:O	14:L:43:THR:HG22	2.10	0.51
3:A:29:ALA:HB1	4:B:1184:GLY:HA2	1.93	0.51
4:B:833:TYR:N	4:B:833:TYR:CD1	2.77	0.51
4:B:343:ILE:HG22	4:B:348:ARG:HG3	1.91	0.51
4:B:336:ARG:CZ	4:B:348:ARG:NH1	2.73	0.51
6:D:8:PHE:CD2	9:G:6:ASP:O	2.63	0.51
3:A:62:ASP:HB3	3:A:64:ASN:HD21	1.74	0.51
5:C:20:PHE:CE1	5:C:22:LEU:HD12	2.45	0.51
3:A:898:ARG:HB2	3:A:933:TYR:CE1	2.46	0.51
3:A:1436:ILE:CD1	4:B:1139:ILE:HG23	2.41	0.51
3:A:903:ASN:C	3:A:903:ASN:ND2	2.64	0.51
4:B:212:LEU:CD2	4:B:480:SER:HB2	2.36	0.51
3:A:332:LYS:HB2	3:A:337:ARG:CZ	2.41	0.51
3:A:382:PRO:HD3	3:A:428:TYR:CD2	2.45	0.51
3:A:794:PRO:C	3:A:796:SER:H	2.13	0.51
4:B:29:ASP:OD1	4:B:658:ILE:HD13	2.10	0.51
3:A:1283:VAL:HG12	3:A:1284:MET:N	2.25	0.51
4:B:168:GLY:HA2	4:B:454:THR:OG1	2.11	0.51
11:I:69:PRO:HG2	11:I:85:PHE:CD2	2.46	0.51
11:I:85:PHE:HD2	11:I:85:PHE:N	2.02	0.51
4:B:839:MET:HE1	4:B:980:PHE:HB2	1.92	0.51
3:A:412:ARG:NH2	4:B:1108:ARG:HH12	2.08	0.51
3:A:148:CYS:O	3:A:168:GLY:HA2	2.09	0.51
4:B:785:TYR:C	4:B:785:TYR:CD1	2.83	0.51
3:A:116:ASP:O	3:A:118:HIS:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:165:LEU:N	7:E:165:LEU:HD23	2.25	0.51
4:B:361:LEU:N	4:B:362:PRO:CD	2.73	0.51
6:D:123:LEU:HD23	6:D:149:THR:HG21	1.93	0.51
4:B:1001:PHE:CE2	5:C:34:ARG:CZ	2.94	0.51
3:A:351:THR:HG22	4:B:1103:ILE:HA	1.91	0.51
3:A:1066:VAL:O	3:A:1070:GLN:HG3	2.10	0.51
5:C:259:LEU:HD13	13:K:91:CYS:CB	2.40	0.51
4:B:460:ALA:HB1	4:B:466:TRP:CZ3	2.46	0.51
4:B:984:HIS:NE2	4:B:1025:HIS:HA	2.26	0.51
7:E:24:LYS:HG3	7:E:25:ASP:N	2.26	0.51
3:A:1371:LEU:O	3:A:1375:MET:HG3	2.10	0.51
8:F:96:THR:O	8:F:100:GLN:HG3	2.11	0.51
4:B:216:GLU:HA	4:B:406:LEU:HD23	1.93	0.51
4:B:944:THR:HG21	4:B:1122:ARG:NH2	2.26	0.51
5:C:213:PRO:O	5:C:214:ASN:CB	2.58	0.51
3:A:896:ARG:NH2	3:A:1030:ARG:NH2	2.59	0.51
7:E:55:ARG:O	7:E:57:MET:N	2.44	0.51
4:B:840:ILE:HG21	4:B:994:TYR:HD1	1.75	0.51
3:A:58:LEU:HD11	3:A:244:PRO:HD2	1.91	0.51
4:B:329:THR:O	4:B:332:ASP:HB3	2.10	0.51
5:C:97:VAL:HB	5:C:159:ALA:HB3	1.93	0.51
10:H:128:ASN:O	10:H:128:ASN:OD1	2.29	0.51
11:I:7:CYS:SG	11:I:8:ARG:O	2.69	0.51
4:B:288:ALA:O	4:B:331:LEU:HD11	2.11	0.51
4:B:640:VAL:O	4:B:641:GLU:C	2.49	0.51
3:A:89:PRO:HB3	3:A:208:LEU:HD12	1.93	0.51
4:B:885:MET:HA	4:B:936:ASP:HB2	1.92	0.51
4:B:176:SER:O	4:B:182:SER:HB3	2.11	0.51
3:A:1220:PHE:O	3:A:1221:LYS:HB2	2.11	0.51
5:C:62:PHE:O	5:C:66:ARG:HG3	2.10	0.50
9:G:127:PRO:HG2	9:G:138:THR:CG2	2.37	0.50
5:C:184:ASN:HD21	5:C:187:LYS:HA	1.76	0.50
4:B:637:LEU:O	4:B:690:VAL:HG13	2.11	0.50
3:A:591:PHE:HA	3:A:595:THR:HG21	1.92	0.50
4:B:23:ALA:H	4:B:654:ARG:HB3	1.77	0.50
4:B:1040:ASN:O	4:B:1042:GLY:N	2.43	0.50
3:A:152:VAL:HG13	3:A:153:PRO:HD2	1.90	0.50
3:A:527:THR:CG2	3:A:650:GLN:HA	2.41	0.50
5:C:112:ASN:HB2	5:C:114:TYR:HE1	1.74	0.50
3:A:75:ASN:O	3:A:76:GLU:CB	2.59	0.50
3:A:347:PHE:H	4:B:1107:ALA:HA	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1149:ALA:HB2	11:I:47:GLU:HA	1.92	0.50
3:A:982:THR:O	3:A:985:ASP:HB2	2.11	0.50
4:B:882:THR:HB	4:B:934:LYS:O	2.11	0.50
11:I:6:PHE:HA	11:I:14:LEU:HG	1.92	0.50
4:B:309:GLN:OE1	11:I:52:ILE:HD11	2.11	0.50
4:B:215:GLN:OE1	4:B:479:VAL:HG22	2.11	0.50
3:A:1410:PHE:HD2	4:B:1212:ILE:HD12	1.76	0.50
4:B:1176:ASN:C	4:B:1178:ASN:H	2.15	0.50
4:B:731:VAL:HG12	4:B:732:SER:H	1.76	0.50
3:A:1197:LEU:HD11	3:A:1238:ILE:HD11	1.93	0.50
3:A:1446:ASP:HB2	8:F:133:VAL:HG23	1.93	0.50
6:D:8:PHE:O	6:D:9:GLN:HB2	2.11	0.50
4:B:822:ASN:ND2	12:J:52:THR:HG21	2.26	0.50
10:H:91:ASP:O	10:H:93:TYR:N	2.41	0.50
12:J:14:VAL:CG1	12:J:50:ILE:HD11	2.39	0.50
3:A:718:VAL:O	3:A:721:PHE:HB2	2.10	0.50
3:A:1425:SER:O	3:A:1429:ILE:HG13	2.11	0.50
5:C:241:ASP:OD1	5:C:242:GLN:N	2.42	0.50
6:D:4:SER:OG	6:D:5:THR:N	2.45	0.50
3:A:357:PRO:HD2	4:B:833:TYR:CE1	2.46	0.50
3:A:1149:ALA:CB	11:I:47:GLU:HA	2.41	0.50
3:A:805:LEU:CD1	4:B:1052:VAL:HG21	2.42	0.50
3:A:648:ASN:O	3:A:649:ILE:C	2.48	0.50
7:E:112:TYR:CE1	7:E:136:ASN:HB2	2.46	0.50
5:C:138:GLU:N	5:C:138:GLU:OE1	2.42	0.50
3:A:317:LYS:O	3:A:318:SER:CB	2.58	0.50
6:D:63:LEU:HD13	6:D:133:THR:OG1	2.10	0.50
9:G:35:GLU:CG	9:G:48:VAL:HG23	2.41	0.50
3:A:719:VAL:C	3:A:721:PHE:H	2.14	0.50
5:C:31:ASN:O	5:C:32:SER:C	2.50	0.50
6:D:153:ARG:C	6:D:154:PHE:CD1	2.85	0.50
3:A:207:ILE:HG22	3:A:211:PHE:CE1	2.47	0.50
4:B:313:MET:HE2	4:B:386:LEU:HD22	1.93	0.50
3:A:720:ARG:HB3	3:A:720:ARG:CZ	2.42	0.50
5:C:263:THR:C	5:C:265:MET:N	2.64	0.50
3:A:325:ILE:HG21	4:B:1210:MET:HG3	1.94	0.50
3:A:31:SER:HA	3:A:81:PHE:O	2.12	0.50
9:G:44:TYR:CD2	9:G:105:PRO:HB2	2.47	0.50
4:B:798:TYR:HE2	5:C:62:PHE:HE2	1.56	0.50
5:C:70:ILE:HD11	5:C:144:ILE:HG12	1.93	0.50
3:A:571:LEU:HD22	10:H:46:LEU:HD11	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:26:ILE:CG2	10:H:27:GLU:N	2.75	0.50
6:D:56:ARG:HD3	6:D:149:THR:HA	1.91	0.50
3:A:837:ILE:HA	3:A:840:ARG:HD3	1.92	0.50
4:B:683:SER:O	4:B:687:GLU:HB2	2.12	0.50
4:B:295:GLY:O	4:B:299:GLU:HG2	2.12	0.50
3:A:295:LEU:O	3:A:298:PHE:HB3	2.11	0.50
3:A:852:TYR:CD1	8:F:136:ARG:HB3	2.46	0.50
9:G:34:VAL:CG1	9:G:45:ILE:HG21	2.37	0.50
4:B:824:ILE:CG2	4:B:1087:PHE:CE2	2.93	0.50
3:A:1120:LEU:O	3:A:1323:ASP:N	2.44	0.50
4:B:638:PHE:HB3	4:B:651:LEU:HD22	1.94	0.50
3:A:675:THR:O	3:A:679:ILE:HG13	2.12	0.50
4:B:526:GLU:OE2	4:B:752:ALA:HB2	2.12	0.50
3:A:16:GLU:HB3	3:A:1418:LEU:HD11	1.94	0.50
5:C:89:GLU:O	5:C:90:ASP:HB3	2.11	0.50
6:D:39:ASN:HD21	6:D:41:GLN:HE21	1.54	0.50
12:J:7:CYS:O	12:J:11:GLY:HA2	2.12	0.50
4:B:100:PRO:HB2	4:B:180:TYR:HE1	1.75	0.50
4:B:169:ARG:HD2	4:B:454:THR:HG21	1.93	0.50
9:G:137:ILE:HG21	9:G:143:ILE:HD11	1.94	0.50
9:G:80:LYS:N	9:G:80:LYS:HD3	2.26	0.50
8:F:68:THR:O	8:F:69:LEU:HB3	2.12	0.50
3:A:1101:LEU:HB2	3:A:1355:VAL:HG11	1.93	0.50
3:A:224:PHE:HD2	3:A:229:SER:O	1.95	0.50
7:E:145:THR:HG21	7:E:187:TYR:CD2	2.46	0.50
6:D:195:ILE:HG22	6:D:198:LEU:HG	1.93	0.50
12:J:55:ASP:OD2	12:J:58:GLU:HG2	2.12	0.50
3:A:920:LEU:HD23	3:A:921:GLY:N	2.27	0.50
3:A:1120:LEU:CD1	3:A:1304:TRP:O	2.60	0.50
3:A:853:ASP:OD1	3:A:855:THR:CB	2.60	0.50
4:B:1162:ILE:HG22	4:B:1163:CYS:H	1.77	0.50
14:L:40:LEU:HD13	14:L:44:ASP:HB3	1.94	0.50
4:B:291:ILE:HD13	4:B:300:HIS:CD2	2.47	0.50
4:B:639:ILE:HG22	4:B:641:GLU:HG2	1.94	0.50
9:G:145:VAL:CG1	9:G:146:LYS:N	2.74	0.50
3:A:606:LEU:HG	3:A:613:ILE:HD12	1.93	0.50
3:A:1144:LYS:HB2	3:A:1268:LEU:O	2.11	0.50
3:A:1364:ASN:O	3:A:1365:TYR:C	2.50	0.50
3:A:180:LYS:NZ	3:A:294:SER:HB3	2.26	0.50
4:B:289:LEU:HD13	4:B:375:ALA:HB2	1.93	0.50
9:G:115:MET:CB	9:G:116:PRO:HD2	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:168:ALA:C	5:C:170:TRP:N	2.65	0.50
3:A:43:GLU:O	3:A:44:THR:HB	2.12	0.50
10:H:55:LEU:HD22	10:H:144:ILE:CG2	2.42	0.50
4:B:281:PRO:O	4:B:283:VAL:N	2.45	0.50
4:B:1045:SER:O	4:B:1046:PRO:O	2.30	0.50
3:A:346:ASP:HB3	4:B:1108:ARG:N	2.25	0.50
4:B:976:ILE:O	4:B:978:ASP:N	2.45	0.50
5:C:11:ARG:HD3	5:C:209:TYR:CZ	2.46	0.50
8:F:114:GLU:OE2	8:F:119:ARG:HG2	2.12	0.50
3:A:852:TYR:CE2	3:A:1060:PRO:HB2	2.47	0.50
4:B:171:PRO:HD2	4:B:457:LEU:CD1	2.42	0.50
4:B:840:ILE:HD13	4:B:994:TYR:HE1	1.77	0.50
3:A:1446:ASP:HB2	8:F:133:VAL:CG2	2.41	0.50
9:G:115:MET:HB3	9:G:116:PRO:HD2	1.93	0.50
12:J:31:ASP:O	12:J:32:GLU:C	2.50	0.50
5:C:18:VAL:CG2	5:C:240:VAL:HB	2.42	0.49
11:I:14:LEU:HD22	11:I:28:GLU:O	2.12	0.49
3:A:7:SER:CB	4:B:1175:LEU:HD22	2.42	0.49
3:A:963:ILE:HD13	3:A:1049:ILE:HG13	1.93	0.49
3:A:845:LEU:O	3:A:846:GLU:C	2.50	0.49
3:A:1017:LEU:HB3	7:E:205:SER:HA	1.93	0.49
9:G:80:LYS:O	9:G:82:PHE:CE1	2.65	0.49
4:B:654:ARG:C	4:B:656:GLY:H	2.15	0.49
7:E:124:VAL:HG13	7:E:132:ILE:CG1	2.42	0.49
8:F:109:VAL:HG23	8:F:124:GLU:HG2	1.94	0.49
3:A:1401:SER:O	3:A:1402:PHE:HB2	2.11	0.49
9:G:96:GLN:HG3	9:G:97:HIS:CD2	2.45	0.49
3:A:827:THR:O	3:A:831:THR:HB	2.11	0.49
4:B:33:VAL:O	4:B:36:ALA:HB3	2.11	0.49
5:C:74:SER:HB2	5:C:77:ILE:HG12	1.95	0.49
4:B:521:LEU:HB3	4:B:633:VAL:HG11	1.94	0.49
3:A:616:VAL:HG12	3:A:617:VAL:N	2.27	0.49
3:A:621:THR:O	3:A:629:LEU:HB2	2.12	0.49
3:A:93:VAL:CG2	3:A:301:ALA:HA	2.41	0.49
4:B:1182:CYS:C	4:B:1183:LYS:HE3	2.32	0.49
3:A:981:LEU:HD21	3:A:1039:LYS:HA	1.94	0.49
3:A:224:PHE:CD2	3:A:231:PRO:HG3	2.47	0.49
3:A:1313:LEU:HD23	3:A:1338:VAL:CG2	2.41	0.49
4:B:1077:THR:HG22	13:K:44:ASN:HD21	1.77	0.49
4:B:640:VAL:O	4:B:640:VAL:HG12	2.11	0.49
3:A:1450:LEU:CG	3:A:1450:LEU:O	2.59	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:720:ARG:O	3:A:724:GLU:HB2	2.11	0.49
5:C:76:ASP:OD2	5:C:128:ASN:N	2.44	0.49
3:A:187:LYS:NZ	3:A:198:GLU:OE2	2.39	0.49
9:G:14:HIS:CD2	9:G:16:SER:CB	2.95	0.49
4:B:281:PRO:HB3	4:B:320:ASP:OD2	2.12	0.49
11:I:15:TYR:N	11:I:15:TYR:CD1	2.80	0.49
3:A:1007:ILE:HD13	7:E:168:TYR:HE2	1.77	0.49
3:A:997:LEU:HD13	3:A:1018:PHE:HE2	1.76	0.49
3:A:322:VAL:HG12	3:A:322:VAL:O	2.11	0.49
3:A:341:MET:HE2	3:A:843:LYS:HZ1	1.77	0.49
10:H:101:ALA:HB2	10:H:116:TYR:CE1	2.48	0.49
3:A:783:THR:HG22	3:A:784:LEU:HG	1.93	0.49
3:A:857:ARG:CZ	8:F:139:PRO:HG3	2.43	0.49
3:A:1006:ILE:HB	7:E:167:ARG:HG3	1.95	0.49
4:B:896:ASP:CG	14:L:58:LYS:HZ2	2.16	0.49
7:E:157:SER:O	7:E:159:ASP:N	2.45	0.49
7:E:156:LEU:HA	7:E:160:GLU:OE1	2.12	0.49
10:H:13:SER:O	10:H:14:GLU:HB2	2.13	0.49
3:A:808:LEU:HD23	3:A:813:PHE:HA	1.93	0.49
4:B:1072:MET:HE3	4:B:1085:ILE:HD13	1.94	0.49
4:B:37:PHE:CD1	4:B:41:LYS:HG3	2.45	0.49
10:H:87:ARG:O	10:H:89:LEU:HG	2.12	0.49
3:A:440:ASP:O	3:A:442:VAL:HG22	2.12	0.49
7:E:22:MET:CE	7:E:26:ARG:NH2	2.74	0.49
4:B:777:ALA:HA	4:B:1095:LEU:HA	1.94	0.49
3:A:106:VAL:HG12	3:A:107:CYS:N	2.28	0.49
3:A:939:ASP:OD1	3:A:1023:ARG:NH1	2.46	0.49
3:A:438:ASP:OD1	3:A:461:LYS:HA	2.12	0.49
4:B:680:THR:O	4:B:684:LEU:HD12	2.12	0.49
14:L:39:SER:O	14:L:40:LEU:HG	2.11	0.49
4:B:1174:LYS:O	4:B:1176:ASN:HB2	2.11	0.49
3:A:1283:VAL:HG12	3:A:1284:MET:H	1.78	0.49
4:B:409:ALA:O	4:B:413:LEU:HG	2.12	0.49
3:A:51:GLY:HA2	3:A:56:PRO:HA	1.94	0.49
4:B:843:GLN:O	4:B:846:ILE:N	2.45	0.49
4:B:745:PRO:C	4:B:747:MET:N	2.66	0.49
7:E:23:VAL:HB	7:E:30:ILE:HD11	1.95	0.49
11:I:51:ASN:O	11:I:54:GLU:HG3	2.12	0.49
11:I:85:PHE:HD1	11:I:99:LEU:HD13	1.75	0.49
3:A:1211:GLN:O	3:A:1212:VAL:C	2.51	0.49
4:B:204:ILE:HG22	4:B:204:ILE:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:35:ILE:HD13	3:A:241:VAL:HG11	1.94	0.49
12:J:56:LEU:O	12:J:59:LYS:N	2.44	0.49
4:B:882:THR:HG21	4:B:884:ARG:HB2	1.93	0.49
4:B:189:LEU:CD1	4:B:196:PRO:HA	2.42	0.49
3:A:578:LEU:O	3:A:578:LEU:HG	2.13	0.49
3:A:1004:ASN:HD21	7:E:167:ARG:HD2	1.73	0.49
9:G:88:ASP:HB3	9:G:144:ARG:CA	2.42	0.49
4:B:1216:LEU:C	4:B:1217:TYR:HD1	2.16	0.49
4:B:784:ASN:O	4:B:788:ARG:HG3	2.13	0.49
9:G:51:TYR:C	9:G:51:TYR:HD2	2.16	0.49
3:A:806:ARG:NH1	4:B:729:ILE:HG13	2.28	0.49
10:H:83:GLN:C	10:H:85:GLY:H	2.15	0.49
3:A:364:VAL:O	3:A:364:VAL:HG13	2.11	0.49
4:B:769:TYR:C	4:B:771:SER:N	2.65	0.49
6:D:39:ASN:HD22	6:D:41:GLN:HB2	1.78	0.49
9:G:7:LEU:CD1	9:G:45:ILE:HD11	2.43	0.49
5:C:146:LYS:HB2	12:J:57:ILE:HD11	1.93	0.49
4:B:280:ILE:CG2	4:B:285:ILE:HG13	2.42	0.49
3:A:1323:ASP:C	3:A:1325:THR:H	2.15	0.49
9:G:129:SER:HB3	9:G:138:THR:OG1	2.12	0.49
3:A:590:ARG:HH21	3:A:620:LYS:CB	2.22	0.49
3:A:605:MET:CE	3:A:612:ILE:HG23	2.42	0.49
3:A:269:ILE:HG23	3:A:300:VAL:CG2	2.43	0.49
9:G:106:MET:CG	9:G:107:LYS:N	2.75	0.49
7:E:13:TRP:CE3	7:E:39:LEU:HD13	2.47	0.49
4:B:642:ASP:CA	4:B:649:LYS:HA	2.40	0.49
7:E:135:PHE:CD2	7:E:140:LEU:HD21	2.48	0.49
3:A:1256:GLU:O	3:A:1260:LEU:HB3	2.12	0.49
13:K:110:ASN:O	13:K:111:LEU:HB3	2.12	0.49
4:B:729:ILE:HG22	4:B:729:ILE:O	2.11	0.49
3:A:1237:ILE:HG22	3:A:1238:ILE:N	2.28	0.49
6:D:210:ILE:O	6:D:214:LEU:HG	2.13	0.49
3:A:1272:THR:C	3:A:1273:LEU:HD12	2.33	0.49
4:B:1220:ARG:HB3	4:B:1220:ARG:CZ	2.43	0.49
3:A:70:CYS:O	3:A:70:CYS:SG	2.71	0.49
9:G:74:TYR:HD2	9:G:74:TYR:H	1.61	0.49
9:G:7:LEU:O	9:G:73:LYS:HD2	2.13	0.49
5:C:234:SER:HB3	5:C:240:VAL:HG13	1.95	0.49
10:H:12:VAL:HB	10:H:52:GLN:H	1.77	0.49
3:A:7:SER:C	3:A:9:ALA:H	2.15	0.49
13:K:47:ARG:O	13:K:47:ARG:HD2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:311:LEU:O	4:B:312:GLU:C	2.49	0.49
3:A:120:GLU:C	3:A:122:MET:N	2.66	0.49
4:B:866:TYR:O	4:B:867:GLY:C	2.52	0.49
3:A:984:LYS:HG2	3:A:988:LEU:CD1	2.43	0.49
5:C:112:ASN:CB	5:C:114:TYR:CE1	2.95	0.49
8:F:128:LYS:HD3	8:F:149:GLU:O	2.12	0.49
3:A:735:VAL:O	3:A:735:VAL:HG12	2.12	0.49
11:I:2:THR:O	11:I:3:THR:C	2.51	0.49
11:I:3:THR:O	11:I:3:THR:HG22	2.13	0.49
5:C:147:LEU:N	5:C:147:LEU:HD23	2.28	0.49
5:C:46:ILE:CD1	5:C:67:LEU:HB3	2.40	0.49
14:L:32:ALA:CB	14:L:55:ILE:HD12	2.33	0.49
7:E:28:TYR:HE1	7:E:78:LEU:HD13	1.78	0.49
4:B:770:GLN:HG2	4:B:983:ARG:O	2.13	0.49
4:B:850:LEU:HD12	4:B:851:PHE:N	2.28	0.49
6:D:19:GLU:O	6:D:21:GLU:N	2.46	0.49
5:C:226:ASP:O	5:C:227:THR:HB	2.12	0.48
4:B:550:ASP:OD1	4:B:551:PRO:HD2	2.13	0.48
11:I:34:TYR:C	11:I:34:TYR:CD2	2.86	0.48
4:B:1084:GLN:OE1	5:C:189:THR:CG2	2.61	0.48
6:D:53:SER:H	6:D:148:LEU:HD23	1.78	0.48
3:A:546:VAL:O	3:A:550:LEU:HG	2.13	0.48
5:C:243:VAL:HG12	5:C:243:VAL:O	2.13	0.48
13:K:61:TYR:C	13:K:61:TYR:CD2	2.85	0.48
4:B:234:ILE:N	4:B:234:ILE:HD12	2.28	0.48
7:E:124:VAL:HB	7:E:125:PRO:HD3	1.95	0.48
3:A:335:ARG:HA	3:A:339:ASN:HD22	1.78	0.48
3:A:527:THR:O	3:A:653:VAL:HG11	2.13	0.48
3:A:981:LEU:HD21	3:A:1038:THR:O	2.13	0.48
3:A:29:ALA:HB1	4:B:1184:GLY:CA	2.43	0.48
4:B:992:ILE:HD11	13:K:66:PRO:HB2	1.95	0.48
7:E:15:ALA:O	7:E:19:VAL:HG23	2.13	0.48
4:B:615:MET:HA	4:B:625:LYS:O	2.13	0.48
3:A:605:MET:HE1	3:A:612:ILE:HG23	1.95	0.48
13:K:65:HIS:HD2	13:K:67:PHE:N	2.03	0.48
3:A:18:GLN:HB3	4:B:1215:ARG:HG3	1.94	0.48
3:A:227:VAL:HG12	6:D:15:LEU:HD23	1.94	0.48
4:B:129:PHE:CD2	4:B:166:PHE:HA	2.48	0.48
3:A:166:GLY:O	3:A:167:CYS:CB	2.61	0.48
3:A:573:SER:OG	3:A:576:GLN:HB2	2.12	0.48
11:I:21:GLU:O	11:I:21:GLU:HG2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:1068:GLY:O	4:B:1069:PHE:O	2.32	0.48
5:C:70:ILE:HG12	5:C:142:VAL:HG11	1.95	0.48
4:B:879:ARG:O	4:B:880:THR:HB	2.13	0.48
3:A:719:VAL:C	3:A:721:PHE:N	2.67	0.48
4:B:806:THR:HA	4:B:1045:SER:OG	2.13	0.48
3:A:618:GLU:O	3:A:621:THR:N	2.41	0.48
4:B:810:GLU:HB3	4:B:811:TYR:CE1	2.48	0.48
4:B:1166:CYS:O	4:B:1166:CYS:SG	2.70	0.48
4:B:737:THR:CG2	11:I:66:PRO:HA	2.43	0.48
3:A:1385:THR:CG2	3:A:1386:ARG:N	2.76	0.48
4:B:1106:ARG:NH2	4:B:1111:MET:CE	2.76	0.48
3:A:1219:THR:HG21	3:A:1271:ILE:HD11	1.94	0.48
4:B:1022:THR:HG23	4:B:1022:THR:O	2.12	0.48
11:I:56:ALA:O	11:I:57:GLY:O	2.31	0.48
4:B:581:PHE:HA	4:B:585:VAL:O	2.13	0.48
3:A:18:GLN:H	4:B:1215:ARG:HB2	1.79	0.48
4:B:1102:LYS:O	4:B:1103:ILE:C	2.52	0.48
8:F:90:ARG:HD3	8:F:155:LEU:HD12	1.93	0.48
3:A:507:VAL:N	3:A:508:PRO:CD	2.77	0.48
4:B:54:PHE:HA	4:B:58:THR:HB	1.93	0.48
10:H:145:ARG:O	10:H:146:ARG:HB2	2.13	0.48
4:B:893:LEU:HD22	4:B:897:GLY:C	2.34	0.48
3:A:1280:GLU:O	3:A:1281:ARG:C	2.52	0.48
5:C:221:TYR:CE1	5:C:222:LYS:HG3	2.49	0.48
4:B:363:HIS:HD2	4:B:585:VAL:HG22	1.78	0.48
12:J:44:TYR:HA	12:J:47:ARG:HB3	1.95	0.48
7:E:78:LEU:C	7:E:78:LEU:HD23	2.33	0.48
7:E:13:TRP:CZ3	7:E:39:LEU:HB2	2.48	0.48
4:B:498:THR:O	4:B:536:VAL:HA	2.13	0.48
4:B:365:THR:HG23	4:B:367:LEU:HG	1.96	0.48
3:A:474:VAL:C	3:A:477:PRO:HD2	2.34	0.48
11:I:111:THR:CG2	11:I:112:SER:N	2.77	0.48
3:A:1094:VAL:HG12	3:A:1095:THR:N	2.26	0.48
5:C:181:ASP:CG	5:C:186:LEU:HD13	2.32	0.48
3:A:1319:VAL:HG13	3:A:1320:PRO:HD2	1.96	0.48
3:A:1029:ARG:HG3	3:A:1029:ARG:HH11	1.79	0.48
4:B:324:ILE:HD13	4:B:330:ALA:HA	1.96	0.48
5:C:249:ASP:O	5:C:252:GLN:HB3	2.13	0.48
4:B:1167:GLY:N	4:B:1217:TYR:HE1	2.11	0.48
3:A:98:LYS:O	3:A:102:VAL:HG23	2.14	0.48
3:A:475:THR:CG2	3:A:476:SER:H	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:981:LEU:HD23	3:A:1039:LYS:HA	1.96	0.48
3:A:423:ASP:O	3:A:424:ILE:CB	2.62	0.48
3:A:1444:MET:CG	9:G:60:ARG:HA	2.43	0.48
7:E:2:ASP:HB3	7:E:3:GLN:H	1.46	0.48
4:B:711:GLU:H	4:B:712:PRO:HD2	1.78	0.48
4:B:913:GLY:HA2	4:B:938:SER:OG	2.13	0.48
4:B:1072:MET:CE	4:B:1087:PHE:HD1	2.26	0.48
10:H:91:ASP:C	10:H:93:TYR:H	2.15	0.48
4:B:954:VAL:O	14:L:55:ILE:O	2.31	0.48
3:A:341:MET:HE1	4:B:1135:ARG:HH12	1.79	0.48
5:C:11:ARG:HH21	5:C:229:TYR:HB3	1.79	0.48
7:E:55:ARG:HD2	7:E:83:CYS:O	2.14	0.48
3:A:185:TRP:CZ3	3:A:200:ARG:HG2	2.48	0.48
3:A:1409:LEU:HD13	4:B:1207:LEU:HD21	1.95	0.48
3:A:167:CYS:O	3:A:167:CYS:SG	2.72	0.48
3:A:1005:GLU:O	3:A:1009:ASN:HB2	2.13	0.48
3:A:666:ILE:CD1	3:A:667:GLY:H	2.20	0.48
4:B:1072:MET:SD	4:B:1087:PHE:HD1	2.37	0.48
5:C:146:LYS:C	5:C:147:LEU:HD23	2.33	0.48
5:C:147:LEU:HD12	5:C:151:GLN:O	2.13	0.48
5:C:174:ALA:O	5:C:175:ALA:HB2	2.14	0.48
12:J:1:MET:H2	12:J:57:ILE:HG22	1.78	0.48
10:H:116:TYR:HE2	10:H:140:ALA:CB	2.27	0.48
4:B:744:HIS:CG	4:B:745:PRO:HD2	2.49	0.48
4:B:314:LEU:O	4:B:317:CYS:HB3	2.14	0.48
4:B:121:ASN:OD1	4:B:963:PHE:HZ	1.96	0.48
6:D:135:GLY:C	6:D:137:ASN:H	2.16	0.48
3:A:442:VAL:CB	3:A:489:LEU:HD11	2.40	0.48
14:L:47:ARG:HH21	14:L:54:ARG:NH2	2.12	0.48
3:A:407:ARG:HD2	3:A:413:ILE:HD11	1.96	0.48
6:D:191:ALA:C	6:D:193:THR:H	2.17	0.48
3:A:207:ILE:CG2	3:A:211:PHE:CE1	2.97	0.48
7:E:213:ILE:HG12	7:E:214:CYS:H	1.78	0.48
3:A:613:ILE:O	3:A:614:PHE:HB3	2.13	0.48
4:B:345:LYS:O	4:B:348:ARG:N	2.47	0.48
3:A:399:HIS:CB	3:A:400:PRO:CD	2.90	0.48
4:B:1097:HIS:N	4:B:1098:MET:HE2	2.29	0.48
10:H:99:GLY:CA	10:H:118:PHE:HA	2.44	0.48
6:D:51:ASN:O	6:D:52:LEU:O	2.32	0.48
3:A:1398:MET:HB2	3:A:1426:GLU:OE2	2.13	0.48
4:B:519:TRP:C	4:B:519:TRP:CD1	2.87	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:790:ASP:OD2	4:B:790:ASP:N	2.45	0.48
3:A:79:GLY:H	4:B:1205:GLN:HE22	1.61	0.48
3:A:1120:LEU:HD13	3:A:1304:TRP:O	2.14	0.48
3:A:568:PRO:HB2	5:C:221:TYR:CZ	2.49	0.48
10:H:20:TYR:O	10:H:22:LYS:N	2.46	0.48
4:B:954:VAL:HA	4:B:964:VAL:HG22	1.95	0.48
14:L:61:THR:HG22	14:L:62:LYS:N	2.28	0.48
4:B:557:PHE:O	4:B:557:PHE:HD2	1.96	0.48
3:A:608:ILE:HD12	3:A:613:ILE:CD1	2.44	0.48
9:G:153:GLN:CG	9:G:154:VAL:HG23	2.44	0.48
8:F:138:LEU:HB3	8:F:139:PRO:HD2	1.95	0.47
3:A:1438:THR:CG2	8:F:92:ARG:HD2	2.44	0.47
3:A:1438:THR:HG22	8:F:92:ARG:HD2	1.96	0.47
9:G:43:GLY:HA3	9:G:80:LYS:HB3	1.96	0.47
4:B:955:THR:HG22	4:B:956:THR:O	2.14	0.47
3:A:98:LYS:O	3:A:99:ILE:C	2.52	0.47
3:A:444:PHE:CB	3:A:458:HIS:HD2	2.26	0.47
5:C:186:LEU:HD12	5:C:186:LEU:N	2.29	0.47
4:B:1023:VAL:O	4:B:1026:LEU:N	2.47	0.47
4:B:801:LYS:O	12:J:52:THR:CG2	2.58	0.47
4:B:193:LYS:HZ3	14:L:32:ALA:HB1	1.74	0.47
3:A:903:ASN:ND2	3:A:905:ASP:H	2.12	0.47
5:C:35:ARG:HH11	13:K:41:THR:CA	2.27	0.47
3:A:1349:TYR:CA	3:A:1372:VAL:HG21	2.44	0.47
4:B:43:LEU:HD11	4:B:811:TYR:O	2.15	0.47
8:F:68:THR:O	8:F:69:LEU:CB	2.62	0.47
3:A:146:MET:HA	3:A:171:GLN:HB2	1.97	0.47
4:B:294:ASP:C	4:B:296:GLU:H	2.16	0.47
3:A:514:PRO:C	3:A:516:SER:H	2.16	0.47
6:D:52:LEU:CD2	6:D:147:TYR:HE2	2.27	0.47
4:B:200:GLY:HA2	4:B:202:TYR:CE2	2.49	0.47
4:B:842:ASN:ND2	4:B:845:SER:OG	2.38	0.47
4:B:878:GLN:O	4:B:879:ARG:C	2.52	0.47
4:B:628:THR:O	4:B:628:THR:HG23	2.14	0.47
4:B:314:LEU:O	4:B:318:VAL:HG23	2.15	0.47
4:B:38:PHE:CD1	4:B:811:TYR:CD2	3.00	0.47
14:L:46:VAL:HG12	14:L:46:VAL:O	2.14	0.47
4:B:557:PHE:O	4:B:557:PHE:CD2	2.67	0.47
3:A:282:ASN:O	3:A:284:ALA:N	2.47	0.47
5:C:263:THR:O	5:C:265:MET:N	2.47	0.47
3:A:352:VAL:O	3:A:467:THR:HG22	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:43:THR:CG2	5:C:44:LEU:N	2.52	0.47
3:A:42:ASP:C	3:A:44:THR:N	2.67	0.47
5:C:18:VAL:CG1	5:C:18:VAL:O	2.56	0.47
10:H:123:MET:HG2	10:H:124:ARG:N	2.28	0.47
3:A:1048:ASN:O	3:A:1049:ILE:C	2.52	0.47
3:A:1376:THR:O	3:A:1377:THR:C	2.53	0.47
7:E:164:LEU:HD11	7:E:211:TYR:CE1	2.50	0.47
4:B:1198:TYR:CD2	4:B:1198:TYR:O	2.67	0.47
4:B:300:HIS:O	4:B:303:TYR:HE2	1.98	0.47
4:B:310:MET:O	4:B:313:MET:HB2	2.13	0.47
3:A:90:VAL:HG13	3:A:297:GLN:CD	2.35	0.47
8:F:74:ILE:HG23	8:F:75:PRO:HD2	1.96	0.47
4:B:44:VAL:O	4:B:45:SER:C	2.52	0.47
4:B:838:SER:HB2	4:B:989:THR:O	2.15	0.47
4:B:897:GLY:O	4:B:898:LEU:HD23	2.13	0.47
5:C:215:GLU:O	5:C:216:GLY:C	2.51	0.47
6:D:185:CYS:O	6:D:211:LEU:HD22	2.14	0.47
3:A:961:ARG:HH11	3:A:961:ARG:HG3	1.80	0.47
4:B:1069:PHE:HA	4:B:1085:ILE:O	2.14	0.47
5:C:22:LEU:O	5:C:227:THR:HA	2.15	0.47
5:C:67:LEU:HD11	5:C:155:LEU:HD12	1.97	0.47
4:B:298:LEU:CD2	4:B:298:LEU:N	2.78	0.47
4:B:604:ARG:C	4:B:606:LYS:H	2.17	0.47
3:A:262:LEU:O	3:A:264:PHE:N	2.47	0.47
4:B:118:ARG:CG	4:B:204:ILE:HD13	2.45	0.47
8:F:77:ASP:C	8:F:79:ARG:H	2.16	0.47
6:D:151:PHE:N	6:D:151:PHE:CD1	2.81	0.47
4:B:376:PHE:O	4:B:586:TRP:HZ3	1.97	0.47
4:B:51:PHE:CD2	4:B:173:MET:HB3	2.49	0.47
5:C:84:ARG:NE	13:K:11:LEU:HD11	2.29	0.47
4:B:293:PRO:HG2	4:B:296:GLU:CB	2.44	0.47
7:E:145:THR:HG21	7:E:187:TYR:CE2	2.50	0.47
4:B:769:TYR:C	4:B:771:SER:H	2.17	0.47
4:B:258:LEU:O	4:B:258:LEU:HG	2.13	0.47
5:C:100:THR:OG1	5:C:121:VAL:HG21	2.14	0.47
5:C:69:LEU:HB3	12:J:6:ARG:HD3	1.97	0.47
4:B:273:LEU:CB	4:B:276:ILE:HD12	2.27	0.47
3:A:567:LYS:CG	3:A:568:PRO:CD	2.80	0.47
5:C:189:THR:CG2	5:C:190:ASP:N	2.69	0.47
4:B:114:PRO:O	4:B:116:GLU:N	2.48	0.47
4:B:247:GLY:C	4:B:249:ARG:H	2.17	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:48:ILE:HG21	9:G:4:ILE:HB	1.96	0.47
6:D:54:GLU:O	6:D:58:VAL:HG23	2.14	0.47
8:F:103:MET:HE3	9:G:66:GLY:H	1.80	0.47
3:A:816:HIS:CD2	4:B:764:SER:HB2	2.50	0.47
3:A:106:VAL:HG13	3:A:112:LYS:C	2.35	0.47
4:B:1152:MET:HE1	4:B:1157:ALA:HA	1.96	0.47
4:B:604:ARG:O	4:B:606:LYS:N	2.47	0.47
3:A:1313:LEU:C	3:A:1315:GLU:H	2.18	0.47
5:C:116:LYS:HD3	5:C:140:ASN:HA	1.96	0.47
4:B:460:ALA:HB1	4:B:466:TRP:CE3	2.50	0.47
4:B:220:GLY:O	4:B:222:ILE:HG13	2.14	0.47
11:I:22:ASN:O	11:I:23:ASN:HB2	2.15	0.47
3:A:55:ASP:N	3:A:56:PRO:CD	2.77	0.47
3:A:47:ARG:O	3:A:48:ALA:HB2	2.15	0.47
5:C:98:VAL:HG12	5:C:99:LEU:N	2.29	0.47
4:B:882:THR:HG21	4:B:934:LYS:O	2.15	0.47
3:A:902:LEU:CG	3:A:926:GLN:HG3	2.43	0.47
14:L:52:GLY:O	14:L:53:HIS:C	2.53	0.47
7:E:205:SER:O	7:E:206:GLY:C	2.54	0.47
3:A:1036:ARG:HH11	3:A:1036:ARG:CG	2.28	0.47
5:C:259:LEU:HD13	13:K:91:CYS:HB2	1.96	0.47
7:E:144:ILE:HG13	7:E:145:THR:H	1.79	0.47
4:B:54:PHE:O	4:B:58:THR:HB	2.15	0.47
7:E:93:MET:SD	7:E:97:VAL:CG2	3.03	0.47
4:B:735:ALA:O	4:B:738:PHE:HE1	1.98	0.47
3:A:1236:LEU:C	3:A:1237:ILE:HG13	2.35	0.47
4:B:485:ARG:HG3	4:B:781:PHE:CD1	2.49	0.47
5:C:100:THR:HG22	5:C:101:LEU:N	2.30	0.47
5:C:121:VAL:HG12	5:C:121:VAL:O	2.15	0.47
4:B:569:TYR:CE1	4:B:589:VAL:HG21	2.49	0.47
4:B:882:THR:CB	4:B:934:LYS:O	2.62	0.47
3:A:1114:PRO:HB2	3:A:1311:VAL:HG23	1.95	0.47
11:I:5:ARG:HD3	11:I:36:GLU:OE2	2.15	0.47
4:B:826:ALA:HB2	4:B:1008:PRO:HB3	1.96	0.47
3:A:590:ARG:HH11	3:A:590:ARG:HG3	1.79	0.47
4:B:839:MET:CE	4:B:980:PHE:HB2	2.44	0.47
4:B:903:VAL:HG12	4:B:904:ARG:N	2.30	0.47
3:A:211:PHE:HA	3:A:214:ILE:CD1	2.45	0.47
14:L:38:LEU:CD1	14:L:49:LYS:HE2	2.44	0.47
3:A:1453:TYR:O	3:A:1454:MET:HB3	2.14	0.47
10:H:99:GLY:HA3	10:H:117:SER:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:185:CYS:HB2	6:D:211:LEU:HD21	1.97	0.47
10:H:7:ASP:O	10:H:8:ASP:HB2	2.15	0.47
3:A:246:VAL:O	3:A:328:ARG:NH1	2.41	0.47
3:A:601:LYS:HB2	3:A:603:ASN:ND2	2.29	0.47
9:G:126:ASN:HD22	9:G:127:PRO:HA	1.80	0.47
7:E:78:LEU:HD11	7:E:109:ILE:HD12	1.97	0.47
4:B:616:ILE:HG12	4:B:697:GLU:HA	1.97	0.47
4:B:1161:HIS:NE2	4:B:1175:LEU:HD21	2.30	0.47
4:B:373:ARG:CG	4:B:566:LEU:HD23	2.45	0.47
4:B:642:ASP:H	4:B:649:LYS:HE3	1.79	0.47
4:B:1167:GLY:H	4:B:1215:ARG:HD2	1.80	0.47
3:A:793:SER:HB2	3:A:794:PRO:HD2	1.96	0.47
3:A:506:ALA:HB1	3:A:508:PRO:HD2	1.96	0.47
5:C:179:GLU:HG2	5:C:180:TYR:H	1.78	0.47
4:B:44:VAL:HG21	4:B:199:MET:O	2.15	0.47
5:C:234:SER:OG	5:C:235:VAL:N	2.46	0.46
3:A:254:GLU:CG	4:B:935:ARG:HH22	2.27	0.46
10:H:26:ILE:HG22	10:H:27:GLU:N	2.31	0.46
4:B:1070:GLU:O	4:B:1084:GLN:HB3	2.16	0.46
11:I:53:GLY:C	11:I:55:THR:H	2.19	0.46
9:G:91:VAL:HA	9:G:101:VAL:HA	1.97	0.46
4:B:860:MET:CB	4:B:965:LYS:HG2	2.43	0.46
4:B:525:ALA:O	4:B:768:THR:HG23	2.15	0.46
5:C:112:ASN:N	5:C:112:ASN:HD22	2.13	0.46
4:B:195:CYS:SG	4:B:197:PHE:HB2	2.55	0.46
9:G:87:VAL:HB	9:G:103:VAL:HG11	1.97	0.46
8:F:131:PRO:C	8:F:132:LEU:HD23	2.36	0.46
4:B:824:ILE:O	4:B:824:ILE:HG22	2.15	0.46
4:B:115:GLN:HG2	4:B:193:LYS:CB	2.40	0.46
3:A:1015:VAL:CG1	3:A:1019:CYS:SG	3.03	0.46
4:B:1183:LYS:HE3	4:B:1183:LYS:O	2.15	0.46
4:B:773:MET:CE	4:B:985:GLY:HA2	2.45	0.46
3:A:347:PHE:HE2	3:A:375:THR:HG23	1.79	0.46
9:G:115:MET:CB	9:G:116:PRO:CD	2.93	0.46
3:A:961:ARG:O	3:A:965:GLN:HG3	2.15	0.46
7:E:151:PRO:HB3	7:E:200:ARG:HB3	1.96	0.46
10:H:139:ASN:O	10:H:140:ALA:CB	2.63	0.46
3:A:567:LYS:CE	10:H:46:LEU:HB2	2.44	0.46
10:H:38:LEU:HD13	10:H:125:LEU:CD1	2.46	0.46
5:C:47:ASP:HA	14:L:69:ALA:CB	2.33	0.46
7:E:35:VAL:C	7:E:37:LEU:H	2.19	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:33:PHE:CE1	9:G:80:LYS:HE3	2.50	0.46
7:E:124:VAL:CA	7:E:132:ILE:HD12	2.46	0.46
3:A:1121:GLU:O	3:A:1122:PRO:C	2.53	0.46
10:H:11:GLN:O	10:H:28:ALA:HB1	2.15	0.46
3:A:90:VAL:HG13	3:A:297:GLN:OE1	2.14	0.46
3:A:350:ARG:NH1	3:A:350:ARG:HG3	2.31	0.46
9:G:99:PHE:CD1	9:G:99:PHE:C	2.87	0.46
3:A:967:ALA:HA	3:A:1044:TRP:CZ3	2.51	0.46
7:E:61:GLN:NE2	7:E:105:PHE:CZ	2.82	0.46
3:A:247:ARG:HH11	3:A:247:ARG:HG3	1.81	0.46
3:A:49:LYS:HZ1	3:A:61:ILE:CG1	2.27	0.46
4:B:372:SER:O	4:B:376:PHE:HD1	1.98	0.46
3:A:537:ARG:NH1	10:H:120:GLY:O	2.47	0.46
3:A:963:ILE:HD13	3:A:1049:ILE:HG12	1.96	0.46
13:K:7:PHE:HA	13:K:10:PHE:CE2	2.50	0.46
3:A:1377:THR:O	3:A:1378:GLN:C	2.53	0.46
3:A:709:THR:HG21	11:I:93:LYS:O	2.15	0.46
9:G:3:PHE:CD1	9:G:80:LYS:NZ	2.72	0.46
9:G:61:ILE:HG23	9:G:66:GLY:O	2.16	0.46
11:I:106:CYS:SG	11:I:107:SER:N	2.89	0.46
14:L:46:VAL:CG1	14:L:56:LEU:HD12	2.46	0.46
5:C:124:LEU:CD2	5:C:129:ILE:HG22	2.46	0.46
4:B:840:ILE:HD13	4:B:994:TYR:CE1	2.51	0.46
3:A:371:ALA:HB2	3:A:462:VAL:HG12	1.97	0.46
3:A:957:PRO:O	3:A:958:VAL:HB	2.16	0.46
5:C:74:SER:CB	5:C:77:ILE:HG12	2.46	0.46
5:C:175:ALA:HB3	12:J:43:ARG:HH22	1.79	0.46
3:A:701:LEU:HD23	11:I:115:LYS:HG3	1.96	0.46
10:H:27:GLU:HA	10:H:38:LEU:O	2.15	0.46
3:A:986:ILE:CG2	3:A:987:VAL:N	2.76	0.46
6:D:154:PHE:CE2	6:D:163:VAL:HG21	2.50	0.46
4:B:563:MET:HE3	4:B:580:VAL:HB	1.96	0.46
3:A:787:PHE:CE1	3:A:796:SER:HA	2.51	0.46
3:A:211:PHE:HA	3:A:214:ILE:CG1	2.46	0.46
6:D:219:THR:HG22	6:D:220:LEU:N	2.30	0.46
2:T:6:C:H2'	2:T:7:G:O4'	2.16	0.46
4:B:973:ILE:HG23	4:B:974:PRO:HD2	1.98	0.46
9:G:48:VAL:HG13	9:G:74:TYR:CD1	2.49	0.46
5:C:234:SER:HB2	5:C:240:VAL:HG13	1.98	0.46
4:B:616:ILE:HG23	4:B:700:SER:OG	2.15	0.46
3:A:562:THR:HA	3:A:563:PRO:HD3	1.82	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:676:MET:O	3:A:679:ILE:HB	2.16	0.46
3:A:683:ILE:HG21	3:A:801:GLU:CG	2.45	0.46
4:B:957:ASN:O	4:B:958:GLN:C	2.54	0.46
4:B:240:ILE:HG23	4:B:240:ILE:O	2.14	0.46
4:B:344:LYS:O	4:B:346:GLU:N	2.48	0.46
3:A:377:PRO:HD3	3:A:493:GLN:OE1	2.15	0.46
6:D:40:HIS:CG	6:D:41:GLN:N	2.83	0.46
12:J:45:CYS:O	12:J:48:ARG:HG3	2.15	0.46
4:B:280:ILE:HD13	4:B:334:ILE:HG12	1.98	0.46
3:A:899:VAL:CB	3:A:929:LEU:HD11	2.39	0.46
3:A:701:LEU:CD2	11:I:115:LYS:HG3	2.45	0.46
9:G:18:PHE:HZ	9:G:68:ALA:HB2	1.81	0.46
6:D:144:THR:HG21	9:G:46:LEU:HD13	1.98	0.46
4:B:189:LEU:HD12	4:B:196:PRO:HA	1.97	0.46
3:A:1345:ARG:HG3	3:A:1376:THR:CG2	2.39	0.46
4:B:212:LEU:HD21	4:B:461:LEU:HG	1.98	0.46
3:A:1279:ILE:CD1	3:A:1316:VAL:HG21	2.46	0.46
3:A:230:ARG:HB2	3:A:233:TRP:CE3	2.51	0.46
4:B:378:LEU:C	4:B:378:LEU:HD12	2.34	0.46
3:A:768:GLN:HG2	3:A:816:HIS:CA	2.42	0.46
14:L:30:ILE:HD11	14:L:59:ALA:HB2	1.98	0.46
7:E:92:THR:O	7:E:95:THR:HB	2.15	0.46
4:B:343:ILE:HG21	4:B:348:ARG:N	2.30	0.46
10:H:95:TYR:CE2	10:H:97:MET:HG3	2.51	0.46
10:H:59:ILE:O	10:H:60:ALA:HB3	2.16	0.46
5:C:242:GLN:C	5:C:244:VAL:N	2.69	0.46
14:L:61:THR:HG21	14:L:63:ARG:CG	2.46	0.46
7:E:90:VAL:O	7:E:93:MET:HB3	2.16	0.46
3:A:241:VAL:HG13	3:A:266:LEU:HD13	1.97	0.46
3:A:302:THR:HA	3:A:305:ASP:O	2.16	0.46
9:G:44:TYR:O	9:G:78:VAL:HG12	2.16	0.46
3:A:65:LEU:O	3:A:66:LYS:O	2.34	0.46
12:J:56:LEU:O	12:J:57:ILE:C	2.55	0.46
4:B:376:PHE:CE2	4:B:569:TYR:HD2	2.34	0.46
3:A:1116:LEU:CD1	3:A:1118:VAL:HG13	2.45	0.46
3:A:1325:THR:OG1	7:E:146:HIS:O	2.27	0.46
9:G:22:MET:O	9:G:23:LYS:C	2.54	0.46
3:A:269:ILE:CG2	3:A:300:VAL:HG22	2.46	0.46
7:E:17:ARG:O	7:E:20:LYS:HB2	2.16	0.46
4:B:96:TYR:N	4:B:129:PHE:O	2.39	0.46
4:B:185:THR:O	4:B:186:GLU:C	2.54	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:179:GLN:HB2	7:E:182:ASP:HB2	1.97	0.46
7:E:90:VAL:HG23	7:E:120:ALA:HA	1.97	0.46
4:B:834:ASN:O	4:B:838:SER:O	2.34	0.46
6:D:185:CYS:HB2	6:D:211:LEU:CD2	2.46	0.46
5:C:160:LYS:O	5:C:161:LYS:O	2.34	0.46
5:C:133:ILE:HD13	5:C:236:GLY:C	2.37	0.46
12:J:6:ARG:HG2	12:J:13:VAL:HA	1.98	0.46
12:J:2:ILE:HG22	12:J:3:VAL:O	2.16	0.46
3:A:900:ASP:HA	3:A:926:GLN:NE2	2.31	0.46
6:D:56:ARG:CA	6:D:148:LEU:HD13	2.45	0.46
3:A:710:LEU:HD12	3:A:710:LEU:N	2.29	0.46
3:A:308:ILE:HG22	3:A:309:ALA:N	2.20	0.46
4:B:1151:LEU:CD1	4:B:1151:LEU:N	2.78	0.46
4:B:758:PHE:HZ	4:B:1031:LEU:HD22	1.81	0.46
3:A:84:ILE:O	3:A:84:ILE:CG2	2.64	0.46
3:A:115:LEU:HB2	3:A:122:MET:HE2	1.97	0.46
3:A:219:PHE:O	3:A:222:LEU:O	2.34	0.46
5:C:256:ALA:O	5:C:259:LEU:N	2.47	0.46
14:L:27:LEU:HD23	14:L:27:LEU:N	2.30	0.46
10:H:44:VAL:O	10:H:44:VAL:HG12	2.16	0.46
5:C:2:SER:N	5:C:3:GLU:O	2.49	0.46
3:A:418:SER:C	3:A:420:ARG:N	2.69	0.46
11:I:19:ASP:OD1	11:I:22:ASN:HB2	2.16	0.46
5:C:22:LEU:HD13	5:C:230:MET:HE1	1.96	0.45
4:B:798:TYR:CE2	5:C:62:PHE:HE2	2.30	0.45
5:C:67:LEU:HD11	5:C:155:LEU:HD13	1.98	0.45
3:A:883:LEU:CD2	3:A:1021:LEU:HB2	2.46	0.45
3:A:728:LYS:HA	3:A:731:ARG:HB2	1.98	0.45
4:B:860:MET:HG2	4:B:861:ASP:N	2.31	0.45
3:A:335:ARG:NH1	4:B:1202:LEU:HD22	2.31	0.45
5:C:254:LYS:O	5:C:256:ALA:N	2.49	0.45
5:C:104:PHE:HD2	5:C:105:GLY:N	2.14	0.45
3:A:852:TYR:HA	3:A:1060:PRO:HB3	1.97	0.45
4:B:570:VAL:HG23	4:B:573:GLN:HB3	1.98	0.45
6:D:195:ILE:HB	6:D:198:LEU:CD1	2.46	0.45
11:I:70:ARG:HA	11:I:83:ASN:O	2.15	0.45
3:A:425:GLN:N	3:A:425:GLN:OE1	2.49	0.45
4:B:827:ILE:HD12	4:B:1086:PHE:CD2	2.51	0.45
4:B:827:ILE:HD12	4:B:1086:PHE:HD2	1.81	0.45
4:B:880:THR:O	4:B:880:THR:HG22	2.17	0.45
4:B:283:VAL:O	4:B:286:PHE:N	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:7:SER:OG	4:B:1193:GLN:NE2	2.50	0.45
11:I:53:GLY:C	11:I:55:THR:N	2.70	0.45
6:D:175:PHE:O	6:D:179:GLN:HG2	2.16	0.45
5:C:11:ARG:NH2	5:C:229:TYR:HB3	2.31	0.45
5:C:40:GLU:HA	5:C:163:ILE:HG22	1.98	0.45
7:E:48:ASP:CG	7:E:49:SER:N	2.68	0.45
7:E:178:ILE:CD1	7:E:185:ALA:HB2	2.47	0.45
3:A:116:ASP:C	3:A:118:HIS:N	2.66	0.45
3:A:964:ILE:O	3:A:967:ALA:HB3	2.16	0.45
3:A:954:TRP:HB3	3:A:955:PRO:HD2	1.98	0.45
4:B:558:LEU:C	4:B:560:GLU:H	2.19	0.45
9:G:37:SER:OG	9:G:45:ILE:HB	2.16	0.45
4:B:579:ARG:HG2	4:B:579:ARG:HH11	1.81	0.45
3:A:901:LEU:O	3:A:921:GLY:N	2.35	0.45
4:B:1159:ARG:CD	4:B:1193:GLN:HE21	2.30	0.45
6:D:156:ASP:C	6:D:158:GLU:N	2.70	0.45
4:B:232:SER:CB	4:B:261:ARG:HH21	2.24	0.45
11:I:111:THR:CG2	11:I:112:SER:H	2.27	0.45
3:A:416:ARG:O	3:A:417:TYR:HD2	2.00	0.45
3:A:683:ILE:HG21	3:A:801:GLU:CD	2.36	0.45
13:K:110:ASN:O	13:K:111:LEU:HD23	2.17	0.45
11:I:68:LEU:HB3	11:I:84:VAL:HG23	1.98	0.45
3:A:1362:TYR:CD1	3:A:1363:VAL:N	2.84	0.45
3:A:33:ALA:CB	3:A:56:PRO:HB2	2.38	0.45
3:A:59:GLY:HA2	3:A:67:CYS:SG	2.56	0.45
6:D:8:PHE:HD1	6:D:8:PHE:O	1.99	0.45
3:A:919:ILE:HD13	3:A:983:ILE:HD12	1.97	0.45
12:J:64:ASN:HB3	12:J:65:PRO:HD2	1.90	0.45
4:B:401:PHE:HB2	4:B:517:THR:OG1	2.16	0.45
9:G:13:LEU:O	9:G:67:SER:HA	2.17	0.45
4:B:980:PHE:HE2	4:B:1094:ARG:HB2	1.81	0.45
14:L:58:LYS:O	14:L:59:ALA:O	2.34	0.45
4:B:25:ILE:HD11	4:B:653:VAL:C	2.36	0.45
11:I:101:PHE:HE1	11:I:112:SER:HB2	1.80	0.45
4:B:603:LEU:HB3	4:B:609:ILE:CD1	2.47	0.45
3:A:878:ILE:HG22	3:A:956:LEU:N	2.30	0.45
4:B:469:GLN:HB2	4:B:470:LYS:H	1.50	0.45
3:A:248:PRO:O	3:A:260:ASP:HB2	2.15	0.45
4:B:520:GLY:H	4:B:748:ILE:HG22	1.81	0.45
4:B:744:HIS:ND1	4:B:745:PRO:HD2	2.31	0.45
3:A:469:ARG:NH1	3:A:469:ARG:HB3	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:61:THR:CG2	14:L:63:ARG:HG2	2.47	0.45
4:B:979:LYS:HG2	4:B:1095:LEU:HD13	1.97	0.45
4:B:63:ILE:O	4:B:67:SER:HB3	2.16	0.45
4:B:95:ILE:CB	4:B:130:VAL:HG22	2.47	0.45
3:A:445:ASN:HB2	3:A:454:SER:O	2.17	0.45
4:B:780:VAL:HG12	4:B:782:LEU:O	2.17	0.45
4:B:265:SER:O	4:B:266:ALA:CB	2.65	0.45
4:B:118:ARG:HG2	4:B:204:ILE:HD13	1.98	0.45
4:B:1197:PRO:HG2	4:B:1200:ALA:HB2	1.99	0.45
3:A:961:ARG:HG2	3:A:965:GLN:HE21	1.81	0.45
3:A:967:ALA:O	3:A:968:GLN:O	2.35	0.45
3:A:21:LEU:HD11	3:A:1414:ALA:HA	1.98	0.45
3:A:634:THR:HG1	3:A:642:CYS:HG	1.63	0.45
3:A:150:THR:HG22	3:A:150:THR:O	2.16	0.45
8:F:147:SER:OG	8:F:150:GLU:HG3	2.16	0.45
5:C:45:ALA:HA	5:C:72:LEU:HD12	1.97	0.45
5:C:16:ASP:O	5:C:17:ASN:CG	2.55	0.45
10:H:43:ASN:OD1	10:H:46:LEU:HG	2.17	0.45
3:A:774:ARG:NH2	3:A:797:LYS:CG	2.78	0.45
4:B:542:MET:CE	4:B:743:ILE:HG13	2.47	0.45
7:E:19:VAL:HG11	7:E:80:VAL:HG11	1.98	0.45
3:A:590:ARG:HH11	3:A:590:ARG:CG	2.29	0.45
9:G:101:VAL:HG12	9:G:102:GLN:N	2.31	0.45
13:K:50:LEU:HD11	13:K:75:ILE:CD1	2.47	0.45
4:B:1034:VAL:O	4:B:1036:ALA:N	2.50	0.45
3:A:185:TRP:HZ3	3:A:200:ARG:HG2	1.81	0.45
3:A:1410:PHE:C	3:A:1412:ALA:H	2.20	0.45
3:A:317:LYS:O	3:A:318:SER:HB3	2.17	0.45
3:A:374:LEU:HD13	3:A:491:VAL:CG2	2.47	0.45
3:A:695:LYS:C	3:A:697:ALA:H	2.20	0.45
10:H:106:GLU:O	10:H:108:SER:N	2.50	0.45
5:C:56:THR:HG22	5:C:57:VAL:H	1.81	0.45
9:G:138:THR:CG2	9:G:139:ILE:N	2.62	0.45
4:B:806:THR:CG2	4:B:808:ALA:HB3	2.47	0.45
7:E:31:THR:O	7:E:35:VAL:HG23	2.16	0.45
4:B:55:VAL:CG1	4:B:97:VAL:HG21	2.47	0.45
3:A:1438:THR:HG23	8:F:92:ARG:HB2	1.99	0.45
3:A:586:ILE:HD11	3:A:633:VAL:HA	1.99	0.45
3:A:399:HIS:O	3:A:400:PRO:C	2.53	0.45
9:G:1:MET:CE	9:G:1:MET:O	2.64	0.45
4:B:980:PHE:CE2	4:B:1094:ARG:HG3	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:24:PRO:HB3	3:A:237:THR:HB	1.99	0.45
3:A:427:GLN:O	3:A:428:TYR:C	2.52	0.45
4:B:758:PHE:HB2	4:B:1024:ALA:HB1	1.98	0.45
3:A:107:CYS:SG	3:A:171:GLN:HG2	2.57	0.45
3:A:547:LEU:HD22	13:K:58:PHE:HE1	1.80	0.45
3:A:1265:ASN:O	3:A:1268:LEU:N	2.48	0.45
4:B:1130:PHE:HZ	4:B:1138:MET:HG2	1.82	0.45
4:B:226:PHE:CD1	4:B:398:ARG:NH2	2.84	0.45
7:E:14:ARG:HH21	7:E:141:VAL:HG12	1.82	0.45
6:D:155:ARG:O	6:D:155:ARG:HG2	2.15	0.45
6:D:64:VAL:C	6:D:66:ARG:N	2.70	0.45
10:H:128:ASN:CG	10:H:128:ASN:O	2.55	0.45
3:A:353:ILE:HG21	3:A:487:MET:HG3	1.98	0.45
4:B:1045:SER:HB3	4:B:1046:PRO:HD2	1.99	0.45
4:B:30:SER:HB3	4:B:743:ILE:O	2.17	0.45
3:A:578:LEU:HD23	3:A:612:ILE:HD11	1.99	0.45
8:F:103:MET:HE1	9:G:65:ASP:HB2	1.99	0.45
4:B:799:PRO:CB	4:B:818:PRO:HG2	2.43	0.45
4:B:860:MET:HG2	4:B:861:ASP:H	1.81	0.45
7:E:124:VAL:HG13	7:E:132:ILE:CB	2.45	0.45
8:F:97:ARG:HA	8:F:97:ARG:HD2	1.82	0.45
3:A:1265:ASN:C	3:A:1267:MET:N	2.68	0.45
9:G:38:CYS:HB3	9:G:155:SER:HA	1.97	0.45
3:A:1389:PHE:C	3:A:1389:PHE:CD1	2.90	0.45
3:A:57:ARG:O	3:A:68:GLN:HG3	2.16	0.45
3:A:78:PRO:HA	4:B:1201:LYS:NZ	2.32	0.45
6:D:67:ARG:CB	6:D:133:THR:HG21	2.45	0.45
4:B:879:ARG:HH11	4:B:883:LEU:CD2	2.20	0.45
3:A:853:ASP:C	3:A:853:ASP:OD1	2.56	0.45
3:A:1341:ILE:CG2	3:A:1342:GLU:N	2.79	0.45
3:A:844:ALA:C	3:A:845:LEU:HD23	2.36	0.45
3:A:560:ILE:HG13	10:H:78:SER:CB	2.40	0.45
8:F:125:LEU:HB2	8:F:130:ILE:CD1	2.47	0.45
13:K:61:TYR:O	13:K:61:TYR:CD2	2.69	0.45
9:G:50:ASP:O	9:G:51:TYR:C	2.54	0.45
3:A:347:PHE:N	3:A:347:PHE:CD1	2.85	0.45
7:E:112:TYR:CZ	7:E:136:ASN:HB2	2.52	0.45
3:A:657:LEU:HD12	3:A:657:LEU:O	2.16	0.45
3:A:1115:SER:OG	3:A:1116:LEU:N	2.50	0.45
10:H:127:GLY:O	10:H:128:ASN:CB	2.59	0.45
2:T:12:G:H4'	2:T:13:U:OP1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:53:HIS:O	14:L:55:ILE:HG12	2.16	0.45
7:E:31:THR:OG1	7:E:34:GLU:N	2.47	0.45
4:B:99:LYS:HB3	4:B:100:PRO:HD2	1.99	0.45
3:A:709:THR:CG2	3:A:710:LEU:N	2.80	0.45
11:I:55:THR:O	11:I:55:THR:HG22	2.16	0.45
3:A:1021:LEU:O	3:A:1024:SER:HB3	2.17	0.45
3:A:417:TYR:CD2	3:A:417:TYR:N	2.85	0.45
3:A:875:ALA:HA	3:A:878:ILE:HD11	1.98	0.45
4:B:1017:ILE:HB	4:B:1018:PRO:HD3	1.98	0.45
3:A:1299:VAL:CG1	3:A:1300:LYS:N	2.79	0.45
3:A:58:LEU:CD1	3:A:59:GLY:N	2.62	0.44
9:G:125:SER:OG	9:G:128:PRO:HA	2.16	0.44
4:B:953:LEU:O	4:B:953:LEU:HD23	2.17	0.44
4:B:1162:ILE:HG22	4:B:1163:CYS:N	2.31	0.44
7:E:151:PRO:CB	7:E:200:ARG:HB3	2.47	0.44
11:I:34:TYR:C	11:I:34:TYR:HD2	2.16	0.44
3:A:590:ARG:HD3	3:A:604:GLY:CA	2.45	0.44
3:A:93:VAL:HG21	3:A:301:ALA:O	2.17	0.44
8:F:86:THR:HG23	8:F:89:GLU:OE1	2.18	0.44
4:B:1182:CYS:O	4:B:1183:LYS:C	2.55	0.44
9:G:117:GLN:C	9:G:119:LEU:N	2.70	0.44
3:A:416:ARG:C	3:A:417:TYR:CD2	2.89	0.44
3:A:1385:THR:C	3:A:1387:HIS:N	2.69	0.44
9:G:20:PRO:HG2	9:G:21:ARG:N	2.32	0.44
3:A:1291:VAL:HG22	3:A:1292:PRO:CD	2.47	0.44
4:B:874:PHE:HA	4:B:913:GLY:O	2.16	0.44
4:B:1079:LYS:CA	5:C:27:LEU:HD21	2.47	0.44
4:B:471:LYS:O	4:B:472:ALA:HB2	2.17	0.44
9:G:48:VAL:HA	9:G:76:ALA:HB2	1.98	0.44
5:C:66:ARG:NH1	5:C:144:ILE:O	2.50	0.44
3:A:786:HIS:CD2	3:A:786:HIS:H	2.35	0.44
7:E:180:ARG:HH21	7:E:192:ARG:CB	2.20	0.44
3:A:341:MET:CE	4:B:1135:ARG:NH1	2.80	0.44
4:B:611:PRO:O	4:B:692:TYR:HB2	2.17	0.44
3:A:207:ILE:HG23	3:A:211:PHE:HE1	1.82	0.44
3:A:1293:SER:OG	3:A:1295:THR:HG23	2.17	0.44
6:D:119:ARG:HD3	6:D:221:TYR:CD2	2.53	0.44
3:A:262:LEU:C	3:A:264:PHE:N	2.71	0.44
4:B:128:LEU:HD11	4:B:170:LEU:CB	2.48	0.44
13:K:12:LEU:HD12	13:K:12:LEU:N	2.32	0.44
3:A:418:SER:O	3:A:420:ARG:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:10:ASN:OD1	9:G:71:ASN:HA	2.18	0.44
3:A:717:ASN:HA	3:A:720:ARG:HH12	1.81	0.44
3:A:1219:THR:HG21	3:A:1271:ILE:CD1	2.47	0.44
9:G:153:GLN:HG2	9:G:154:VAL:HG23	1.97	0.44
5:C:87:PHE:CD1	5:C:87:PHE:N	2.86	0.44
5:C:87:PHE:HD1	5:C:87:PHE:H	1.65	0.44
4:B:339:THR:HG22	4:B:339:THR:O	2.16	0.44
3:A:34:LYS:HG2	3:A:57:ARG:NH2	2.32	0.44
3:A:1445:ILE:HG12	9:G:18:PHE:HE2	1.83	0.44
10:H:40:LEU:HB2	10:H:123:MET:HG3	1.98	0.44
9:G:126:ASN:HA	9:G:126:ASN:HD22	1.60	0.44
3:A:543:LEU:N	3:A:572:TRP:HZ3	2.15	0.44
3:A:1072:ILE:O	3:A:1075:PRO:HG2	2.17	0.44
4:B:1095:LEU:HD12	4:B:1095:LEU:N	2.25	0.44
3:A:343:LYS:NZ	4:B:1151:LEU:O	2.41	0.44
4:B:1165:ILE:HG22	4:B:1166:CYS:N	2.32	0.44
3:A:693:VAL:HA	3:A:696:GLU:HB3	2.00	0.44
3:A:829:VAL:C	3:A:831:THR:N	2.70	0.44
3:A:806:ARG:HD3	4:B:728:ARG:HA	1.99	0.44
4:B:833:TYR:N	4:B:833:TYR:HD1	2.15	0.44
9:G:110:VAL:HG22	9:G:161:GLY:O	2.16	0.44
3:A:406:ILE:HG13	3:A:431:LYS:HB2	2.00	0.44
5:C:69:LEU:N	5:C:69:LEU:CD1	2.81	0.44
5:C:35:ARG:HH11	13:K:41:THR:N	2.13	0.44
11:I:98:VAL:HG12	11:I:99:LEU:N	2.33	0.44
4:B:205:ILE:N	4:B:205:ILE:CD1	2.74	0.44
4:B:94:LYS:HG2	4:B:95:ILE:N	2.32	0.44
3:A:310:GLY:C	3:A:312:PRO:HD2	2.38	0.44
4:B:834:ASN:HB3	4:B:840:ILE:HG13	1.98	0.44
5:C:90:ASP:O	5:C:91:HIS:HB3	2.17	0.44
3:A:608:ILE:HG13	3:A:613:ILE:HD12	1.99	0.44
7:E:186:LEU:O	7:E:189:GLY:N	2.50	0.44
1:P:13:A:O2'	1:P:14:G:H5'	2.18	0.44
3:A:415:LEU:HA	3:A:415:LEU:HD23	1.80	0.44
5:C:44:LEU:HD21	5:C:159:ALA:HB1	1.99	0.44
4:B:562:GLY:HA3	4:B:590:HIS:CE1	2.52	0.44
11:I:12:ASN:HB3	11:I:13:MET:H	1.55	0.44
6:D:47:LEU:HD11	9:G:3:PHE:HD2	1.81	0.44
9:G:106:MET:HB3	9:G:106:MET:HE2	1.90	0.44
7:E:42:PHE:CE1	7:E:58:MET:HE3	2.53	0.44
4:B:234:ILE:HG21	4:B:237:VAL:CG2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:124:VAL:CG1	7:E:132:ILE:HD12	2.43	0.44
5:C:8:VAL:O	5:C:9:LYS:HG3	2.17	0.44
4:B:1116:ARG:HD2	4:B:1198:TYR:CD1	2.53	0.44
14:L:28:LYS:HB2	14:L:39:SER:CB	2.48	0.44
4:B:957:ASN:HD22	4:B:961:LEU:HD12	1.83	0.44
3:A:1213:GLY:O	3:A:1214:GLU:C	2.56	0.44
3:A:1409:LEU:HD13	4:B:1207:LEU:CD2	2.48	0.44
7:E:182:ASP:OD1	7:E:183:PRO:HD2	2.17	0.44
3:A:31:SER:OG	3:A:82:GLY:HA2	2.18	0.44
9:G:154:VAL:HG12	9:G:155:SER:N	2.32	0.44
5:C:193:TYR:HD2	5:C:197:SER:HB3	1.83	0.44
3:A:108:MET:O	3:A:109:HIS:HB2	2.18	0.44
4:B:882:THR:O	4:B:883:LEU:HB2	2.17	0.44
3:A:1116:LEU:HD12	3:A:1116:LEU:C	2.38	0.44
3:A:1445:ILE:HG21	9:G:18:PHE:CD2	2.53	0.44
10:H:89:LEU:HB3	10:H:91:ASP:OD1	2.18	0.44
3:A:1436:ILE:HD11	4:B:1139:ILE:HG23	2.00	0.44
4:B:1001:PHE:CD1	4:B:1001:PHE:C	2.91	0.44
4:B:401:PHE:HA	4:B:404:LYS:HG3	1.99	0.44
11:I:78:CYS:SG	11:I:106:CYS:HB3	2.58	0.44
3:A:1226:VAL:HG13	3:A:1239:ARG:O	2.17	0.44
9:G:20:PRO:CG	9:G:21:ARG:H	2.31	0.44
10:H:99:GLY:N	10:H:118:PHE:CD2	2.86	0.44
3:A:889:SER:HB3	3:A:1297:GLU:HG2	1.99	0.44
4:B:387:LEU:O	4:B:392:ARG:HB2	2.17	0.44
6:D:8:PHE:CE2	9:G:6:ASP:O	2.71	0.44
3:A:600:PRO:HA	10:H:25:ARG:NH2	2.32	0.44
10:H:4:THR:HG22	10:H:5:LEU:H	1.83	0.44
3:A:719:VAL:O	3:A:721:PHE:N	2.50	0.44
3:A:1345:ARG:HD2	3:A:1373:ASP:OD1	2.17	0.44
3:A:867:ILE:N	3:A:867:ILE:HD12	2.32	0.44
3:A:738:LYS:CD	3:A:740:LEU:HD21	2.46	0.44
3:A:821:ARG:HD2	3:A:825:ILE:CD1	2.47	0.44
5:C:254:LYS:C	5:C:256:ALA:N	2.70	0.44
3:A:818:MET:N	4:B:514:LEU:HD23	2.33	0.44
13:K:55:LYS:HB3	13:K:81:TYR:CE1	2.52	0.44
6:D:51:ASN:O	6:D:52:LEU:C	2.56	0.44
4:B:1106:ARG:HH21	4:B:1111:MET:HE1	1.82	0.44
4:B:1207:LEU:HB3	4:B:1212:ILE:HG22	2.00	0.44
4:B:766:ARG:HD3	4:B:766:ARG:HA	1.69	0.44
3:A:1209:MET:SD	3:A:1236:LEU:HD22	2.57	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:82:ASP:O	13:K:85:ASP:HB2	2.18	0.44
10:H:142:LEU:C	10:H:143:LEU:HD12	2.37	0.44
10:H:12:VAL:HB	10:H:52:GLN:N	2.33	0.44
12:J:41:LEU:HD23	12:J:41:LEU:N	2.33	0.44
3:A:1011:GLN:HE21	3:A:1015:VAL:HG21	1.83	0.44
13:K:68:PHE:CD2	13:K:68:PHE:N	2.83	0.44
3:A:986:ILE:HD12	3:A:1032:LEU:HD11	1.99	0.44
3:A:442:VAL:O	3:A:457:ALA:HA	2.18	0.44
3:A:332:LYS:C	3:A:334:GLY:H	2.20	0.44
3:A:382:PRO:HD3	3:A:428:TYR:HD2	1.83	0.44
3:A:14:VAL:HG21	4:B:1216:LEU:CD1	2.48	0.44
3:A:896:ARG:HB3	3:A:897:TYR:CD1	2.53	0.44
4:B:298:LEU:N	4:B:298:LEU:HD22	2.33	0.44
4:B:408:LEU:HA	4:B:408:LEU:HD12	1.75	0.44
3:A:224:PHE:CZ	3:A:234:MET:HE2	2.52	0.44
3:A:1191:TRP:HB3	3:A:1260:LEU:HD23	2.00	0.44
7:E:169:ARG:HB3	8:F:140:ASP:OD2	2.17	0.44
3:A:1410:PHE:HA	4:B:1212:ILE:HD11	2.00	0.44
4:B:199:MET:N	4:B:199:MET:SD	2.88	0.44
3:A:608:ILE:C	3:A:610:GLY:H	2.21	0.44
5:C:26:ASP:O	5:C:27:LEU:C	2.56	0.44
4:B:274:PRO:O	4:B:275:TYR:HB2	2.18	0.44
3:A:42:ASP:HB3	3:A:45:GLN:N	2.33	0.43
5:C:113:VAL:O	5:C:144:ILE:N	2.50	0.43
5:C:98:VAL:CG2	5:C:122:SER:HB3	2.48	0.43
12:J:1:MET:HG3	12:J:1:MET:O	2.17	0.43
3:A:621:THR:HG22	3:A:621:THR:O	2.18	0.43
7:E:168:TYR:HB2	7:E:170:LEU:HG	2.00	0.43
4:B:515:HIS:HD2	4:B:516:ASN:N	2.14	0.43
13:K:10:PHE:HA	13:K:37:LYS:HB3	2.00	0.43
13:K:7:PHE:CD1	13:K:7:PHE:C	2.91	0.43
3:A:164:ARG:CG	3:A:165:GLY:H	2.12	0.43
13:K:43:GLY:HA3	13:K:61:TYR:CE1	2.53	0.43
4:B:1166:CYS:SG	4:B:1168:LEU:HD12	2.57	0.43
3:A:897:TYR:CD1	3:A:897:TYR:N	2.86	0.43
3:A:285:PRO:CG	3:A:288:ALA:HB3	2.44	0.43
7:E:178:ILE:HG22	7:E:213:ILE:O	2.18	0.43
14:L:40:LEU:HD22	14:L:44:ASP:HB3	1.99	0.43
3:A:1225:PHE:CE2	3:A:1227:ILE:HD11	2.52	0.43
3:A:805:LEU:HD11	4:B:1052:VAL:HG21	1.98	0.43
3:A:814:PHE:O	3:A:817:ALA:HB3	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:129:PRO:O	7:E:130:ALA:C	2.57	0.43
8:F:72:LYS:O	8:F:142:SER:HA	2.18	0.43
4:B:210:LYS:HE2	4:B:462:ALA:HA	2.00	0.43
5:C:131:HIS:HA	5:C:132:PRO:HD3	1.89	0.43
6:D:8:PHE:CE1	6:D:37:GLN:HB2	2.53	0.43
9:G:34:VAL:HG11	9:G:74:TYR:CE1	2.54	0.43
5:C:101:LEU:HA	5:C:101:LEU:HD12	1.79	0.43
5:C:113:VAL:HG23	5:C:147:LEU:HD21	1.99	0.43
4:B:593:PRO:HG2	4:B:617:ARG:NH2	2.33	0.43
5:C:242:GLN:C	5:C:244:VAL:H	2.20	0.43
4:B:1115:THR:CG2	4:B:1117:GLN:HG3	2.43	0.43
3:A:514:PRO:CB	3:A:875:ALA:HB3	2.47	0.43
3:A:1076:ALA:HA	3:A:1079:MET:HE3	2.00	0.43
3:A:279:LEU:O	3:A:284:ALA:HB2	2.17	0.43
3:A:1147:THR:O	11:I:48:LEU:HD12	2.18	0.43
4:B:1197:PRO:O	4:B:1200:ALA:N	2.48	0.43
3:A:523:ILE:CD1	3:A:649:ILE:HG21	2.48	0.43
4:B:769:TYR:O	4:B:771:SER:N	2.51	0.43
3:A:966:ASN:O	3:A:967:ALA:C	2.56	0.43
4:B:497:ARG:NH2	4:B:775:LYS:NZ	2.66	0.43
3:A:1151:GLU:HA	11:I:44:TYR:O	2.17	0.43
6:D:40:HIS:HB2	9:G:73:LYS:HZ2	1.83	0.43
3:A:1153:TYR:CE1	11:I:42:LEU:HD13	2.54	0.43
10:H:82:PRO:C	10:H:84:ALA:H	2.21	0.43
11:I:7:CYS:HB2	11:I:34:TYR:CD1	2.53	0.43
3:A:858:ASN:ND2	3:A:861:GLY:H	2.15	0.43
12:J:41:LEU:HD11	12:J:50:ILE:HG13	2.00	0.43
4:B:996:ARG:HG2	4:B:1007:VAL:HG11	1.99	0.43
3:A:546:VAL:HA	3:A:549:MET:HE2	1.99	0.43
4:B:309:GLN:CG	11:I:52:ILE:HD11	2.48	0.43
4:B:773:MET:HB3	4:B:1095:LEU:HD23	2.01	0.43
3:A:18:GLN:HB2	4:B:1215:ARG:CB	2.47	0.43
4:B:756:ILE:O	4:B:759:PRO:HD3	2.19	0.43
4:B:95:ILE:HB	4:B:130:VAL:HG22	2.00	0.43
4:B:1156:ASP:HB3	4:B:1198:TYR:H	1.84	0.43
14:L:34:CYS:O	14:L:35:SER:C	2.57	0.43
3:A:218:ASP:O	3:A:219:PHE:C	2.57	0.43
4:B:278:GLN:HG2	4:B:279:ASP:N	2.33	0.43
8:F:81:THR:HB	8:F:136:ARG:HH11	1.83	0.43
3:A:278:THR:O	3:A:282:ASN:HB2	2.18	0.43
3:A:965:GLN:HA	3:A:968:GLN:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:147:HIS:CD2	7:E:149:LEU:H	2.36	0.43
3:A:244:PRO:CG	3:A:245:PRO:CD	2.92	0.43
3:A:58:LEU:O	3:A:59:GLY:O	2.37	0.43
5:C:82:TYR:O	5:C:83:SER:C	2.56	0.43
12:J:3:VAL:CG2	12:J:18:TRP:CG	3.02	0.43
3:A:753:GLY:HA2	3:A:757:ASN:ND2	2.33	0.43
4:B:542:MET:SD	4:B:747:MET:HE2	2.59	0.43
4:B:1001:PHE:HD2	5:C:34:ARG:NH2	2.14	0.43
3:A:560:ILE:CG1	10:H:78:SER:HB2	2.39	0.43
3:A:351:THR:CB	4:B:1103:ILE:HD12	2.46	0.43
3:A:1095:THR:OG1	3:A:1113:THR:HB	2.19	0.43
3:A:1409:LEU:HA	3:A:1409:LEU:HD23	1.87	0.43
3:A:1410:PHE:HA	4:B:1212:ILE:CD1	2.48	0.43
4:B:885:MET:HA	4:B:936:ASP:CB	2.47	0.43
7:E:149:LEU:HD23	7:E:149:LEU:N	2.33	0.43
3:A:86:LEU:HD12	3:A:236:LEU:O	2.18	0.43
12:J:53:HIS:CD2	12:J:54:VAL:N	2.86	0.43
6:D:20:GLU:HA	6:D:20:GLU:OE2	2.19	0.43
7:E:94:LYS:CE	7:E:98:ILE:HD11	2.26	0.43
4:B:221:ASN:OD1	4:B:242:SER:HA	2.18	0.43
4:B:102:VAL:O	4:B:109:THR:HA	2.18	0.43
4:B:114:PRO:HG2	4:B:115:GLN:N	2.28	0.43
3:A:1011:GLN:O	3:A:1015:VAL:HG23	2.19	0.43
3:A:401:GLY:C	3:A:435:HIS:CD2	2.89	0.43
13:K:10:PHE:CD1	13:K:11:LEU:CD2	3.01	0.43
3:A:1349:TYR:O	3:A:1350:LYS:C	2.56	0.43
7:E:204:THR:HG23	7:E:205:SER:N	2.34	0.43
4:B:53:GLN:HG2	4:B:547:VAL:CG2	2.45	0.43
4:B:351:TYR:CD1	4:B:355:ILE:HD11	2.54	0.43
4:B:46:GLN:OE1	4:B:47:GLN:HG2	2.19	0.43
4:B:977:GLY:HA3	4:B:1099:VAL:HB	2.01	0.43
4:B:303:TYR:N	4:B:303:TYR:CD2	2.86	0.43
10:H:48:PRO:O	10:H:49:VAL:CG2	2.66	0.43
3:A:806:ARG:HH12	4:B:729:ILE:HD12	1.83	0.43
4:B:383:ASN:O	4:B:384:ARG:C	2.57	0.43
5:C:12:GLU:O	5:C:13:ALA:HB2	2.18	0.43
3:A:1162:VAL:HG12	3:A:1162:VAL:O	2.17	0.43
3:A:667:GLY:HA3	5:C:192:TRP:CH2	2.54	0.43
3:A:1285:MET:O	3:A:1304:TRP:HA	2.18	0.43
3:A:1311:VAL:HG11	3:A:1329:THR:HG21	1.99	0.43
4:B:97:VAL:HG12	4:B:178:ASN:ND2	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:225:VAL:HG11	4:B:385:LEU:HA	2.01	0.43
3:A:17:VAL:HA	4:B:1215:ARG:O	2.18	0.43
5:C:8:VAL:CG1	5:C:9:LYS:N	2.80	0.43
3:A:1171:GLN:HA	3:A:1174:PHE:CE1	2.54	0.43
3:A:1315:GLU:C	3:A:1317:MET:N	2.70	0.43
7:E:178:ILE:HD11	7:E:185:ALA:HB2	2.01	0.43
4:B:29:ASP:HB3	4:B:658:ILE:CD1	2.49	0.43
3:A:325:ILE:HG22	4:B:1210:MET:HE1	2.00	0.43
4:B:519:TRP:HE1	4:B:635:ARG:NH2	2.16	0.43
3:A:247:ARG:HG3	3:A:247:ARG:O	2.18	0.43
4:B:383:ASN:O	4:B:387:LEU:HD13	2.18	0.43
3:A:402:ALA:CB	3:A:434:ARG:HA	2.49	0.43
4:B:1074:ASN:HB2	4:B:1081:LEU:CD2	2.49	0.43
5:C:22:LEU:HD13	5:C:230:MET:HE3	2.00	0.43
3:A:1118:VAL:HG12	3:A:1327:ILE:CG1	2.43	0.43
13:K:49:GLU:OE2	13:K:97:LYS:HE3	2.19	0.43
4:B:700:SER:O	4:B:701:ILE:HG22	2.19	0.43
3:A:577:ILE:C	3:A:579:SER:N	2.71	0.43
3:A:604:GLY:O	3:A:605:MET:HB2	2.19	0.43
4:B:1159:ARG:NH1	4:B:1159:ARG:HB3	2.34	0.43
7:E:175:LEU:HD23	7:E:176:PRO:HD2	2.00	0.43
14:L:61:THR:CG2	14:L:63:ARG:CG	2.97	0.43
4:B:282:ILE:CD1	4:B:382:ILE:HD13	2.48	0.43
3:A:477:PRO:HG3	3:A:521:MET:HG2	1.98	0.43
10:H:2:SER:HA	10:H:62:SER:OG	2.19	0.43
11:I:101:PHE:HD1	11:I:101:PHE:H	1.66	0.43
6:D:4:SER:C	6:D:5:THR:HG22	2.39	0.43
3:A:818:MET:HG2	4:B:514:LEU:HG	2.01	0.43
3:A:647:GLY:O	3:A:651:LYS:HG3	2.19	0.43
4:B:1034:VAL:C	4:B:1036:ALA:N	2.71	0.43
6:D:119:ARG:HG2	6:D:120:GLU:H	1.81	0.43
3:A:369:SER:CB	13:K:2:ASN:OD1	2.67	0.43
7:E:72:PHE:CE2	7:E:155:ARG:NH2	2.87	0.43
3:A:50:ILE:HG22	3:A:52:GLY:N	2.33	0.43
3:A:567:LYS:HB3	10:H:95:TYR:CA	2.46	0.43
3:A:658:LEU:HD12	4:B:830:TYR:CD1	2.53	0.43
4:B:701:ILE:HD11	4:B:703:ILE:HD11	2.01	0.43
4:B:168:GLY:N	4:B:450:ALA:HB1	2.29	0.43
3:A:541:ILE:HD13	3:A:549:MET:HE3	2.00	0.43
4:B:839:MET:HG3	4:B:1010:LEU:HD11	2.01	0.43
7:E:42:PHE:O	7:E:43:LYS:C	2.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:1031:LEU:HD11	4:B:1042:GLY:CA	2.48	0.43
3:A:1193:LEU:HB2	3:A:1260:LEU:HD11	2.01	0.43
3:A:717:ASN:HA	3:A:720:ARG:NH1	2.34	0.43
3:A:89:PRO:HB2	3:A:204:THR:CG2	2.49	0.43
3:A:971:PHE:HE2	3:A:1040:GLN:HG2	1.83	0.43
3:A:1156:PRO:HA	3:A:1190:PRO:CB	2.49	0.43
3:A:302:THR:HG22	3:A:303:TYR:N	2.34	0.43
3:A:37:PHE:H	3:A:37:PHE:HD1	1.66	0.43
6:D:66:ARG:HD2	6:D:133:THR:HB	2.00	0.43
3:A:722:LEU:HD22	3:A:799:PHE:CG	2.54	0.43
3:A:535:THR:CG2	3:A:575:LYS:HE2	2.48	0.43
5:C:47:ASP:CA	14:L:69:ALA:HB3	2.36	0.43
11:I:99:LEU:C	11:I:100:PHE:HD1	2.21	0.43
4:B:980:PHE:CE2	4:B:1094:ARG:HB2	2.54	0.43
4:B:38:PHE:HD1	4:B:811:TYR:HD2	1.64	0.43
3:A:335:ARG:HH11	4:B:1202:LEU:HD13	1.82	0.43
4:B:758:PHE:N	4:B:759:PRO:CD	2.82	0.43
3:A:1066:VAL:HG11	4:B:1136:ASP:O	2.19	0.43
3:A:515:GLN:O	3:A:516:SER:HB3	2.18	0.43
5:C:120:ILE:CD1	5:C:124:LEU:HD11	2.48	0.43
3:A:1215:ARG:HH11	3:A:1215:ARG:HG2	1.83	0.43
3:A:208:LEU:C	3:A:208:LEU:HD23	2.39	0.43
4:B:1079:LYS:HA	5:C:27:LEU:HD21	2.01	0.43
3:A:184:SER:HB3	3:A:199:LEU:CD2	2.48	0.43
3:A:551:TYR:CE2	13:K:62:LYS:HG2	2.53	0.43
7:E:177:ARG:HD3	7:E:215:MET:HG3	2.01	0.43
3:A:765:VAL:HG23	3:A:802:ASN:O	2.18	0.43
4:B:597:MET:CE	4:B:597:MET:HA	2.49	0.43
4:B:1060:ARG:HD2	4:B:1060:ARG:HA	1.57	0.43
11:I:53:GLY:O	11:I:55:THR:N	2.52	0.43
8:F:93:ILE:HD13	8:F:148:VAL:HG12	2.01	0.43
5:C:252:GLN:HB2	13:K:98:LEU:HD13	2.01	0.43
3:A:866:PHE:O	3:A:867:ILE:HD12	2.19	0.43
4:B:764:SER:HB3	4:B:765:PRO:CD	2.49	0.43
5:C:8:VAL:CG1	5:C:9:LYS:H	2.27	0.43
3:A:527:THR:HG23	3:A:650:GLN:HA	2.00	0.43
8:F:111:LEU:H	8:F:111:LEU:CD1	2.29	0.43
4:B:412:LEU:HB3	4:B:466:TRP:CZ2	2.54	0.43
3:A:789:LYS:NZ	4:B:620:ARG:HH11	2.17	0.43
4:B:1065:GLN:NE2	4:B:1067:ARG:H	2.11	0.42
9:G:14:HIS:ND1	9:G:15:PRO:CD	2.77	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:470:LEU:HD22	3:A:487:MET:HE1	2.01	0.42
3:A:1424:VAL:HG11	4:B:1139:ILE:CD1	2.40	0.42
3:A:1004:ASN:HD21	3:A:1007:ILE:HG12	1.84	0.42
11:I:100:PHE:N	11:I:100:PHE:CD1	2.87	0.42
5:C:238:ILE:HD11	5:C:246:ARG:CZ	2.47	0.42
4:B:205:ILE:O	4:B:207:GLY:N	2.52	0.42
4:B:642:ASP:CA	4:B:649:LYS:HG3	2.48	0.42
3:A:939:ASP:O	3:A:940:ARG:C	2.58	0.42
14:L:40:LEU:HD13	14:L:44:ASP:CB	2.49	0.42
3:A:478:TYR:O	3:A:479:ASN:CB	2.65	0.42
3:A:1434:ALA:HA	3:A:1435:PRO:HD3	1.90	0.42
4:B:769:TYR:O	4:B:772:ALA:N	2.52	0.42
7:E:105:PHE:O	7:E:106:GLN:HB2	2.19	0.42
3:A:37:PHE:HB2	3:A:52:GLY:HA3	2.01	0.42
3:A:65:LEU:O	3:A:66:LYS:C	2.57	0.42
3:A:1163:ILE:HG22	3:A:1164:PRO:HD2	2.01	0.42
4:B:360:PHE:CD2	4:B:360:PHE:C	2.92	0.42
3:A:767:GLN:OE1	3:A:799:PHE:HB2	2.19	0.42
4:B:100:PRO:HB2	4:B:180:TYR:CE1	2.53	0.42
4:B:51:PHE:HE2	4:B:172:ILE:HG23	1.84	0.42
3:A:629:LEU:HD22	3:A:633:VAL:CG2	2.50	0.42
4:B:952:VAL:CG1	4:B:953:LEU:N	2.81	0.42
3:A:336:ILE:HG22	3:A:337:ARG:N	2.33	0.42
3:A:1191:TRP:CD1	3:A:1256:GLU:HB2	2.54	0.42
3:A:1280:GLU:O	3:A:1281:ARG:O	2.37	0.42
3:A:367:PRO:HB3	3:A:465:TYR:O	2.19	0.42
10:H:31:THR:O	10:H:31:THR:HG22	2.19	0.42
5:C:133:ILE:HD13	5:C:236:GLY:O	2.18	0.42
3:A:353:ILE:HD13	3:A:487:MET:CE	2.49	0.42
4:B:360:PHE:O	4:B:361:LEU:C	2.58	0.42
6:D:56:ARG:CB	6:D:148:LEU:HD22	2.36	0.42
4:B:515:HIS:CD2	4:B:517:THR:HG23	2.54	0.42
4:B:515:HIS:N	4:B:518:HIS:HD2	2.03	0.42
3:A:560:ILE:HG12	3:A:560:ILE:H	1.55	0.42
3:A:1239:ARG:HH22	3:A:1241:ARG:NH2	2.15	0.42
4:B:502:ILE:N	4:B:502:ILE:CD1	2.82	0.42
4:B:867:GLY:C	4:B:869:SER:H	2.22	0.42
7:E:157:SER:HG	7:E:160:GLU:HG3	1.82	0.42
3:A:172:PRO:HB3	3:A:185:TRP:CE2	2.54	0.42
3:A:1215:ARG:HA	3:A:1218:GLN:HE21	1.84	0.42
3:A:645:LEU:CD1	3:A:649:ILE:HG13	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:608:ILE:C	3:A:610:GLY:N	2.72	0.42
3:A:614:PHE:C	3:A:614:PHE:CD1	2.92	0.42
3:A:1280:GLU:O	3:A:1282:VAL:HG23	2.19	0.42
1:P:14:G:O2'	1:P:15:G:H5'	2.19	0.42
3:A:742:ASN:O	3:A:745:GLN:HB2	2.19	0.42
3:A:55:ASP:C	3:A:57:ARG:N	2.71	0.42
3:A:40:THR:C	3:A:41:MET:HG3	2.37	0.42
3:A:41:MET:HB2	3:A:42:ASP:H	1.39	0.42
5:C:69:LEU:HB3	12:J:6:ARG:CD	2.49	0.42
5:C:147:LEU:HA	12:J:61:LEU:HD21	2.01	0.42
3:A:894:GLU:HG3	3:A:933:TYR:OH	2.18	0.42
3:A:598:LEU:O	3:A:599:SER:C	2.57	0.42
10:H:84:ALA:HB1	10:H:87:ARG:HB2	1.98	0.42
3:A:1424:VAL:HG13	3:A:1436:ILE:HD12	2.02	0.42
3:A:577:ILE:HG13	3:A:578:LEU:N	2.33	0.42
4:B:467:GLY:CA	4:B:475:SER:HB3	2.48	0.42
6:D:29:LEU:HD23	6:D:29:LEU:N	2.33	0.42
3:A:896:ARG:HB3	3:A:897:TYR:HD1	1.84	0.42
4:B:1096:ARG:CG	4:B:1097:HIS:N	2.82	0.42
4:B:707:PRO:HG2	4:B:708:GLU:H	1.82	0.42
3:A:553:VAL:HG22	3:A:652:VAL:CG2	2.49	0.42
3:A:626:ASN:C	3:A:628:GLY:H	2.22	0.42
3:A:224:PHE:CD2	3:A:231:PRO:HD3	2.54	0.42
3:A:1394:THR:CG2	3:A:1398:MET:SD	3.06	0.42
7:E:149:LEU:O	7:E:151:PRO:HD3	2.19	0.42
4:B:259:TYR:HB2	4:B:268:THR:HG23	2.01	0.42
3:A:481:ASP:OD1	3:A:483:ASP:OD2	2.37	0.42
5:C:73:GLN:HB2	5:C:131:HIS:HB2	2.00	0.42
3:A:1164:PRO:HG2	3:A:1165:GLU:HG3	2.02	0.42
10:H:95:TYR:HE2	10:H:97:MET:CG	2.31	0.42
10:H:110:ASP:O	10:H:128:ASN:ND2	2.53	0.42
10:H:4:THR:O	10:H:5:LEU:HD23	2.19	0.42
3:A:1015:VAL:O	3:A:1016:THR:C	2.57	0.42
4:B:1010:LEU:HD12	4:B:1010:LEU:HA	1.74	0.42
3:A:332:LYS:HG3	3:A:333:GLU:CG	2.43	0.42
3:A:1332:PHE:HA	3:A:1335:ILE:HB	2.00	0.42
4:B:1167:GLY:O	4:B:1215:ARG:HA	2.20	0.42
9:G:117:GLN:O	9:G:119:LEU:N	2.53	0.42
3:A:120:GLU:C	3:A:122:MET:H	2.23	0.42
7:E:117:THR:C	7:E:119:SER:H	2.22	0.42
3:A:514:PRO:HB2	3:A:875:ALA:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:103:THR:HG22	13:K:104:ASN:N	2.34	0.42
3:A:977:LYS:HB3	3:A:978:PRO:HD2	2.00	0.42
9:G:83:LYS:HE2	9:G:150:CYS:H	1.84	0.42
3:A:362:ASP:OD2	3:A:459:ARG:HD3	2.19	0.42
4:B:455:SER:O	4:B:456:GLY:C	2.58	0.42
3:A:244:PRO:CB	3:A:245:PRO:HD3	2.49	0.42
6:D:67:ARG:CA	6:D:133:THR:HG21	2.49	0.42
4:B:578:THR:C	4:B:589:VAL:HG13	2.40	0.42
3:A:1161:THR:C	3:A:1163:ILE:H	2.22	0.42
4:B:377:PHE:HE1	4:B:581:PHE:HE2	1.66	0.42
3:A:780:VAL:O	3:A:780:VAL:HG12	2.19	0.42
14:L:53:HIS:HB3	14:L:55:ILE:HD11	2.01	0.42
4:B:1159:ARG:HD3	4:B:1193:GLN:CG	2.39	0.42
4:B:96:TYR:HE1	4:B:131:ASP:OD2	2.02	0.42
3:A:346:ASP:OD1	4:B:1108:ARG:HA	2.19	0.42
3:A:794:PRO:C	3:A:796:SER:N	2.73	0.42
10:H:62:SER:C	10:H:64:ASN:N	2.73	0.42
11:I:101:PHE:CE1	11:I:112:SER:HB2	2.55	0.42
5:C:114:TYR:CD2	5:C:140:ASN:HB2	2.55	0.42
13:K:111:LEU:O	13:K:112:GLN:CB	2.67	0.42
7:E:85:GLU:O	7:E:88:VAL:HG23	2.19	0.42
7:E:179:GLN:O	7:E:182:ASP:HB2	2.20	0.42
11:I:90:GLN:HE21	11:I:92:ARG:HB2	1.85	0.42
3:A:1444:MET:N	3:A:1444:MET:HE2	2.35	0.42
5:C:27:LEU:O	5:C:28:ALA:C	2.58	0.42
3:A:622:VAL:O	3:A:622:VAL:HG13	2.19	0.42
3:A:68:GLN:C	3:A:70:CYS:N	2.70	0.42
4:B:332:ASP:OD1	4:B:336:ARG:NE	2.53	0.42
6:D:39:ASN:ND2	6:D:41:GLN:NE2	2.60	0.42
5:C:18:VAL:O	5:C:19:ASP:C	2.58	0.42
12:J:7:CYS:SG	12:J:49:MET:CE	3.05	0.42
3:A:919:ILE:HD13	3:A:983:ILE:CD1	2.50	0.42
10:H:42:ILE:HG12	10:H:95:TYR:CE1	2.55	0.42
3:A:960:ILE:HA	3:A:963:ILE:CG2	2.50	0.42
6:D:179:GLN:NE2	6:D:179:GLN:HA	2.33	0.42
4:B:205:ILE:O	4:B:206:ASN:C	2.58	0.42
3:A:388:LEU:HD22	3:A:432:VAL:HB	2.01	0.42
8:F:118:LEU:HD12	8:F:118:LEU:O	2.20	0.42
8:F:94:LEU:HD21	8:F:122:MET:HA	2.02	0.42
3:A:154:SER:OG	3:A:162:VAL:HG21	2.20	0.42
13:K:88:LYS:O	13:K:91:CYS:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1385:THR:O	3:A:1387:HIS:N	2.52	0.42
4:B:1039:GLY:HA2	12:J:51:LEU:CD2	2.48	0.42
7:E:136:ASN:OD1	7:E:137:GLU:N	2.52	0.42
3:A:1265:ASN:O	3:A:1267:MET:N	2.53	0.42
11:I:2:THR:O	11:I:4:PHE:N	2.52	0.42
3:A:20:GLY:O	3:A:21:LEU:HD23	2.20	0.42
3:A:890:ASP:H	3:A:1296:GLY:HA3	1.84	0.42
6:D:118:THR:O	6:D:118:THR:HG22	2.20	0.42
3:A:1107:VAL:HG12	3:A:1107:VAL:O	2.19	0.42
6:D:7:THR:O	6:D:9:GLN:N	2.52	0.42
10:H:102:TYR:N	10:H:102:TYR:HD2	2.16	0.42
11:I:13:MET:HG3	11:I:14:LEU:N	2.34	0.42
3:A:870:GLU:HB2	7:E:204:THR:HG21	2.02	0.42
3:A:1059:HIS:ND1	8:F:86:THR:HA	2.33	0.42
4:B:911:ILE:HG22	4:B:966:VAL:HG21	2.02	0.42
3:A:652:VAL:O	3:A:653:VAL:C	2.58	0.42
3:A:453:MET:C	3:A:455:MET:H	2.23	0.42
4:B:854:LEU:HB3	4:B:856:PHE:HE1	1.85	0.42
4:B:293:PRO:C	4:B:294:ASP:O	2.58	0.42
5:C:250:THR:O	5:C:253:LYS:N	2.53	0.42
4:B:492:LEU:HD13	4:B:812:LEU:HD23	2.02	0.42
3:A:90:VAL:HG12	3:A:91:PHE:N	2.35	0.42
3:A:1339:LEU:HD13	7:E:147:HIS:CD2	2.54	0.42
4:B:356:LEU:O	4:B:374:LYS:NZ	2.48	0.42
4:B:31:TRP:CE3	4:B:34:ILE:HD12	2.54	0.42
3:A:664:THR:CG2	3:A:665:GLY:N	2.82	0.42
4:B:828:ALA:HB2	4:B:1085:ILE:HG23	2.01	0.42
5:C:46:ILE:HD13	5:C:157:CYS:SG	2.60	0.42
5:C:66:ARG:CZ	12:J:2:ILE:CG2	2.98	0.42
5:C:93:ASP:OD1	5:C:122:SER:HB2	2.20	0.42
10:H:107:VAL:HG21	10:H:126:GLU:OE2	2.20	0.42
4:B:1070:GLU:OE1	12:J:44:TYR:OH	2.37	0.42
3:A:605:MET:HG2	3:A:621:THR:HG21	2.01	0.42
3:A:354:SER:O	3:A:469:ARG:HA	2.19	0.42
3:A:883:LEU:HD11	3:A:1017:LEU:HD11	2.02	0.42
4:B:461:LEU:HD12	4:B:461:LEU:N	2.35	0.42
6:D:27:LEU:HD22	6:D:173:HIS:CD2	2.54	0.42
11:I:105:SER:O	11:I:106:CYS:CB	2.68	0.42
3:A:1279:ILE:HD11	3:A:1316:VAL:CG2	2.49	0.42
4:B:234:ILE:O	4:B:261:ARG:NH2	2.53	0.42
4:B:611:PRO:CB	4:B:685:LEU:HD21	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:114:LEU:O	3:A:115:LEU:HG	2.19	0.42
3:A:940:ARG:HG2	3:A:940:ARG:NH1	2.34	0.42
4:B:293:PRO:HG2	4:B:296:GLU:HB3	2.02	0.42
13:K:55:LYS:HB2	13:K:81:TYR:HE1	1.83	0.42
3:A:1154:TYR:HD1	3:A:1191:TRP:CH2	2.38	0.42
9:G:21:ARG:HD3	9:G:21:ARG:HA	1.79	0.42
3:A:1219:THR:CB	3:A:1271:ILE:HD11	2.50	0.42
3:A:1297:GLU:H	3:A:1297:GLU:HG3	1.56	0.42
3:A:1150:SER:O	3:A:1151:GLU:HG3	2.20	0.42
3:A:367:PRO:HA	3:A:463:ILE:O	2.20	0.42
4:B:449:ASN:C	4:B:451:LYS:H	2.23	0.42
5:C:174:ALA:O	12:J:10:CYS:HB2	2.19	0.42
5:C:191:TYR:CD2	5:C:201:TRP:CD1	3.00	0.42
3:A:1120:LEU:HD11	3:A:1305:VAL:HA	2.01	0.42
10:H:80:ARG:HA	10:H:81:PRO:HD3	1.87	0.42
3:A:1437:GLY:HA3	8:F:88:TYR:CD2	2.55	0.42
4:B:1002:THR:HG21	4:B:1006:ILE:HD12	2.01	0.42
3:A:532:ARG:HD3	3:A:749:ALA:HB2	2.02	0.42
4:B:582:VAL:HG23	4:B:626:ILE:CB	2.46	0.42
9:G:39:THR:CG2	9:G:40:GLY:H	2.18	0.42
3:A:1348:LEU:HD21	3:A:1375:MET:SD	2.60	0.42
4:B:307:ASP:O	4:B:308:TRP:C	2.57	0.42
5:C:6:PRO:HB3	5:C:25:VAL:CG1	2.40	0.42
3:A:1441:PHE:CZ	8:F:89:GLU:HA	2.55	0.42
3:A:979:SER:HG	3:A:980:ASP:H	1.66	0.42
3:A:1074:GLU:HB3	3:A:1075:PRO:CD	2.50	0.42
3:A:1226:VAL:HG22	3:A:1240:CYS:CB	2.49	0.42
4:B:603:LEU:HB3	4:B:609:ILE:HG13	2.01	0.42
14:L:40:LEU:HD22	14:L:44:ASP:CG	2.40	0.42
10:H:11:GLN:C	10:H:28:ALA:HB1	2.41	0.42
3:A:1260:LEU:CG	3:A:1260:LEU:O	2.68	0.42
6:D:24:ALA:C	6:D:26:THR:N	2.73	0.42
4:B:222:ILE:O	4:B:240:ILE:HA	2.19	0.42
10:H:83:GLN:O	10:H:85:GLY:N	2.51	0.42
4:B:383:ASN:C	4:B:387:LEU:HD13	2.40	0.42
3:A:370:ILE:O	3:A:373:THR:N	2.45	0.42
4:B:841:MET:SD	4:B:846:ILE:HD11	2.59	0.41
5:C:77:ILE:HD13	5:C:77:ILE:HA	1.84	0.41
4:B:376:PHE:HB3	4:B:586:TRP:CZ3	2.55	0.41
3:A:699:ALA:O	3:A:700:ASN:HB3	2.20	0.41
10:H:95:TYR:CE2	10:H:97:MET:CG	3.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:470:LEU:HD22	3:A:487:MET:HE3	2.01	0.41
4:B:806:THR:HG22	4:B:808:ALA:CB	2.50	0.41
13:K:67:PHE:C	13:K:68:PHE:HD2	2.24	0.41
8:F:89:GLU:HB3	8:F:134:ILE:HD13	2.02	0.41
5:C:246:ARG:HA	5:C:249:ASP:HB3	2.02	0.41
4:B:22:SER:HA	4:B:654:ARG:CG	2.50	0.41
4:B:654:ARG:C	4:B:656:GLY:N	2.72	0.41
4:B:839:MET:HG3	4:B:1010:LEU:CD1	2.50	0.41
3:A:383:TYR:CD2	3:A:383:TYR:N	2.88	0.41
4:B:60:GLN:NE2	4:B:94:LYS:HA	2.31	0.41
3:A:494:SER:O	3:A:497:THR:N	2.53	0.41
13:K:46:ILE:O	13:K:46:ILE:HG22	2.20	0.41
3:A:500:GLU:O	3:A:504:LEU:HD13	2.20	0.41
3:A:404:TYR:CD2	3:A:414:ASP:HA	2.54	0.41
3:A:875:ALA:HB2	3:A:1366:ARG:HD2	2.02	0.41
5:C:107:SER:C	5:C:109:SER:N	2.72	0.41
4:B:1106:ARG:HD2	4:B:1125:ASP:O	2.20	0.41
7:E:177:ARG:HD3	7:E:215:MET:CG	2.49	0.41
4:B:736:THR:O	4:B:736:THR:HG22	2.20	0.41
5:C:45:ALA:O	5:C:159:ALA:HA	2.19	0.41
6:D:8:PHE:HE1	6:D:37:GLN:HB2	1.86	0.41
3:A:567:LYS:HD3	10:H:95:TYR:HA	2.02	0.41
3:A:857:ARG:HD3	3:A:861:GLY:O	2.20	0.41
5:C:187:LYS:HG3	5:C:219:PHE:CE1	2.54	0.41
3:A:719:VAL:CG2	3:A:774:ARG:HD3	2.50	0.41
3:A:714:PHE:HE2	3:A:792:TYR:HD2	1.67	0.41
11:I:50:THR:CG2	11:I:51:ASN:N	2.83	0.41
3:A:870:GLU:HG2	7:E:208:TYR:CD1	2.55	0.41
3:A:269:ILE:HG23	3:A:300:VAL:HG22	2.02	0.41
6:D:156:ASP:HB3	6:D:159:THR:H	1.85	0.41
3:A:18:GLN:CB	4:B:1215:ARG:HG3	2.50	0.41
4:B:761:HIS:HB2	4:B:1024:ALA:HB2	2.02	0.41
3:A:289:ILE:C	3:A:291:GLU:H	2.23	0.41
5:C:254:LYS:C	5:C:256:ALA:H	2.23	0.41
4:B:1208:MET:HA	4:B:1212:ILE:O	2.19	0.41
7:E:93:MET:HE2	7:E:120:ALA:HB1	2.01	0.41
5:C:89:GLU:O	5:C:90:ASP:CB	2.68	0.41
3:A:1053:PHE:O	3:A:1055:ARG:N	2.53	0.41
3:A:822:GLU:HG3	4:B:513:GLN:NE2	2.35	0.41
3:A:1010:ALA:O	3:A:1013:ASP:HB2	2.19	0.41
3:A:510:GLN:HA	3:A:510:GLN:OE1	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:48:ALA:O	3:A:49:LYS:HG2	2.20	0.41
4:B:1064:TYR:O	4:B:1065:GLN:C	2.59	0.41
4:B:1085:ILE:CD1	4:B:1085:ILE:N	2.79	0.41
12:J:16:ASP:O	12:J:18:TRP:N	2.54	0.41
6:D:13:ARG:CA	6:D:17:LYS:NZ	2.83	0.41
4:B:616:ILE:HG13	4:B:697:GLU:HA	2.03	0.41
8:F:103:MET:CE	9:G:65:ASP:HB2	2.50	0.41
5:C:239:PRO:O	5:C:241:ASP:N	2.53	0.41
3:A:1072:ILE:HG23	3:A:1356:ILE:HD11	2.02	0.41
6:D:156:ASP:C	6:D:158:GLU:H	2.23	0.41
4:B:906:SER:O	4:B:907:GLY:O	2.38	0.41
14:L:61:THR:HG22	14:L:63:ARG:HG2	2.01	0.41
4:B:165:VAL:HG11	4:B:448:ILE:HD13	2.02	0.41
3:A:182:VAL:CG2	3:A:201:VAL:HA	2.49	0.41
3:A:809:THR:OG1	3:A:812:GLU:HG3	2.21	0.41
3:A:746:MET:CE	4:B:1018:PRO:CG	2.98	0.41
13:K:55:LYS:CB	13:K:81:TYR:CE1	3.03	0.41
3:A:1192:LEU:HG	3:A:1193:LEU:N	2.35	0.41
8:F:101:ILE:HD13	8:F:120:ILE:CG2	2.51	0.41
3:A:1025:ARG:HG3	3:A:1025:ARG:NH1	2.34	0.41
3:A:492:PRO:O	3:A:493:GLN:NE2	2.53	0.41
6:D:139:LYS:O	6:D:143:ASN:ND2	2.50	0.41
3:A:34:LYS:CG	3:A:57:ARG:HH22	2.33	0.41
6:D:38:ILE:HG22	6:D:39:ASN:O	2.20	0.41
3:A:532:ARG:O	3:A:535:THR:HB	2.20	0.41
4:B:806:THR:HG22	4:B:808:ALA:HB3	2.02	0.41
3:A:577:ILE:O	3:A:578:LEU:C	2.59	0.41
9:G:79:PHE:HZ	9:G:106:MET:CE	2.31	0.41
6:D:154:PHE:HB2	6:D:160:VAL:HG22	2.02	0.41
7:E:164:LEU:HD21	7:E:211:TYR:CG	2.54	0.41
3:A:1205:LYS:O	3:A:1206:ASP:C	2.58	0.41
3:A:1450:LEU:CD1	8:F:108:PHE:CZ	3.04	0.41
4:B:1207:LEU:HD23	4:B:1207:LEU:HA	1.93	0.41
8:F:82:THR:HG23	8:F:83:PRO:HD2	2.03	0.41
3:A:1209:MET:CE	3:A:1236:LEU:HB3	2.50	0.41
3:A:1263:ILE:O	3:A:1267:MET:HG3	2.20	0.41
3:A:965:GLN:O	3:A:968:GLN:HB2	2.20	0.41
5:C:94:LYS:HE3	5:C:94:LYS:HB2	1.76	0.41
5:C:168:ALA:O	5:C:170:TRP:N	2.54	0.41
5:C:73:GLN:CD	5:C:74:SER:H	2.24	0.41
4:B:1085:ILE:HG22	4:B:1086:PHE:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:929:LEU:HD23	3:A:983:ILE:HG21	2.02	0.41
14:L:55:ILE:H	14:L:55:ILE:HG12	1.45	0.41
11:I:100:PHE:N	11:I:100:PHE:HD1	2.18	0.41
9:G:65:ASP:OD2	9:G:67:SER:HB2	2.20	0.41
4:B:654:ARG:N	4:B:657:HIS:HD2	2.05	0.41
4:B:1167:GLY:CA	4:B:1217:TYR:HE1	2.34	0.41
4:B:990:ILE:HG22	4:B:991:GLY:N	2.36	0.41
8:F:119:ARG:NH1	8:F:119:ARG:CG	2.83	0.41
4:B:1034:VAL:C	4:B:1036:ALA:H	2.22	0.41
3:A:1289:ARG:HH12	3:A:1326:ARG:NH1	2.18	0.41
3:A:693:VAL:HG12	3:A:693:VAL:O	2.20	0.41
4:B:259:TYR:H	4:B:259:TYR:HD1	1.68	0.41
13:K:27:ALA:HB1	13:K:28:PRO:HD2	2.03	0.41
10:H:91:ASP:CG	10:H:91:ASP:O	2.57	0.41
9:G:39:THR:CG2	9:G:41:LYS:H	2.29	0.41
11:I:54:GLU:HB3	11:I:100:PHE:CE2	2.55	0.41
5:C:252:GLN:HE21	13:K:95:ILE:HG23	1.85	0.41
6:D:137:ASN:C	6:D:137:ASN:HD22	2.23	0.41
4:B:21:GLU:O	4:B:22:SER:O	2.38	0.41
5:C:217:ASP:HA	5:C:218:PRO:HD3	1.85	0.41
3:A:412:ARG:HH21	4:B:1108:ARG:NH1	2.17	0.41
3:A:172:PRO:HB3	3:A:185:TRP:CD2	2.55	0.41
14:L:43:THR:C	14:L:45:ALA:H	2.24	0.41
3:A:1152:ILE:HG13	11:I:44:TYR:HB3	2.03	0.41
9:G:23:LYS:HG3	9:G:56:ILE:CD1	2.50	0.41
4:B:1033:LYS:NZ	4:B:1070:GLU:OE1	2.48	0.41
7:E:30:ILE:HG22	7:E:31:THR:N	2.35	0.41
4:B:464:GLY:O	4:B:477:ALA:HA	2.21	0.41
6:D:48:ILE:CG2	9:G:4:ILE:HB	2.51	0.41
4:B:23:ALA:H	4:B:654:ARG:HD2	1.86	0.41
7:E:17:ARG:O	7:E:21:GLU:HG3	2.21	0.41
4:B:864:LYS:HB2	4:B:872:GLU:OE1	2.21	0.41
3:A:474:VAL:HG22	3:A:474:VAL:O	2.21	0.41
10:H:61:SER:O	10:H:62:SER:CB	2.64	0.41
3:A:404:TYR:CE2	3:A:414:ASP:HA	2.56	0.41
7:E:114:ASN:O	7:E:115:ASN:CB	2.63	0.41
3:A:958:VAL:O	3:A:958:VAL:HG12	2.20	0.41
3:A:684:ALA:O	3:A:687:LYS:HB2	2.21	0.41
3:A:77:CYS:C	3:A:78:PRO:O	2.58	0.41
6:D:63:LEU:O	6:D:129:LEU:HD11	2.21	0.41
3:A:42:ASP:O	3:A:44:THR:N	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:666:ILE:HD11	4:B:1086:PHE:CE1	2.55	0.41
4:B:800:GLN:O	4:B:801:LYS:C	2.58	0.41
3:A:667:GLY:HA3	5:C:192:TRP:HH2	1.85	0.41
3:A:1115:SER:HB3	3:A:1330:ASN:HD21	1.86	0.41
9:G:59:GLY:CA	9:G:70:PHE:CD2	3.02	0.41
3:A:1019:CYS:O	3:A:1022:LEU:HB3	2.21	0.41
7:E:168:TYR:CB	7:E:170:LEU:HG	2.50	0.41
4:B:307:ASP:O	4:B:309:GLN:N	2.54	0.41
3:A:341:MET:HE2	3:A:843:LYS:NZ	2.34	0.41
3:A:335:ARG:HE	3:A:335:ARG:HB2	1.58	0.41
3:A:43:GLU:HB2	3:A:46:THR:HB	2.03	0.41
3:A:899:VAL:CG2	3:A:1029:ARG:HG2	2.51	0.41
3:A:1153:TYR:CD2	3:A:1163:ILE:HD11	2.55	0.41
9:G:15:PRO:O	9:G:18:PHE:HB2	2.21	0.41
5:C:221:TYR:CD1	5:C:222:LYS:HG3	2.56	0.41
4:B:284:ILE:HG23	4:B:324:ILE:HD12	2.03	0.41
4:B:324:ILE:CG2	4:B:325:GLN:N	2.82	0.41
11:I:6:PHE:C	11:I:14:LEU:HD11	2.41	0.41
3:A:784:LEU:HB3	3:A:785:PRO:HD2	2.03	0.41
3:A:399:HIS:CG	3:A:400:PRO:N	2.88	0.41
11:I:86:PHE:CE1	11:I:100:PHE:HB2	2.55	0.41
9:G:102:GLN:HG3	9:G:106:MET:O	2.21	0.41
3:A:866:PHE:HE1	7:E:211:TYR:H	1.68	0.41
3:A:384:ASN:O	3:A:385:ILE:C	2.59	0.41
3:A:385:ILE:HG22	3:A:386:ASP:N	2.35	0.41
4:B:211:VAL:HG23	4:B:483:LEU:HB2	2.03	0.41
3:A:1101:LEU:HD11	3:A:1105:LEU:HD11	2.02	0.41
3:A:102:VAL:O	3:A:105:CYS:HB2	2.21	0.41
7:E:114:ASN:HD22	7:E:114:ASN:HA	1.62	0.41
3:A:818:MET:HE2	3:A:818:MET:HB3	1.88	0.41
4:B:487:THR:H	4:B:490:SER:HB3	1.85	0.41
3:A:1214:GLU:O	3:A:1218:GLN:HG2	2.21	0.41
8:F:82:THR:HA	8:F:83:PRO:HD3	1.80	0.41
7:E:116:ILE:CG2	7:E:120:ALA:HB3	2.50	0.41
9:G:114:LEU:HD12	9:G:114:LEU:HA	1.96	0.41
3:A:608:ILE:HD12	3:A:613:ILE:HD11	2.03	0.41
4:B:711:GLU:HB2	4:B:712:PRO:CD	2.51	0.41
4:B:890:TYR:CZ	4:B:910:VAL:HG21	2.55	0.41
4:B:619:ILE:HD12	11:I:65:ASP:HB2	2.02	0.41
3:A:1126:ALA:O	3:A:1128:GLN:N	2.54	0.41
5:C:33:LEU:O	5:C:37:MET:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:244:PRO:O	3:A:246:VAL:N	2.53	0.41
3:A:53:LEU:O	3:A:54:ASN:C	2.60	0.41
5:C:167:HIS:CD2	5:C:168:ALA:H	2.39	0.41
3:A:898:ARG:O	3:A:1029:ARG:NH1	2.54	0.41
3:A:899:VAL:CG2	3:A:908:LEU:HD21	2.51	0.41
11:I:15:TYR:O	11:I:28:GLU:HG2	2.20	0.41
4:B:1000:PRO:O	4:B:1000:PRO:HG2	2.21	0.41
4:B:693:ILE:HG22	4:B:694:ASP:O	2.20	0.41
3:A:709:THR:HB	3:A:712:GLU:H	1.86	0.41
11:I:58:VAL:HG12	11:I:58:VAL:O	2.21	0.41
4:B:818:PRO:HB2	4:B:1091:TYR:OH	2.21	0.41
4:B:622:LYS:HE2	11:I:59:VAL:CG2	2.42	0.41
4:B:1132:GLU:O	4:B:1135:ARG:HB3	2.20	0.41
6:D:14:ARG:O	6:D:15:LEU:HB3	2.21	0.41
3:A:207:ILE:CG2	3:A:211:PHE:HE1	2.33	0.41
3:A:298:PHE:HD2	3:A:299:HIS:CD2	2.39	0.41
13:K:78:THR:O	13:K:81:TYR:HB3	2.21	0.41
3:A:852:TYR:CD2	3:A:1060:PRO:CB	3.03	0.41
4:B:1106:ARG:NH2	4:B:1111:MET:HE2	2.36	0.41
10:H:56:THR:HB	10:H:145:ARG:HG2	2.02	0.41
3:A:781:ASP:O	3:A:789:LYS:HA	2.21	0.41
6:D:176:GLU:C	6:D:178:ALA:N	2.73	0.41
6:D:176:GLU:O	6:D:178:ALA:N	2.54	0.41
3:A:306:ASN:HB2	3:A:324:SER:HB3	2.02	0.41
4:B:555:ILE:HG22	4:B:556:THR:N	2.35	0.41
5:C:82:TYR:CD2	5:C:161:LYS:HB3	2.55	0.40
9:G:7:LEU:CB	9:G:74:TYR:CE2	2.97	0.40
5:C:174:ALA:O	12:J:10:CYS:O	2.39	0.40
2:T:12:G:C2'	2:T:13:U:O5'	2.69	0.40
4:B:826:ALA:O	4:B:1011:ILE:HA	2.21	0.40
4:B:542:MET:CG	4:B:747:MET:HB3	2.51	0.40
4:B:899:ILE:HG22	4:B:903:VAL:CG2	2.50	0.40
3:A:497:THR:HG23	4:B:1146:PHE:HD1	1.85	0.40
4:B:681:TRP:O	4:B:683:SER:N	2.54	0.40
4:B:46:GLN:CG	4:B:47:GLN:H	2.32	0.40
5:C:259:LEU:CD1	13:K:91:CYS:HB2	2.51	0.40
11:I:61:ASP:C	11:I:63:GLY:N	2.73	0.40
3:A:1025:ARG:HG3	3:A:1025:ARG:HH11	1.85	0.40
4:B:175:ARG:HH11	4:B:175:ARG:HG2	1.87	0.40
3:A:241:VAL:HG13	3:A:266:LEU:CD1	2.51	0.40
3:A:874:ASP:CA	3:A:1058:VAL:HG22	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:591:ARG:O	4:B:592:ASN:C	2.59	0.40
9:G:111:THR:HG22	9:G:113:HIS:N	2.20	0.40
9:G:82:PHE:N	9:G:82:PHE:CD1	2.89	0.40
8:F:99:LEU:HD21	9:G:64:THR:O	2.21	0.40
13:K:95:ILE:O	13:K:98:LEU:HB2	2.21	0.40
3:A:738:LYS:HB2	3:A:740:LEU:CG	2.45	0.40
3:A:821:ARG:CB	3:A:821:ARG:HH11	2.27	0.40
3:A:84:ILE:HD11	3:A:270:LEU:HD22	2.02	0.40
3:A:503:GLN:OE1	8:F:90:ARG:NH2	2.48	0.40
14:L:40:LEU:HB3	14:L:41:SER:H	1.47	0.40
4:B:250:PHE:HA	4:B:250:PHE:HD2	1.69	0.40
4:B:732:SER:HB2	4:B:734:HIS:CD2	2.56	0.40
3:A:89:PRO:C	3:A:204:THR:HG21	2.42	0.40
4:B:728:ARG:HH12	4:B:1047:PHE:HB3	1.86	0.40
3:A:961:ARG:HG3	3:A:961:ARG:NH1	2.35	0.40
4:B:558:LEU:O	4:B:560:GLU:N	2.54	0.40
3:A:108:MET:SD	3:A:108:MET:N	2.94	0.40
4:B:552:MET:HA	4:B:555:ILE:HB	2.03	0.40
4:B:950:ASP:O	4:B:951:GLN:HB2	2.21	0.40
4:B:388:CYS:O	4:B:391:ASP:N	2.51	0.40
4:B:376:PHE:CZ	4:B:569:TYR:HB3	2.56	0.40
3:A:699:ALA:O	3:A:700:ASN:CB	2.69	0.40
10:H:113:ALA:CB	10:H:125:LEU:O	2.70	0.40
12:J:47:ARG:HH11	12:J:47:ARG:HG2	1.85	0.40
4:B:1080:LYS:HD2	5:C:188:HIS:HB2	2.04	0.40
13:K:67:PHE:C	13:K:68:PHE:CD2	2.94	0.40
4:B:311:LEU:O	4:B:314:LEU:N	2.51	0.40
9:G:88:ASP:CB	9:G:144:ARG:HA	2.44	0.40
6:D:154:PHE:CE2	6:D:163:VAL:CG2	3.04	0.40
4:B:953:LEU:CD2	4:B:965:LYS:HB2	2.50	0.40
4:B:610:ASN:HA	4:B:611:PRO:HD3	1.89	0.40
14:L:58:LYS:CG	14:L:58:LYS:O	2.65	0.40
4:B:835:GLN:HB2	4:B:835:GLN:HE21	1.65	0.40
4:B:791:THR:O	4:B:792:MET:O	2.38	0.40
8:F:111:LEU:C	8:F:113:GLY:N	2.73	0.40
4:B:446:LEU:HD23	4:B:446:LEU:N	2.36	0.40
6:D:195:ILE:O	6:D:198:LEU:HG	2.21	0.40
4:B:984:HIS:CD2	4:B:1025:HIS:HB2	2.56	0.40
3:A:1364:ASN:HD22	3:A:1365:TYR:N	2.19	0.40
4:B:258:LEU:CG	4:B:258:LEU:O	2.69	0.40
12:J:3:VAL:HA	12:J:4:PRO:HD3	1.92	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:100:THR:CG2	10:H:101:ALA:N	2.83	0.40
4:B:1159:ARG:HB3	4:B:1159:ARG:HH11	1.87	0.40
7:E:212:ARG:CG	7:E:212:ARG:HH11	2.34	0.40
3:A:1441:PHE:HB2	8:F:135:ARG:O	2.21	0.40
4:B:382:ILE:O	4:B:385:LEU:HB3	2.21	0.40
4:B:680:THR:O	4:B:684:LEU:CD1	2.69	0.40
13:K:29:ASN:O	13:K:76:GLN:HG3	2.21	0.40
5:C:179:GLU:CG	5:C:180:TYR:N	2.84	0.40
4:B:26:THR:O	4:B:29:ASP:HB2	2.21	0.40
8:F:77:ASP:C	8:F:79:ARG:N	2.75	0.40
6:D:24:ALA:HB3	6:D:26:THR:OG1	2.21	0.40
4:B:984:HIS:CG	4:B:1025:HIS:HB2	2.56	0.40
3:A:576:GLN:HG3	10:H:119:GLY:HA3	2.04	0.40
3:A:491:VAL:HG12	3:A:492:PRO:O	2.21	0.40
3:A:95:PHE:O	3:A:96:ILE:C	2.58	0.40
9:G:112:LYS:NZ	9:G:120:THR:HA	2.37	0.40
4:B:236:HIS:CE1	4:B:389:ALA:HA	2.57	0.40
3:A:43:GLU:O	3:A:44:THR:CB	2.68	0.40
3:A:49:LYS:NZ	3:A:60:SER:HA	2.36	0.40
2:T:12:G:HO2'	2:T:13:U:C4'	2.35	0.40
4:B:114:PRO:O	4:B:115:GLN:C	2.60	0.40
3:A:1369:ALA:O	3:A:1370:LEU:C	2.58	0.40
9:G:3:PHE:CE1	9:G:80:LYS:HE2	2.56	0.40
7:E:58:MET:O	7:E:59:SER:O	2.39	0.40
3:A:24:PRO:HD2	3:A:233:TRP:NE1	2.36	0.40
3:A:1097:GLY:HA2	3:A:1355:VAL:HG13	2.04	0.40
6:D:191:ALA:C	6:D:193:THR:N	2.75	0.40
4:B:1017:ILE:HA	4:B:1017:ILE:HD13	1.92	0.40
3:A:1291:VAL:HG13	3:A:1292:PRO:N	2.36	0.40
4:B:802:PRO:HG2	4:B:805:THR:HG22	2.03	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	
3	A	1412/1733 (82%)	1030 (73%)	249 (18%)	133 (9%)	1	15
4	B	1094/1224 (89%)	780 (71%)	214 (20%)	100 (9%)	1	16
5	C	264/318 (83%)	164 (62%)	64 (24%)	36 (14%)	0	6
6	D	174/221 (79%)	126 (72%)	30 (17%)	18 (10%)	1	12
7	E	212/215 (99%)	158 (74%)	36 (17%)	18 (8%)	1	17
8	F	86/155 (56%)	69 (80%)	9 (10%)	8 (9%)	1	15
9	G	169/171 (99%)	130 (77%)	33 (20%)	6 (4%)	4	41
10	H	131/146 (90%)	74 (56%)	36 (28%)	21 (16%)	0	5
11	I	114/122 (93%)	69 (60%)	30 (26%)	15 (13%)	0	6
12	J	63/70 (90%)	39 (62%)	10 (16%)	14 (22%)	0	1
13	K	110/120 (92%)	87 (79%)	15 (14%)	8 (7%)	1	22
14	L	44/70 (63%)	18 (41%)	10 (23%)	16 (36%)	0	0
All	All	3873/4565 (85%)	2744 (71%)	736 (19%)	393 (10%)	1	13

All (393) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	4	GLN
3	A	44	THR
3	A	48	ALA
3	A	54	ASN
3	A	57	ARG
3	A	58	LEU
3	A	62	ASP
3	A	65	LEU
3	A	66	LYS
3	A	70	CYS
3	A	74	MET
3	A	93	VAL
3	A	154	SER
3	A	167	CYS
3	A	223	GLY
3	A	250	ILE
3	A	255	SER
3	A	286	HIS
3	A	311	GLN

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Mol	Chain	Res	Type
3	A	318	SER
3	A	335	ARG
3	A	399	HIS
3	A	516	SER
3	A	517	ASN
3	A	536	LEU
3	A	567	LYS
3	A	597	LEU
3	A	619	LYS
3	A	626	ASN
3	A	666	ILE
3	A	780	VAL
3	A	968	GLN
3	A	986	ILE
3	A	1016	THR
3	A	1036	ARG
3	A	1115	SER
3	A	1116	LEU
3	A	1120	LEU
3	A	1122	PRO
3	A	1124	HIS
3	A	1127	ASP
3	A	1176	LEU
3	A	1212	VAL
3	A	1223	ASP
3	A	1233	ASP
3	A	1314	SER
3	A	1365	TYR
3	A	1378	GLN
3	A	1405	THR
4	B	22	SER
4	B	28	GLU
4	B	45	SER
4	B	108	VAL
4	B	186	GLU
4	B	206	ASN
4	B	258	LEU
4	B	266	ALA
4	B	367	LEU
4	B	467	GLY
4	B	643	ASP
4	B	709	ASP

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Mol	Chain	Res	Type
4	B	731	VAL
4	B	792	MET
4	B	879	ARG
4	B	881	ASN
4	B	907	GLY
4	B	958	GLN
4	B	1003	ALA
4	B	1041	GLU
4	B	1046	PRO
4	B	1069	PHE
4	B	1097	HIS
4	B	1156	ASP
4	B	1171	VAL
4	B	1175	LEU
4	B	1181	GLU
4	B	1182	CYS
4	B	1188	LYS
5	C	4	GLU
5	C	18	VAL
5	C	110	THR
5	C	132	PRO
5	C	149	LYS
5	C	156	THR
5	C	161	LYS
5	C	184	ASN
5	C	214	ASN
5	C	215	GLU
5	C	216	GLY
6	D	5	THR
6	D	8	PHE
6	D	20	GLU
6	D	131	GLU
6	D	199	ASN
7	E	3	GLN
7	E	45	LYS
7	E	59	SER
7	E	73	PRO
7	E	106	GLN
7	E	130	ALA
8	F	81	THR
9	G	63	PRO
10	H	21	ASN

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Mol	Chain	Res	Type
10	H	62	SER
10	H	78	SER
10	H	128	ASN
10	H	140	ALA
11	I	3	THR
11	I	57	GLY
11	I	106	CYS
12	J	2	ILE
12	J	28	ASP
12	J	32	GLU
12	J	41	LEU
12	J	64	ASN
13	K	109	TRP
13	K	110	ASN
13	K	111	LEU
14	L	50	ASP
14	L	59	ALA
3	A	42	ASP
3	A	59	GLY
3	A	61	ILE
3	A	71	GLN
3	A	76	GLU
3	A	117	GLU
3	A	128	ILE
3	A	253	ASN
3	A	257	ARG
3	A	283	GLY
3	A	312	PRO
3	A	322	VAL
3	A	331	GLY
3	A	332	LYS
3	A	419	LYS
3	A	543	LEU
3	A	592	ASP
3	A	649	ILE
3	A	753	GLY
3	A	765	VAL
3	A	888	GLY
3	A	969	GLN
3	A	1002	GLY
3	A	1281	ARG
3	A	1377	THR

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Mol	Chain	Res	Type
3	A	1438	THR
4	B	46	GLN
4	B	58	THR
4	B	65	GLU
4	B	100	PRO
4	B	115	GLN
4	B	261	ARG
4	B	282	ILE
4	B	345	LYS
4	B	543	SER
4	B	605	ARG
4	B	641	GLU
4	B	655	LYS
4	B	746	SER
4	B	751	VAL
4	B	831	SER
4	B	848	ARG
4	B	867	GLY
4	B	891	ASP
4	B	1065	GLN
4	B	1075	GLY
4	B	1155	SER
4	B	1186	ASP
5	C	78	GLU
5	C	141	GLY
5	C	142	VAL
5	C	213	PRO
5	C	231	ASN
6	D	9	GLN
6	D	12	ARG
6	D	16	LYS
6	D	19	GLU
6	D	21	GLU
6	D	30	GLY
6	D	52	LEU
6	D	192	LYS
7	E	36	GLU
7	E	44	ALA
7	E	74	ASP
7	E	76	GLY
7	E	192	ARG
7	E	206	GLY

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Mol	Chain	Res	Type
8	F	69	LEU
8	F	70	LYS
8	F	150	GLU
8	F	151	LEU
9	G	139	ILE
10	H	17	PRO
10	H	59	ILE
10	H	77	ARG
10	H	81	PRO
10	H	82	PRO
10	H	84	ALA
10	H	90	ALA
10	H	107	VAL
10	H	108	SER
11	I	11	ASN
11	I	59	VAL
11	I	95	THR
12	J	6	ARG
12	J	9	SER
12	J	14	VAL
12	J	17	LYS
12	J	29	GLU
12	J	33	GLY
13	K	15	GLY
14	L	53	HIS
14	L	60	ARG
3	A	67	CYS
3	A	169	ASN
3	A	219	PHE
3	A	263	THR
3	A	336	ILE
3	A	424	ILE
3	A	465	TYR
3	A	591	PHE
3	A	652	VAL
3	A	846	GLU
3	A	847	ASP
3	A	871	ASP
3	A	875	ALA
3	A	926	GLN
3	A	972	HIS
3	A	1054	LEU

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Mol	Chain	Res	Type
3	A	1221	LYS
4	B	184	ALA
4	B	257	LYS
4	B	259	TYR
4	B	264	SER
4	B	401	PHE
4	B	470	LYS
4	B	642	ASP
4	B	708	GLU
4	B	711	GLU
4	B	943	SER
4	B	1100	ASP
4	B	1178	ASN
4	B	1183	LYS
5	C	90	ASP
5	C	117	ASP
5	C	217	ASP
5	C	233	GLU
6	D	47	LEU
7	E	43	LYS
7	E	115	ASN
7	E	158	SER
8	F	128	LYS
9	G	20	PRO
9	G	118	ASP
9	G	154	VAL
10	H	52	GLN
10	H	63	LEU
10	H	64	ASN
10	H	92	ASP
11	I	9	ASP
11	I	78	CYS
11	I	91	ARG
11	I	107	SER
12	J	8	PHE
13	K	29	ASN
14	L	35	SER
14	L	37	LYS
3	A	69	THR
3	A	84	ILE
3	A	410	GLY
3	A	439	ASN

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Mol	Chain	Res	Type
3	A	483	ASP
3	A	648	ASN
3	A	706	HIS
3	A	775	ILE
3	A	789	LYS
3	A	1114	PRO
3	A	1136	SER
4	B	48	LEU
4	B	114	PRO
4	B	249	ARG
4	B	260	GLY
4	B	308	TRP
4	B	362	PRO
4	B	450	ALA
4	B	474	SER
4	B	483	LEU
4	B	559	SER
4	B	575	PRO
4	B	764	SER
4	B	880	THR
4	B	977	GLY
4	B	1017	ILE
4	B	1035	ALA
4	B	1074	ASN
4	B	1108	ARG
4	B	1144	ALA
4	B	1157	ALA
5	C	11	ARG
5	C	87	PHE
5	C	175	ALA
5	C	188	HIS
5	C	240	VAL
6	D	218	GLU
7	E	40	GLU
7	E	56	LYS
9	G	115	MET
10	H	32	THR
10	H	44	VAL
11	I	47	GLU
11	I	79	HIS
12	J	62	ARG
13	K	7	PHE

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Mol	Chain	Res	Type
14	L	26	THR
14	L	28	LYS
14	L	40	LEU
14	L	43	THR
14	L	45	ALA
3	A	35	ILE
3	A	43	GLU
3	A	55	ASP
3	A	113	LEU
3	A	130	ASP
3	A	164	ARG
3	A	317	LYS
3	A	605	MET
3	A	739	ASP
3	A	783	THR
3	A	891	ALA
3	A	1366	ARG
3	A	1392	SER
4	B	27	ALA
4	B	365	THR
4	B	383	ASN
4	B	513	GLN
4	B	551	PRO
4	B	705	MET
4	B	712	PRO
4	B	1045	SER
5	C	10	ILE
5	C	13	ALA
5	C	108	GLU
5	C	264	GLN
8	F	104	ASN
11	I	4	PHE
11	I	54	GLU
11	I	62	ILE
13	K	103	THR
14	L	41	SER
14	L	44	ASP
14	L	54	ARG
3	A	5	GLN
3	A	245	PRO
3	A	249	SER
3	A	830	LYS

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Mol	Chain	Res	Type
3	A	958	VAL
3	A	1094	VAL
3	A	1123	GLY
3	A	1454	MET
4	B	20	ASP
4	B	94	LYS
4	B	295	GLY
5	C	70	ILE
5	C	133	ILE
5	C	137	LYS
5	C	209	TYR
6	D	139	LYS
10	H	36	CYS
12	J	57	ILE
14	L	56	LEU
3	A	400	PRO
3	A	604	GLY
3	A	1164	PRO
4	B	1167	GLY
5	C	51	VAL
3	A	599	SER
3	A	1324	PRO
5	C	126	GLY
5	C	202	PRO
3	A	51	GLY
3	A	825	ILE
6	D	59	ILE
8	F	131	PRO
13	K	43	GLY
3	A	600	PRO
3	A	622	VAL
4	B	411	PRO
4	B	613	VAL
4	B	976	ILE
6	D	202	ILE
14	L	55	ILE
4	B	524	PRO
7	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	
3	A	1245/1520 (82%)	1129 (91%)	116 (9%)	11	47
4	B	964/1061 (91%)	890 (92%)	74 (8%)	16	56
5	C	235/274 (86%)	212 (90%)	23 (10%)	10	44
6	D	160/200 (80%)	142 (89%)	18 (11%)	7	38
7	E	196/197 (100%)	188 (96%)	8 (4%)	37	74
8	F	78/137 (57%)	75 (96%)	3 (4%)	40	76
9	G	152/152 (100%)	140 (92%)	12 (8%)	15	55
10	H	119/128 (93%)	113 (95%)	6 (5%)	30	70
11	I	110/116 (95%)	99 (90%)	11 (10%)	9	43
12	J	60/65 (92%)	55 (92%)	5 (8%)	14	52
13	K	97/102 (95%)	87 (90%)	10 (10%)	9	42
14	L	40/57 (70%)	36 (90%)	4 (10%)	9	43
All	All	3456/4009 (86%)	3166 (92%)	290 (8%)	14	52

All (290) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	2	VAL
3	A	11	LEU
3	A	37	PHE
3	A	38	PRO
3	A	41	MET
3	A	54	ASN
3	A	62	ASP
3	A	67	CYS
3	A	83	HIS
3	A	93	VAL
3	A	108	MET
3	A	122	MET
3	A	131	SER
3	A	188	ASP

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Mol	Chain	Res	Type
3	A	200	ARG
3	A	221	SER
3	A	236	LEU
3	A	245	PRO
3	A	261	ASP
3	A	265	LYS
3	A	270	LEU
3	A	302	THR
3	A	312	PRO
3	A	326	ARG
3	A	335	ARG
3	A	337	ARG
3	A	345	VAL
3	A	381	THR
3	A	385	ILE
3	A	406	ILE
3	A	408	ASP
3	A	425	GLN
3	A	434	ARG
3	A	442	VAL
3	A	443	LEU
3	A	445	ASN
3	A	450	LEU
3	A	462	VAL
3	A	469	ARG
3	A	470	LEU
3	A	481	ASP
3	A	504	LEU
3	A	515	GLN
3	A	518	LYS
3	A	524	VAL
3	A	560	ILE
3	A	562	THR
3	A	584	ASN
3	A	618	GLU
3	A	622	VAL
3	A	626	ASN
3	A	629	LEU
3	A	635	ARG
3	A	659	HIS
3	A	666	ILE
3	A	685	GLU

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Mol	Chain	Res	Type
3	A	741	ASN
3	A	768	GLN
3	A	779	PHE
3	A	786	HIS
3	A	821	ARG
3	A	827	THR
3	A	831	THR
3	A	834	THR
3	A	852	TYR
3	A	858	ASN
3	A	871	ASP
3	A	886	ILE
3	A	890	ASP
3	A	903	ASN
3	A	907	THR
3	A	929	LEU
3	A	940	ARG
3	A	941	LYS
3	A	969	GLN
3	A	992	ASP
3	A	1001	ARG
3	A	1029	ARG
3	A	1035	TYR
3	A	1052	GLN
3	A	1067	LEU
3	A	1116	LEU
3	A	1122	PRO
3	A	1138	ILE
3	A	1170	ILE
3	A	1176	LEU
3	A	1177	LEU
3	A	1193	LEU
3	A	1206	ASP
3	A	1240	CYS
3	A	1245	PRO
3	A	1264	GLU
3	A	1271	ILE
3	A	1291	VAL
3	A	1295	THR
3	A	1309	ASP
3	A	1325	THR
3	A	1332	PHE

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Mol	Chain	Res	Type
3	A	1333	ILE
3	A	1336	MET
3	A	1359	ASP
3	A	1364	ASN
3	A	1366	ARG
3	A	1372	VAL
3	A	1386	ARG
3	A	1389	PHE
3	A	1393	ASN
3	A	1394	THR
3	A	1405	THR
3	A	1433	MET
3	A	1436	ILE
3	A	1442	ASP
3	A	1443	VAL
3	A	1444	MET
3	A	1445	ILE
3	A	1447	GLU
4	B	37	PHE
4	B	57	TYR
4	B	61	ASP
4	B	100	PRO
4	B	106	ASP
4	B	178	ASN
4	B	203	PHE
4	B	217	ARG
4	B	250	PHE
4	B	268	THR
4	B	283	VAL
4	B	298	LEU
4	B	365	THR
4	B	371	GLU
4	B	378	LEU
4	B	393	LYS
4	B	396	ASP
4	B	401	PHE
4	B	427	ASP
4	B	429	PHE
4	B	466	TRP
4	B	482	VAL
4	B	485	ARG
4	B	496	ARG

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Mol	Chain	Res	Type
4	B	498	THR
4	B	502	ILE
4	B	516	ASN
4	B	557	PHE
4	B	582	VAL
4	B	591	ARG
4	B	603	LEU
4	B	628	THR
4	B	635	ARG
4	B	644	GLU
4	B	682	SER
4	B	724	ASP
4	B	737	THR
4	B	742	GLU
4	B	790	ASP
4	B	791	THR
4	B	811	TYR
4	B	830	TYR
4	B	835	GLN
4	B	839	MET
4	B	878	GLN
4	B	894	ASP
4	B	909	ASP
4	B	939	THR
4	B	944	THR
4	B	978	ASP
4	B	986	GLN
4	B	997	GLU
4	B	999	MET
4	B	1002	THR
4	B	1006	ILE
4	B	1047	PHE
4	B	1060	ARG
4	B	1069	PHE
4	B	1087	PHE
4	B	1095	LEU
4	B	1096	ARG
4	B	1098	MET
4	B	1099	VAL
4	B	1103	ILE
4	B	1108	ARG
4	B	1123	SER

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Mol	Chain	Res	Type
4	B	1159	ARG
4	B	1169	MET
4	B	1176	ASN
4	B	1183	LYS
4	B	1202	LEU
4	B	1212	ILE
4	B	1216	LEU
4	B	1220	ARG
5	C	22	LEU
5	C	23	SER
5	C	56	THR
5	C	58	LEU
5	C	62	PHE
5	C	72	LEU
5	C	75	MET
5	C	77	ILE
5	C	104	PHE
5	C	129	ILE
5	C	140	ASN
5	C	145	CYS
5	C	147	LEU
5	C	163	ILE
5	C	166	GLU
5	C	170	TRP
5	C	193	TYR
5	C	209	TYR
5	C	229	TYR
5	C	233	GLU
5	C	238	ILE
5	C	240	VAL
5	C	266	ASP
6	D	3	VAL
6	D	13	ARG
6	D	17	LYS
6	D	21	GLU
6	D	22	GLU
6	D	63	LEU
6	D	70	PHE
6	D	137	ASN
6	D	139	LYS
6	D	148	LEU
6	D	149	THR

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Mol	Chain	Res	Type
6	D	152	SER
6	D	156	ASP
6	D	170	THR
6	D	192	LYS
6	D	193	THR
6	D	208	GLU
6	D	221	TYR
7	E	60	PHE
7	E	74	ASP
7	E	78	LEU
7	E	104	ASN
7	E	114	ASN
7	E	132	ILE
7	E	165	LEU
7	E	175	LEU
8	F	79	ARG
8	F	90	ARG
8	F	99	LEU
9	G	1	MET
9	G	13	LEU
9	G	51	TYR
9	G	52	ASP
9	G	74	TYR
9	G	78	VAL
9	G	80	LYS
9	G	88	ASP
9	G	99	PHE
9	G	115	MET
9	G	126	ASN
9	G	171	ILE
10	H	7	ASP
10	H	17	PRO
10	H	91	ASP
10	H	95	TYR
10	H	102	TYR
10	H	130	ARG
11	I	4	PHE
11	I	8	ARG
11	I	15	TYR
11	I	34	TYR
11	I	75	CYS
11	I	78	CYS

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Mol	Chain	Res	Type
11	I	85	PHE
11	I	86	PHE
11	I	94	ASP
11	I	101	PHE
11	I	106	CYS
12	J	7	CYS
12	J	43	ARG
12	J	44	TYR
12	J	46	CYS
12	J	48	ARG
13	K	1	MET
13	K	5	ASP
13	K	10	PHE
13	K	25	THR
13	K	42	LEU
13	K	47	ARG
13	K	50	LEU
13	K	61	TYR
13	K	111	LEU
13	K	112	GLN
14	L	27	LEU
14	L	51	CYS
14	L	55	ILE
14	L	70	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (95) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	54	ASN
3	A	64	ASN
3	A	71	GLN
3	A	225	ASN
3	A	256	GLN
3	A	299	HIS
3	A	339	ASN
3	A	358	ASN
3	A	394	ASN
3	A	435	HIS
3	A	479	ASN
3	A	525	GLN
3	A	603	ASN
3	A	631	HIS

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Mol	Chain	Res	Type
3	A	654	ASN
3	A	723	ASN
3	A	736	ASN
3	A	741	ASN
3	A	745	GLN
3	A	757	ASN
3	A	768	GLN
3	A	786	HIS
3	A	838	GLN
3	A	858	ASN
3	A	877	HIS
3	A	903	ASN
3	A	926	GLN
3	A	935	GLN
3	A	994	GLN
3	A	1130	GLN
3	A	1140	HIS
3	A	1188	GLN
3	A	1218	GLN
3	A	1364	ASN
3	A	1432	GLN
4	B	60	GLN
4	B	121	ASN
4	B	178	ASN
4	B	215	GLN
4	B	236	HIS
4	B	350	GLN
4	B	363	HIS
4	B	366	GLN
4	B	465	ASN
4	B	513	GLN
4	B	515	HIS
4	B	516	ASN
4	B	518	HIS
4	B	538	ASN
4	B	706	GLN
4	B	744	HIS
4	B	821	GLN
4	B	842	ASN
4	B	957	ASN
4	B	975	GLN
4	B	1015	HIS

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Mol	Chain	Res	Type
4	B	1025	HIS
4	B	1065	GLN
4	B	1117	GLN
4	B	1176	ASN
4	B	1179	GLN
4	B	1193	GLN
5	C	24	ASN
5	C	73	GLN
5	C	112	ASN
5	C	167	HIS
5	C	252	GLN
6	D	39	ASN
6	D	40	HIS
6	D	41	GLN
6	D	137	ASN
6	D	179	GLN
7	E	8	ASN
7	E	101	GLN
7	E	104	ASN
7	E	114	ASN
7	E	147	HIS
9	G	53	ASN
9	G	57	GLN
9	G	97	HIS
9	G	122	ASN
9	G	126	ASN
10	H	64	ASN
10	H	133	ASN
10	H	137	GLN
11	I	12	ASN
11	I	46	HIS
11	I	90	GLN
11	I	108	HIS
12	J	53	HIS
12	J	64	ASN
13	K	44	ASN
13	K	65	HIS
13	K	76	GLN
13	K	112	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	P	8/16 (50%)	1 (12%)	0
2	T	9/17 (52%)	5 (55%)	2 (22%)
All	All	17/33 (51%)	6 (35%)	2 (11%)

All (6) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	P	9	G
2	T	11	G
2	T	12	G
2	T	13	U
2	T	14	C
2	T	15	A

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	T	12	G
2	T	13	U

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

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

5.5 Carbohydrates [i](#)

There are no 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

There are no such residues in this entry.

5.8 Polymer linkage issues

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	P	9/16 (56%)	1.97	2 (22%) 1 1	194, 200, 200, 200	0
2	T	10/17 (58%)	2.17	7 (70%) 0 1	180, 190, 200, 200	0
3	A	1422/1733 (82%)	-0.24	8 (0%) 90 82	56, 116, 175, 200	0
4	B	1112/1224 (90%)	-0.17	11 (0%) 84 72	57, 126, 188, 200	0
5	C	267/318 (83%)	-0.26	0 100 100	74, 110, 158, 180	0
6	D	178/221 (80%)	-0.23	1 (0%) 90 82	87, 133, 184, 198	0
7	E	214/215 (99%)	-0.22	4 (1%) 70 54	90, 159, 197, 200	0
8	F	88/155 (56%)	-0.49	0 100 100	65, 91, 129, 140	0
9	G	171/171 (100%)	-0.28	0 100 100	88, 112, 155, 163	0
10	H	135/146 (92%)	0.37	5 (3%) 45 30	139, 166, 190, 200	0
11	I	116/122 (95%)	0.09	0 100 100	114, 163, 191, 200	0
12	J	65/70 (92%)	-0.46	0 100 100	79, 108, 146, 153	0
13	K	112/120 (93%)	-0.28	0 100 100	81, 114, 139, 167	0
14	L	46/70 (65%)	0.04	1 (2%) 65 50	111, 166, 194, 196	0
All	All	3945/4598 (85%)	-0.18	39 (0%) 84 72	56, 123, 187, 200	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	B	471	LYS	5.1
1	P	9	G	4.5
3	A	1092	LYS	3.7
1	P	8	A	3.5
2	T	15	A	3.4
2	T	6	C	3.3
10	H	140	ALA	3.1
4	B	882	THR	3.0

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Mol	Chain	Res	Type	RSRZ
4	B	132	VAL	2.9
3	A	1455	PRO	2.9
4	B	883	LEU	2.9
3	A	188	ASP	2.8
4	B	733	HIS	2.8
7	E	82	PHE	2.8
2	T	14	C	2.8
14	L	54	ARG	2.7
3	A	253	ASN	2.5
10	H	86	ASP	2.5
3	A	1256	GLU	2.5
10	H	50	ALA	2.4
7	E	110	PHE	2.4
7	E	81	GLU	2.4
7	E	97	VAL	2.4
2	T	12	G	2.3
10	H	139	ASN	2.3
3	A	115	LEU	2.3
2	T	7	G	2.3
10	H	142	LEU	2.3
2	T	11	G	2.1
6	D	76	LYS	2.1
4	B	133	LYS	2.1
2	T	8	C	2.1
4	B	679	TYR	2.1
4	B	340	ALA	2.1
4	B	341	LEU	2.1
4	B	870	ILE	2.0
3	A	1244	ARG	2.0
4	B	470	LYS	2.0
3	A	1225	PHE	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

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(Å ²)	Q<0.9
15	ZN	B	1307	1/1	1.00	0.22	0.80	83,83,83,83	0
15	ZN	I	203	1/1	0.99	0.16	0.27	120,120,120,120	0
15	ZN	C	302	1/1	1.00	0.13	-0.56	82,82,82,82	0
15	ZN	A	1508	1/1	1.00	0.14	-0.96	83,83,83,83	0
15	ZN	J	101	1/1	1.00	0.25	-0.97	100,100,100,100	0
15	ZN	L	105	1/1	0.97	0.10	-1.12	155,155,155,155	0
15	ZN	I	204	1/1	0.99	0.04	-1.70	181,181,181,181	0
15	ZN	A	1506	1/1	0.95	0.08	-2.66	121,121,121,121	0
16	MG	A	1	1/1	0.97	0.18	-	79,79,79,79	0

6.5 Other polymers

There are no such residues in this entry.