



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:35 AM GMT

PDB ID : 2R7Z
Title : Cisplatin lesion containing RNA polymerase II elongation complex
Authors : Damsma, G.E.; Alt, A.; Brueckner, F.; Carell, T.; Cramer, P.
Deposited on : 2007-09-10
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

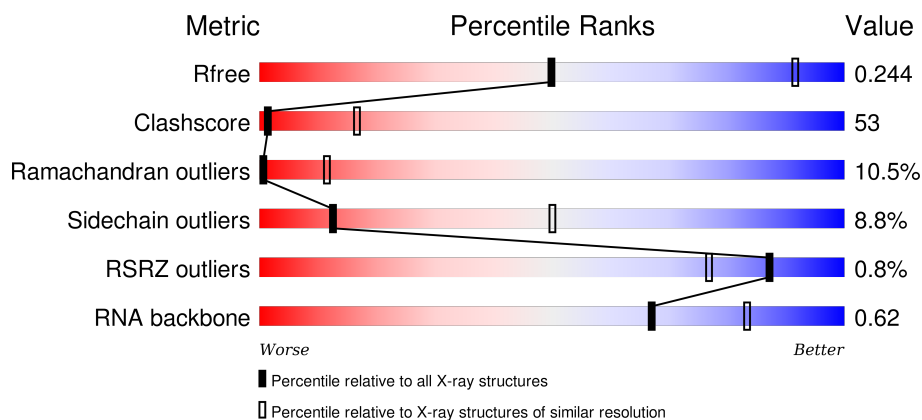
1 Overall quality at a glance

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	T	17	
2	N	7	
3	P	10	
4	A	1733	

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Mol	Chain	Length	Quality of chain
5	B	1224	
6	C	318	
7	D	221	
8	E	215	
9	F	155	
10	G	171	
11	H	146	
12	I	122	
13	J	70	
14	K	120	
15	L	70	

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 31804 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 DNA chain called 5'-D(*TP*AP*CP*TP*TP*GUP*CP*CP*CP*TP*CP*CP*TP*CP*AP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	T	17	Total	C	N	O	P	0	0	0
			336	163	53	104	16			

- Molecule 2 is a DNA chain called 5'-D(*CP*AP*AP*GP*TP*AP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	N	7	Total	C	N	O	P	0	0	0
			143	69	30	38	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	10	Total	C	N	O	P	0	0	0
			216	97	41	69	9			

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit RPB1.

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

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	B	1108	Total	C	N	O	S	0	0	0
			8810	5580	1541	1634	55			

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit RPB3.

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

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	D	177	Total	C	N	O	S	0	0	0
			1427	882	256	287	2			

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

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

- Molecule 9 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

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

- Molecule 10 is a protein called DNA-directed RNA polymerase II subunit RPB7.

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

- Molecule 11 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

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

- Molecule 12 is a protein called DNA-directed RNA polymerase II subunit RPB9.

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

- Molecule 13 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

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

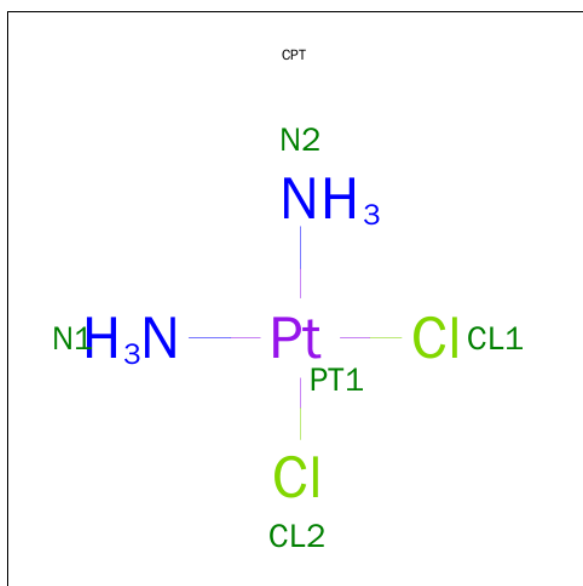
- Molecule 14 is a protein called DNA-directed RNA polymerase II subunit RPB11.

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

- Molecule 15 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

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

- Molecule 16 is CISPLATIN (three-letter code: CPT) (formula: $\text{Cl}_2\text{H}_6\text{N}_2\text{Pt}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
16	T	1	Total	N	Pt	0	0
			3	2	1		

- Molecule 17 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	J	1	Total	Zn	0	0
			1	1		

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

- Molecule 18 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

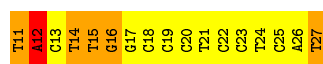
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
18	A	1	Total 1	Mg 1	0	0

3 Residue-property plots

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

- Molecule 1: 5'-D(*TP*AP*CP*TP*TP*GUP*CP*CP*CP*TP*CP*CP*TP*CP*AP*T)-3',

Chain T: 

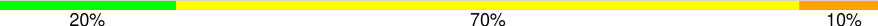


- Molecule 2: 5'-D(*CP*AP*AP*GP*TP*AP*G)-3'

Chain N: 



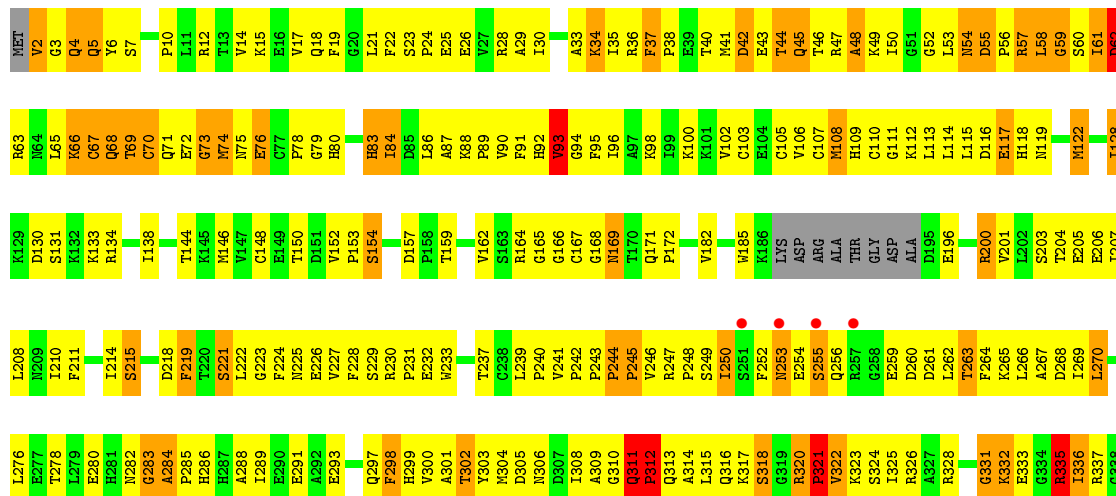
- Molecule 3: 5'-R(*UP*UP*UP*GP*AP*GP*GP*AP*GP*G)-3'

Chain P: 

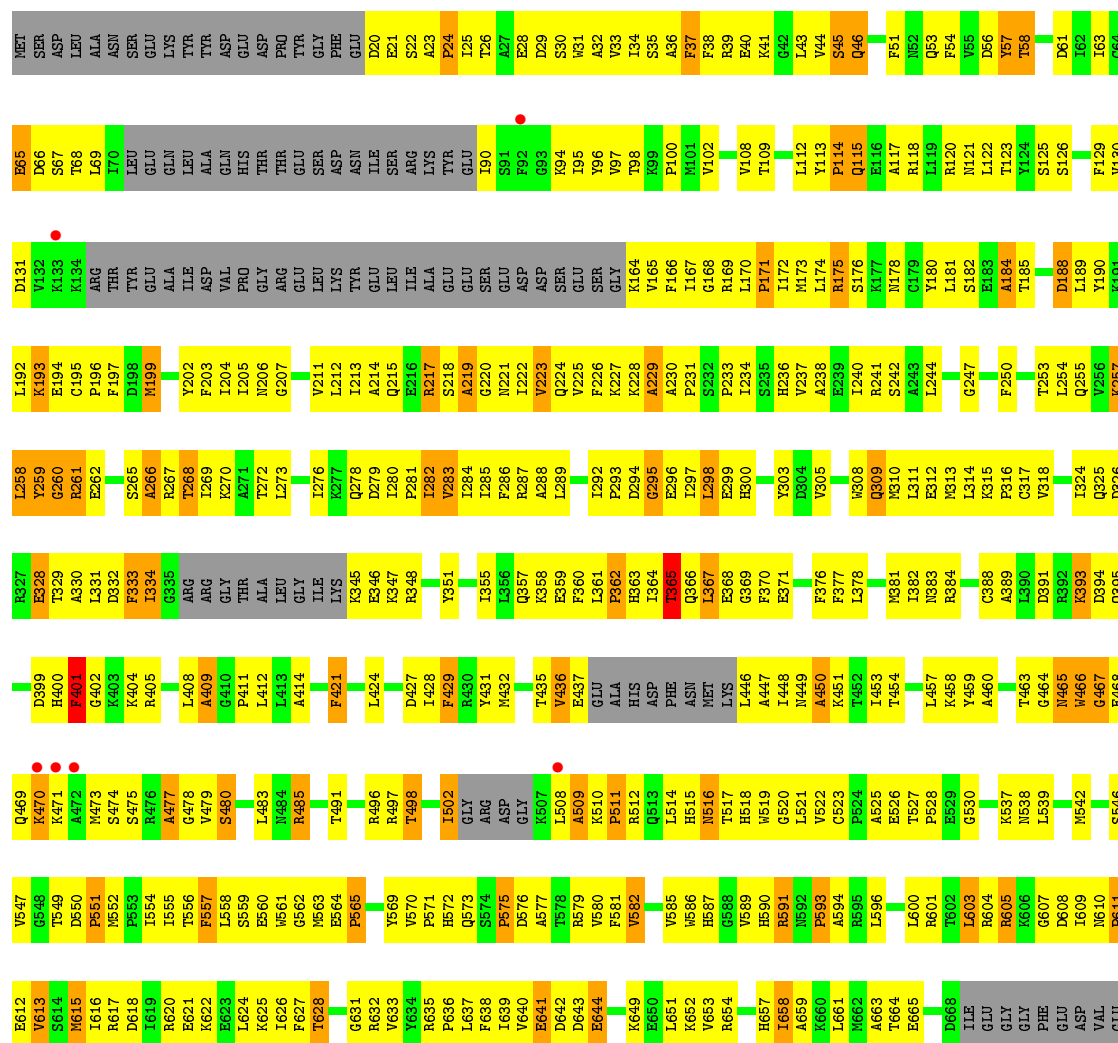


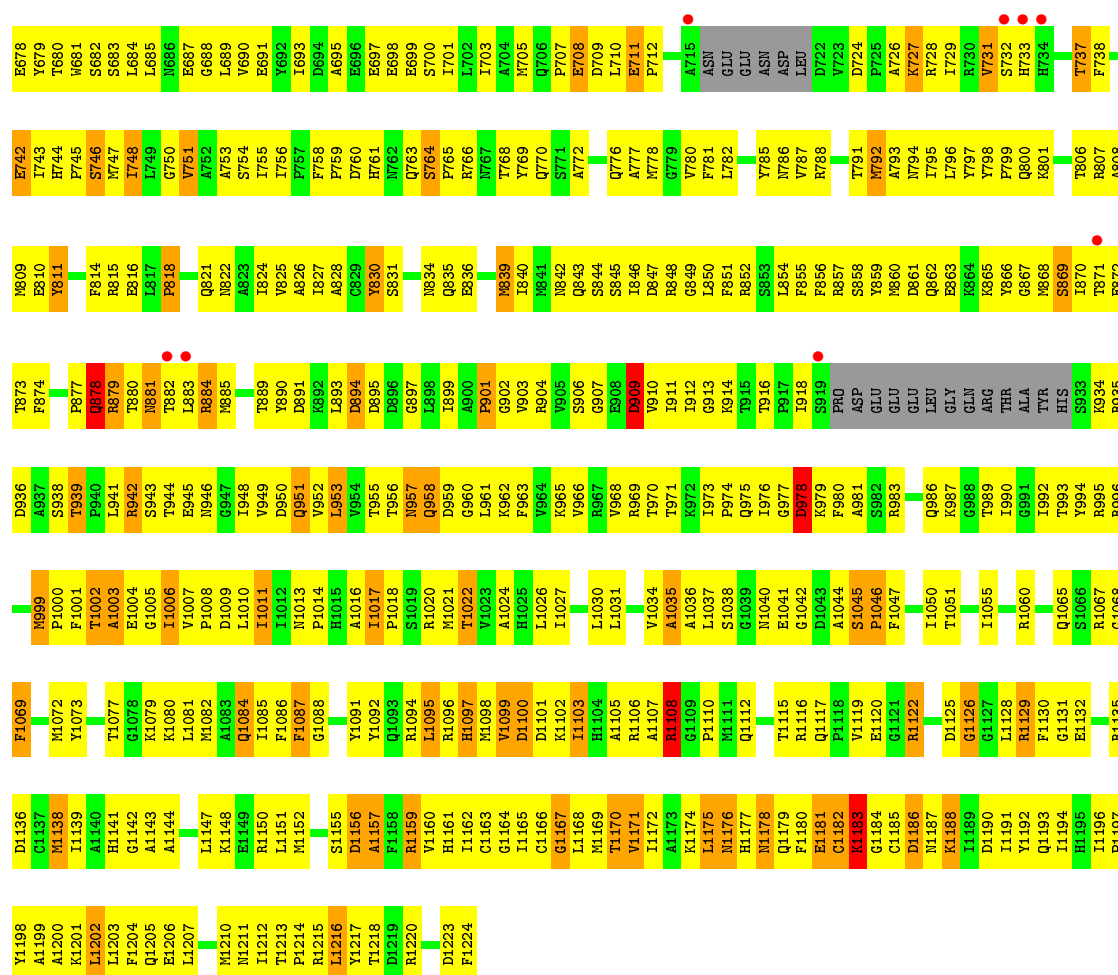
- Molecule 4: DNA-directed RNA polymerase II subunit RPB1

Chain A: 



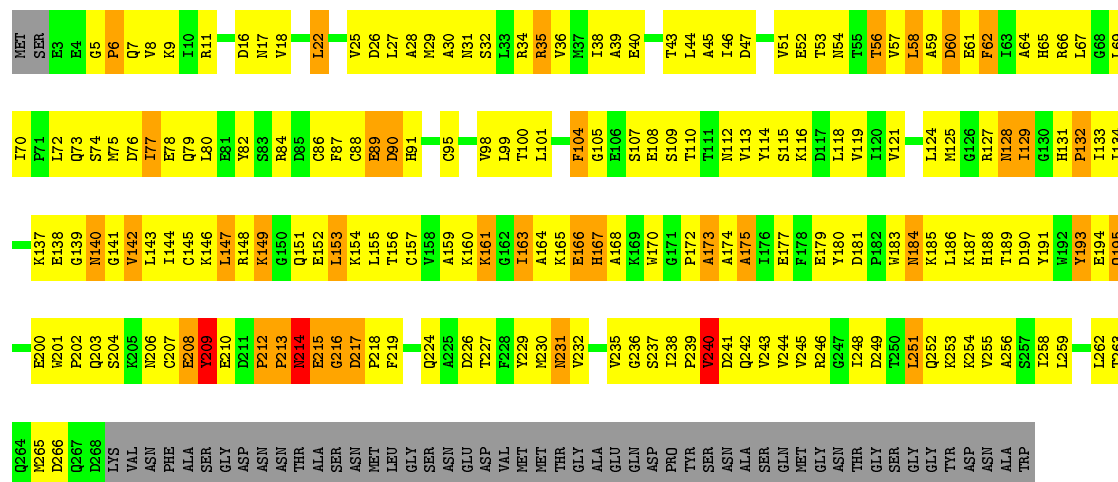
V1355	P1294	D1223	V1098	R1025	V359	I386	R821	V747	T675	L606	L536	R469	D408	I339
I1356	T1295	L1224	V1099	R1026	I960	G887	I825	S751	M676	L607	R537	L470	S409	L340
D1359	E1296	F1225	P1099	R1027	R961	G888	D826	K752	I679	I608	I541	I471	D410	R341
Y1362	E1297	V1226	R1100	P1029	R962	S889	T827	K753	I679	D609	E542	S473	D411	G342
V1363	V1298	P1228	K1101	V1031	I963	D890	E828	S754	E681	I613	E543	V474	I413	R343
M364	K1300	S1229	L1166	L1032	Q965	R896	R829	I757	T682	F614	D544	T475	D414	V345
Y1365	E1301	L1236	E1167	Q1033	R966	I997	T830	I757	I683	G615	Q545	S476	L415	D346
R1366	P1302	E1237	E1168	E1034	A967	R898	T831	I757	A684	V616	V546	P477	L416	F347
R1367	E1303	I1237	R1100	E1035	Q968	V899	A832	K761	E685	E617	L547	V478	R416	Y417
M368	W1304	I1238	L1101	R1036	Q969	D900	E833	S762	A686	E618	M548	V479	S418	A349
A1369	V1305	R1239	Q1171	L1037	T970	I901	T834	A763	D692	K619	M549	A480	K419	R350
M369	L1306	G1240	L1172	L1038	R971	I902	G835	G764	D693	K620	L550	D481	L551	T351
E1307	E1307	H1173	H1173	K1039	R972	N903	R836	V765	V693	T621	Y551	F482	R420	V352
T1371	T1308	V1242	S1175	Q1040	I973	T904	I837	G766	T694	T622	W552	D423	D423	I353
V1372	D1309	F1174	L1106	A1041	D905	Q835	I838	G767	K695	G623	W556	D485	I424	S354
D1373	T1310	L1176	V1107	F1042	R906	R839	R839	Q768	E696	S624	D557	N487	Q426	G355
V1311	G1310	ARG	L1176	D1043	D980	T907	L841	R774	Q698	N626	G558	N488	Q427	P357
M1312	M1110	LYS	ASP	V1044	I981	I908	R842	I775	A699	G627	V559	L489	Y428	E360
L1313	M1111	GLU	GLU	V1045	T982	D909	R843	I775	A699	G627	V559	L489	Y428	L361
T1376	L1314	LEU	GLU	L1046	T983	P910	K843	I775	A699	G627	V559	L489	Y428	G365
T1377	S1314	LEU	GLU	L1047	T984	S911	A844	F779	L701	L629	P561	V491	W430	G366
Q1378	E1315	ALA	ALA	S1047	K984	S911	L845	V780	L701	L629	P561	V491	W430	G367
G1379	V1316	ALA	GLU	N1048	D985	I912	L845	V780	L701	L629	P561	V491	W430	G368
M1317	M1317	GLN	GLN	I1049	I986	I913	E846	D781	D716	G632	P563	Q493	V432	G369
T1318	T1318	THR	THR	E1050	I987	E914	D847	R782	D716	G632	A564	Q493	V432	G370
V1319	V1319	GLU	PHE	A1051	L988	S915	L848	T783	D716	G632	I565	E494	R434	G371
P1320	P1320	ASP	ASP	Q1052	G989	G916	M849	L784	R711	T634	I566	E496	R435	G372
G1321	G1321	ASP	ASP	Q1052	G989	G916	M849	L784	R711	T634	I566	E496	R435	G373
T1322	T1322	E1255	Y1119	Q1052	V990	S917	V850	F785	E712	T635	K567	T497	I436	G374
D1323	S1188	E1256	Y1119	Q1052	V990	S917	V850	F785	E712	T635	K567	T497	I436	G375
P1324	Q1189	Q1188	E1121	V1058	D992	I919	H851	H787	S713	P639	P568	R498	M437	K372
T1325	P1122	S1189	E1121	V1059	D992	I919	H851	H787	S713	P639	P568	R498	M437	K373
R1326	P1123	Q1190	P1122	P1060	L993	I920	D853	S783	E715	Q640	P570	E500	M439	G374
M1327	H1124	W1191	G1061	G1061	Q994	G921	I854	K789	D716	G641	I571	Q503	D440	L374
T1328	H1124	L1192	E1062	E995	D922	D922	T855	K789	D716	G641	I571	Q503	D440	L375
T1329	L1195	L1195	M1063	L996	Q926	Q926	R856	S793	V719	F646	S573	L504	L443	V376
M1330	E1196	E1196	V1066	L998	I929	I929	R857	E795	R720	G647	K575	L504	L443	P377
S1331	L1197	L1197	L1067	L999	Q929	Q929	R858	S796	F721	G648	Q576	V507	F444	T381
F1332	D1198	D1198	L1067	L999	I929	I929	R859	S796	F721	G648	Q576	V507	F444	P382
I1333	Q1130	Q1130	A1068	L1000	E932	E932	R860	K797	L722	Q650	L577	V512	R446	I383
D1334	L1133	L1133	A1069	L1000	Y933	Y933	R861	G798	N723	Q650	L577	V512	R446	I384
I1335	L1134	L1134	Q1070	M1004	Q934	Q934	R862	G799	E724	R651	V580	P514	S449	I385
M1336	I1138	I1138	S1071	M1004	Q935	Q935	R863	V800	A725	N654	N594	Q515	L450	I386
E1337	E1139	E1139	I1072	E1005	L936	L936	R864	N802	R726	N654	N594	Q515	L450	I387
G1340	H1140	H1140	G1073	I1006	Y937	Y937	R865	S803	K728	F655	I588	N517	K452	L388
E1341	L1143	L1143	E1074	I1007	Q938	Q938	R866	V804	A729	L658	L588	N517	K452	L389
E1342	K1144	K1144	P1075	Q1008	D939	D939	R867	R806	G730	H659	Q589	P519	S454	V392
F1343	S1145	S1145	T1077	M1009	R940	R940	R868	R806	R731	N660	R590	C520	M455	I393
G1344	V1146	V1146	Q1078	Q1011	I942	I942	R871	G807	L732	G661	F591	N521	M456	I394
R1345	T1147	T1147	M1079	Q1012	F942	F942	R872	L408	N736	F662	D592	G522	A457	I395
R1346	E1214	E1214	T1080	D1013	L943	L943	R873	T809	L737	S663	T895	V523	R458	P396
A1347	R1215	R1215	L1081	A1013	V946	V946	R874	P810	K738	G665	T896	V524	V460	R399
L1348	I1148	I1148	ASN	V1015	F947	F947	R875	Q811	D739	I666	L597	D526	V461	P400
V1349	T1150	T1150	THR	T1016	I947	I947	R876	E812	L740	G667	L598	T527	V462	I401
R1350	S1150	S1150	PHE	L1017	N953	N953	R877	P814	N741	G667	S599	L528	I463	G401
E1351	H1151	H1151	THR	L1018	Q954	Q954	R878	P815	N742	G670	P600	L528	I463	G401
P1352	I1152	I1152	PHE	C1019	P855	P855	R879	R816	V743	A671	K601	L531	Y465	Y404
R1353	Y1153	Y1153	ALA	C1020	P856	P856	R880	H816	V744	A672	D602	L534	S466	V405
V1354	D1155	D1155	GLY	L1021	P857	P857	R881	N818	Q745	G673	L605	L534	T467	I406
R1355	N1222	N1222	VAL	L1022	V958	V958	R882	N818	M746	P874	M605	T535	F468	R407





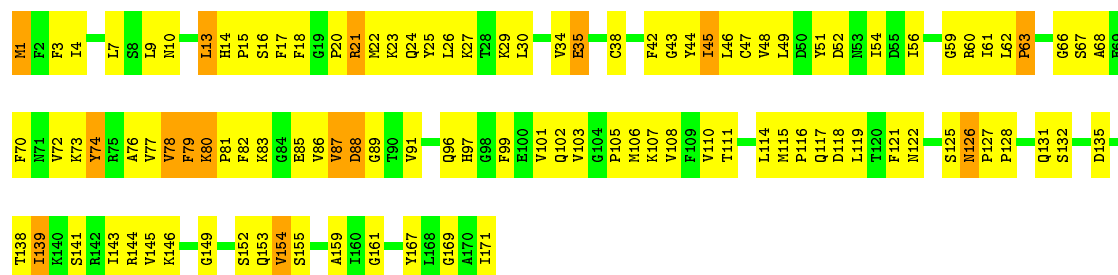
• Molecule 6: DNA-directed RNA polymerase II subunit RPB3

Chain C: 23% 48% 11% 16%

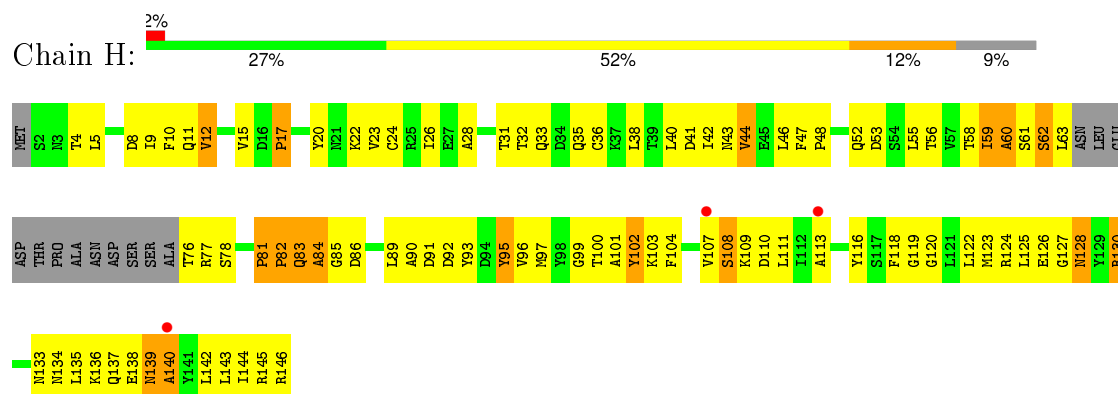


• Molecule 7: DNA-directed RNA polymerase II subunit RPB4

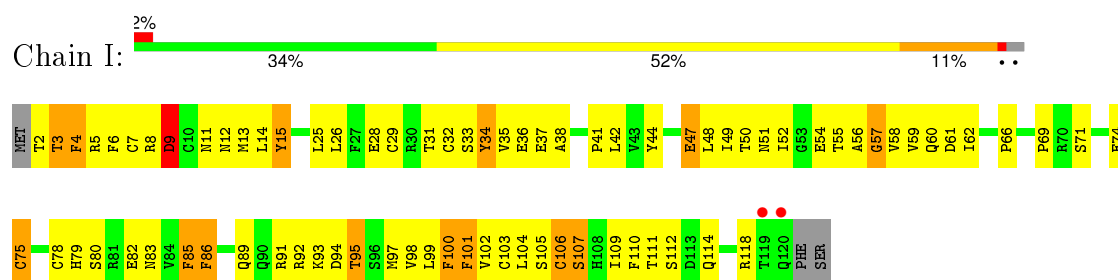
Chain D: 28% 38% 11% 20%



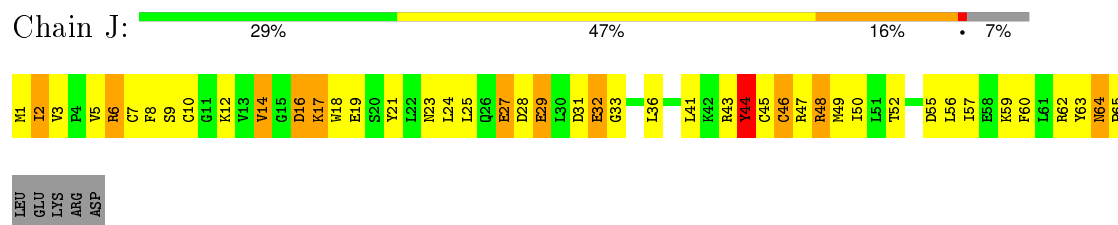
- Molecule 11: DNA-directed RNA polymerases I, II, and III subunit RPABC3



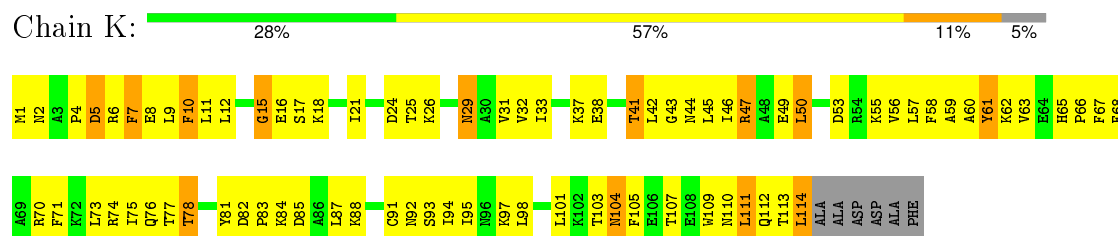
- Molecule 12: DNA-directed RNA polymerase II subunit RPB9



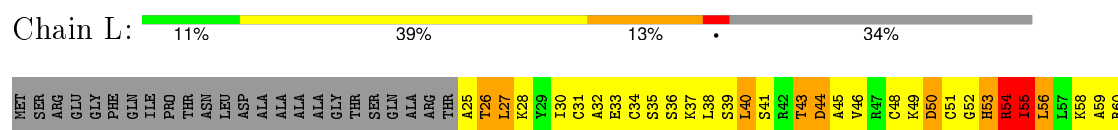
- Molecule 13: DNA-directed RNA polymerases I, II, and III subunit RPABC5



- Molecule 14: DNA-directed RNA polymerase II subunit RPB11



- Molecule 15: 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	222.06 Å 393.12 Å 283.73 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.80 49.14 – 3.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-3.80) 99.8 (49.14-3.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.95 (at 3.77 Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.215 , 0.240 0.225 , 0.244	Depositor DCC
R_{free} test set	2410 reflections (1.98%)	DCC
Wilson B-factor (Å ²)	106.6	Xtriage
Anisotropy	0.442	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 58.8	EDS
Estimated twinning fraction	0.045 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.045 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 121417 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	31804	wwPDB-VP
Average B, all atoms (Å ²)	116.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.84% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, CPT, 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	T	1.41	5/373 (1.3%)	1.79	11/572 (1.9%)
2	N	1.38	0/161	1.10	0/247
3	P	0.95	0/242	0.98	0/377
4	A	0.43	0/11339	0.72	4/15334 (0.0%)
5	B	0.42	0/8981	0.68	0/12108
6	C	0.44	0/2133	0.72	0/2891
7	D	0.42	0/1437	0.69	1/1925 (0.1%)
8	E	0.41	0/1788	0.65	0/2406
9	F	0.49	0/691	0.77	0/933
10	G	0.45	0/1368	0.72	0/1844
11	H	0.38	0/1086	0.65	0/1470
12	I	0.36	0/989	0.65	0/1331
13	J	0.47	0/541	0.74	0/727
14	K	0.45	0/937	0.68	0/1265
15	L	0.47	0/366	0.71	0/485
All	All	0.46	5/32432 (0.0%)	0.73	16/43915 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	T	0	2
2	N	0	2
6	C	0	1
13	J	0	1
All	All	0	6

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	T	16	DG	N3-C4	8.85	1.41	1.35
1	T	17	DG	N3-C4	7.68	1.40	1.35
1	T	17	DG	C2-N3	6.93	1.38	1.32
1	T	16	DG	N1-C2	5.71	1.42	1.37
1	T	14	DT	O3'-P	5.20	1.67	1.61

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	17	DG	O4'-C1'-N9	11.85	116.29	108.00
1	T	16	DG	O4'-C1'-N9	9.50	114.65	108.00
1	T	17	DG	N3-C2-N2	7.61	125.22	119.90
4	A	567	LYS	C-N-CD	6.05	141.11	128.40
1	T	16	DG	N1-C2-N3	-5.93	120.34	123.90
1	T	15	DT	C4'-C3'-C2'	5.50	108.05	103.10
1	T	17	DG	O4'-C4'-C3'	5.42	109.25	106.00
1	T	12	DA	O4'-C1'-N9	5.42	111.79	108.00
4	A	425	GLN	N-CA-C	-5.42	96.38	111.00
4	A	466	SER	N-CA-C	5.31	125.33	111.00
1	T	16	DG	C4'-C3'-C2'	-5.09	98.52	103.10
7	D	26	THR	N-CA-C	-5.06	97.33	111.00
1	T	27	DT	C4'-C3'-C2'	5.04	107.63	103.10
4	A	311	GLN	N-CA-C	5.01	124.53	111.00
1	T	17	DG	N1-C2-N3	-5.00	120.90	123.90
1	T	16	DG	C8-N9-C1'	5.00	133.50	127.00

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	C	82	TYR	Sidechain
13	J	44	TYR	Sidechain
2	N	5	DT	Sidechain
2	N	6	DA	Sidechain
1	T	11	DT	Sidechain
1	T	12	DA	Sidechain

5.2 Too-close contacts ⓘ

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

the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	T	336	0	195	46	0
2	N	143	0	80	20	0
3	P	216	0	108	13	0
4	A	11140	0	11217	1294	0
5	B	8810	0	8847	1025	0
6	C	2095	0	2052	253	0
7	D	1427	0	1451	136	0
8	E	1752	0	1776	149	0
9	F	679	0	701	79	0
10	G	1340	0	1357	152	0
11	H	1068	0	1040	131	0
12	I	971	0	930	102	0
13	J	532	0	543	106	0
14	K	919	0	929	115	0
15	L	364	0	388	57	0
16	T	3	0	0	1	0
17	A	2	0	0	0	0
17	B	1	0	0	0	0
17	C	1	0	0	0	0
17	I	2	0	0	0	0
17	J	1	0	0	0	0
17	L	1	0	0	0	0
18	A	1	0	0	0	0
All	All	31804	0	31614	3347	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 53.

All (3347) 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)
11:H:100:THR:HG23	11:H:138:GLU:HA	1.26	1.16
10:G:138:THR:HG22	10:G:139:ILE:H	1.09	1.12
4:A:53:LEU:HD23	4:A:54:ASN:H	0.99	1.12
4:A:1094:VAL:HG13	4:A:1113:THR:HG21	1.32	1.11
5:B:510:LYS:HG3	5:B:511:PRO:HD3	1.12	1.11
5:B:273:LEU:HB2	5:B:276:ILE:HD12	1.30	1.09
1:T:22:DC:H2"	1:T:23:DC:H5"	1.16	1.08
4:A:1438:THR:HB	5:B:1144:ALA:HB3	1.37	1.06
5:B:792:MET:HE2	5:B:857:ARG:HH12	1.16	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1017:LEU:HB2	8:E:206:GLY:H	1.17	1.05
5:B:806:THR:HG22	5:B:808:ALA:H	1.22	1.03
4:A:855:THR:HG21	4:A:857:ARG:HE	1.17	1.02
8:E:22:MET:HE3	8:E:26:ARG:HH21	1.18	1.02
12:I:111:THR:HG22	12:I:112:SER:H	1.25	1.02
5:B:882:THR:HG22	5:B:884:ARG:H	1.26	1.01
4:A:1161:THR:HG22	4:A:1163:ILE:H	1.26	1.01
5:B:589:VAL:HG12	5:B:590:HIS:H	1.22	1.01
5:B:172:ILE:HD13	5:B:178:ASN:HB3	1.42	1.01
7:D:40:HIS:HB3	10:G:73:LYS:HZ3	1.22	1.00
14:K:47:ARG:HB3	14:K:47:ARG:HH11	1.24	1.00
6:C:116:LYS:HD3	6:C:140:ASN:HB3	1.40	1.00
4:A:828:ALA:CB	5:B:530:GLY:HA2	1.92	1.00
6:C:43:THR:HG22	6:C:44:LEU:H	1.24	1.00
4:A:40:THR:HG22	4:A:41:MET:HG3	1.44	1.00
5:B:918:ILE:HB	5:B:935:ARG:HD2	1.43	0.99
4:A:475:THR:HG23	4:A:476:SER:H	1.27	0.99
1:T:22:DC:H2''	1:T:23:DC:C5'	1.92	0.99
4:A:535:THR:HG21	4:A:616:VAL:HA	1.46	0.98
4:A:53:LEU:HD23	4:A:54:ASN:N	1.76	0.98
8:E:19:VAL:O	8:E:23:VAL:HG23	1.63	0.98
5:B:510:LYS:CG	5:B:511:PRO:HD3	1.92	0.98
4:A:1445:ILE:HD12	4:A:1445:ILE:H	1.23	0.98
7:D:40:HIS:HB3	10:G:73:LYS:NZ	1.80	0.96
6:C:39:ALA:HA	6:C:164:ALA:HB3	1.45	0.96
6:C:44:LEU:HB2	6:C:77:ILE:HD11	1.48	0.95
5:B:879:ARG:HH11	5:B:883:LEU:HD22	1.29	0.95
10:G:7:LEU:HB2	10:G:74:TYR:CE2	2.02	0.95
4:A:399:HIS:HB3	4:A:400:PRO:HD3	1.46	0.95
6:C:166:GLU:HG3	14:K:10:PHE:HZ	1.32	0.95
5:B:563:MET:HE3	5:B:580:VAL:HB	1.49	0.95
5:B:365:THR:HG23	5:B:367:LEU:H	1.30	0.94
5:B:233:PRO:HG2	5:B:234:ILE:HD12	1.48	0.94
8:E:94:LYS:HE2	8:E:98:ILE:HD11	1.50	0.94
11:H:4:THR:HA	11:H:60:ALA:HB2	1.49	0.94
4:A:779:PHE:HE1	4:A:785:PRO:HD3	1.32	0.93
5:B:169:ARG:HB2	5:B:454:THR:HG23	1.47	0.93
4:A:1189:SER:O	4:A:1241:ARG:HD3	1.67	0.93
6:C:47:ASP:HA	15:L:69:ALA:HB3	1.51	0.93
4:A:1127:ASP:HB3	4:A:1130:GLN:HB3	1.48	0.93
5:B:98:THR:O	5:B:126:SER:HB2	1.69	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:903:ASN:HD22	4:A:904:THR:N	1.68	0.92
6:C:45:ALA:HA	6:C:72:LEU:HD12	1.51	0.91
5:B:483:LEU:HD11	5:B:491:THR:HG23	1.51	0.91
5:B:579:ARG:HB2	5:B:586:TRP:NE1	1.85	0.91
4:A:1004:ASN:ND2	8:E:167:ARG:HD2	1.86	0.91
4:A:828:ALA:HB2	5:B:530:GLY:HA2	1.51	0.91
5:B:217:ARG:HE	5:B:405:ARG:HB2	1.33	0.91
5:B:1159:ARG:HB3	5:B:1159:ARG:HH11	1.35	0.91
10:G:1:MET:SD	10:G:79:PHE:HD1	1.93	0.90
4:A:829:VAL:HG21	5:B:508:LEU:HD13	1.50	0.90
4:A:239:LEU:HD12	4:A:240:PRO:HD2	1.52	0.90
13:J:64:ASN:HB3	13:J:65:PRO:CD	2.00	0.90
5:B:579:ARG:HB2	5:B:586:TRP:HE1	1.35	0.90
5:B:577:ALA:HB1	5:B:589:VAL:HG11	1.52	0.90
6:C:98:VAL:O	6:C:99:LEU:HD23	1.72	0.90
9:F:86:THR:OG1	9:F:89:GLU:HG3	1.72	0.90
5:B:510:LYS:HG3	5:B:511:PRO:CD	2.02	0.89
4:A:963:ILE:HD11	4:A:1048:ASN:HB3	1.54	0.89
5:B:25:ILE:HD11	5:B:653:VAL:O	1.72	0.89
1:T:11:DT:H2''	1:T:12:DA:O5'	1.71	0.89
13:J:44:TYR:HA	13:J:47:ARG:HB2	1.53	0.89
5:B:594:ALA:HA	5:B:617:ARG:HH12	1.38	0.89
4:A:763:ALA:O	4:A:803:SER:HB3	1.72	0.89
13:J:5:VAL:HG12	13:J:6:ARG:HG3	1.53	0.89
14:K:53:ASP:HB3	14:K:56:VAL:HG23	1.53	0.89
4:A:567:LYS:CG	4:A:568:PRO:HD2	2.02	0.89
4:A:709:THR:HG22	4:A:711:ARG:H	1.36	0.89
5:B:364:ILE:HG12	5:B:585:VAL:HG13	1.55	0.89
4:A:1116:LEU:N	4:A:1308:THR:HG22	1.88	0.88
6:C:7:GLN:HG2	14:K:104:ASN:HD22	1.38	0.88
9:F:93:ILE:HD11	9:F:134:ILE:HD11	1.56	0.88
4:A:646:PHE:O	4:A:650:GLN:HG3	1.73	0.88
8:E:153:HIS:HB3	8:E:196:VAL:HG11	1.56	0.88
15:L:32:ALA:HB3	15:L:55:ILE:HD12	1.54	0.88
5:B:879:ARG:NH1	5:B:883:LEU:HD22	1.87	0.88
4:A:1312:ASN:O	4:A:1316:VAL:HG23	1.74	0.88
10:G:13:LEU:HD21	10:G:17:PHE:HB2	1.55	0.88
4:A:356:ASP:HB2	4:A:469:ARG:NH1	1.89	0.88
4:A:366:VAL:HG21	4:A:460:VAL:HG22	1.56	0.88
4:A:901:LEU:H	4:A:926:GLN:NE2	1.72	0.88
6:C:133:ILE:HD11	6:C:237:SER:HA	1.54	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:211:VAL:O	5:B:480:SER:HA	1.73	0.87
5:B:1166:CYS:HB2	5:B:1215:ARG:NH1	1.90	0.87
1:T:24:DT:H2"	1:T:25:DC:O5'	1.74	0.87
8:E:14:ARG:HH21	8:E:141:VAL:HG12	1.37	0.87
5:B:1002:THR:HG21	5:B:1006:ILE:HD12	1.57	0.87
5:B:1159:ARG:HB3	5:B:1159:ARG:NH1	1.89	0.87
4:A:49:LYS:NZ	4:A:61:ILE:HG13	1.89	0.87
4:A:321:PRO:O	4:A:322:VAL:HB	1.73	0.87
4:A:225:ASN:HD22	4:A:228:PHE:H	1.23	0.86
6:C:57:VAL:HG11	13:J:60:PHE:HB3	1.54	0.86
10:G:127:PRO:HG2	10:G:138:THR:HG21	1.58	0.86
5:B:1165:ILE:HG22	5:B:1166:CYS:N	1.90	0.86
4:A:441:PRO:HD2	4:A:498:ARG:NH2	1.90	0.86
9:F:82:THR:HG22	9:F:84:TYR:H	1.36	0.86
5:B:594:ALA:HA	5:B:617:ARG:NH1	1.89	0.86
4:A:754:SER:H	4:A:757:ASN:HD22	1.23	0.86
8:E:177:ARG:HD3	8:E:215:MET:HG3	1.57	0.86
4:A:537:ARG:HD2	11:H:20:TYR:HE1	1.39	0.85
5:B:1159:ARG:HD3	5:B:1193:GLN:HG3	1.56	0.85
4:A:427:GLN:HG3	4:A:430:TRP:CZ2	2.11	0.85
9:F:111:LEU:H	9:F:111:LEU:HD12	1.41	0.85
5:B:467:GLY:H	5:B:475:SER:HB3	1.40	0.85
5:B:516:ASN:N	5:B:516:ASN:HD22	1.74	0.85
8:E:22:MET:HE3	8:E:26:ARG:NH2	1.91	0.85
10:G:18:PHE:HA	10:G:22:MET:CE	2.07	0.84
5:B:798:TYR:HE2	6:C:62:PHE:CE2	1.95	0.84
10:G:138:THR:HG22	10:G:139:ILE:N	1.91	0.84
1:T:22:DC:C2'	1:T:23:DC:H5"	2.06	0.84
2:N:6:DA:H2"	2:N:7:DG:OP2	1.76	0.84
4:A:249:SER:O	4:A:250:ILE:HG13	1.76	0.84
6:C:32:SER:O	6:C:36:VAL:HG23	1.78	0.84
4:A:567:LYS:HB3	11:H:96:VAL:H	1.43	0.84
11:H:4:THR:HA	11:H:60:ALA:CB	2.08	0.83
4:A:1283:VAL:HG12	4:A:1284:MET:H	1.42	0.83
5:B:1224:PHE:HE2	8:E:171:LYS:HG3	1.43	0.83
10:G:34:VAL:HG12	10:G:45:ILE:HG21	1.60	0.83
11:H:42:ILE:HG23	11:H:95:TYR:HE1	1.40	0.83
5:B:1065:GLN:HE21	5:B:1067:ARG:N	1.75	0.83
10:G:23:LYS:HG3	10:G:56:ILE:HD11	1.61	0.83
5:B:1180:PHE:HB3	5:B:1191:ILE:HD12	1.61	0.83
12:I:26:LEU:HD23	12:I:37:GLU:HA	1.60	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:48:ILE:HG21	10:G:4:ILE:HB	1.60	0.83
1:T:18:DC:H2"	1:T:19:DC:O5'	1.79	0.83
8:E:117:THR:HG22	8:E:119:SER:H	1.44	0.83
4:A:93:VAL:HG22	4:A:301:ALA:HA	1.61	0.83
11:H:130:ARG:H	11:H:130:ARG:HD2	1.44	0.83
4:A:55:ASP:C	4:A:57:ARG:H	1.81	0.83
6:C:38:ILE:HA	6:C:173:ALA:HB2	1.61	0.83
11:H:100:THR:OG1	11:H:138:GLU:HG3	1.78	0.82
6:C:43:THR:HG22	6:C:44:LEU:N	1.93	0.82
4:A:1242:VAL:HG12	4:A:1243:VAL:H	1.45	0.82
4:A:809:THR:HG23	4:A:812:GLU:OE1	1.78	0.82
4:A:860:LEU:HD11	4:A:1393:ASN:HB2	1.59	0.82
4:A:56:PRO:O	4:A:57:ARG:HG3	1.80	0.82
10:G:14:HIS:ND1	10:G:15:PRO:HD2	1.94	0.82
8:E:16:PHE:CZ	8:E:20:LYS:HE2	2.14	0.82
1:T:20:DC:H2"	1:T:21:DT:O5'	1.80	0.82
4:A:1017:LEU:HB2	8:E:206:GLY:N	1.95	0.82
7:D:144:THR:O	7:D:148:LEU:HB2	1.79	0.82
5:B:613:VAL:HG13	5:B:627:PHE:O	1.79	0.82
13:J:12:LYS:O	13:J:14:VAL:HG23	1.79	0.82
4:A:70:CYS:O	4:A:72:GLU:HG2	1.79	0.82
11:H:93:TYR:HB3	11:H:144:ILE:O	1.80	0.82
5:B:801:LYS:O	13:J:52:THR:HG23	1.78	0.82
4:A:743:VAL:O	4:A:747:VAL:HG23	1.79	0.82
4:A:23:SER:HA	4:A:233:TRP:NE1	1.94	0.82
4:A:353:ILE:HG21	4:A:487:MET:HE3	1.61	0.82
5:B:189:LEU:HA	5:B:192:LEU:HD12	1.62	0.82
4:A:458:HIS:CE1	4:A:507:VAL:HG21	2.15	0.82
5:B:23:ALA:HB1	5:B:24:PRO:HD2	1.62	0.82
1:T:25:DC:H2"	1:T:26:DA:O5'	1.79	0.81
13:J:57:ILE:HA	13:J:60:PHE:HD2	1.43	0.81
4:A:1127:ASP:HB3	4:A:1130:GLN:CB	2.09	0.81
4:A:567:LYS:CD	4:A:568:PRO:HD2	2.11	0.81
5:B:792:MET:HE2	5:B:857:ARG:NH1	1.94	0.81
5:B:839:MET:HE3	5:B:1010:LEU:HD21	1.63	0.81
5:B:821:GLN:HE22	5:B:851:PHE:HA	1.45	0.81
5:B:521:LEU:HD22	5:B:633:VAL:HG12	1.60	0.80
6:C:6:PRO:HB3	6:C:25:VAL:HG12	1.64	0.80
4:A:886:ILE:HG22	4:A:887:GLY:N	1.95	0.80
5:B:53:GLN:HG2	5:B:547:VAL:HG22	1.61	0.80
5:B:563:MET:CE	5:B:580:VAL:HB	2.11	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:611:PRO:HB3	5:B:685:LEU:HD11	1.63	0.80
8:E:202:SER:OG	8:E:204:THR:HG22	1.81	0.80
11:H:102:TYR:OH	11:H:122:LEU:HD22	1.81	0.80
4:A:858:ASN:ND2	4:A:860:LEU:H	1.80	0.80
5:B:710:LEU:HA	5:B:733:HIS:HB3	1.64	0.80
6:C:172:PRO:O	6:C:235:VAL:HG23	1.81	0.80
11:H:59:ILE:HG22	11:H:60:ALA:N	1.97	0.80
5:B:244:LEU:HD21	5:B:366:GLN:NE2	1.97	0.80
4:A:868:TYR:HD2	4:A:1058:VAL:HG21	1.46	0.80
4:A:598:LEU:HA	11:H:122:LEU:HD13	1.64	0.79
7:D:35:LEU:HD23	7:D:174:PRO:HD2	1.65	0.79
4:A:524:VAL:HG12	4:A:525:GLN:H	1.47	0.79
4:A:475:THR:HG23	4:A:476:SER:N	1.96	0.79
5:B:782:LEU:HD12	5:B:788:ARG:HH11	1.46	0.79
3:P:3:U:H2'	3:P:4:G:C8	2.17	0.79
10:G:81:PRO:HG3	10:G:106:MET:SD	2.23	0.79
4:A:534:LEU:O	4:A:574:GLY:HA3	1.82	0.79
5:B:999:MET:HG3	5:B:1000:PRO:HD2	1.63	0.79
4:A:902:LEU:HG	4:A:926:GLN:HG3	1.64	0.79
12:I:55:THR:HG21	12:I:109:ILE:HD13	1.65	0.79
5:B:847:ASP:HB3	6:C:167:HIS:NE2	1.98	0.79
5:B:33:VAL:HG21	5:B:638:PHE:HZ	1.48	0.79
4:A:265:LYS:HD2	4:A:265:LYS:H	1.47	0.79
5:B:859:TYR:OH	5:B:941:LEU:HD12	1.83	0.78
5:B:882:THR:CG2	5:B:884:ARG:HB2	2.12	0.78
4:A:741:ASN:HD22	4:A:744:LYS:H	1.31	0.78
5:B:549:THR:HG22	5:B:550:ASP:H	1.46	0.78
5:B:125:SER:HA	5:B:171:PRO:HA	1.63	0.78
10:G:122:ASN:ND2	10:G:125:SER:HB3	1.98	0.78
1:T:11:DT:H2''	1:T:12:DA:C5'	2.12	0.78
12:I:85:PHE:HD2	12:I:85:PHE:H	1.27	0.78
7:D:49:ALA:HB2	7:D:174:PRO:HB3	1.66	0.78
14:K:45:LEU:HG	14:K:94:ILE:HD13	1.63	0.78
8:E:213:ILE:HG12	8:E:214:CYS:H	1.47	0.78
5:B:953:LEU:HD21	5:B:965:LYS:HB2	1.65	0.78
5:B:35:SER:HA	5:B:811:TYR:HE2	1.46	0.78
8:E:135:PHE:HB3	8:E:140:LEU:HD11	1.64	0.78
7:D:40:HIS:CB	10:G:73:LYS:NZ	2.47	0.78
4:A:828:ALA:HB1	5:B:530:GLY:HA2	1.64	0.78
14:K:65:HIS:CD2	14:K:67:PHE:H	2.01	0.78
4:A:670:ILE:HG23	4:A:805:LEU:HD21	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:217:ARG:NE	5:B:405:ARG:HB2	1.99	0.78
4:A:886:ILE:HD11	4:A:943:LEU:HB3	1.64	0.78
5:B:615:MET:HB3	5:B:626:ILE:HG12	1.66	0.78
7:D:189:ASP:O	7:D:193:THR:HB	1.84	0.78
4:A:855:THR:HG23	4:A:857:ARG:HG3	1.66	0.77
4:A:446:ARG:CD	4:A:480:ALA:HB2	2.14	0.77
13:J:1:MET:N	13:J:57:ILE:H	1.81	0.77
4:A:53:LEU:CD2	4:A:54:ASN:H	1.91	0.77
5:B:520:GLY:H	5:B:748:ILE:HG22	1.49	0.77
5:B:603:LEU:HD13	5:B:608:ASP:HB2	1.65	0.77
7:D:17:LYS:HE2	7:D:17:LYS:N	1.99	0.77
9:F:111:LEU:C	9:F:113:GLY:H	1.86	0.77
14:K:47:ARG:HB3	14:K:47:ARG:NH1	1.99	0.77
4:A:563:PRO:HG3	4:A:572:TRP:CZ2	2.19	0.77
4:A:779:PHE:CE1	4:A:785:PRO:HD3	2.18	0.77
5:B:1017:ILE:HB	5:B:1018:PRO:HD3	1.65	0.77
8:E:179:GLN:HB2	8:E:182:ASP:HB2	1.67	0.77
12:I:75:CYS:HG	12:I:78:CYS:HG	1.32	0.77
4:A:885:THR:O	4:A:940:ARG:HD2	1.84	0.77
10:G:80:LYS:HD3	10:G:80:LYS:N	1.98	0.77
10:G:15:PRO:HA	10:G:18:PHE:CD1	2.19	0.77
4:A:1420:ASP:HB3	4:A:1422:ARG:HG3	1.65	0.77
13:J:1:MET:N	13:J:56:LEU:N	2.33	0.77
5:B:1085:ILE:HD12	5:B:1085:ILE:N	1.99	0.77
13:J:3:VAL:HG21	13:J:18:TRP:HB2	1.65	0.77
4:A:49:LYS:HZ1	4:A:61:ILE:HG13	1.48	0.77
4:A:718:VAL:O	4:A:722:LEU:HD12	1.85	0.77
5:B:978:ASP:OD2	5:B:1098:MET:HG2	1.84	0.77
10:G:80:LYS:HD3	10:G:80:LYS:H	1.50	0.76
4:A:853:ASP:O	4:A:854:ASN:HB2	1.85	0.76
13:J:16:ASP:OD1	13:J:17:LYS:HD2	1.84	0.76
5:B:1065:GLN:HE21	5:B:1067:ARG:H	1.30	0.76
4:A:709:THR:HG23	12:I:94:ASP:HA	1.68	0.76
14:K:113:THR:O	14:K:114:LEU:HB2	1.83	0.76
6:C:66:ARG:NH1	13:J:2:ILE:HG21	2.00	0.76
5:B:996:ARG:NH2	6:C:175:ALA:H	1.84	0.76
9:F:103:MET:O	9:F:104:ASN:HB2	1.84	0.76
5:B:1162:ILE:HD11	5:B:1194:ILE:HD13	1.66	0.76
10:G:18:PHE:HA	10:G:22:MET:HE3	1.65	0.76
4:A:496:GLU:HG2	9:F:99:LEU:HD23	1.67	0.76
4:A:1208:THR:HG22	4:A:1210:GLY:H	1.51	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1116:LEU:HB2	4:A:1329:THR:OG1	1.86	0.76
5:B:705:MET:H	5:B:710:LEU:HD12	1.51	0.76
5:B:778:MET:CE	5:B:1094:ARG:HD3	2.15	0.76
4:A:414:ASP:OD1	4:A:416:ARG:HG2	1.86	0.76
5:B:862:GLN:HG2	5:B:963:PHE:HD1	1.51	0.76
5:B:467:GLY:N	5:B:475:SER:HB3	2.01	0.76
5:B:957:ASN:HD22	5:B:961:LEU:HD12	1.49	0.76
8:E:2:ASP:O	8:E:3:GLN:HG2	1.84	0.76
11:H:89:LEU:HB3	11:H:91:ASP:OD1	1.86	0.76
8:E:180:ARG:HH21	8:E:192:ARG:HB2	1.51	0.76
11:H:38:LEU:HD12	11:H:124:ARG:O	1.85	0.76
5:B:309:GLN:OE1	12:I:52:ILE:HD11	1.86	0.76
4:A:1341:ILE:HD12	4:A:1379:GLY:O	1.86	0.75
4:A:1424:VAL:HG13	4:A:1436:ILE:CD1	2.17	0.75
9:F:90:ARG:HD3	9:F:155:LEU:HD12	1.67	0.75
5:B:278:GLN:HG2	5:B:279:ASP:H	1.49	0.75
5:B:882:THR:HG22	5:B:884:ARG:N	1.98	0.75
5:B:800:GLN:HB3	13:J:52:THR:HG21	1.66	0.75
13:J:8:PHE:H	13:J:49:MET:HE3	1.50	0.75
4:A:590:ARG:HH21	4:A:620:LYS:CB	1.99	0.75
10:G:43:GLY:HA3	10:G:80:LYS:HB3	1.69	0.75
4:A:866:PHE:C	4:A:867:ILE:HD12	2.07	0.75
6:C:239:PRO:HB2	6:C:241:ASP:OD1	1.87	0.75
12:I:8:ARG:HG3	12:I:34:TYR:HE1	1.52	0.75
5:B:806:THR:HG22	5:B:808:ALA:N	2.01	0.75
13:J:44:TYR:H	13:J:44:TYR:HD2	1.34	0.75
8:E:14:ARG:HH21	8:E:141:VAL:CG1	1.99	0.75
4:A:567:LYS:HG3	4:A:568:PRO:HD2	1.67	0.75
14:K:7:PHE:HA	14:K:10:PHE:CE2	2.22	0.75
5:B:363:HIS:O	5:B:364:ILE:HB	1.84	0.75
4:A:537:ARG:HD2	11:H:20:TYR:CE1	2.21	0.74
4:A:466:SER:O	5:B:1103:ILE:HD11	1.86	0.74
12:I:111:THR:HG22	12:I:112:SER:N	2.02	0.74
5:B:758:PHE:HB3	5:B:761:HIS:HD2	1.52	0.74
3:P:3:U:H2'	3:P:4:G:H8	1.50	0.74
6:C:7:GLN:HG2	14:K:104:ASN:ND2	2.03	0.74
6:C:147:LEU:HB2	6:C:151:GLN:HB2	1.69	0.74
14:K:65:HIS:HD2	14:K:67:PHE:H	1.36	0.74
4:A:1239:ARG:HH22	4:A:1241:ARG:NH2	1.86	0.74
5:B:1072:MET:CE	5:B:1085:ILE:HB	2.18	0.74
4:A:1341:ILE:HG23	4:A:1342:GLU:N	2.01	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:1152:MET:CE	5:B:1157:ALA:HA	2.18	0.74
4:A:981:LEU:CD2	4:A:1039:LYS:HA	2.17	0.74
4:A:1279:ILE:HD11	4:A:1316:VAL:CG2	2.17	0.74
6:C:5:GLY:O	6:C:7:GLN:HG3	1.88	0.74
5:B:214:ALA:HB3	5:B:498:THR:HA	1.69	0.74
5:B:1182:CYS:O	5:B:1182:CYS:SG	2.45	0.74
7:D:12:ARG:NH2	7:D:12:ARG:HB3	2.03	0.74
5:B:637:LEU:HD12	5:B:693:ILE:HD12	1.68	0.74
11:H:23:VAL:HG22	11:H:43:ASN:HA	1.70	0.74
5:B:971:THR:OG1	6:C:61:GLU:HG3	1.88	0.74
4:A:185:TRP:CZ3	4:A:200:ARG:HG2	2.22	0.74
7:D:52:LEU:HD21	7:D:147:TYR:HE2	1.52	0.74
4:A:1004:ASN:O	4:A:1008:GLN:HB2	1.87	0.74
4:A:19:PHE:O	4:A:1416:ALA:HA	1.86	0.74
5:B:770:GLN:OE1	5:B:983:ARG:HA	1.87	0.74
4:A:528:LEU:O	4:A:531:ILE:HG22	1.88	0.74
4:A:855:THR:HG21	4:A:857:ARG:NE	2.00	0.73
4:A:836:TYR:CE2	4:A:840:ARG:HD2	2.22	0.73
4:A:808:LEU:HD23	4:A:813:PHE:HA	1.70	0.73
7:D:9:GLN:HE21	7:D:38:ILE:HD12	1.53	0.73
4:A:982:THR:HB	4:A:985:ASP:H	1.53	0.73
4:A:1444:MET:HG2	10:G:60:ARG:HA	1.70	0.73
5:B:273:LEU:CB	5:B:276:ILE:HD12	2.16	0.73
4:A:567:LYS:HB3	11:H:95:TYR:HA	1.70	0.73
4:A:288:ALA:HA	4:A:291:GLU:OE2	1.89	0.73
4:A:518:LYS:HE2	4:A:624:SER:O	1.88	0.73
5:B:1077:THR:HG22	14:K:44:ASN:HD21	1.52	0.73
5:B:1077:THR:HG22	14:K:44:ASN:ND2	2.03	0.73
4:A:164:ARG:HG3	4:A:165:GLY:N	2.03	0.73
4:A:682:THR:HG23	4:A:728:LYS:HE3	1.70	0.73
5:B:1065:GLN:NE2	5:B:1067:ARG:HG2	2.03	0.73
5:B:287:ARG:HG2	5:B:292:ILE:HA	1.70	0.73
4:A:55:ASP:CG	4:A:55:ASP:O	2.22	0.73
5:B:642:ASP:HA	5:B:649:LYS:HA	1.68	0.73
4:A:351:THR:HB	5:B:1103:ILE:HD12	1.71	0.73
4:A:960:ILE:HA	4:A:963:ILE:HG22	1.69	0.73
4:A:283:GLY:O	4:A:285:PRO:HD3	1.88	0.73
4:A:849:MET:HE1	4:A:1061:GLY:HA2	1.70	0.73
13:J:43:ARG:HG3	13:J:45:CYS:SG	2.28	0.73
5:B:521:LEU:HB3	5:B:633:VAL:HG11	1.70	0.73
7:D:12:ARG:HH21	7:D:12:ARG:HB3	1.53	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:628:GLY:O	4:A:632:VAL:HG23	1.88	0.73
8:E:153:HIS:HB3	8:E:196:VAL:CG1	2.18	0.73
7:D:56:ARG:HB2	7:D:148:LEU:HD22	1.69	0.73
6:C:194:GLU:O	6:C:195:GLN:HG3	1.87	0.73
4:A:963:ILE:HD11	4:A:1048:ASN:CB	2.19	0.72
5:B:603:LEU:HB3	5:B:609:ILE:HD11	1.70	0.72
6:C:262:LEU:HD11	14:K:87:LEU:HD23	1.71	0.72
5:B:175:ARG:HH11	5:B:175:ARG:HG2	1.53	0.72
5:B:798:TYR:HE2	6:C:62:PHE:CZ	2.07	0.72
6:C:47:ASP:HA	15:L:69:ALA:CB	2.17	0.72
4:A:23:SER:HB3	4:A:233:TRP:CZ2	2.24	0.72
3:P:10:G:H4'	4:A:485:ASP:OD1	1.89	0.72
4:A:446:ARG:HD3	4:A:480:ALA:HB2	1.71	0.72
5:B:401:PHE:HA	5:B:404:LYS:HG3	1.70	0.72
5:B:737:THR:HG21	12:I:66:PRO:HA	1.71	0.72
11:H:81:PRO:CB	11:H:82:PRO:HD2	2.19	0.72
5:B:1201:LYS:HE2	5:B:1205:GLN:OE1	1.89	0.72
5:B:190:TYR:CE2	13:J:62:ARG:HB3	2.24	0.72
4:A:794:PRO:HG2	4:A:795:GLU:OE2	1.89	0.72
5:B:911:ILE:HD11	5:B:941:LEU:HD13	1.70	0.72
4:A:590:ARG:NH2	4:A:620:LYS:HB3	2.05	0.72
7:D:18:VAL:O	7:D:19:GLU:HB2	1.89	0.72
6:C:212:PRO:HB3	6:C:213:PRO:HD2	1.70	0.72
5:B:791:THR:HG22	5:B:858:SER:O	1.88	0.72
5:B:542:MET:HE2	5:B:743:ILE:HG13	1.72	0.72
5:B:613:VAL:HG22	5:B:628:THR:HA	1.70	0.72
5:B:810:GLU:HA	5:B:815:ARG:HH12	1.53	0.72
5:B:542:MET:CE	5:B:743:ILE:HG13	2.20	0.71
5:B:957:ASN:O	5:B:959:ASP:N	2.23	0.71
5:B:1001:PHE:CE1	5:B:1073:TYR:HB2	2.25	0.71
7:D:170:THR:CG2	7:D:172:LEU:HG	2.20	0.71
5:B:847:ASP:HB3	6:C:167:HIS:CD2	2.25	0.71
8:E:124:VAL:HG13	8:E:132:ILE:HB	1.71	0.71
5:B:980:PHE:HE1	5:B:990:ILE:HD11	1.53	0.71
4:A:87:ALA:HB3	4:A:276:LEU:HD23	1.70	0.71
4:A:798:GLY:HA2	4:A:815:PHE:CD1	2.25	0.71
3:P:8:A:O2'	3:P:9:G:H5'	1.91	0.71
4:A:244:PRO:HG2	4:A:245:PRO:HD3	1.71	0.71
1:T:16:DG:H4'	4:A:1403:GLU:OE2	1.91	0.71
5:B:996:ARG:HH22	6:C:175:ALA:H	1.35	0.71
4:A:1118:VAL:HG12	4:A:1327:ILE:HG13	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:35:LEU:H	7:D:35:LEU:HD12	1.55	0.71
4:A:34:LYS:HG2	4:A:36:ARG:HH21	1.54	0.71
1:T:23:DC:H2'	1:T:24:DT:C6	2.26	0.71
4:A:446:ARG:HB2	4:A:487:MET:SD	2.31	0.71
5:B:830:TYR:CE2	5:B:1000:PRO:HD3	2.26	0.71
13:J:64:ASN:HB3	13:J:65:PRO:HD3	1.71	0.71
13:J:64:ASN:HD22	13:J:65:PRO:HD3	1.54	0.71
5:B:284:ILE:HD13	5:B:333:PHE:HD2	1.56	0.71
11:H:81:PRO:HB2	11:H:82:PRO:HD2	1.71	0.71
7:D:134:THR:HG22	7:D:135:GLY:N	2.06	0.71
5:B:515:HIS:H	5:B:518:HIS:CD2	2.09	0.71
4:A:164:ARG:HG3	4:A:165:GLY:H	1.56	0.71
5:B:295:GLY:H	5:B:298:LEU:HD23	1.55	0.71
5:B:899:ILE:HD11	5:B:911:ILE:HA	1.73	0.71
10:G:115:MET:HB2	10:G:116:PRO:HD2	1.72	0.71
11:H:55:LEU:HD22	11:H:144:ILE:CG2	2.21	0.70
4:A:1279:ILE:HD11	4:A:1316:VAL:HG21	1.72	0.70
5:B:653:VAL:CG2	5:B:689:LEU:HB3	2.21	0.70
4:A:115:LEU:O	4:A:122:MET:HE3	1.92	0.70
11:H:83:GLN:C	11:H:85:GLY:H	1.92	0.70
4:A:265:LYS:HD2	4:A:265:LYS:N	2.04	0.70
6:C:36:VAL:HG21	6:C:251:LEU:HD22	1.72	0.70
10:G:143:ILE:HG22	10:G:144:ARG:N	2.06	0.70
5:B:221:ASN:N	5:B:241:ARG:O	2.24	0.70
11:H:15:VAL:HG22	11:H:26:ILE:HD11	1.73	0.70
5:B:393:LYS:HA	5:B:393:LYS:HE3	1.71	0.70
9:F:97:ARG:O	9:F:101:ILE:HG13	1.91	0.70
13:J:1:MET:H1	13:J:57:ILE:H	1.37	0.70
4:A:1118:VAL:HG23	4:A:1306:LEU:HB2	1.74	0.70
4:A:666:ILE:HD12	4:A:667:GLY:H	1.57	0.70
7:D:9:GLN:NE2	7:D:38:ILE:HD12	2.07	0.70
7:D:170:THR:HG21	7:D:172:LEU:HG	1.73	0.70
5:B:168:GLY:H	5:B:450:ALA:HB1	1.56	0.70
4:A:450:LEU:HD12	4:A:450:LEU:H	1.55	0.70
4:A:541:ILE:HD13	4:A:549:MET:CE	2.22	0.70
4:A:590:ARG:HH21	4:A:620:LYS:HB2	1.55	0.70
4:A:285:PRO:HG2	4:A:288:ALA:HB3	1.73	0.70
10:G:1:MET:SD	10:G:79:PHE:CD1	2.83	0.70
4:A:351:THR:HB	5:B:1103:ILE:CD1	2.22	0.70
5:B:977:GLY:HA3	5:B:1099:VAL:HB	1.74	0.70
6:C:145:CYS:HA	13:J:2:ILE:HD11	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:3:VAL:HG21	13:J:18:TRP:CB	2.22	0.70
9:F:82:THR:HG22	9:F:84:TYR:N	2.06	0.70
6:C:179:GLU:HG2	6:C:180:TYR:N	2.07	0.70
5:B:1159:ARG:HD3	5:B:1193:GLN:CG	2.22	0.70
4:A:981:LEU:HD21	4:A:1039:LYS:HA	1.73	0.70
10:G:145:VAL:HG12	10:G:146:LYS:N	2.05	0.70
4:A:853:ASP:OD1	4:A:855:THR:HB	1.90	0.70
5:B:1165:ILE:HG22	5:B:1166:CYS:H	1.57	0.70
4:A:567:LYS:NZ	11:H:46:LEU:HB2	2.07	0.70
4:A:1283:VAL:HG12	4:A:1284:MET:N	2.07	0.70
4:A:1349:TYR:HB2	4:A:1372:VAL:HG21	1.74	0.70
14:K:12:LEU:HD12	14:K:12:LEU:H	1.57	0.70
4:A:92:HIS:O	4:A:94:GLY:N	2.25	0.69
6:C:114:TYR:HB3	6:C:140:ASN:O	1.92	0.69
7:D:7:THR:HB	10:G:42:PHE:CZ	2.26	0.69
5:B:798:TYR:CE2	6:C:62:PHE:CE2	2.81	0.69
5:B:616:ILE:HD12	5:B:616:ILE:N	2.07	0.69
11:H:111:LEU:HD23	11:H:127:GLY:O	1.93	0.69
6:C:209:TYR:H	6:C:209:TYR:HD1	1.39	0.69
4:A:1161:THR:HG22	4:A:1163:ILE:N	2.04	0.69
5:B:846:ILE:HG23	5:B:974:PRO:HG2	1.74	0.69
4:A:224:PHE:CZ	4:A:231:PRO:HG3	2.28	0.69
4:A:590:ARG:NH2	4:A:620:LYS:CB	2.55	0.69
4:A:1373:ASP:HA	4:A:1376:THR:HG22	1.75	0.69
15:L:27:LEU:HD13	15:L:37:LYS:HE2	1.74	0.69
10:G:138:THR:CG2	10:G:139:ILE:H	1.92	0.69
4:A:1329:THR:CG2	4:A:1331:SER:H	2.04	0.69
6:C:179:GLU:HG2	6:C:180:TYR:H	1.56	0.69
4:A:855:THR:CG2	4:A:857:ARG:HE	2.01	0.69
4:A:1332:PHE:H	4:A:1332:PHE:HD2	1.39	0.69
6:C:66:ARG:HH21	13:J:5:VAL:HG23	1.57	0.69
11:H:89:LEU:C	11:H:91:ASP:H	1.96	0.69
4:A:382:PRO:HB3	4:A:428:TYR:HE2	1.57	0.69
5:B:950:ASP:O	5:B:951:GLN:HB2	1.91	0.69
4:A:311:GLN:O	4:A:312:PRO:C	2.31	0.69
14:K:47:ARG:HH11	14:K:47:ARG:CB	2.04	0.69
11:H:4:THR:CA	11:H:60:ALA:HB2	2.22	0.69
5:B:701:ILE:HD11	5:B:703:ILE:HD11	1.74	0.69
5:B:653:VAL:HG22	5:B:689:LEU:HB3	1.75	0.69
4:A:567:LYS:HD2	4:A:568:PRO:HD2	1.74	0.69
4:A:567:LYS:HD3	11:H:95:TYR:CD2	2.27	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:567:LYS:HB3	11:H:96:VAL:N	2.07	0.69
5:B:770:GLN:CD	5:B:983:ARG:HA	2.13	0.69
7:D:7:THR:HB	10:G:42:PHE:CE2	2.28	0.69
5:B:411:PRO:O	5:B:414:ALA:HB3	1.93	0.69
5:B:515:HIS:H	5:B:518:HIS:HD2	1.40	0.69
5:B:852:ARG:NH2	15:L:70:ARG:OXT	2.23	0.69
4:A:407:ARG:HB3	4:A:430:TRP:CE2	2.28	0.69
5:B:975:GLN:O	5:B:990:ILE:HD12	1.93	0.69
5:B:957:ASN:ND2	5:B:961:LEU:HD12	2.08	0.69
7:D:40:HIS:CE1	7:D:41:GLN:HG3	2.29	0.68
4:A:809:THR:H	4:A:812:GLU:HB2	1.58	0.68
9:F:72:LYS:HD2	9:F:142:SER:HB3	1.75	0.68
6:C:213:PRO:O	6:C:214:ASN:HB2	1.90	0.68
7:D:130:LEU:O	7:D:132:GLN:N	2.25	0.68
4:A:1394:THR:HG21	4:A:1398:MET:SD	2.34	0.68
4:A:7:SER:HB3	5:B:1193:GLN:NE2	2.08	0.68
5:B:1180:PHE:HB3	5:B:1191:ILE:CD1	2.23	0.68
6:C:244:VAL:O	6:C:248:ILE:HG13	1.94	0.68
4:A:679:ILE:HG12	4:A:732:LEU:HD12	1.75	0.68
5:B:882:THR:HB	5:B:934:LYS:O	1.94	0.68
4:A:341:MET:HE1	4:A:843:LYS:NZ	2.07	0.68
4:A:913:LEU:HD12	4:A:914:GLU:H	1.58	0.68
6:C:226:ASP:O	6:C:227:THR:HB	1.92	0.68
14:K:63:VAL:O	14:K:63:VAL:HG23	1.94	0.68
4:A:546:VAL:O	4:A:550:LEU:HG	1.94	0.68
4:A:463:ILE:CD1	4:A:469:ARG:HG3	2.23	0.68
5:B:745:PRO:O	5:B:748:ILE:HG12	1.93	0.68
5:B:746:SER:HB2	5:B:1046:PRO:HG2	1.75	0.68
4:A:567:LYS:CB	11:H:95:TYR:HA	2.24	0.68
5:B:1095:LEU:HD12	5:B:1095:LEU:H	1.58	0.68
5:B:44:VAL:HG11	5:B:199:MET:HG2	1.74	0.68
10:G:49:LEU:HG	10:G:76:ALA:HA	1.75	0.68
6:C:164:ALA:HA	6:C:167:HIS:O	1.93	0.68
5:B:435:THR:C	5:B:437:GLU:H	1.97	0.68
7:D:153:ARG:HB3	7:D:154:PHE:CE1	2.28	0.68
5:B:542:MET:HG2	5:B:747:MET:HB3	1.74	0.68
7:D:53:SER:HB3	7:D:152:SER:CB	2.24	0.68
5:B:603:LEU:HB3	5:B:609:ILE:CD1	2.23	0.68
5:B:642:ASP:O	5:B:644:GLU:N	2.26	0.68
4:A:12:ARG:HD2	5:B:1218:THR:HB	1.74	0.68
10:G:35:GLU:OE2	10:G:48:VAL:HG23	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:751:SER:O	4:A:752:LYS:HG2	1.94	0.68
4:A:475:THR:CG2	4:A:476:SER:H	2.03	0.68
4:A:524:VAL:HG12	4:A:525:GLN:N	2.08	0.68
4:A:1066:VAL:O	4:A:1070:GLN:HG3	1.94	0.68
11:H:17:PRO:HB3	11:H:24:CYS:SG	2.34	0.68
5:B:589:VAL:HG12	5:B:590:HIS:N	2.03	0.68
12:I:34:TYR:CD2	12:I:35:VAL:N	2.62	0.68
4:A:106:VAL:HG13	4:A:112:LYS:O	1.94	0.68
7:D:130:LEU:C	7:D:132:GLN:H	1.97	0.68
8:E:78:LEU:HD21	8:E:80:VAL:HG23	1.74	0.67
11:H:59:ILE:HG22	11:H:60:ALA:H	1.59	0.67
5:B:1072:MET:HE3	5:B:1085:ILE:HB	1.75	0.67
4:A:1438:THR:HB	5:B:1144:ALA:CB	2.19	0.67
4:A:901:LEU:O	4:A:921:GLY:N	2.28	0.67
12:I:54:GLU:HB3	12:I:100:PHE:HE2	1.58	0.67
4:A:591:PHE:HA	4:A:595:THR:HG21	1.74	0.67
4:A:107:CYS:N	4:A:114:LEU:HD21	2.09	0.67
5:B:1166:CYS:HB2	5:B:1215:ARG:HH12	1.57	0.67
5:B:693:ILE:HD13	5:B:701:ILE:HD13	1.76	0.67
15:L:32:ALA:HB3	15:L:55:ILE:CD1	2.21	0.67
8:E:198:ILE:HD11	8:E:212:ARG:HG3	1.75	0.67
5:B:516:ASN:H	5:B:516:ASN:HD22	1.39	0.67
8:E:90:VAL:HG23	8:E:120:ALA:HA	1.76	0.67
5:B:705:MET:H	5:B:710:LEU:CD1	2.07	0.67
5:B:65:GLU:HG3	5:B:66:ASP:H	1.59	0.67
5:B:184:ALA:HB1	5:B:188:ASP:HB3	1.76	0.67
4:A:673:GLY:O	4:A:676:MET:HB2	1.95	0.67
8:E:180:ARG:NH2	8:E:192:ARG:HB2	2.08	0.67
5:B:758:PHE:CE1	5:B:1027:ILE:HG22	2.30	0.67
4:A:107:CYS:SG	4:A:171:GLN:HG2	2.35	0.67
4:A:1333:ILE:O	4:A:1337:GLU:HG3	1.95	0.67
4:A:381:THR:HG23	4:A:383:TYR:H	1.59	0.67
4:A:1293:SER:OG	4:A:1294:PRO:HD2	1.94	0.67
4:A:50:ILE:C	4:A:52:GLY:H	1.96	0.67
4:A:1325:THR:O	8:E:148:GLU:HB2	1.94	0.67
5:B:800:GLN:HB3	13:J:52:THR:CG2	2.24	0.67
14:K:21:ILE:HG12	14:K:33:ILE:HG12	1.77	0.67
4:A:675:THR:O	4:A:679:ILE:HG13	1.95	0.67
14:K:50:LEU:HD11	14:K:75:ILE:HD13	1.77	0.67
9:F:132:LEU:O	9:F:148:VAL:HG22	1.95	0.67
4:A:535:THR:CG2	4:A:616:VAL:HA	2.22	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1324:PRO:HB2	8:E:142:VAL:HG11	1.76	0.67
4:A:1299:VAL:HG12	4:A:1300:LYS:N	2.10	0.67
4:A:1063:MET:CG	4:A:1436:ILE:HG23	2.24	0.67
4:A:547:LEU:HD22	14:K:58:PHE:CD1	2.30	0.67
4:A:172:PRO:HD3	4:A:185:TRP:NE1	2.10	0.67
4:A:1444:MET:CG	10:G:60:ARG:HA	2.25	0.67
4:A:1206:ASP:O	4:A:1274:ARG:NH1	2.27	0.67
4:A:984:LYS:O	4:A:988:LEU:HB2	1.94	0.67
4:A:683:ILE:HG21	4:A:801:GLU:HG3	1.75	0.67
4:A:1143:LEU:HD12	4:A:1146:VAL:HG23	1.75	0.67
6:C:43:THR:CG2	6:C:44:LEU:H	2.03	0.66
4:A:1206:ASP:HB3	4:A:1274:ARG:HH12	1.60	0.66
5:B:240:ILE:CG2	5:B:254:LEU:HB3	2.25	0.66
4:A:356:ASP:HB2	4:A:469:ARG:HH12	1.58	0.66
4:A:849:MET:CE	4:A:1061:GLY:HA2	2.25	0.66
4:A:679:ILE:O	4:A:683:ILE:HG13	1.95	0.66
4:A:353:ILE:HD13	4:A:487:MET:HE2	1.77	0.66
2:N:3:DA:H2"	2:N:4:DG:OP2	1.95	0.66
4:A:1005:GLU:O	4:A:1009:ASN:HB2	1.95	0.66
4:A:1291:VAL:HG13	4:A:1292:PRO:HD2	1.77	0.66
10:G:34:VAL:HG11	10:G:74:TYR:HE1	1.59	0.66
5:B:778:MET:HE2	5:B:1094:ARG:HG2	1.77	0.66
5:B:756:ILE:O	5:B:759:PRO:HD3	1.96	0.66
9:F:125:LEU:O	9:F:125:LEU:HG	1.95	0.66
4:A:79:GLY:HA3	4:A:243:PRO:CG	2.26	0.66
2:N:1:DC:H1'	2:N:2:DA:O5'	1.96	0.66
4:A:567:LYS:HD3	11:H:95:TYR:CG	2.30	0.66
4:A:225:ASN:ND2	4:A:228:PHE:H	1.90	0.66
9:F:111:LEU:N	9:F:111:LEU:HD12	2.11	0.66
4:A:590:ARG:HG3	4:A:590:ARG:NH1	2.10	0.66
8:E:114:ASN:O	8:E:115:ASN:HB3	1.95	0.66
10:G:47:CYS:O	10:G:76:ALA:HB1	1.95	0.66
4:A:67:CYS:O	4:A:70:CYS:HB3	1.95	0.66
12:I:54:GLU:HB3	12:I:100:PHE:CE2	2.30	0.66
9:F:130:ILE:O	9:F:148:VAL:HG21	1.95	0.66
4:A:1121:GLU:HG2	4:A:1122:PRO:HD2	1.78	0.66
5:B:37:PHE:CE1	5:B:41:LYS:HG3	2.31	0.66
4:A:499:ALA:O	4:A:503:GLN:HB2	1.96	0.66
7:D:128:VAL:O	7:D:132:GLN:HG3	1.96	0.66
6:C:67:LEU:HD11	6:C:155:LEU:CD1	2.26	0.66
4:A:14:VAL:HG21	5:B:1216:LEU:HD12	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:2:ILE:HG12	13:J:57:ILE:HD12	1.77	0.66
14:K:6:ARG:O	14:K:9:LEU:HG	1.96	0.66
13:J:48:ARG:HD2	13:J:49:MET:N	2.10	0.66
10:G:23:LYS:HG3	10:G:56:ILE:CD1	2.25	0.66
12:I:8:ARG:HG3	12:I:34:TYR:CE1	2.31	0.66
14:K:10:PHE:CD2	14:K:10:PHE:N	2.64	0.66
4:A:982:THR:HG22	4:A:984:LYS:H	1.60	0.66
12:I:62:ILE:HG12	12:I:62:ILE:O	1.94	0.66
4:A:265:LYS:HZ3	4:A:322:VAL:HG13	1.59	0.66
5:B:758:PHE:HB3	5:B:761:HIS:CD2	2.30	0.66
4:A:340:LEU:HD21	5:B:1200:ALA:N	2.11	0.66
7:D:52:LEU:HD21	7:D:147:TYR:CE2	2.31	0.66
7:D:7:THR:O	7:D:9:GLN:N	2.29	0.66
5:B:737:THR:CG2	12:I:66:PRO:HA	2.26	0.66
5:B:798:TYR:CE2	6:C:62:PHE:HE2	2.15	0.65
5:B:121:ASN:HA	5:B:207:GLY:CA	2.26	0.65
6:C:73:GLN:HB3	6:C:131:HIS:H	1.61	0.65
4:A:68:GLN:C	4:A:70:CYS:H	1.99	0.65
4:A:541:ILE:HG22	4:A:546:VAL:HG23	1.79	0.65
9:F:89:GLU:OE2	9:F:134:ILE:HG21	1.96	0.65
4:A:960:ILE:O	4:A:963:ILE:HG22	1.96	0.65
4:A:376:TYR:OH	4:A:498:ARG:HD2	1.97	0.65
4:A:248:PRO:O	4:A:260:ASP:HB2	1.95	0.65
4:A:58:LEU:HD22	4:A:80:HIS:O	1.96	0.65
4:A:1445:ILE:HD11	10:G:68:ALA:HB1	1.79	0.65
13:J:3:VAL:HG21	13:J:18:TRP:CG	2.31	0.65
6:C:133:ILE:CD1	6:C:237:SER:HA	2.26	0.65
4:A:61:ILE:HG22	4:A:62:ASP:H	1.61	0.65
5:B:333:PHE:O	5:B:334:ILE:HG13	1.96	0.65
5:B:220:GLY:O	5:B:222:ILE:HG13	1.97	0.65
8:E:47:CYS:HA	8:E:52:ARG:O	1.97	0.65
4:A:269:ILE:HD11	4:A:300:VAL:HA	1.77	0.65
5:B:1099:VAL:CG1	5:B:1100:ASP:N	2.60	0.65
4:A:588:LEU:O	4:A:606:LEU:HA	1.95	0.65
6:C:18:VAL:O	6:C:18:VAL:HG12	1.96	0.65
5:B:69:LEU:HD22	5:B:429:PHE:CE1	2.32	0.65
11:H:100:THR:HG22	11:H:101:ALA:N	2.12	0.65
4:A:1224:LEU:HD12	4:A:1241:ARG:O	1.97	0.65
13:J:44:TYR:HA	13:J:47:ARG:CB	2.24	0.65
4:A:868:TYR:CE1	4:A:1064:VAL:HG11	2.31	0.65
5:B:120:ARG:HG2	5:B:955:THR:HG21	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:K:101:LEU:HD23	14:K:101:LEU:O	1.96	0.65
15:L:70:ARG:HG2	15:L:70:ARG:HH11	1.62	0.65
5:B:1065:GLN:HB2	6:C:201:TRP:CZ3	2.32	0.65
4:A:728:LYS:HA	4:A:731:ARG:HB2	1.79	0.65
4:A:107:CYS:H	4:A:114:LEU:HD21	1.61	0.65
6:C:183:TRP:O	6:C:185:LYS:N	2.29	0.65
4:A:298:PHE:HZ	4:A:314:ALA:HB2	1.61	0.65
4:A:306:ASN:HB2	4:A:324:SER:HB3	1.77	0.65
4:A:852:TYR:CD2	4:A:1060:PRO:HB2	2.32	0.65
5:B:916:THR:O	5:B:935:ARG:HG3	1.97	0.65
5:B:96:TYR:HB2	5:B:129:PHE:HB2	1.77	0.65
4:A:548:ASN:HA	14:K:60:ALA:HB1	1.79	0.65
5:B:902:GLY:O	15:L:65:VAL:HG11	1.97	0.65
6:C:232:VAL:HG21	6:C:244:VAL:HG22	1.79	0.65
1:T:23:DC:H2''	1:T:24:DT:H5'	1.78	0.65
5:B:797:TYR:HB2	5:B:852:ARG:O	1.97	0.65
4:A:1424:VAL:HG11	5:B:1139:ILE:HD13	1.78	0.65
4:A:224:PHE:CE2	4:A:231:PRO:HG3	2.32	0.65
5:B:102:VAL:HG23	5:B:112:LEU:HB2	1.79	0.65
5:B:708:GLU:O	5:B:710:LEU:N	2.30	0.65
14:K:49:GLU:HG3	14:K:94:ILE:HG12	1.79	0.65
4:A:1100:ARG:NH2	4:A:1351:GLU:HG2	2.12	0.65
5:B:172:ILE:HG22	5:B:173:MET:N	2.12	0.64
5:B:233:PRO:HG2	5:B:234:ILE:CD1	2.26	0.64
4:A:901:LEU:H	4:A:926:GLN:HE21	1.45	0.64
4:A:746:MET:HE3	5:B:1018:PRO:HG2	1.79	0.64
4:A:680:THR:HA	4:A:683:ILE:HD12	1.79	0.64
15:L:40:LEU:HD13	15:L:44:ASP:HB3	1.79	0.64
5:B:282:ILE:HD12	5:B:382:ILE:HD13	1.79	0.64
4:A:1227:ILE:HG22	4:A:1228:TRP:H	1.62	0.64
4:A:698:GLN:HA	12:I:97:MET:O	1.97	0.64
4:A:54:ASN:HB3	4:A:247:ARG:HH12	1.63	0.64
13:J:1:MET:H1	13:J:57:ILE:N	1.95	0.64
5:B:1166:CYS:O	5:B:1168:LEU:N	2.28	0.64
5:B:684:LEU:H	5:B:684:LEU:HD12	1.61	0.64
14:K:29:ASN:O	14:K:76:GLN:HG3	1.98	0.64
4:A:416:ARG:C	4:A:417:TYR:HD2	2.00	0.64
5:B:1197:PRO:HG2	5:B:1200:ALA:HB2	1.78	0.64
4:A:172:PRO:HD3	4:A:185:TRP:HE1	1.62	0.64
4:A:84:ILE:HD11	4:A:270:LEU:HD22	1.78	0.64
1:T:20:DC:H4'	4:A:447:GLN:NE2	2.12	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:562:GLY:HA3	5:B:590:HIS:CE1	2.31	0.64
5:B:593:PRO:HG2	5:B:617:ARG:NH2	2.12	0.64
5:B:467:GLY:H	5:B:475:SER:CB	2.08	0.64
4:A:102:VAL:HG11	4:A:211:PHE:CE2	2.32	0.64
5:B:185:THR:H	5:B:188:ASP:HB2	1.62	0.64
15:L:28:LYS:HB2	15:L:39:SER:HA	1.79	0.64
4:A:560:ILE:HG13	11:H:78:SER:HB2	1.78	0.64
10:G:91:VAL:HG23	10:G:141:SER:O	1.97	0.64
5:B:1065:GLN:HG3	5:B:1067:ARG:H	1.62	0.64
5:B:114:PRO:HG2	5:B:115:GLN:H	1.63	0.64
6:C:208:GLU:O	6:C:210:GLU:N	2.30	0.64
4:A:965:GLN:O	4:A:968:GLN:HB2	1.97	0.64
6:C:214:ASN:HB3	6:C:217:ASP:OD2	1.98	0.64
4:A:1002:GLY:HA3	4:A:1007:ILE:HG21	1.79	0.64
4:A:1227:ILE:HG22	4:A:1228:TRP:N	2.12	0.64
4:A:1410:PHE:HA	5:B:1212:ILE:HD11	1.79	0.64
4:A:30:ILE:HG23	5:B:1170:THR:HG23	1.79	0.64
4:A:1341:ILE:HG23	4:A:1342:GLU:H	1.62	0.64
4:A:1100:ARG:HH21	4:A:1351:GLU:CG	2.11	0.64
7:D:202:ILE:HG21	7:D:207:LEU:HB2	1.79	0.64
4:A:768:GLN:HG2	4:A:816:HIS:HA	1.79	0.64
5:B:824:ILE:CG2	5:B:1087:PHE:HE2	2.10	0.64
13:J:36:LEU:HD12	13:J:47:ARG:NH1	2.13	0.64
13:J:8:PHE:H	13:J:49:MET:CE	2.11	0.64
5:B:1138:MET:HA	5:B:1138:MET:HE3	1.80	0.64
13:J:1:MET:H1	13:J:56:LEU:N	1.96	0.64
4:A:399:HIS:CB	4:A:400:PRO:HD3	2.24	0.64
4:A:1329:THR:HG22	4:A:1331:SER:N	2.13	0.64
4:A:1299:VAL:HG12	4:A:1300:LYS:H	1.63	0.64
5:B:361:LEU:HD21	5:B:377:PHE:CD2	2.33	0.64
13:J:23:ASN:C	13:J:25:LEU:H	2.01	0.64
6:C:76:ASP:O	6:C:79:GLN:HG2	1.97	0.64
6:C:166:GLU:HG3	14:K:10:PHE:CZ	2.24	0.64
6:C:251:LEU:HD12	6:C:251:LEU:O	1.98	0.64
13:J:14:VAL:HG12	13:J:50:ILE:HD11	1.78	0.64
5:B:515:HIS:HD2	5:B:517:THR:H	1.44	0.64
4:A:114:LEU:O	4:A:115:LEU:HG	1.98	0.64
5:B:465:ASN:HD22	5:B:465:ASN:N	1.95	0.64
4:A:346:ASP:HB3	5:B:1108:ARG:H	1.63	0.64
7:D:170:THR:HB	7:D:172:LEU:H	1.62	0.64
4:A:341:MET:HE1	4:A:843:LYS:HZ3	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:41:ASP:O	11:H:42:ILE:HG13	1.98	0.63
8:E:213:ILE:HG12	8:E:214:CYS:N	2.13	0.63
11:H:82:PRO:O	11:H:84:ALA:N	2.27	0.63
5:B:378:LEU:O	5:B:382:ILE:HG13	1.98	0.63
4:A:720:ARG:O	4:A:724:GLU:HB2	1.98	0.63
4:A:55:ASP:N	4:A:56:PRO:HD3	2.12	0.63
7:D:8:PHE:CZ	7:D:40:HIS:HA	2.33	0.63
5:B:744:HIS:HD2	5:B:746:SER:OG	1.81	0.63
5:B:822:ASN:ND2	13:J:52:THR:HG21	2.12	0.63
5:B:1183:LYS:HE3	5:B:1183:LYS:N	2.13	0.63
10:G:3:PHE:CD1	10:G:80:LYS:NZ	2.65	0.63
5:B:850:LEU:HD12	5:B:851:PHE:N	2.12	0.63
5:B:822:ASN:HD22	13:J:52:THR:HG21	1.62	0.63
4:A:1329:THR:CG2	4:A:1331:SER:HB3	2.28	0.63
4:A:406:ILE:HG22	4:A:412:ARG:HA	1.81	0.63
5:B:1152:MET:HE3	5:B:1157:ALA:HA	1.79	0.63
5:B:526:GLU:HG2	5:B:538:ASN:HD22	1.64	0.63
6:C:105:GLY:HA3	6:C:149:LYS:O	1.99	0.63
7:D:31:GLN:O	7:D:34:GLN:HG3	1.99	0.63
1:T:23:DC:H2'	1:T:24:DT:H71	1.81	0.63
4:A:1166:ASP:OD2	4:A:1239:ARG:HD2	1.98	0.63
6:C:177:GLU:HB2	6:C:231:ASN:HB3	1.81	0.63
11:H:42:ILE:HG23	11:H:95:TYR:CE1	2.30	0.63
5:B:1001:PHE:CZ	5:B:1073:TYR:HB2	2.33	0.63
5:B:827:ILE:HD12	5:B:1086:PHE:HD2	1.64	0.63
4:A:339:ASN:O	4:A:343:LYS:HG2	1.98	0.63
5:B:44:VAL:CG1	5:B:199:MET:HG2	2.28	0.63
4:A:1198:ASP:O	4:A:1202:MET:HG2	1.99	0.63
4:A:35:ILE:HG22	4:A:84:ILE:HD12	1.81	0.63
5:B:879:ARG:HH11	5:B:883:LEU:CD2	2.06	0.63
4:A:1420:ASP:O	4:A:1421:CYS:HB2	1.98	0.63
5:B:65:GLU:HG3	5:B:66:ASP:N	2.14	0.63
5:B:95:ILE:HG13	5:B:130:VAL:HG22	1.80	0.63
15:L:40:LEU:HD22	15:L:44:ASP:CG	2.19	0.63
4:A:1209:MET:SD	4:A:1236:LEU:HD22	2.38	0.63
5:B:345:LYS:O	5:B:347:LYS:HG2	1.98	0.63
7:D:47:LEU:HD12	7:D:48:ILE:H	1.62	0.63
5:B:579:ARG:CB	5:B:586:TRP:HE1	2.08	0.63
7:D:35:LEU:CD2	7:D:173:HIS:HB3	2.28	0.63
5:B:1197:PRO:HG2	5:B:1200:ALA:CB	2.28	0.63
4:A:356:ASP:OD2	14:K:65:HIS:HE1	1.82	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:438:ASP:O	4:A:439:ASN:HB2	1.97	0.63
10:G:15:PRO:HA	10:G:18:PHE:CE1	2.34	0.63
10:G:18:PHE:HA	10:G:22:MET:HE2	1.81	0.63
4:A:144:THR:O	4:A:146:MET:HG3	1.98	0.63
4:A:1148:ILE:HG23	12:I:49:ILE:HB	1.80	0.63
12:I:25:LEU:HB3	12:I:38:ALA:HB2	1.79	0.63
4:A:90:VAL:CG1	4:A:297:GLN:HA	2.28	0.63
4:A:1424:VAL:HG13	4:A:1436:ILE:HD11	1.80	0.63
4:A:1329:THR:HG22	4:A:1331:SER:H	1.63	0.63
9:F:109:VAL:HG12	9:F:110:ASP:N	2.14	0.63
13:J:64:ASN:HB3	13:J:65:PRO:HD2	1.80	0.63
4:A:341:MET:CE	4:A:843:LYS:NZ	2.61	0.63
5:B:1224:PHE:CE2	8:E:171:LYS:HG3	2.31	0.63
12:I:80:SER:HB2	12:I:103:CYS:SG	2.39	0.63
5:B:1096:ARG:O	5:B:1097:HIS:HB2	1.99	0.63
4:A:450:LEU:N	4:A:450:LEU:HD12	2.14	0.63
4:A:381:THR:CG2	4:A:383:TYR:H	2.12	0.63
5:B:424:LEU:O	5:B:428:ILE:HG13	1.99	0.63
5:B:866:TYR:HD1	5:B:870:ILE:O	1.82	0.63
4:A:993:LEU:HD22	4:A:1046:LEU:HD22	1.80	0.63
10:G:79:PHE:CE2	10:G:105:PRO:HD2	2.34	0.62
4:A:857:ARG:HD3	4:A:861:GLY:O	1.99	0.62
12:I:111:THR:CG2	12:I:112:SER:H	2.07	0.62
6:C:146:LYS:C	6:C:147:LEU:HD23	2.20	0.62
4:A:903:ASN:HD22	4:A:904:THR:H	1.47	0.62
15:L:53:HIS:O	15:L:55:ILE:HG12	1.99	0.62
4:A:870:GLU:HB2	8:E:204:THR:HG21	1.80	0.62
7:D:17:LYS:HE2	7:D:17:LYS:H	1.62	0.62
5:B:955:THR:HG22	5:B:956:THR:O	1.98	0.62
5:B:324:ILE:HD13	5:B:330:ALA:HA	1.79	0.62
5:B:753:ALA:O	5:B:756:ILE:HG13	1.99	0.62
4:A:117:GLU:H	4:A:117:GLU:CD	2.01	0.62
4:A:40:THR:CG2	4:A:41:MET:HG3	2.25	0.62
5:B:850:LEU:HD12	5:B:851:PHE:H	1.65	0.62
4:A:1370:LEU:O	4:A:1374:VAL:HG23	1.98	0.62
4:A:826:ASP:O	4:A:830:LYS:HB2	1.99	0.62
1:T:23:DC:H2''	1:T:24:DT:C5'	2.30	0.62
6:C:38:ILE:HA	6:C:173:ALA:CB	2.30	0.62
5:B:1081:LEU:HD12	5:B:1085:ILE:HD11	1.80	0.62
7:D:63:LEU:HD12	7:D:129:LEU:HG	1.81	0.62
10:G:1:MET:O	10:G:3:PHE:CE1	2.52	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:19:DC:H2''	1:T:20:DC:O5'	1.99	0.62
5:B:999:MET:HG2	5:B:1007:VAL:HG22	1.80	0.62
4:A:783:THR:HG21	4:A:815:PHE:CZ	2.35	0.62
4:A:7:SER:HB2	5:B:1175:LEU:HD22	1.81	0.62
4:A:901:LEU:HA	4:A:907:THR:OG1	1.99	0.62
4:A:382:PRO:CB	4:A:428:TYR:HE2	2.12	0.62
3:P:2:U:C2'	3:P:3:U:O5'	2.48	0.62
11:H:44:VAL:HG12	11:H:44:VAL:O	2.00	0.62
5:B:400:HIS:O	5:B:402:GLY:N	2.32	0.62
10:G:96:GLN:HG3	10:G:97:HIS:HD2	1.64	0.62
4:A:90:VAL:HG13	4:A:297:GLN:HA	1.81	0.62
5:B:376:PHE:HB3	5:B:586:TRP:CZ3	2.35	0.62
4:A:1206:ASP:HB3	4:A:1274:ARG:NH1	2.15	0.62
4:A:298:PHE:CZ	4:A:314:ALA:HB2	2.35	0.62
4:A:541:ILE:HG21	4:A:549:MET:HE3	1.81	0.62
5:B:821:GLN:NE2	5:B:851:PHE:HA	2.14	0.62
4:A:1323:ASP:C	4:A:1325:THR:H	2.03	0.62
4:A:590:ARG:O	4:A:591:PHE:HB2	2.00	0.62
6:C:100:THR:HG22	6:C:101:LEU:N	2.15	0.62
5:B:579:ARG:HH11	5:B:579:ARG:HG2	1.65	0.62
5:B:1073:TYR:CE2	5:B:1080:LYS:HG2	2.35	0.62
7:D:134:THR:HG22	7:D:135:GLY:H	1.65	0.62
4:A:513:SER:HB2	4:A:520:CYS:HB3	1.80	0.62
4:A:856:THR:HB	4:A:865:GLN:HB2	1.81	0.62
4:A:782:ARG:NH2	5:B:699:GLU:O	2.32	0.62
5:B:899:ILE:CD1	5:B:911:ILE:HA	2.29	0.62
5:B:1008:PRO:HB2	5:B:1010:LEU:O	1.99	0.62
8:E:176:PRO:O	8:E:212:ARG:HA	1.99	0.62
4:A:746:MET:CE	5:B:1018:PRO:HG2	2.29	0.62
4:A:1208:THR:HG22	4:A:1210:GLY:N	2.14	0.62
4:A:34:LYS:HB3	4:A:36:ARG:HE	1.65	0.62
5:B:429:PHE:HA	5:B:432:MET:HE3	1.82	0.62
10:G:51:TYR:C	10:G:51:TYR:CD2	2.72	0.62
10:G:91:VAL:HA	10:G:101:VAL:HA	1.82	0.62
6:C:113:VAL:O	6:C:144:ILE:HB	2.00	0.62
4:A:1323:ASP:O	4:A:1325:THR:N	2.33	0.62
4:A:17:VAL:HA	5:B:1215:ARG:O	1.99	0.62
5:B:520:GLY:N	5:B:748:ILE:HG22	2.14	0.62
1:T:11:DT:H2''	1:T:12:DA:H5'	1.81	0.62
4:A:23:SER:HA	4:A:233:TRP:CD1	2.35	0.62
4:A:1454:MET:HG3	4:A:1454:MET:O	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:I:82:GLU:HB3	12:I:104:LEU:HD12	1.81	0.62
7:D:33:PHE:CE1	10:G:80:LYS:HE3	2.35	0.62
4:A:1017:LEU:HB3	8:E:205:SER:HA	1.82	0.62
11:H:91:ASP:C	11:H:93:TYR:H	2.04	0.62
4:A:265:LYS:HE2	4:A:322:VAL:CG1	2.29	0.62
5:B:1073:TYR:OH	6:C:179:GLU:HG3	1.99	0.62
4:A:761:MET:HA	4:A:804:TYR:HB2	1.82	0.62
4:A:1124:HIS:HB3	4:A:1130:GLN:HG2	1.82	0.61
7:D:14:ARG:O	7:D:16:LYS:HD3	2.00	0.61
6:C:101:LEU:HD22	6:C:118:LEU:HD21	1.81	0.61
5:B:766:ARG:HH22	5:B:1020:ARG:HH11	1.48	0.61
6:C:66:ARG:NH2	13:J:5:VAL:HG23	2.15	0.61
4:A:903:ASN:ND2	4:A:904:THR:N	2.46	0.61
4:A:663:SER:OG	4:A:664:THR:N	2.32	0.61
8:E:195:VAL:HG22	8:E:213:ILE:HG13	1.81	0.61
7:D:153:ARG:NH2	7:D:184:ALA:HA	2.15	0.61
5:B:1084:GLN:NE2	5:B:1084:GLN:H	1.98	0.61
5:B:807:ARG:HG2	5:B:1045:SER:OG	1.99	0.61
8:E:157:SER:OG	8:E:160:GLU:HG3	2.01	0.61
7:D:47:LEU:CD1	7:D:48:ILE:H	2.13	0.61
5:B:569:TYR:CE1	5:B:589:VAL:HG21	2.35	0.61
4:A:728:LYS:O	4:A:732:LEU:HG	2.00	0.61
5:B:69:LEU:HD13	5:B:429:PHE:HD1	1.65	0.61
4:A:961:ARG:HG3	4:A:961:ARG:HH11	1.66	0.61
4:A:842:VAL:HG11	5:B:1136:ASP:OD2	2.00	0.61
10:G:153:GLN:HG2	10:G:154:VAL:HG23	1.82	0.61
4:A:1356:ILE:HD13	4:A:1363:VAL:HG21	1.81	0.61
10:G:117:GLN:C	10:G:119:LEU:H	2.03	0.61
5:B:37:PHE:CD1	5:B:41:LYS:HG3	2.36	0.61
4:A:718:VAL:HG12	4:A:722:LEU:HD11	1.82	0.61
5:B:705:MET:N	5:B:710:LEU:HD12	2.14	0.61
4:A:1039:LYS:HE3	4:A:1043:ASP:OD2	2.01	0.61
4:A:19:PHE:HB3	4:A:1413:GLY:HA2	1.81	0.61
11:H:61:SER:O	11:H:62:SER:HB3	2.01	0.61
7:D:5:THR:HG23	10:G:9:LEU:HD13	1.82	0.61
10:G:128:PRO:O	10:G:138:THR:HG23	2.01	0.61
4:A:784:LEU:HD11	4:A:815:PHE:CE2	2.35	0.61
4:A:321:PRO:O	4:A:322:VAL:CB	2.48	0.61
4:A:138:ILE:CD1	4:A:222:LEU:HD23	2.31	0.61
4:A:269:ILE:HD13	4:A:300:VAL:HG22	1.81	0.61
4:A:21:LEU:HD11	4:A:1414:ALA:HA	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:108:PHE:HE1	9:F:131:PRO:HG3	1.66	0.61
5:B:1164:GLY:HA3	5:B:1190:ASP:OD2	1.99	0.61
4:A:353:ILE:HG21	4:A:487:MET:CE	2.31	0.61
4:A:470:LEU:HD22	4:A:487:MET:CE	2.30	0.61
6:C:147:LEU:N	6:C:147:LEU:HD23	2.14	0.61
4:A:870:GLU:HG2	8:E:208:TYR:CG	2.35	0.61
4:A:87:ALA:CB	4:A:276:LEU:HD23	2.31	0.61
5:B:295:GLY:N	5:B:298:LEU:HD23	2.16	0.61
4:A:29:ALA:HB1	5:B:1184:GLY:CA	2.31	0.61
4:A:1035:TYR:O	4:A:1037:LEU:N	2.34	0.61
5:B:1165:ILE:CG2	5:B:1166:CYS:N	2.61	0.61
3:P:2:U:H2'	3:P:3:U:O5'	2.00	0.61
4:A:172:PRO:HB3	4:A:185:TRP:CE2	2.35	0.61
4:A:1444:MET:HG2	10:G:60:ARG:CA	2.29	0.61
5:B:359:GLU:O	5:B:362:PRO:HD3	2.00	0.61
6:C:186:LEU:HD21	6:C:224:GLN:O	2.01	0.61
5:B:508:LEU:O	5:B:509:ALA:CB	2.49	0.61
5:B:654:ARG:HH11	5:B:654:ARG:HG3	1.65	0.61
5:B:1096:ARG:O	5:B:1097:HIS:CB	2.48	0.61
6:C:238:ILE:HG22	6:C:243:VAL:HG23	1.83	0.61
6:C:241:ASP:O	6:C:245:VAL:HG23	2.00	0.61
4:A:896:ARG:NH2	4:A:1030:ARG:NH2	2.49	0.61
4:A:4:GLN:O	4:A:5:GLN:HB2	2.00	0.61
6:C:45:ALA:HA	6:C:72:LEU:CD1	2.28	0.61
8:E:15:ALA:O	8:E:19:VAL:HG23	2.01	0.61
1:T:11:DT:O2	2:N:7:DG:N2	2.33	0.61
4:A:427:GLN:HG3	4:A:430:TRP:CE2	2.36	0.61
7:D:17:LYS:H	7:D:17:LYS:CE	2.14	0.61
5:B:121:ASN:HA	5:B:207:GLY:HA2	1.83	0.61
4:A:1373:ASP:HA	4:A:1376:THR:CG2	2.30	0.61
4:A:1450:LEU:HG	4:A:1450:LEU:O	2.01	0.61
4:A:1094:VAL:HG13	4:A:1113:THR:CG2	2.21	0.60
4:A:337:ARG:HD3	5:B:1132:GLU:OE1	2.00	0.60
4:A:345:VAL:HG23	4:A:346:ASP:O	2.01	0.60
5:B:955:THR:CG2	5:B:956:THR:N	2.64	0.60
6:C:100:THR:HG22	6:C:101:LEU:H	1.65	0.60
5:B:948:ILE:HG22	5:B:949:VAL:O	2.02	0.60
4:A:1424:VAL:HG22	4:A:1436:ILE:HD11	1.83	0.60
10:G:145:VAL:CG1	10:G:146:LYS:N	2.64	0.60
4:A:269:ILE:CD1	4:A:300:VAL:HA	2.30	0.60
5:B:872:GLU:CD	5:B:914:LYS:HE2	2.21	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:152:VAL:HG13	4:A:153:PRO:HD2	1.82	0.60
4:A:1063:MET:SD	4:A:1436:ILE:HG12	2.42	0.60
13:J:9:SER:HB2	13:J:45:CYS:HB2	1.83	0.60
8:E:10:SER:O	8:E:14:ARG:HG3	2.00	0.60
5:B:1097:HIS:H	5:B:1098:MET:HE2	1.66	0.60
4:A:694:THR:O	4:A:698:GLN:HG3	2.02	0.60
5:B:842:ASN:ND2	5:B:845:SER:OG	2.35	0.60
4:A:50:ILE:O	4:A:52:GLY:N	2.32	0.60
2:N:2:DA:OP1	2:N:2:DA:H3'	2.01	0.60
13:J:44:TYR:CD2	13:J:44:TYR:N	2.68	0.60
8:E:124:VAL:HA	8:E:132:ILE:HD12	1.82	0.60
4:A:29:ALA:HB1	5:B:1184:GLY:HA2	1.84	0.60
4:A:882:SER:HB3	4:A:953:ASN:OD1	2.00	0.60
9:F:119:ARG:HH11	9:F:119:ARG:HG3	1.66	0.60
8:E:135:PHE:HD2	8:E:140:LEU:HD21	1.66	0.60
4:A:1121:GLU:CG	4:A:1122:PRO:HD2	2.31	0.60
4:A:896:ARG:HD3	4:A:897:TYR:CE1	2.36	0.60
4:A:384:ASN:CG	4:A:388:LEU:HD12	2.22	0.60
5:B:582:VAL:HG23	5:B:626:ILE:HB	1.82	0.60
4:A:49:LYS:HZ1	4:A:61:ILE:N	1.99	0.60
3:P:3:U:O2'	4:A:320:ARG:NH2	2.35	0.60
5:B:1182:CYS:O	5:B:1183:LYS:O	2.20	0.60
11:H:81:PRO:CB	11:H:82:PRO:CD	2.80	0.60
4:A:1030:ARG:HG3	4:A:1034:GLU:OE2	2.00	0.60
4:A:958:VAL:HG11	4:A:1049:ILE:HG23	1.83	0.60
5:B:611:PRO:HG2	5:B:685:LEU:HD21	1.83	0.60
4:A:590:ARG:HG3	4:A:590:ARG:HH11	1.65	0.60
4:A:672:ASP:HB2	4:A:736:ASN:OD1	2.01	0.60
4:A:1410:PHE:HA	5:B:1212:ILE:CD1	2.31	0.60
4:A:384:ASN:OD1	4:A:388:LEU:HD12	2.01	0.60
5:B:912:ILE:HB	5:B:939:THR:OG1	2.01	0.60
5:B:601:ARG:O	5:B:605:ARG:HG3	2.01	0.60
4:A:377:PRO:HG3	4:A:493:GLN:HG3	1.83	0.60
4:A:1323:ASP:OD1	4:A:1325:THR:HB	2.02	0.60
4:A:1290:LYS:O	4:A:1291:VAL:HG23	2.02	0.60
8:E:48:ASP:CG	8:E:49:SER:H	2.05	0.60
5:B:294:ASP:O	5:B:296:GLU:N	2.31	0.60
5:B:825:VAL:CG1	5:B:826:ALA:N	2.65	0.60
5:B:570:VAL:CG2	5:B:573:GLN:HB3	2.31	0.60
5:B:1115:THR:O	5:B:1116:ARG:HB2	2.02	0.60
5:B:882:THR:HG21	5:B:884:ARG:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:45:ILE:HG22	10:G:45:ILE:O	2.02	0.60
4:A:903:ASN:HD22	4:A:903:ASN:C	2.04	0.60
5:B:1163:CYS:SG	5:B:1165:ILE:HB	2.41	0.60
4:A:567:LYS:HZ1	11:H:46:LEU:HB2	1.67	0.60
15:L:38:LEU:O	15:L:39:SER:HB3	2.02	0.60
4:A:466:SER:HA	14:K:2:ASN:HD22	1.67	0.59
5:B:744:HIS:CG	5:B:745:PRO:HD2	2.36	0.59
5:B:522:VAL:HG11	5:B:537:LYS:HB3	1.82	0.59
7:D:172:LEU:HD22	7:D:176:GLU:OE1	2.01	0.59
4:A:781:ASP:O	4:A:789:LYS:HA	2.02	0.59
4:A:344:ARG:HA	5:B:1129:ARG:HA	1.84	0.59
4:A:1032:LEU:O	4:A:1036:ARG:HD3	2.01	0.59
6:C:124:LEU:O	6:C:127:ARG:HG2	2.02	0.59
5:B:799:PRO:HB3	5:B:818:PRO:HG2	1.83	0.59
4:A:1102:LYS:HG2	4:A:1106:ASN:HD21	1.65	0.59
10:G:91:VAL:HB	10:G:139:ILE:O	2.01	0.59
4:A:858:ASN:HD22	4:A:858:ASN:C	2.04	0.59
6:C:66:ARG:NH2	13:J:3:VAL:O	2.35	0.59
4:A:960:ILE:HA	4:A:963:ILE:CG2	2.32	0.59
4:A:841:LEU:O	4:A:845:LEU:HG	2.02	0.59
14:K:21:ILE:HG23	14:K:31:VAL:HG11	1.84	0.59
8:E:14:ARG:NH2	8:E:141:VAL:HG12	2.13	0.59
9:F:111:LEU:C	9:F:113:GLY:N	2.53	0.59
15:L:31:CYS:SG	15:L:34:CYS:SG	3.00	0.59
4:A:1102:LYS:HG2	4:A:1106:ASN:ND2	2.16	0.59
4:A:1149:ALA:HB2	12:I:47:GLU:HA	1.83	0.59
11:H:40:LEU:HD13	11:H:123:MET:HB2	1.85	0.59
4:A:53:LEU:HD22	4:A:54:ASN:HD22	1.66	0.59
4:A:1317:MET:O	4:A:1322:ILE:HD11	2.01	0.59
5:B:115:GLN:HG2	5:B:193:LYS:HB2	1.82	0.59
5:B:192:LEU:O	5:B:193:LYS:HB2	2.02	0.59
12:I:55:THR:HG22	12:I:58:VAL:HG21	1.84	0.59
8:E:161:LYS:HD2	8:E:195:VAL:HG23	1.84	0.59
5:B:408:LEU:O	5:B:411:PRO:HD2	2.02	0.59
4:A:1151:GLU:HA	12:I:44:TYR:O	2.01	0.59
10:G:34:VAL:HG11	10:G:74:TYR:CE1	2.37	0.59
6:C:98:VAL:C	6:C:99:LEU:HD23	2.22	0.59
15:L:55:ILE:O	15:L:56:LEU:HB2	2.02	0.59
8:E:17:ARG:O	8:E:21:GLU:HG3	2.02	0.59
7:D:63:LEU:HD13	7:D:133:THR:OG1	2.02	0.59
10:G:51:TYR:O	10:G:54:ILE:HG13	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:119:LEU:HD12	10:G:131:GLN:O	2.03	0.59
4:A:1153:TYR:CE1	12:I:42:LEU:HD13	2.36	0.59
10:G:27:LYS:O	10:G:30:LEU:HB3	2.02	0.59
4:A:86:LEU:HG	4:A:237:THR:O	2.03	0.59
4:A:37:PHE:HB2	4:A:52:GLY:HA3	1.84	0.59
4:A:1445:ILE:H	4:A:1445:ILE:CD1	2.00	0.59
4:A:869:GLY:O	8:E:204:THR:HG21	2.01	0.59
12:I:55:THR:CG2	12:I:58:VAL:HG21	2.33	0.59
12:I:106:CYS:O	12:I:107:SER:HB2	2.01	0.59
5:B:167:ILE:HG22	5:B:453:ILE:HD12	1.84	0.59
5:B:347:LYS:HG3	5:B:348:ARG:H	1.67	0.59
4:A:1015:VAL:HG12	4:A:1019:CYS:SG	2.43	0.59
5:B:57:TYR:N	5:B:57:TYR:HD1	2.01	0.59
8:E:144:ILE:HG13	8:E:145:THR:N	2.17	0.59
5:B:1000:PRO:O	5:B:1007:VAL:HG23	2.02	0.59
4:A:399:HIS:HB3	4:A:400:PRO:CD	2.27	0.59
5:B:824:ILE:HG23	5:B:1087:PHE:HE2	1.67	0.59
4:A:1116:LEU:HD11	4:A:1118:VAL:HG13	1.84	0.59
4:A:1343:ALA:HB2	8:E:150:VAL:HG22	1.83	0.59
10:G:1:MET:SD	10:G:1:MET:C	2.81	0.59
9:F:130:ILE:O	9:F:148:VAL:CG2	2.51	0.59
4:A:1114:PRO:HB2	4:A:1311:VAL:HG23	1.84	0.59
4:A:37:PHE:N	4:A:37:PHE:CD1	2.69	0.59
6:C:77:ILE:HG23	6:C:161:LYS:HE3	1.85	0.59
4:A:1341:ILE:CG2	4:A:1342:GLU:N	2.66	0.59
4:A:42:ASP:HA	4:A:46:THR:O	2.03	0.59
4:A:1041:ALA:O	4:A:1045:VAL:HG23	2.01	0.59
4:A:252:PHE:O	4:A:253:ASN:HB2	2.03	0.59
6:C:69:LEU:HD12	6:C:69:LEU:N	2.18	0.59
5:B:35:SER:O	5:B:39:ARG:HG3	2.03	0.59
4:A:341:MET:CE	4:A:843:LYS:HZ3	2.16	0.59
5:B:827:ILE:HD12	5:B:1086:PHE:CD2	2.37	0.59
8:E:178:ILE:HG22	8:E:213:ILE:O	2.03	0.59
4:A:1349:TYR:CA	4:A:1372:VAL:HG21	2.32	0.59
4:A:596:THR:O	4:A:598:LEU:N	2.35	0.59
5:B:918:ILE:HG21	5:B:935:ARG:NH1	2.17	0.59
5:B:542:MET:HB3	5:B:636:PRO:HD2	1.85	0.59
1:T:13:DC:H2'	1:T:14:DT:H71	1.85	0.59
4:A:49:LYS:HZ3	4:A:61:ILE:HG13	1.63	0.59
4:A:63:ARG:HA	4:A:74:MET:SD	2.43	0.59
4:A:503:GLN:NE2	9:F:90:ARG:HH21	2.00	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:954:TRP:HB3	4:A:955:PRO:HD2	1.85	0.59
10:G:106:MET:CG	10:G:107:LYS:N	2.66	0.58
4:A:84:ILE:CD1	4:A:270:LEU:HD22	2.32	0.58
4:A:1313:LEU:HD23	4:A:1338:VAL:HG21	1.85	0.58
4:A:222:LEU:O	4:A:224:PHE:N	2.36	0.58
4:A:2:VAL:HG21	5:B:1157:ALA:C	2.23	0.58
5:B:642:ASP:HB3	5:B:649:LYS:CD	2.32	0.58
5:B:502:ILE:HD12	5:B:502:ILE:H	1.68	0.58
6:C:8:VAL:HG12	6:C:9:LYS:N	2.18	0.58
4:A:774:ARG:HB2	4:A:797:LYS:O	2.02	0.58
4:A:1130:GLN:HE21	4:A:1134:ILE:HD11	1.67	0.58
4:A:741:ASN:HD21	4:A:743:VAL:HB	1.68	0.58
11:H:83:GLN:O	11:H:85:GLY:N	2.36	0.58
5:B:168:GLY:N	5:B:450:ALA:HB1	2.17	0.58
15:L:40:LEU:HD22	15:L:44:ASP:CB	2.34	0.58
4:A:1410:PHE:HD2	5:B:1212:ILE:HD12	1.69	0.58
4:A:890:ASP:H	4:A:1296:GLY:HA3	1.68	0.58
5:B:326:ASP:OD2	5:B:328:GLU:HB2	2.02	0.58
5:B:792:MET:HG3	5:B:855:PHE:HE1	1.68	0.58
11:H:93:TYR:CD2	11:H:143:LEU:HB3	2.38	0.58
13:J:45:CYS:O	13:J:48:ARG:HG3	2.03	0.58
4:A:547:LEU:HD22	14:K:58:PHE:CE1	2.38	0.58
13:J:14:VAL:HG12	13:J:14:VAL:O	2.03	0.58
4:A:852:TYR:CE2	4:A:1060:PRO:HB2	2.39	0.58
4:A:1409:LEU:HD13	5:B:1207:LEU:HD21	1.85	0.58
10:G:49:LEU:HD21	10:G:77:VAL:HG23	1.85	0.58
6:C:66:ARG:NH1	13:J:2:ILE:CG2	2.67	0.58
6:C:174:ALA:O	6:C:175:ALA:HB3	2.04	0.58
13:J:44:TYR:HD2	13:J:44:TYR:N	1.99	0.58
14:K:53:ASP:OD1	14:K:55:LYS:HB2	2.02	0.58
5:B:1065:GLN:NE2	5:B:1067:ARG:H	1.99	0.58
4:A:185:TRP:HZ3	4:A:200:ARG:HG2	1.65	0.58
10:G:149:GLY:O	10:G:159:ALA:HB1	2.02	0.58
14:K:31:VAL:HG12	14:K:32:VAL:N	2.17	0.58
9:F:111:LEU:O	9:F:113:GLY:N	2.34	0.58
5:B:254:LEU:HD23	5:B:381:MET:HE1	1.85	0.58
5:B:293:PRO:HG2	5:B:296:GLU:HB3	1.86	0.58
4:A:369:SER:HB2	14:K:2:ASN:OD1	2.03	0.58
4:A:541:ILE:HG21	4:A:549:MET:CE	2.33	0.58
14:K:6:ARG:O	14:K:8:GLU:N	2.37	0.58
4:A:785:PRO:HG2	4:A:786:HIS:HD2	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:31:ASN:O	6:C:34:ARG:HB3	2.04	0.58
4:A:1114:PRO:O	4:A:1115:SER:O	2.21	0.58
4:A:910:PRO:HB3	4:A:917:SER:H	1.68	0.58
5:B:20:ASP:O	5:B:22:SER:N	2.37	0.58
1:T:22:DC:OP1	5:B:1122:ARG:HB3	2.04	0.58
4:A:858:ASN:ND2	4:A:861:GLY:H	2.01	0.58
5:B:1006:ILE:HG23	13:J:45:CYS:SG	2.44	0.58
8:E:177:ARG:HD3	8:E:215:MET:CG	2.31	0.58
4:A:666:ILE:HG23	5:B:1026:LEU:HB3	1.86	0.58
6:C:238:ILE:CG2	6:C:242:GLN:HB2	2.34	0.58
5:B:345:LYS:O	5:B:347:LYS:N	2.35	0.58
5:B:265:SER:O	5:B:266:ALA:HB3	2.03	0.58
4:A:1017:LEU:CB	8:E:205:SER:HA	2.34	0.58
4:A:63:ARG:HA	4:A:74:MET:CE	2.34	0.58
5:B:828:ALA:HB2	5:B:1085:ILE:HG23	1.85	0.58
7:D:145:MET:O	7:D:149:THR:HB	2.03	0.58
12:I:55:THR:O	12:I:55:THR:HG22	2.02	0.58
5:B:863:GLU:OE2	5:B:873:THR:HA	2.03	0.58
4:A:1334:ASP:O	4:A:1337:GLU:N	2.36	0.58
4:A:152:VAL:CG1	4:A:153:PRO:HD2	2.33	0.58
4:A:92:HIS:CD2	4:A:304:MET:HE3	2.39	0.58
1:T:21:DT:H2''	1:T:22:DC:O5'	2.03	0.58
4:A:372:LYS:HA	4:A:435:HIS:ND1	2.19	0.58
4:A:1313:LEU:HD23	4:A:1338:VAL:CG2	2.34	0.58
5:B:980:PHE:CA	5:B:1095:LEU:HD11	2.34	0.58
4:A:675:THR:OG1	4:A:736:ASN:ND2	2.37	0.58
4:A:55:ASP:C	4:A:57:ARG:N	2.52	0.58
4:A:445:ASN:HB2	4:A:454:SER:O	2.03	0.58
9:F:89:GLU:O	9:F:93:ILE:HG13	2.04	0.58
11:H:22:LYS:O	11:H:23:VAL:HG23	2.04	0.58
4:A:347:PHE:HE2	4:A:375:THR:HG23	1.69	0.58
5:B:969:ARG:NH1	6:C:61:GLU:OE1	2.37	0.58
6:C:249:ASP:O	6:C:252:GLN:HB3	2.04	0.58
6:C:107:SER:C	6:C:109:SER:H	2.07	0.58
8:E:145:THR:HG21	8:E:187:TYR:CD2	2.39	0.57
5:B:172:ILE:HD13	5:B:178:ASN:CB	2.25	0.57
4:A:541:ILE:HD13	4:A:549:MET:HE1	1.85	0.57
13:J:1:MET:N	13:J:56:LEU:H	2.00	0.57
13:J:64:ASN:CB	13:J:65:PRO:CD	2.78	0.57
4:A:1116:LEU:CD1	4:A:1118:VAL:HG13	2.34	0.57
15:L:27:LEU:HB3	15:L:37:LYS:HD3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:494:SER:O	4:A:497:THR:N	2.37	0.57
10:G:106:MET:HG2	10:G:107:LYS:N	2.19	0.57
4:A:49:LYS:HE2	4:A:61:ILE:HD12	1.84	0.57
4:A:685:GLU:HG3	4:A:686:ALA:N	2.18	0.57
5:B:57:TYR:CD1	5:B:57:TYR:N	2.69	0.57
5:B:576:ASP:HA	5:B:622:LYS:NZ	2.20	0.57
5:B:525:ALA:O	5:B:768:THR:HG23	2.05	0.57
5:B:54:PHE:HA	5:B:58:THR:HB	1.85	0.57
5:B:1031:LEU:HD11	5:B:1042:GLY:HA3	1.85	0.57
5:B:758:PHE:HZ	5:B:1031:LEU:HD22	1.69	0.57
7:D:54:GLU:O	7:D:58:VAL:HG23	2.03	0.57
4:A:626:ASN:O	4:A:631:HIS:CD2	2.57	0.57
4:A:577:ILE:O	4:A:580:VAL:HG23	2.04	0.57
4:A:701:LEU:HD21	12:I:114:GLN:HB2	1.86	0.57
10:G:79:PHE:HE2	10:G:105:PRO:HG2	1.69	0.57
5:B:100:PRO:HD2	5:B:180:TYR:CE1	2.40	0.57
14:K:65:HIS:CD2	14:K:67:PHE:HB2	2.39	0.57
11:H:58:THR:HB	11:H:143:LEU:HD13	1.86	0.57
13:J:47:ARG:HG2	13:J:47:ARG:HH11	1.69	0.57
4:A:382:PRO:HB3	4:A:428:TYR:CE2	2.38	0.57
4:A:1447:GLU:OE2	10:G:23:LYS:HB2	2.04	0.57
4:A:863:VAL:HG11	4:A:866:PHE:CD2	2.38	0.57
3:P:3:U:H4'	4:A:323:LYS:NZ	2.19	0.57
8:E:101:GLN:NE2	8:E:127:ILE:HG21	2.19	0.57
5:B:217:ARG:C	5:B:217:ARG:HD2	2.24	0.57
4:A:1313:LEU:O	4:A:1315:GLU:N	2.37	0.57
4:A:1341:ILE:O	4:A:1344:GLY:N	2.38	0.57
4:A:34:LYS:HG2	4:A:36:ARG:NH2	2.19	0.57
4:A:102:VAL:O	4:A:105:CYS:HB2	2.04	0.57
4:A:268:ASP:HB3	4:A:299:HIS:CE1	2.39	0.57
9:F:118:LEU:O	9:F:118:LEU:HD12	2.05	0.57
7:D:175:PHE:HZ	10:G:85:GLU:HG3	1.68	0.57
11:H:142:LEU:C	11:H:143:LEU:HD12	2.25	0.57
4:A:138:ILE:HD13	4:A:222:LEU:HD23	1.86	0.57
4:A:215:SER:O	4:A:218:ASP:HB2	2.04	0.57
4:A:868:TYR:CD2	4:A:1058:VAL:HG21	2.35	0.57
9:F:90:ARG:HD3	9:F:155:LEU:CD1	2.35	0.57
4:A:647:GLY:O	4:A:651:LYS:HG3	2.04	0.57
4:A:565:ILE:O	4:A:570:PRO:HA	2.05	0.57
5:B:579:ARG:N	5:B:589:VAL:HG13	2.18	0.57
8:E:94:LYS:CE	8:E:98:ILE:HD11	2.30	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:844:ALA:O	4:A:845:LEU:HD23	2.04	0.57
5:B:604:ARG:NH1	5:B:691:GLU:OE2	2.38	0.57
9:F:90:ARG:HG3	9:F:91:ALA:N	2.18	0.57
7:D:52:LEU:O	7:D:54:GLU:N	2.36	0.57
6:C:213:PRO:HG2	6:C:214:ASN:H	1.69	0.57
4:A:34:LYS:CG	4:A:36:ARG:HH21	2.18	0.57
10:G:143:ILE:CG2	10:G:144:ARG:N	2.67	0.57
5:B:557:PHE:C	5:B:557:PHE:CD2	2.77	0.57
4:A:1220:PHE:O	4:A:1221:LYS:HB2	2.03	0.57
4:A:71:GLN:C	4:A:73:GLY:H	2.08	0.57
4:A:477:PRO:HG2	4:A:521:MET:HG2	1.87	0.57
5:B:1069:PHE:HD1	5:B:1069:PHE:H	1.52	0.57
5:B:955:THR:HG22	5:B:956:THR:N	2.20	0.57
4:A:1336:MET:CE	4:A:1381:LEU:HG	2.35	0.57
4:A:600:PRO:C	4:A:602:ASP:H	2.05	0.57
5:B:794:ASN:C	5:B:795:ILE:HD12	2.25	0.57
5:B:847:ASP:C	5:B:849:GLY:H	2.07	0.57
5:B:594:ALA:CA	5:B:617:ARG:HH12	2.15	0.57
5:B:357:GLN:O	5:B:366:GLN:HA	2.04	0.57
8:E:134:THR:C	8:E:135:PHE:HD1	2.08	0.57
6:C:212:PRO:CB	6:C:213:PRO:HD2	2.35	0.57
4:A:385:ILE:HG22	4:A:386:ASP:N	2.20	0.57
10:G:1:MET:SD	10:G:1:MET:O	2.63	0.57
5:B:1099:VAL:O	5:B:1101:ASP:N	2.38	0.57
4:A:477:PRO:CG	4:A:521:MET:HG2	2.35	0.57
4:A:1239:ARG:HH22	4:A:1241:ARG:HH22	1.51	0.57
5:B:31:TRP:CE3	5:B:34:ILE:HD12	2.40	0.57
4:A:1116:LEU:H	4:A:1308:THR:HG22	1.69	0.57
7:D:17:LYS:HG2	7:D:17:LYS:O	2.04	0.57
6:C:238:ILE:HG23	6:C:242:GLN:HB2	1.85	0.57
5:B:190:TYR:HD2	13:J:62:ARG:O	1.88	0.57
5:B:552:MET:HA	5:B:555:ILE:HB	1.87	0.56
4:A:590:ARG:HB3	4:A:605:MET:N	2.20	0.56
15:L:34:CYS:SG	15:L:34:CYS:O	2.63	0.56
4:A:44:THR:O	4:A:45:GLN:HB2	2.04	0.56
4:A:442:VAL:O	4:A:457:ALA:HA	2.05	0.56
4:A:93:VAL:HG11	4:A:305:ASP:HB3	1.86	0.56
10:G:59:GLY:HA3	10:G:70:PHE:CD2	2.41	0.56
6:C:70:ILE:HG12	6:C:142:VAL:HG11	1.87	0.56
4:A:444:PHE:CB	4:A:458:HIS:HD2	2.17	0.56
4:A:886:ILE:CG2	4:A:887:GLY:N	2.67	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:642:ASP:HB3	5:B:649:LYS:HD2	1.87	0.56
4:A:115:LEU:HB2	4:A:122:MET:HE2	1.87	0.56
4:A:946:VAL:HG13	8:E:201:LYS:HB3	1.85	0.56
5:B:1102:LYS:O	5:B:1103:ILE:C	2.44	0.56
5:B:792:MET:HA	5:B:856:PHE:O	2.06	0.56
5:B:616:ILE:HG23	5:B:700:SER:OG	2.06	0.56
11:H:110:ASP:O	11:H:128:ASN:ND2	2.38	0.56
5:B:635:ARG:NH2	5:B:742:GLU:OE2	2.38	0.56
13:J:21:TYR:CE1	13:J:36:LEU:HD21	2.40	0.56
4:A:886:ILE:HD11	4:A:943:LEU:CB	2.35	0.56
5:B:603:LEU:HD13	5:B:608:ASP:CB	2.33	0.56
8:E:3:GLN:HG3	8:E:4:GLU:N	2.20	0.56
9:F:135:ARG:HD3	9:F:143:PHE:CD2	2.39	0.56
6:C:73:GLN:NE2	6:C:75:MET:HB2	2.20	0.56
6:C:181:ASP:OD1	6:C:186:LEU:HD13	2.05	0.56
5:B:912:ILE:O	5:B:938:SER:HB3	2.05	0.56
12:I:14:LEU:HA	12:I:28:GLU:O	2.06	0.56
8:E:55:ARG:HD2	8:E:83:CYS:O	2.05	0.56
4:A:168:GLY:O	4:A:169:ASN:C	2.44	0.56
10:G:25:TYR:HE2	10:G:29:LYS:HD2	1.70	0.56
5:B:97:VAL:HG12	5:B:178:ASN:HD21	1.70	0.56
10:G:74:TYR:H	10:G:74:TYR:HD2	1.51	0.56
6:C:77:ILE:HA	6:C:129:ILE:HD11	1.88	0.56
11:H:89:LEU:O	11:H:91:ASP:N	2.36	0.56
14:K:49:GLU:HG3	14:K:94:ILE:CG1	2.35	0.56
5:B:1183:LYS:HA	5:B:1186:ASP:HA	1.88	0.56
4:A:282:ASN:O	4:A:284:ALA:N	2.38	0.56
5:B:880:THR:O	5:B:881:ASN:HB2	2.05	0.56
5:B:1072:MET:HE1	5:B:1085:ILE:HB	1.87	0.56
5:B:195:CYS:SG	5:B:196:PRO:HD2	2.46	0.56
7:D:7:THR:HG21	7:D:32:GLU:CD	2.25	0.56
4:A:42:ASP:HB3	4:A:45:GLN:H	1.70	0.56
7:D:195:ILE:HG22	7:D:198:LEU:HG	1.85	0.56
6:C:40:GLU:HA	6:C:163:ILE:HG21	1.87	0.56
4:A:860:LEU:CD1	4:A:1393:ASN:HB2	2.31	0.56
7:D:40:HIS:CB	10:G:73:LYS:HZ3	2.05	0.56
4:A:356:ASP:HB2	4:A:469:ARG:HH11	1.71	0.56
5:B:839:MET:HG3	5:B:1010:LEU:HD11	1.86	0.56
11:H:23:VAL:HG13	11:H:42:ILE:O	2.05	0.56
5:B:1085:ILE:H	5:B:1085:ILE:HD12	1.70	0.56
9:F:143:PHE:C	9:F:143:PHE:HD1	2.09	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:94:LYS:HG2	5:B:95:ILE:N	2.20	0.56
4:A:384:ASN:O	4:A:385:ILE:C	2.43	0.56
5:B:225:VAL:HG12	5:B:238:ALA:HB2	1.88	0.56
6:C:254:LYS:O	6:C:258:ILE:HD13	2.05	0.56
4:A:75:ASN:O	4:A:76:GLU:CB	2.54	0.56
5:B:906:SER:O	5:B:941:LEU:HD23	2.05	0.56
13:J:64:ASN:ND2	13:J:65:PRO:HD3	2.21	0.56
5:B:39:ARG:NH2	5:B:665:GLU:HG2	2.20	0.56
3:P:3:U:H4'	4:A:323:LYS:HZ3	1.71	0.56
4:A:965:GLN:HA	4:A:968:GLN:HG3	1.87	0.56
5:B:707:PRO:O	5:B:711:GLU:HG3	2.06	0.56
5:B:620:ARG:NH2	12:I:89:GLN:NE2	2.54	0.56
7:D:160:VAL:O	7:D:164:ILE:HG13	2.06	0.56
5:B:258:LEU:HG	5:B:258:LEU:O	2.05	0.56
5:B:113:TYR:CD2	5:B:192:LEU:HD22	2.41	0.56
5:B:981:ALA:HB2	5:B:987:LYS:HA	1.87	0.56
4:A:1341:ILE:CG2	4:A:1342:GLU:H	2.18	0.56
10:G:117:GLN:O	10:G:119:LEU:N	2.37	0.56
4:A:262:LEU:O	4:A:264:PHE:N	2.39	0.56
4:A:68:GLN:O	4:A:70:CYS:N	2.34	0.56
9:F:138:LEU:HB3	9:F:139:PRO:HD2	1.87	0.56
14:K:10:PHE:HD2	14:K:10:PHE:N	2.03	0.56
5:B:365:THR:HG23	5:B:367:LEU:N	2.13	0.56
4:A:1063:MET:HG3	4:A:1436:ILE:HG23	1.88	0.56
14:K:46:ILE:O	14:K:50:LEU:HB2	2.04	0.56
4:A:269:ILE:HG12	4:A:299:HIS:HB3	1.86	0.56
5:B:299:GLU:HB3	5:B:571:PRO:HG3	1.87	0.56
5:B:176:SER:O	5:B:182:SER:HB3	2.05	0.56
5:B:405:ARG:CZ	5:B:632:ARG:HG2	2.36	0.56
1:T:12:DA:H2''	1:T:13:DC:O5'	2.05	0.56
5:B:1087:PHE:HD2	5:B:1088:GLY:N	2.04	0.56
9:F:111:LEU:H	9:F:111:LEU:CD1	2.15	0.56
5:B:516:ASN:ND2	5:B:516:ASN:N	2.47	0.56
6:C:248:ILE:HD13	14:K:101:LEU:HD22	1.88	0.56
12:I:33:SER:O	12:I:35:VAL:HG23	2.06	0.56
6:C:203:GLN:HG2	6:C:207:CYS:SG	2.46	0.56
9:F:81:THR:HB	9:F:136:ARG:HH11	1.70	0.56
4:A:1100:ARG:HH21	4:A:1351:GLU:HG2	1.69	0.56
4:A:947:PHE:HD2	4:A:954:TRP:CZ2	2.24	0.56
4:A:442:VAL:HB	4:A:489:LEU:HD11	1.87	0.56
4:A:1164:PRO:HG2	4:A:1165:GLU:H	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:260:GLY:O	5:B:267:ARG:HD3	2.06	0.56
5:B:731:VAL:HG12	5:B:732:SER:N	2.20	0.56
5:B:305:VAL:HG12	5:B:305:VAL:O	2.05	0.56
5:B:637:LEU:HD21	5:B:742:GLU:OE2	2.05	0.55
14:K:58:PHE:HB3	14:K:76:GLN:HB3	1.87	0.55
12:I:85:PHE:CD1	12:I:99:LEU:HD13	2.41	0.55
14:K:45:LEU:HG	14:K:94:ILE:CD1	2.33	0.55
4:A:1214:GLU:O	4:A:1218:GLN:HG2	2.05	0.55
5:B:861:ASP:OD1	5:B:862:GLN:N	2.39	0.55
4:A:605:MET:HE3	4:A:614:PHE:O	2.06	0.55
5:B:758:PHE:CE2	5:B:1044:ALA:HA	2.40	0.55
4:A:335:ARG:NH1	5:B:1202:LEU:HD13	2.21	0.55
14:K:42:LEU:HD21	14:K:46:ILE:HD11	1.88	0.55
4:A:1149:ALA:CB	12:I:47:GLU:HA	2.36	0.55
11:H:135:LEU:HD13	11:H:137:GLN:HE21	1.71	0.55
5:B:906:SER:HA	5:B:946:ASN:HB2	1.88	0.55
13:J:1:MET:H1	13:J:56:LEU:CA	2.20	0.55
1:T:12:DA:C2	2:N:6:DA:C2	2.94	0.55
10:G:14:HIS:CD2	10:G:16:SER:HB2	2.41	0.55
5:B:1196:ILE:HB	5:B:1197:PRO:HD2	1.88	0.55
5:B:222:ILE:O	5:B:240:ILE:HA	2.06	0.55
4:A:44:THR:HG22	4:A:44:THR:O	2.06	0.55
4:A:482:PHE:O	5:B:989:THR:HG23	2.06	0.55
5:B:259:TYR:HB2	5:B:268:THR:HG23	1.88	0.55
5:B:310:MET:O	5:B:313:MET:HB2	2.06	0.55
6:C:152:GLU:HG2	6:C:153:LEU:H	1.72	0.55
11:H:116:TYR:HE2	11:H:140:ALA:CB	2.19	0.55
8:E:78:LEU:C	8:E:78:LEU:HD23	2.27	0.55
4:A:709:THR:HG21	12:I:93:LYS:O	2.06	0.55
8:E:198:ILE:CD1	8:E:212:ARG:HG3	2.36	0.55
5:B:1065:GLN:HE21	5:B:1067:ARG:HG2	1.72	0.55
5:B:515:HIS:CD2	5:B:517:THR:H	2.23	0.55
4:A:867:ILE:HG22	4:A:872:GLY:N	2.22	0.55
3:P:2:U:O2'	3:P:3:U:H5'	2.06	0.55
4:A:768:GLN:CG	4:A:816:HIS:HA	2.36	0.55
10:G:9:LEU:HG	10:G:10:ASN:N	2.20	0.55
5:B:226:PHE:HA	5:B:395:GLN:HG3	1.86	0.55
5:B:1135:ARG:O	5:B:1139:ILE:HG13	2.07	0.55
4:A:416:ARG:O	4:A:417:TYR:HD2	1.89	0.55
5:B:332:ASP:O	5:B:334:ILE:N	2.37	0.55
8:E:124:VAL:HG13	8:E:132:ILE:CB	2.35	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:22:PHE:CE1	5:B:1213:THR:HG22	2.42	0.55
12:I:71:SER:OG	12:I:83:ASN:HB2	2.07	0.55
5:B:446:LEU:O	5:B:447:ALA:HB3	2.06	0.55
4:A:278:THR:O	4:A:278:THR:HG22	2.07	0.55
10:G:44:TYR:O	10:G:78:VAL:HG12	2.07	0.55
4:A:567:LYS:HB3	11:H:95:TYR:CA	2.35	0.55
4:A:34:LYS:CB	4:A:36:ARG:HE	2.18	0.55
4:A:1260:LEU:HG	4:A:1260:LEU:O	2.07	0.55
10:G:1:MET:HE3	10:G:80:LYS:O	2.06	0.55
4:A:1445:ILE:HD12	10:G:59:GLY:O	2.07	0.55
11:H:127:GLY:O	11:H:128:ASN:HB2	2.06	0.55
4:A:1402:PHE:CE1	4:A:1403:GLU:HG3	2.42	0.55
4:A:317:LYS:O	4:A:318:SER:CB	2.55	0.55
5:B:778:MET:CE	5:B:1094:ARG:CD	2.85	0.55
4:A:1349:TYR:CB	4:A:1372:VAL:HG21	2.36	0.55
5:B:94:LYS:O	5:B:130:VAL:HG13	2.07	0.55
8:E:42:PHE:HZ	8:E:58:MET:HE3	1.72	0.55
4:A:1155:ASP:OD2	4:A:1161:THR:HG23	2.06	0.55
5:B:637:LEU:O	5:B:690:VAL:HG13	2.06	0.55
4:A:843:LYS:HD3	4:A:846:GLU:OE2	2.07	0.55
4:A:845:LEU:HD22	4:A:1374:VAL:HG21	1.89	0.55
6:C:31:ASN:O	6:C:34:ARG:N	2.40	0.55
5:B:358:LYS:HA	5:B:366:GLN:HB3	1.89	0.55
4:A:590:ARG:HH11	4:A:590:ARG:CG	2.19	0.55
4:A:816:HIS:CD2	5:B:764:SER:HB2	2.42	0.55
4:A:154:SER:HB3	4:A:162:VAL:HG21	1.89	0.55
5:B:215:GLN:HA	5:B:215:GLN:NE2	2.21	0.55
4:A:93:VAL:HG13	4:A:301:ALA:HB1	1.89	0.55
5:B:806:THR:CG2	5:B:808:ALA:HB3	2.37	0.55
4:A:767:GLN:HB2	4:A:799:PHE:HD1	1.71	0.55
4:A:785:PRO:HG2	4:A:786:HIS:CD2	2.41	0.55
4:A:10:PRO:O	5:B:1193:GLN:HB3	2.06	0.55
2:N:1:DC:H1'	2:N:2:DA:C5'	2.37	0.55
7:D:176:GLU:C	7:D:178:ALA:H	2.10	0.55
5:B:361:LEU:N	5:B:362:PRO:CD	2.70	0.55
4:A:1035:TYR:O	4:A:1037:LEU:HD23	2.07	0.55
15:L:25:ALA:O	15:L:26:THR:HB	2.07	0.55
6:C:45:ALA:O	6:C:159:ALA:HA	2.07	0.55
6:C:147:LEU:HD12	6:C:151:GLN:O	2.07	0.55
4:A:709:THR:HB	4:A:712:GLU:HG3	1.88	0.55
4:A:265:LYS:HE2	4:A:322:VAL:HG13	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:981:LEU:HD23	4:A:1039:LYS:HA	1.87	0.55
5:B:866:TYR:O	5:B:868:MET:N	2.40	0.55
4:A:308:ILE:HG22	4:A:309:ALA:H	1.71	0.55
5:B:351:TYR:CE1	5:B:355:ILE:HD11	2.42	0.55
9:F:76:LYS:O	9:F:79:ARG:HD3	2.07	0.55
4:A:853:ASP:OD1	4:A:855:THR:CB	2.55	0.55
10:G:73:LYS:HE2	10:G:74:TYR:O	2.07	0.55
5:B:473:MET:O	5:B:475:SER:N	2.40	0.55
5:B:758:PHE:CE1	5:B:1027:ILE:CG2	2.90	0.55
5:B:69:LEU:HD22	5:B:429:PHE:HE1	1.71	0.55
5:B:874:PHE:HA	5:B:913:GLY:O	2.06	0.55
5:B:640:VAL:HG12	5:B:640:VAL:O	2.07	0.55
5:B:1172:ILE:O	5:B:1172:ILE:HG22	2.07	0.55
5:B:1099:VAL:HG12	5:B:1100:ASP:H	1.71	0.54
15:L:30:ILE:O	15:L:56:LEU:HA	2.07	0.54
5:B:953:LEU:CD2	5:B:965:LYS:HB2	2.35	0.54
12:I:52:ILE:HG13	12:I:52:ILE:O	2.06	0.54
6:C:11:ARG:HD3	6:C:209:TYR:CE2	2.42	0.54
15:L:49:LYS:O	15:L:50:ASP:CB	2.54	0.54
15:L:58:LYS:HG2	15:L:58:LYS:O	2.06	0.54
1:T:20:DC:H4'	4:A:447:GLN:HE22	1.71	0.54
5:B:180:TYR:HD1	5:B:180:TYR:H	1.54	0.54
4:A:718:VAL:O	4:A:721:PHE:HB2	2.08	0.54
4:A:1308:THR:HG23	4:A:1309:ASP:N	2.22	0.54
4:A:19:PHE:HE1	4:A:1396:ALA:HB3	1.71	0.54
4:A:1336:MET:HE3	4:A:1381:LEU:HG	1.88	0.54
4:A:1291:VAL:HG13	4:A:1292:PRO:CD	2.35	0.54
5:B:570:VAL:HG23	5:B:573:GLN:HB3	1.88	0.54
4:A:1191:TRP:CD1	4:A:1256:GLU:HB2	2.41	0.54
13:J:5:VAL:O	13:J:6:ARG:O	2.26	0.54
12:I:60:GLN:NE2	12:I:107:SER:OG	2.40	0.54
4:A:244:PRO:CG	4:A:245:PRO:HD3	2.38	0.54
4:A:767:GLN:NE2	4:A:774:ARG:HB3	2.22	0.54
4:A:1441:PHE:CE2	9:F:89:GLU:HG2	2.42	0.54
5:B:1006:ILE:HD13	13:J:44:TYR:CE2	2.43	0.54
4:A:61:ILE:HG22	4:A:62:ASP:N	2.23	0.54
5:B:1223:ASP:O	5:B:1224:PHE:HB2	2.08	0.54
4:A:808:LEU:HG	4:A:812:GLU:HB3	1.89	0.54
7:D:56:ARG:HD3	7:D:149:THR:HA	1.88	0.54
8:E:124:VAL:HG13	8:E:132:ILE:HD12	1.88	0.54
4:A:3:GLY:O	4:A:4:GLN:CB	2.56	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:865:LYS:HE2	5:B:871:THR:OG1	2.06	0.54
1:T:18:DC:P	1:T:18:DC:H3'	2.48	0.54
1:T:12:DA:H2''	1:T:13:DC:C5'	2.37	0.54
4:A:219:PHE:O	4:A:222:LEU:O	2.25	0.54
6:C:73:GLN:HE21	6:C:75:MET:N	2.05	0.54
5:B:459:TYR:CE1	5:B:469:GLN:HG2	2.42	0.54
4:A:69:THR:C	4:A:71:GLN:N	2.61	0.54
7:D:40:HIS:CB	10:G:73:LYS:HZ2	2.18	0.54
5:B:1004:GLU:O	6:C:177:GLU:HG2	2.08	0.54
4:A:366:VAL:CG2	4:A:460:VAL:HG22	2.34	0.54
5:B:1038:SER:C	5:B:1040:ASN:H	2.10	0.54
4:A:979:SER:OG	4:A:980:ASP:N	2.41	0.54
9:F:119:ARG:HG3	9:F:119:ARG:NH1	2.23	0.54
4:A:1074:GLU:N	4:A:1075:PRO:HD2	2.23	0.54
7:D:209:ARG:O	7:D:212:LYS:HB2	2.08	0.54
5:B:825:VAL:HG12	5:B:826:ALA:N	2.21	0.54
5:B:39:ARG:HH21	5:B:665:GLU:CD	2.11	0.54
4:A:1435:PRO:HA	4:A:1439:GLY:O	2.06	0.54
5:B:309:GLN:CD	12:I:52:ILE:HD11	2.28	0.54
4:A:3:GLY:O	4:A:4:GLN:HB2	2.08	0.54
4:A:182:VAL:HG22	4:A:201:VAL:HA	1.89	0.54
4:A:829:VAL:C	4:A:831:THR:H	2.10	0.54
7:D:39:ASN:ND2	7:D:41:GLN:HB2	2.23	0.54
5:B:796:LEU:HD12	5:B:852:ARG:O	2.08	0.54
4:A:401:GLY:C	4:A:435:HIS:CD2	2.81	0.54
4:A:265:LYS:NZ	4:A:322:VAL:HG13	2.23	0.54
5:B:1069:PHE:HA	5:B:1085:ILE:O	2.07	0.54
12:I:51:ASN:O	12:I:54:GLU:HG3	2.08	0.54
15:L:39:SER:O	15:L:40:LEU:HG	2.08	0.54
4:A:1346:ALA:HB3	8:E:149:LEU:HD13	1.89	0.54
11:H:102:TYR:N	11:H:102:TYR:CD2	2.76	0.54
4:A:41:MET:HB3	4:A:48:ALA:O	2.08	0.54
4:A:831:THR:HG23	4:A:832:ALA:N	2.21	0.54
14:K:65:HIS:HD2	14:K:67:PHE:N	2.05	0.54
4:A:774:ARG:O	4:A:775:ILE:C	2.46	0.54
4:A:774:ARG:NH2	4:A:797:LYS:HB2	2.23	0.54
5:B:205:ILE:N	5:B:205:ILE:HD12	2.23	0.54
5:B:1152:MET:HE1	5:B:1157:ALA:HA	1.89	0.54
9:F:143:PHE:C	9:F:143:PHE:CD1	2.78	0.54
7:D:167:LEU:O	7:D:170:THR:OG1	2.26	0.54
5:B:185:THR:O	5:B:188:ASP:HB2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:46:ILE:HD12	6:C:67:LEU:HB3	1.89	0.54
5:B:130:VAL:HB	5:B:167:ILE:CD1	2.38	0.54
6:C:8:VAL:HG12	6:C:9:LYS:H	1.73	0.54
8:E:85:GLU:HB2	8:E:88:VAL:HG22	1.89	0.54
5:B:1099:VAL:HG12	5:B:1100:ASP:N	2.23	0.54
5:B:948:ILE:O	5:B:968:VAL:HG13	2.08	0.54
6:C:116:LYS:HD3	6:C:140:ASN:CB	2.27	0.54
5:B:653:VAL:HG22	5:B:689:LEU:HD13	1.90	0.54
5:B:658:ILE:HG22	5:B:659:ALA:N	2.22	0.54
12:I:103:CYS:HB3	12:I:106:CYS:SG	2.48	0.54
4:A:910:PRO:HB3	4:A:917:SER:N	2.22	0.54
5:B:576:ASP:HA	5:B:622:LYS:HZ2	1.73	0.54
14:K:15:GLY:O	14:K:16:GLU:HG3	2.08	0.54
11:H:99:GLY:HA3	11:H:118:PHE:HA	1.89	0.53
7:D:39:ASN:HD22	7:D:41:GLN:HB2	1.73	0.53
4:A:472:LEU:O	4:A:475:THR:HG22	2.07	0.53
4:A:401:GLY:C	4:A:435:HIS:HD2	2.10	0.53
9:F:89:GLU:HB3	9:F:134:ILE:CD1	2.39	0.53
4:A:1329:THR:HG23	4:A:1331:SER:H	1.73	0.53
4:A:899:VAL:HB	4:A:929:LEU:CD1	2.38	0.53
5:B:1001:PHE:CD2	6:C:34:ARG:NH2	2.76	0.53
4:A:172:PRO:HG3	4:A:185:TRP:CZ2	2.43	0.53
7:D:7:THR:HG21	7:D:32:GLU:OE2	2.08	0.53
4:A:1254:ALA:O	4:A:1255:GLU:HB2	2.07	0.53
11:H:58:THR:HG22	11:H:59:ILE:N	2.23	0.53
5:B:39:ARG:HG2	5:B:39:ARG:HH11	1.73	0.53
4:A:714:PHE:O	4:A:718:VAL:HG23	2.08	0.53
6:C:259:LEU:HD13	14:K:91:CYS:HB2	1.90	0.53
5:B:1084:GLN:OE1	6:C:189:THR:CG2	2.57	0.53
4:A:806:ARG:HH12	5:B:729:ILE:CD1	2.20	0.53
13:J:27:GLU:C	13:J:29:GLU:H	2.12	0.53
4:A:130:ASP:O	4:A:133:LYS:N	2.39	0.53
6:C:142:VAL:H	13:J:16:ASP:HB3	1.72	0.53
11:H:5:LEU:HD22	11:H:133:ASN:O	2.09	0.53
5:B:1162:ILE:O	5:B:1171:VAL:HG21	2.08	0.53
5:B:485:ARG:NH2	5:B:782:LEU:HD11	2.23	0.53
4:A:940:ARG:HH11	4:A:940:ARG:HG2	1.72	0.53
4:A:347:PHE:CE2	4:A:375:THR:HG23	2.43	0.53
7:D:52:LEU:C	7:D:54:GLU:H	2.11	0.53
10:G:88:ASP:OD2	10:G:88:ASP:N	2.42	0.53
4:A:1225:PHE:HE2	4:A:1227:ILE:HD11	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:167:CYS:SG	4:A:167:CYS:O	2.66	0.53
4:A:858:ASN:HD22	4:A:861:GLY:H	1.56	0.53
4:A:846:GLU:OE1	4:A:1425:SER:OG	2.27	0.53
4:A:335:ARG:HA	4:A:339:ASN:HB2	1.90	0.53
6:C:35:ARG:NH1	14:K:41:THR:H	2.06	0.53
5:B:810:GLU:HB2	5:B:815:ARG:HH22	1.74	0.53
8:E:124:VAL:HG13	8:E:132:ILE:CG1	2.39	0.53
6:C:101:LEU:HD13	6:C:118:LEU:HD23	1.90	0.53
6:C:125:MET:HB2	6:C:127:ARG:NH2	2.23	0.53
11:H:56:THR:HB	11:H:145:ARG:HG2	1.90	0.53
10:G:61:ILE:HG23	10:G:66:GLY:O	2.08	0.53
10:G:102:GLN:HG3	10:G:106:MET:O	2.08	0.53
7:D:53:SER:HB3	7:D:152:SER:HB2	1.91	0.53
7:D:49:ALA:HB2	7:D:174:PRO:CB	2.37	0.53
4:A:504:LEU:HD12	4:A:504:LEU:N	2.24	0.53
14:K:50:LEU:HD11	14:K:75:ILE:CD1	2.37	0.53
4:A:130:ASP:O	4:A:131:SER:C	2.47	0.53
5:B:1176:ASN:C	5:B:1178:ASN:H	2.10	0.53
5:B:449:ASN:C	5:B:451:LYS:H	2.12	0.53
4:A:68:GLN:HE22	4:A:80:HIS:CG	2.27	0.53
4:A:84:ILE:HG23	4:A:84:ILE:O	2.07	0.53
8:E:207:ARG:CB	8:E:207:ARG:HH11	2.20	0.53
4:A:541:ILE:HD13	4:A:549:MET:HE3	1.91	0.53
4:A:332:LYS:O	4:A:333:GLU:HB2	2.09	0.53
13:J:44:TYR:CA	13:J:47:ARG:HB2	2.33	0.53
4:A:1329:THR:H	4:A:1335:ILE:HD11	1.73	0.53
4:A:665:GLY:HA2	5:B:1026:LEU:HD22	1.91	0.53
12:I:85:PHE:N	12:I:85:PHE:CD2	2.74	0.53
4:A:416:ARG:C	4:A:417:TYR:CD2	2.81	0.53
4:A:504:LEU:HD11	9:F:91:ALA:HB1	1.91	0.53
4:A:971:PHE:CE2	4:A:1040:GLN:HG2	2.44	0.53
4:A:658:LEU:HD13	5:B:831:SER:HA	1.90	0.53
4:A:786:HIS:CD2	4:A:786:HIS:N	2.74	0.53
5:B:483:LEU:HD11	5:B:491:THR:CG2	2.32	0.53
9:F:86:THR:HG23	9:F:89:GLU:OE1	2.09	0.53
4:A:1372:VAL:O	4:A:1376:THR:HG22	2.07	0.53
15:L:48:CYS:HB3	15:L:51:CYS:O	2.08	0.53
10:G:34:VAL:CG1	10:G:45:ILE:HG21	2.36	0.53
8:E:78:LEU:HD21	8:E:80:VAL:CG2	2.37	0.53
4:A:464:PRO:HG2	4:A:465:TYR:HD1	1.72	0.53
4:A:1120:LEU:CD1	4:A:1120:LEU:H	2.22	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:745:PRO:O	5:B:747:MET:N	2.41	0.53
14:K:55:LYS:HB3	14:K:81:TYR:CD1	2.44	0.53
4:A:1283:VAL:CG1	4:A:1284:MET:H	2.17	0.53
4:A:503:GLN:HE21	9:F:90:ARG:HH21	1.55	0.53
5:B:287:ARG:NH1	5:B:324:ILE:O	2.41	0.53
11:H:83:GLN:C	11:H:85:GLY:N	2.60	0.53
11:H:15:VAL:HG22	11:H:26:ILE:CD1	2.39	0.53
4:A:1198:ASP:HB3	4:A:1201:ALA:HB3	1.90	0.53
4:A:42:ASP:C	4:A:44:THR:H	2.12	0.53
11:H:103:LYS:HG2	11:H:104:PHE:N	2.24	0.53
4:A:1289:ARG:NH1	4:A:1326:ARG:NH1	2.56	0.53
10:G:85:GLU:HG2	10:G:86:VAL:N	2.24	0.53
8:E:207:ARG:HH11	8:E:207:ARG:HB3	1.74	0.53
5:B:126:SER:O	5:B:169:ARG:HA	2.09	0.53
5:B:744:HIS:ND1	5:B:745:PRO:HD2	2.24	0.53
13:J:7:CYS:SG	13:J:46:CYS:HA	2.49	0.53
4:A:682:THR:CG2	4:A:728:LYS:HE3	2.37	0.53
5:B:286:PHE:CD1	5:B:297:ILE:HG23	2.44	0.53
12:I:2:THR:O	12:I:3:THR:C	2.46	0.53
1:T:19:DC:H2''	1:T:20:DC:C5'	2.39	0.53
6:C:144:ILE:O	6:C:145:CYS:HB3	2.09	0.53
4:A:1325:THR:HG23	8:E:146:HIS:O	2.08	0.53
4:A:567:LYS:HB2	4:A:568:PRO:CD	2.39	0.53
5:B:1001:PHE:CE2	6:C:34:ARG:NE	2.77	0.53
12:I:13:MET:CE	12:I:14:LEU:H	2.22	0.53
4:A:1140:HIS:CE1	4:A:1272:THR:HG23	2.43	0.53
4:A:1076:ALA:HA	4:A:1079:MET:CE	2.38	0.53
14:K:82:ASP:OD1	14:K:84:LYS:N	2.41	0.53
4:A:50:ILE:C	4:A:52:GLY:N	2.60	0.52
5:B:999:MET:HB3	5:B:1007:VAL:HG21	1.91	0.52
5:B:33:VAL:HG21	5:B:638:PHE:CZ	2.36	0.52
10:G:13:LEU:CD2	10:G:17:PHE:HB2	2.34	0.52
4:A:901:LEU:HG	4:A:926:GLN:HE21	1.74	0.52
4:A:901:LEU:HB2	4:A:926:GLN:HG2	1.90	0.52
4:A:899:VAL:HB	4:A:929:LEU:HD12	1.90	0.52
4:A:665:GLY:HA2	5:B:1026:LEU:CD2	2.39	0.52
5:B:112:LEU:HD12	5:B:113:TYR:H	1.73	0.52
4:A:524:VAL:CG1	4:A:525:GLN:H	2.21	0.52
4:A:1356:ILE:HG21	4:A:1363:VAL:HG23	1.90	0.52
5:B:315:LYS:N	5:B:316:PRO:HD2	2.24	0.52
13:J:27:GLU:O	13:J:29:GLU:N	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:157:ASP:C	4:A:159:THR:H	2.12	0.52
4:A:352:VAL:O	4:A:467:THR:HB	2.09	0.52
4:A:79:GLY:HA3	4:A:243:PRO:HG3	1.91	0.52
10:G:34:VAL:HG12	10:G:45:ILE:CG2	2.34	0.52
4:A:1120:LEU:CD1	4:A:1120:LEU:N	2.72	0.52
4:A:18:GLN:O	5:B:1215:ARG:HG2	2.10	0.52
4:A:527:THR:CG2	4:A:650:GLN:HA	2.40	0.52
4:A:24:PRO:HD2	4:A:233:TRP:HE1	1.74	0.52
8:E:192:ARG:HG3	8:E:192:ARG:HH11	1.73	0.52
4:A:1409:LEU:CD1	5:B:1207:LEU:HD21	2.39	0.52
8:E:83:CYS:HG	8:E:110:PHE:HZ	1.54	0.52
6:C:53:THR:O	6:C:153:LEU:HA	2.09	0.52
4:A:523:ILE:CD1	4:A:649:ILE:HG21	2.38	0.52
7:D:151:PHE:N	7:D:151:PHE:CD1	2.77	0.52
6:C:39:ALA:CA	6:C:164:ALA:HB3	2.29	0.52
10:G:143:ILE:HG23	10:G:169:GLY:O	2.09	0.52
9:F:118:LEU:O	9:F:122:MET:HG3	2.09	0.52
4:A:997:LEU:N	4:A:997:LEU:HD23	2.23	0.52
5:B:464:GLY:HA2	5:B:479:VAL:O	2.09	0.52
4:A:35:ILE:CG2	4:A:84:ILE:HD12	2.39	0.52
5:B:880:THR:HB	5:B:934:LYS:HD2	1.92	0.52
5:B:811:TYR:N	5:B:811:TYR:CD1	2.78	0.52
4:A:1329:THR:HG21	4:A:1331:SER:HB3	1.92	0.52
8:E:16:PHE:CE2	8:E:20:LYS:HE2	2.44	0.52
4:A:1364:ASN:O	4:A:1365:TYR:C	2.47	0.52
5:B:558:LEU:HD21	5:B:600:LEU:HD11	1.91	0.52
5:B:130:VAL:HB	5:B:167:ILE:HD12	1.91	0.52
9:F:116:ASP:O	9:F:120:ILE:HG13	2.10	0.52
11:H:12:VAL:HA	11:H:28:ALA:HB2	1.92	0.52
4:A:255:SER:OG	5:B:918:ILE:HG23	2.09	0.52
11:H:126:GLU:C	11:H:130:ARG:HH22	2.13	0.52
4:A:567:LYS:HD2	4:A:568:PRO:CD	2.40	0.52
5:B:1095:LEU:CD1	5:B:1095:LEU:H	2.19	0.52
5:B:860:MET:HG2	5:B:861:ASP:N	2.25	0.52
4:A:1377:THR:O	4:A:1379:GLY:N	2.42	0.52
4:A:1348:LEU:O	4:A:1352:VAL:HG23	2.09	0.52
6:C:252:GLN:HG3	14:K:95:ILE:HG23	1.92	0.52
4:A:699:ALA:HB3	4:A:701:LEU:HG	1.91	0.52
9:F:77:ASP:C	9:F:79:ARG:H	2.12	0.52
7:D:66:ARG:O	7:D:70:PHE:HB2	2.09	0.52
11:H:40:LEU:HD22	11:H:123:MET:CE	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:853:ASP:OD2	4:A:855:THR:CG2	2.58	0.52
4:A:1445:ILE:HD12	4:A:1445:ILE:N	2.07	0.52
13:J:1:MET:H3	13:J:56:LEU:H	1.57	0.52
5:B:25:ILE:HD11	5:B:653:VAL:C	2.29	0.52
5:B:638:PHE:HB3	5:B:651:LEU:HD22	1.90	0.52
4:A:1389:PHE:C	4:A:1389:PHE:CD1	2.82	0.52
1:T:16:DG:N2	2:N:2:DA:C2	2.78	0.52
5:B:1031:LEU:CD2	5:B:1044:ALA:HB2	2.40	0.52
4:A:298:PHE:CD2	4:A:299:HIS:N	2.78	0.52
5:B:763:GLN:HG2	5:B:765:PRO:HD2	1.92	0.52
14:K:61:TYR:C	14:K:61:TYR:CD2	2.80	0.52
4:A:254:GLU:O	4:A:256:GLN:N	2.41	0.52
10:G:7:LEU:HB2	10:G:74:TYR:HE2	1.67	0.52
11:H:36:CYS:HA	11:H:126:GLU:O	2.09	0.52
10:G:83:LYS:HG2	10:G:149:GLY:HA2	1.91	0.52
12:I:7:CYS:HB3	12:I:14:LEU:HD21	1.90	0.52
9:F:75:PRO:HG2	9:F:78:GLN:HB2	1.92	0.52
6:C:263:THR:C	6:C:265:MET:H	2.12	0.52
4:A:40:THR:HG22	4:A:41:MET:CG	2.28	0.52
5:B:899:ILE:CG2	5:B:949:VAL:HG21	2.40	0.52
5:B:846:ILE:HA	5:B:850:LEU:HB3	1.91	0.52
4:A:438:ASP:OD1	4:A:461:LYS:HA	2.10	0.52
5:B:29:ASP:OD1	5:B:658:ILE:HD13	2.10	0.52
4:A:1313:LEU:HB3	4:A:1338:VAL:HG21	1.92	0.52
7:D:191:ALA:C	7:D:193:THR:H	2.12	0.52
5:B:983:ARG:HD2	5:B:1091:TYR:HB3	1.92	0.52
4:A:982:THR:N	4:A:985:ASP:HB2	2.25	0.52
4:A:262:LEU:HD12	4:A:328:ARG:NH2	2.24	0.52
11:H:107:VAL:O	11:H:108:SER:O	2.28	0.52
4:A:1021:LEU:O	4:A:1025:ARG:HG2	2.10	0.52
5:B:890:TYR:CZ	5:B:910:VAL:HG21	2.45	0.52
5:B:806:THR:HB	5:B:809:MET:HG3	1.92	0.52
6:C:161:LYS:O	6:C:170:TRP:NE1	2.42	0.52
5:B:616:ILE:HG13	5:B:697:GLU:HG3	1.92	0.52
11:H:113:ALA:HB2	11:H:126:GLU:HG3	1.91	0.52
11:H:58:THR:HG22	11:H:59:ILE:H	1.74	0.52
4:A:767:GLN:HE21	4:A:774:ARG:HB3	1.75	0.52
5:B:782:LEU:HD12	5:B:788:ARG:NH1	2.20	0.52
15:L:28:LYS:HB2	15:L:39:SER:CA	2.39	0.52
4:A:1011:GLN:NE2	4:A:1015:VAL:HG21	2.25	0.52
4:A:1259:MET:C	4:A:1261:LYS:H	2.12	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:210:ILE:O	7:D:214:LEU:HG	2.10	0.52
5:B:213:ILE:HD12	5:B:497:ARG:HB3	1.92	0.52
1:T:23:DC:H2'	1:T:24:DT:H6	1.71	0.52
10:G:7:LEU:HD11	10:G:45:ILE:HD11	1.92	0.52
5:B:843:GLN:HB2	5:B:993:THR:HB	1.91	0.52
11:H:89:LEU:C	11:H:91:ASP:N	2.63	0.52
6:C:175:ALA:CB	13:J:43:ARG:HH12	2.23	0.52
6:C:175:ALA:CB	13:J:43:ARG:NH1	2.72	0.52
14:K:41:THR:HG22	14:K:42:LEU:N	2.25	0.52
12:I:82:GLU:HB3	12:I:104:LEU:CD1	2.39	0.52
12:I:6:PHE:HA	12:I:14:LEU:HG	1.92	0.52
4:A:148:CYS:O	4:A:168:GLY:HA2	2.09	0.52
11:H:104:PHE:CE2	11:H:136:LYS:HG2	2.45	0.52
6:C:86:CYS:O	6:C:88:CYS:N	2.41	0.52
4:A:825:ILE:O	4:A:829:VAL:HG23	2.10	0.51
5:B:899:ILE:HD11	5:B:910:VAL:O	2.10	0.51
5:B:945:GLU:O	5:B:946:ASN:HB3	2.10	0.51
4:A:360:GLU:HG3	4:A:459:ARG:HH12	1.73	0.51
5:B:992:ILE:HG12	5:B:993:THR:N	2.25	0.51
5:B:1180:PHE:O	5:B:1181:GLU:O	2.27	0.51
4:A:230:ARG:H	4:A:233:TRP:HE3	1.52	0.51
4:A:868:TYR:CE1	4:A:1064:VAL:CG1	2.92	0.51
5:B:753:ALA:HA	5:B:756:ILE:CD1	2.40	0.51
4:A:961:ARG:HG3	4:A:961:ARG:NH1	2.24	0.51
4:A:1168:GLU:O	4:A:1172:LEU:HG	2.10	0.51
5:B:368:GLU:O	5:B:370:PHE:N	2.42	0.51
12:I:110:PHE:H	12:I:110:PHE:HD2	1.58	0.51
4:A:471:ASN:OD1	4:A:472:LEU:N	2.43	0.51
5:B:843:GLN:O	5:B:846:ILE:N	2.43	0.51
6:C:59:ALA:O	6:C:62:PHE:HB3	2.10	0.51
6:C:99:LEU:HA	6:C:119:VAL:O	2.10	0.51
4:A:958:VAL:HG22	4:A:1052:GLN:HB3	1.92	0.51
5:B:687:GLU:O	5:B:689:LEU:HG	2.11	0.51
5:B:549:THR:HB	5:B:628:THR:OG1	2.10	0.51
5:B:189:LEU:O	5:B:192:LEU:N	2.39	0.51
4:A:320:ARG:NH1	4:A:320:ARG:HG3	2.25	0.51
15:L:28:LYS:HB2	15:L:39:SER:CB	2.41	0.51
5:B:20:ASP:C	5:B:22:SER:H	2.14	0.51
4:A:451:HIS:CD2	4:A:1074:GLU:HG3	2.45	0.51
4:A:765:VAL:HG23	4:A:802:ASN:O	2.10	0.51
7:D:137:ASN:HD22	7:D:137:ASN:C	2.13	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:35:ILE:HD13	4:A:241:VAL:HG11	1.93	0.51
1:T:19:DC:C4	1:T:20:DC:N4	2.79	0.51
4:A:903:ASN:ND2	4:A:903:ASN:C	2.63	0.51
4:A:567:LYS:CE	11:H:46:LEU:HB2	2.40	0.51
8:E:175:LEU:HD23	8:E:176:PRO:HD2	1.91	0.51
7:D:17:LYS:H	7:D:17:LYS:CD	2.23	0.51
6:C:248:ILE:HG23	14:K:98:LEU:HD22	1.92	0.51
4:A:730:GLY:O	4:A:732:LEU:N	2.43	0.51
4:A:511:ILE:O	4:A:519:PRO:HA	2.10	0.51
7:D:185:CYS:CB	7:D:211:LEU:HD22	2.40	0.51
4:A:69:THR:O	4:A:71:GLN:N	2.43	0.51
4:A:853:ASP:OD2	4:A:855:THR:HG22	2.10	0.51
4:A:18:GLN:HB2	5:B:1215:ARG:HB2	1.93	0.51
2:N:6:DA:C2'	2:N:7:DG:OP2	2.55	0.51
15:L:46:VAL:O	15:L:46:VAL:HG12	2.10	0.51
6:C:29:MET:HE1	14:K:98:LEU:HG	1.93	0.51
7:D:21:GLU:HB2	7:D:22:GLU:OE1	2.11	0.51
4:A:244:PRO:O	4:A:246:VAL:N	2.43	0.51
1:T:18:DC:H3'	1:T:18:DC:OP1	2.11	0.51
5:B:1045:SER:O	5:B:1046:PRO:O	2.27	0.51
4:A:567:LYS:HE3	11:H:46:LEU:HB2	1.93	0.51
11:H:47:PHE:CD2	11:H:95:TYR:HD1	2.28	0.51
4:A:23:SER:HB3	4:A:233:TRP:CE2	2.46	0.51
4:A:1208:THR:O	4:A:1212:VAL:HG23	2.10	0.51
4:A:388:LEU:O	4:A:392:VAL:HG23	2.10	0.51
4:A:261:ASP:O	4:A:264:PHE:HB2	2.11	0.51
5:B:288:ALA:HA	5:B:331:LEU:HD12	1.91	0.51
5:B:610:ASN:O	5:B:612:GLU:N	2.44	0.51
6:C:253:LYS:O	6:C:256:ALA:HB3	2.10	0.51
4:A:93:VAL:CG2	4:A:301:ALA:HA	2.36	0.51
4:A:831:THR:CG2	4:A:832:ALA:N	2.72	0.51
5:B:1103:ILE:O	5:B:1122:ARG:NH1	2.43	0.51
4:A:470:LEU:HD12	4:A:471:ASN:O	2.11	0.51
13:J:48:ARG:HE	13:J:49:MET:HE2	1.75	0.51
5:B:1085:ILE:CD1	5:B:1085:ILE:N	2.69	0.51
4:A:320:ARG:HG3	4:A:320:ARG:HH11	1.74	0.51
4:A:34:LYS:H	4:A:34:LYS:HD3	1.75	0.51
9:F:116:ASP:HB3	9:F:119:ARG:HB2	1.93	0.51
5:B:640:VAL:O	5:B:641:GLU:C	2.49	0.51
7:D:47:LEU:HD12	7:D:48:ILE:N	2.25	0.51
5:B:1099:VAL:C	5:B:1101:ASP:H	2.14	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:792:MET:H	5:B:857:ARG:HA	1.74	0.51
5:B:33:VAL:HG12	5:B:681:TRP:HZ3	1.76	0.51
5:B:980:PHE:CD2	5:B:1094:ARG:HA	2.46	0.51
4:A:1332:PHE:N	4:A:1332:PHE:CD2	2.74	0.51
4:A:913:LEU:HD12	4:A:914:GLU:N	2.23	0.51
4:A:1209:MET:CE	4:A:1236:LEU:HB3	2.40	0.51
4:A:367:PRO:HD3	4:A:467:THR:O	2.10	0.51
4:A:567:LYS:CB	4:A:568:PRO:CD	2.88	0.51
4:A:567:LYS:CG	4:A:568:PRO:CD	2.83	0.51
6:C:36:VAL:HG21	6:C:251:LEU:HB2	1.93	0.51
4:A:666:ILE:HD11	5:B:1067:ARG:O	2.11	0.51
5:B:102:VAL:CG2	5:B:112:LEU:HD22	2.41	0.51
4:A:1364:ASN:C	4:A:1364:ASN:HD22	2.14	0.51
4:A:276:LEU:HD13	4:A:293:GLU:HA	1.93	0.51
4:A:577:ILE:C	4:A:579:SER:N	2.62	0.51
4:A:1144:LYS:HB2	4:A:1268:LEU:O	2.11	0.51
4:A:1265:ASN:C	4:A:1267:MET:N	2.64	0.51
4:A:108:MET:N	4:A:108:MET:SD	2.84	0.51
5:B:903:VAL:HG12	5:B:904:ARG:N	2.26	0.51
5:B:882:THR:CB	5:B:934:LYS:O	2.59	0.51
8:E:28:TYR:CE1	8:E:78:LEU:HD13	2.46	0.51
5:B:1011:ILE:O	5:B:1011:ILE:HG22	2.10	0.51
11:H:130:ARG:N	11:H:130:ARG:HD2	2.21	0.51
4:A:1125:ALA:C	4:A:1127:ASP:H	2.14	0.51
5:B:996:ARG:NH2	6:C:175:ALA:N	2.56	0.51
4:A:317:LYS:O	4:A:318:SER:HB3	2.11	0.51
5:B:197:PHE:CZ	5:B:816:GLU:HG2	2.46	0.51
12:I:34:TYR:HD2	12:I:35:VAL:N	2.08	0.51
4:A:1444:MET:CE	9:F:135:ARG:HB2	2.41	0.51
7:D:134:THR:CG2	7:D:135:GLY:N	2.74	0.51
4:A:466:SER:HB2	5:B:1099:VAL:HG11	1.93	0.51
5:B:1002:THR:O	5:B:1004:GLU:N	2.44	0.51
4:A:382:PRO:CA	4:A:428:TYR:HE2	2.24	0.51
5:B:516:ASN:ND2	5:B:516:ASN:H	2.08	0.51
5:B:521:LEU:HD13	5:B:633:VAL:CG1	2.41	0.51
4:A:227:VAL:HG21	7:D:14:ARG:HH12	1.76	0.51
6:C:259:LEU:HD13	14:K:91:CYS:CB	2.41	0.51
4:A:852:TYR:CD1	9:F:136:ARG:HB3	2.45	0.51
8:E:83:CYS:SG	8:E:110:PHE:HZ	2.34	0.51
4:A:37:PHE:H	4:A:37:PHE:HD1	1.58	0.50
5:B:859:TYR:CZ	5:B:941:LEU:HD12	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:234:ILE:HD12	5:B:234:ILE:N	2.26	0.50
5:B:680:THR:O	5:B:684:LEU:HD12	2.11	0.50
4:A:849:MET:HB3	4:A:1063:MET:SD	2.50	0.50
1:T:13:DC:H2"	1:T:14:DT:O5'	2.11	0.50
5:B:957:ASN:O	5:B:960:GLY:N	2.44	0.50
5:B:44:VAL:O	5:B:45:SER:C	2.49	0.50
7:D:34:GLN:C	7:D:36:LYS:H	2.14	0.50
5:B:894:ASP:HB2	15:L:58:LYS:NZ	2.25	0.50
4:A:166:GLY:O	4:A:167:CYS:SG	2.69	0.50
5:B:1050:ILE:HG22	5:B:1051:THR:N	2.25	0.50
4:A:69:THR:C	4:A:71:GLN:H	2.15	0.50
4:A:92:HIS:HD2	4:A:304:MET:HE3	1.75	0.50
5:B:579:ARG:HG2	5:B:579:ARG:NH1	2.26	0.50
4:A:7:SER:HB3	5:B:1193:GLN:HE21	1.76	0.50
13:J:43:ARG:HG2	13:J:46:CYS:SG	2.52	0.50
4:A:870:GLU:HG2	8:E:208:TYR:CD2	2.46	0.50
5:B:205:ILE:O	5:B:207:GLY:N	2.44	0.50
4:A:283:GLY:O	4:A:285:PRO:CD	2.58	0.50
5:B:284:ILE:HG23	5:B:324:ILE:HD12	1.93	0.50
5:B:1198:TYR:O	5:B:1201:LYS:HB3	2.10	0.50
4:A:1143:LEU:O	4:A:1146:VAL:HG23	2.12	0.50
4:A:852:TYR:CD2	4:A:1060:PRO:CB	2.95	0.50
6:C:101:LEU:HD22	6:C:118:LEU:CD2	2.41	0.50
4:A:878:ILE:HG21	4:A:955:PRO:HB2	1.93	0.50
4:A:89:PRO:O	4:A:204:THR:HG21	2.10	0.50
4:A:537:ARG:NH1	11:H:120:GLY:O	2.43	0.50
5:B:657:HIS:CE1	5:B:689:LEU:HD11	2.47	0.50
5:B:661:LEU:HD23	5:B:679:TYR:O	2.11	0.50
4:A:907:THR:HG23	4:A:908:LEU:N	2.26	0.50
7:D:153:ARG:C	7:D:154:PHE:CD1	2.85	0.50
15:L:40:LEU:HD13	15:L:44:ASP:CB	2.40	0.50
11:H:76:THR:HG22	11:H:76:THR:O	2.10	0.50
4:A:446:ARG:HB3	4:A:478:TYR:HB3	1.93	0.50
4:A:18:GLN:CB	5:B:1215:ARG:HB2	2.42	0.50
8:E:198:ILE:HD11	8:E:212:ARG:CG	2.42	0.50
4:A:492:PRO:O	4:A:493:GLN:NE2	2.45	0.50
5:B:446:LEU:N	5:B:446:LEU:HD23	2.26	0.50
5:B:885:MET:HA	5:B:936:ASP:HB2	1.94	0.50
4:A:471:ASN:O	4:A:474:VAL:HG12	2.11	0.50
4:A:535:THR:HG23	4:A:575:LYS:HE2	1.93	0.50
4:A:1445:ILE:HD11	10:G:68:ALA:CB	2.39	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:797:TYR:C	5:B:798:TYR:HD2	2.15	0.50
6:C:66:ARG:NH1	6:C:144:ILE:O	2.43	0.50
5:B:1162:ILE:HG22	5:B:1163:CYS:H	1.76	0.50
4:A:1116:LEU:N	4:A:1308:THR:CG2	2.69	0.50
9:F:99:LEU:HD12	9:F:103:MET:HG3	1.94	0.50
4:A:172:PRO:HB3	4:A:185:TRP:CD2	2.46	0.50
4:A:106:VAL:HG13	4:A:112:LYS:N	2.26	0.50
4:A:146:MET:HB3	4:A:171:GLN:O	2.12	0.50
4:A:1343:ALA:O	4:A:1346:ALA:HB3	2.12	0.50
11:H:103:LYS:HG2	11:H:104:PHE:H	1.75	0.50
6:C:22:LEU:HD13	6:C:230:MET:CE	2.41	0.50
4:A:942:PHE:C	4:A:942:PHE:CD2	2.85	0.50
10:G:80:LYS:HG2	10:G:80:LYS:O	2.12	0.50
5:B:780:VAL:HG21	13:J:56:LEU:HD11	1.92	0.50
6:C:174:ALA:O	6:C:175:ALA:CB	2.59	0.50
7:D:56:ARG:HA	7:D:148:LEU:HD13	1.94	0.50
4:A:873:MET:C	4:A:1058:VAL:HG23	2.31	0.50
5:B:956:THR:CG2	5:B:960:GLY:HA2	2.42	0.50
5:B:190:TYR:HE2	13:J:62:ARG:HB3	1.72	0.50
4:A:146:MET:HA	4:A:171:GLN:HB2	1.91	0.50
5:B:240:ILE:O	5:B:240:ILE:HG23	2.10	0.50
5:B:69:LEU:HD13	5:B:429:PHE:CD1	2.47	0.50
6:C:187:LYS:C	6:C:189:THR:H	2.15	0.50
4:A:1152:ILE:HG13	12:I:44:TYR:HD2	1.76	0.50
4:A:600:PRO:HG2	4:A:601:LYS:H	1.75	0.50
4:A:1006:ILE:CD1	8:E:163:GLU:HG3	2.42	0.50
10:G:4:ILE:HG12	10:G:77:VAL:HG22	1.92	0.50
4:A:331:GLY:O	4:A:332:LYS:O	2.30	0.50
4:A:265:LYS:NZ	4:A:322:VAL:HG22	2.27	0.50
8:E:20:LYS:NZ	8:E:60:PHE:CE1	2.79	0.50
4:A:335:ARG:HA	4:A:339:ASN:HD22	1.76	0.50
4:A:982:THR:O	4:A:985:ASP:HB2	2.12	0.50
15:L:27:LEU:HD13	15:L:37:LYS:CE	2.41	0.50
4:A:1146:VAL:HG11	4:A:1207:LEU:HD12	1.94	0.50
5:B:766:ARG:NH2	5:B:1020:ARG:HD3	2.26	0.50
4:A:204:THR:O	4:A:206:GLU:N	2.45	0.50
12:I:101:PHE:N	12:I:101:PHE:CD1	2.79	0.50
4:A:598:LEU:O	4:A:599:SER:C	2.49	0.50
4:A:241:VAL:HG13	4:A:266:LEU:HD13	1.93	0.50
4:A:37:PHE:HD1	4:A:37:PHE:N	2.09	0.50
5:B:172:ILE:CG2	5:B:173:MET:N	2.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:167:HIS:HA	14:K:6:ARG:HH12	1.76	0.50
5:B:25:ILE:HG23	5:B:658:ILE:CD1	2.41	0.50
10:G:17:PHE:N	10:G:17:PHE:CD2	2.78	0.50
4:A:901:LEU:N	4:A:926:GLN:NE2	2.52	0.50
4:A:265:LYS:CE	4:A:322:VAL:HG13	2.42	0.50
8:E:17:ARG:O	8:E:20:LYS:HB2	2.11	0.50
4:A:670:ILE:HG23	4:A:805:LEU:CD2	2.40	0.50
4:A:888:GLY:O	4:A:940:ARG:NH2	2.45	0.50
6:C:242:GLN:HB3	6:C:246:ARG:HG3	1.94	0.50
4:A:1431:GLY:HA3	5:B:1152:MET:SD	2.52	0.50
14:K:60:ALA:O	14:K:73:LEU:HD12	2.11	0.50
5:B:1020:ARG:HB2	5:B:1022:THR:HG22	1.94	0.50
5:B:299:GLU:OE2	5:B:572:HIS:HE1	1.94	0.50
12:I:59:VAL:C	12:I:61:ASP:H	2.15	0.50
4:A:325:ILE:HG21	5:B:1210:MET:HG3	1.93	0.50
5:B:546:SER:OG	5:B:631:GLY:N	2.38	0.50
10:G:1:MET:CE	10:G:80:LYS:O	2.60	0.50
4:A:351:THR:HG22	5:B:1103:ILE:HA	1.94	0.50
8:E:205:SER:O	8:E:207:ARG:N	2.45	0.50
5:B:582:VAL:HA	5:B:626:ILE:O	2.12	0.50
5:B:117:ALA:HA	5:B:122:LEU:HD12	1.93	0.50
5:B:1106:ARG:HD3	5:B:1126:GLY:O	2.12	0.50
12:I:86:PHE:CE1	12:I:100:PHE:HB2	2.47	0.50
14:K:46:ILE:HG21	14:K:87:LEU:HD11	1.94	0.50
4:A:119:ASN:O	4:A:122:MET:HB3	2.11	0.50
4:A:98:LYS:O	4:A:102:VAL:HG23	2.12	0.50
4:A:816:HIS:CD2	5:B:764:SER:H	2.29	0.50
5:B:347:LYS:HG3	5:B:348:ARG:N	2.27	0.50
4:A:630:ILE:HG23	4:A:642:CYS:SG	2.52	0.50
4:A:1111:MET:CE	4:A:1330:ASN:OD1	2.60	0.50
4:A:58:LEU:O	4:A:59:GLY:O	2.30	0.49
14:K:7:PHE:O	14:K:11:LEU:HB2	2.12	0.49
4:A:1062:GLU:OE2	9:F:88:TYR:OH	2.30	0.49
5:B:824:ILE:CG2	5:B:1087:PHE:CE2	2.93	0.49
14:K:53:ASP:C	14:K:55:LYS:H	2.16	0.49
6:C:251:LEU:O	6:C:255:VAL:HG23	2.11	0.49
12:I:26:LEU:CD2	12:I:37:GLU:HA	2.39	0.49
13:J:14:VAL:CG1	13:J:50:ILE:HD11	2.41	0.49
4:A:345:VAL:HG11	5:B:1130:PHE:HB2	1.95	0.49
4:A:973:ILE:HD13	4:A:1036:ARG:O	2.11	0.49
4:A:88:LYS:HE3	4:A:280:GLU:OE2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:116:TYR:HB2	11:H:123:MET:HB3	1.95	0.49
10:G:38:CYS:SG	10:G:44:TYR:CE1	3.03	0.49
4:A:49:LYS:NZ	4:A:61:ILE:CG1	2.71	0.49
6:C:18:VAL:CG2	6:C:240:VAL:HB	2.42	0.49
5:B:378:LEU:HD12	5:B:378:LEU:O	2.12	0.49
5:B:621:GLU:HG3	5:B:621:GLU:O	2.12	0.49
4:A:244:PRO:HG2	4:A:245:PRO:CD	2.41	0.49
5:B:977:GLY:HA3	5:B:1099:VAL:CB	2.42	0.49
4:A:332:LYS:HG3	4:A:333:GLU:HG2	1.94	0.49
10:G:14:HIS:CE1	10:G:15:PRO:HD2	2.46	0.49
5:B:1183:LYS:C	5:B:1185:CYS:H	2.16	0.49
6:C:73:GLN:HE21	6:C:75:MET:H	1.59	0.49
4:A:1164:PRO:HG2	4:A:1165:GLU:HG3	1.94	0.49
8:E:12:LEU:HD21	8:E:58:MET:SD	2.53	0.49
4:A:1319:VAL:HG13	4:A:1320:PRO:HD2	1.93	0.49
4:A:696:GLU:OE2	4:A:702:LEU:HD21	2.13	0.49
5:B:918:ILE:HG21	5:B:935:ARG:HH11	1.76	0.49
5:B:846:ILE:CG2	5:B:974:PRO:HG2	2.41	0.49
6:C:70:ILE:HD11	6:C:144:ILE:HG12	1.93	0.49
5:B:1161:HIS:HB3	5:B:1171:VAL:HG11	1.95	0.49
5:B:658:ILE:O	5:B:661:LEU:HB2	2.11	0.49
4:A:840:ARG:O	4:A:841:LEU:C	2.51	0.49
13:J:7:CYS:HB3	13:J:10:CYS:SG	2.51	0.49
14:K:58:PHE:HE2	14:K:74:ARG:HE	1.57	0.49
5:B:171:PRO:HD2	5:B:457:LEU:HD13	1.95	0.49
4:A:1098:VAL:N	4:A:1099:PRO:HD2	2.27	0.49
8:E:79:TRP:CD1	8:E:96:PHE:HE1	2.30	0.49
8:E:168:TYR:HB3	8:E:170:LEU:HG	1.94	0.49
11:H:40:LEU:HD12	11:H:122:LEU:O	2.12	0.49
4:A:302:THR:HA	4:A:305:ASP:O	2.12	0.49
5:B:882:THR:HG22	5:B:884:ARG:HB2	1.93	0.49
14:K:47:ARG:HD2	14:K:47:ARG:C	2.32	0.49
11:H:58:THR:HB	11:H:143:LEU:HB2	1.95	0.49
4:A:779:PHE:O	4:A:780:VAL:C	2.51	0.49
5:B:35:SER:HA	5:B:811:TYR:CE2	2.37	0.49
4:A:527:THR:HG21	4:A:650:GLN:HA	1.95	0.49
4:A:929:LEU:CD2	4:A:983:ILE:HG21	2.42	0.49
4:A:417:TYR:CD2	4:A:417:TYR:N	2.80	0.49
5:B:121:ASN:ND2	5:B:207:GLY:HA3	2.28	0.49
4:A:590:ARG:HB2	4:A:605:MET:HB3	1.94	0.49
5:B:175:ARG:NH1	5:B:175:ARG:HG2	2.24	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:96:GLN:HA	10:G:121:PHE:CE2	2.48	0.49
6:C:137:LYS:HB3	6:C:138:GLU:OE1	2.13	0.49
10:G:1:MET:O	10:G:3:PHE:CD1	2.65	0.49
5:B:237:VAL:HG22	5:B:257:LYS:HA	1.95	0.49
5:B:1166:CYS:HB2	5:B:1215:ARG:HH11	1.75	0.49
4:A:1317:MET:HG3	4:A:1327:ILE:HG21	1.93	0.49
4:A:316:GLN:O	4:A:317:LYS:C	2.51	0.49
4:A:2:VAL:HG21	5:B:1157:ALA:O	2.11	0.49
5:B:224:GLN:O	5:B:238:ALA:HA	2.12	0.49
4:A:262:LEU:C	4:A:264:PHE:N	2.66	0.49
4:A:54:ASN:HB3	4:A:247:ARG:HH22	1.78	0.49
6:C:70:ILE:HD13	6:C:115:SER:HB3	1.94	0.49
6:C:70:ILE:HD11	6:C:144:ILE:CG1	2.43	0.49
4:A:798:GLY:HA2	4:A:815:PHE:HD1	1.72	0.49
4:A:1189:SER:OG	4:A:1190:PRO:HD2	2.13	0.49
5:B:31:TRP:CZ3	5:B:34:ILE:HD12	2.48	0.49
7:D:27:LEU:HD13	7:D:173:HIS:HD2	1.78	0.49
8:E:135:PHE:CB	8:E:140:LEU:HD11	2.37	0.49
4:A:412:ARG:HH22	5:B:1108:ARG:HH22	1.61	0.49
4:A:590:ARG:NH2	4:A:620:LYS:HB2	2.22	0.49
7:D:130:LEU:C	7:D:132:GLN:N	2.65	0.49
4:A:1394:THR:HG22	4:A:1395:GLY:N	2.27	0.49
4:A:1334:ASP:O	4:A:1336:MET:N	2.45	0.49
4:A:852:TYR:HA	4:A:1060:PRO:HB3	1.94	0.49
6:C:184:ASN:HD21	6:C:187:LYS:HA	1.77	0.49
4:A:526:ASP:OD1	5:B:1013:ASN:ND2	2.44	0.49
4:A:55:ASP:N	4:A:56:PRO:CD	2.76	0.49
5:B:843:GLN:O	5:B:844:SER:C	2.51	0.49
5:B:364:ILE:HG12	5:B:585:VAL:CG1	2.36	0.49
4:A:63:ARG:HA	4:A:74:MET:HE2	1.94	0.49
8:E:24:LYS:HB3	8:E:30:ILE:HD12	1.95	0.49
4:A:417:TYR:O	4:A:418:SER:C	2.50	0.49
12:I:100:PHE:CD1	12:I:100:PHE:N	2.81	0.49
14:K:110:ASN:C	14:K:112:GLN:H	2.16	0.49
4:A:537:ARG:HH12	11:H:122:LEU:HG	1.77	0.49
11:H:40:LEU:HD22	11:H:123:MET:HE3	1.94	0.49
5:B:806:THR:HG22	5:B:808:ALA:CB	2.43	0.49
5:B:973:ILE:HG23	5:B:974:PRO:HD2	1.95	0.49
5:B:654:ARG:H	5:B:657:HIS:HD2	1.61	0.49
4:A:711:ARG:NH1	12:I:95:THR:HB	2.27	0.49
6:C:191:TYR:CD2	6:C:201:TRP:CD1	3.01	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:758:PHE:CZ	5:B:1031:LEU:HD22	2.48	0.49
5:B:1156:ASP:HB3	5:B:1197:PRO:HA	1.95	0.49
4:A:381:THR:HG21	4:A:383:TYR:CD1	2.47	0.49
4:A:1001:ARG:O	4:A:1002:GLY:O	2.31	0.49
6:C:258:ILE:N	6:C:258:ILE:HD12	2.28	0.49
4:A:909:ASP:C	4:A:911:SER:H	2.16	0.49
4:A:1273:LEU:N	4:A:1273:LEU:HD12	2.28	0.49
7:D:47:LEU:HD11	10:G:3:PHE:CD2	2.48	0.49
4:A:474:VAL:HG22	4:A:478:TYR:HE1	1.77	0.49
5:B:796:LEU:HD21	5:B:821:GLN:HE21	1.77	0.49
4:A:767:GLN:OE1	4:A:799:PHE:HB2	2.13	0.49
5:B:661:LEU:HD11	5:B:684:LEU:HD21	1.93	0.49
5:B:824:ILE:HG12	13:J:48:ARG:HH12	1.77	0.49
4:A:1305:VAL:HG12	4:A:1306:LEU:N	2.28	0.49
5:B:1068:GLY:O	5:B:1069:PHE:O	2.31	0.49
12:I:100:PHE:N	12:I:100:PHE:HD1	2.11	0.49
5:B:1202:LEU:HD23	5:B:1206:GLU:HG3	1.93	0.49
7:D:202:ILE:CG2	7:D:207:LEU:HB2	2.43	0.49
4:A:699:ALA:O	4:A:700:ASN:HB3	2.13	0.49
6:C:40:GLU:HA	6:C:163:ILE:CG2	2.43	0.49
4:A:597:LEU:HD12	4:A:597:LEU:N	2.28	0.49
4:A:655:PHE:O	4:A:658:LEU:HB3	2.13	0.48
6:C:113:VAL:HG23	6:C:147:LEU:HD21	1.95	0.48
13:J:57:ILE:HA	13:J:60:PHE:CD2	2.34	0.48
15:L:70:ARG:HG2	15:L:70:ARG:NH1	2.27	0.48
4:A:18:GLN:HB3	5:B:1215:ARG:HG3	1.93	0.48
5:B:652:LYS:HB3	5:B:689:LEU:CD2	2.43	0.48
2:N:5:DT:H2"	2:N:6:DA:OP2	2.13	0.48
5:B:996:ARG:NH1	6:C:38:ILE:HG23	2.27	0.48
15:L:52:GLY:O	15:L:54:ARG:N	2.46	0.48
5:B:181:LEU:HD22	5:B:189:LEU:HD22	1.95	0.48
4:A:416:ARG:HG3	4:A:417:TYR:CD2	2.48	0.48
4:A:105:CYS:O	4:A:114:LEU:HG	2.13	0.48
6:C:183:TRP:CE2	6:C:207:CYS:HB3	2.47	0.48
9:F:109:VAL:HG12	9:F:110:ASP:H	1.78	0.48
10:G:117:GLN:C	10:G:119:LEU:N	2.67	0.48
8:E:42:PHE:HZ	8:E:58:MET:CE	2.25	0.48
5:B:894:ASP:HB2	15:L:58:LYS:HZ3	1.78	0.48
4:A:150:THR:O	4:A:150:THR:HG22	2.13	0.48
4:A:244:PRO:O	4:A:247:ARG:N	2.42	0.48
4:A:266:LEU:HD21	4:A:303:TYR:CE1	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:35:ILE:O	4:A:35:ILE:HG22	2.11	0.48
14:K:47:ARG:O	14:K:47:ARG:HD2	2.13	0.48
4:A:353:ILE:HB	4:A:470:LEU:HD23	1.96	0.48
11:H:127:GLY:HA3	11:H:130:ARG:NH2	2.28	0.48
4:A:722:LEU:HD21	4:A:794:PRO:HB3	1.95	0.48
7:D:59:ILE:HG21	7:D:145:MET:SD	2.53	0.48
12:I:55:THR:HG22	12:I:58:VAL:CG2	2.44	0.48
4:A:1210:GLY:O	4:A:1214:GLU:HG2	2.13	0.48
5:B:1034:VAL:HG12	5:B:1035:ALA:N	2.27	0.48
7:D:51:ASN:O	7:D:52:LEU:O	2.31	0.48
4:A:285:PRO:CG	4:A:288:ALA:HB3	2.43	0.48
4:A:912:LEU:O	4:A:979:SER:N	2.44	0.48
5:B:435:THR:CG2	5:B:437:GLU:HB2	2.43	0.48
5:B:253:THR:HG22	5:B:254:LEU:N	2.27	0.48
11:H:62:SER:O	11:H:63:LEU:C	2.52	0.48
5:B:265:SER:O	5:B:266:ALA:CB	2.61	0.48
10:G:25:TYR:CE2	10:G:29:LYS:HD2	2.48	0.48
8:E:168:TYR:CB	8:E:170:LEU:HG	2.43	0.48
7:D:219:THR:HG22	7:D:220:LEU:O	2.13	0.48
7:D:47:LEU:CD1	10:G:3:PHE:HD2	2.26	0.48
5:B:942:ARG:O	5:B:944:THR:N	2.46	0.48
1:T:24:DT:H2''	1:T:25:DC:C5'	2.44	0.48
1:T:26:DA:H2''	1:T:27:DT:O5'	2.11	0.48
4:A:470:LEU:HD22	4:A:487:MET:HE3	1.94	0.48
5:B:840:ILE:HD13	5:B:994:TYR:CE1	2.49	0.48
11:H:128:ASN:CG	11:H:128:ASN:O	2.51	0.48
4:A:921:GLY:O	4:A:922:ASP:C	2.51	0.48
7:D:144:THR:HG21	10:G:46:LEU:HD13	1.95	0.48
9:F:81:THR:HB	9:F:136:ARG:NH1	2.28	0.48
5:B:95:ILE:CG1	5:B:130:VAL:HG22	2.42	0.48
11:H:139:ASN:O	11:H:140:ALA:HB2	2.13	0.48
4:A:1441:PHE:CZ	9:F:89:GLU:HA	2.48	0.48
5:B:1132:GLU:O	5:B:1135:ARG:HB3	2.13	0.48
4:A:441:PRO:HD2	4:A:498:ARG:CZ	2.43	0.48
5:B:827:ILE:O	5:B:1085:ILE:HG23	2.13	0.48
4:A:444:PHE:HB3	4:A:458:HIS:CD2	2.49	0.48
12:I:34:TYR:C	12:I:34:TYR:CD2	2.87	0.48
6:C:132:PRO:O	6:C:134:ILE:HG13	2.14	0.48
5:B:56:ASP:CB	5:B:57:TYR:HD1	2.26	0.48
4:A:1115:SER:O	4:A:1311:VAL:HG22	2.14	0.48
6:C:215:GLU:O	6:C:216:GLY:C	2.51	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:769:TYR:O	5:B:772:ALA:N	2.45	0.48
4:A:41:MET:O	4:A:50:ILE:HG13	2.14	0.48
6:C:142:VAL:O	6:C:142:VAL:HG12	2.13	0.48
4:A:1437:GLY:HA3	9:F:88:TYR:CD2	2.49	0.48
4:A:567:LYS:HD3	11:H:95:TYR:HA	1.95	0.48
4:A:663:SER:HA	5:B:1014:PRO:HB3	1.95	0.48
12:I:29:CYS:SG	12:I:32:CYS:SG	3.12	0.48
7:D:12:ARG:HH21	7:D:12:ARG:CB	2.22	0.48
4:A:1007:ILE:O	4:A:1010:ALA:N	2.46	0.48
4:A:44:THR:O	4:A:45:GLN:CB	2.62	0.48
5:B:63:ILE:HA	5:B:421:PHE:CE2	2.49	0.48
11:H:8:ASP:HB3	11:H:10:PHE:CE1	2.49	0.48
5:B:843:GLN:O	5:B:846:ILE:HB	2.14	0.48
13:J:8:PHE:N	13:J:49:MET:HE3	2.24	0.48
4:A:1242:VAL:HG12	4:A:1243:VAL:N	2.21	0.48
10:G:88:ASP:HB3	10:G:144:ARG:HA	1.95	0.48
9:F:97:ARG:HG3	9:F:101:ILE:HD11	1.95	0.48
5:B:65:GLU:HG3	5:B:66:ASP:OD1	2.13	0.48
6:C:184:ASN:ND2	6:C:187:LYS:HA	2.29	0.48
8:E:39:LEU:O	8:E:42:PHE:HB3	2.12	0.48
4:A:1385:THR:HG22	4:A:1386:ARG:N	2.29	0.48
12:I:15:TYR:CD1	12:I:15:TYR:N	2.82	0.48
11:H:101:ALA:HB2	11:H:116:TYR:CE1	2.49	0.48
5:B:589:VAL:CG1	5:B:590:HIS:H	2.04	0.48
5:B:51:PHE:CD2	5:B:173:MET:HB3	2.48	0.48
4:A:1134:ILE:O	4:A:1138:ILE:HG13	2.13	0.48
5:B:654:ARG:NH1	5:B:654:ARG:HG3	2.28	0.48
5:B:1002:THR:O	5:B:1005:GLY:N	2.43	0.48
15:L:33:GLU:OE2	15:L:55:ILE:HD11	2.14	0.48
10:G:14:HIS:CD2	10:G:16:SER:CB	2.96	0.48
5:B:521:LEU:HD13	5:B:633:VAL:HG12	1.95	0.48
4:A:289:ILE:C	4:A:291:GLU:H	2.17	0.48
14:K:85:ASP:O	14:K:88:LYS:HB2	2.13	0.48
4:A:116:ASP:O	4:A:118:HIS:N	2.47	0.48
4:A:1389:PHE:CD1	4:A:1390:ASN:N	2.82	0.48
4:A:836:TYR:CD2	4:A:840:ARG:HD2	2.49	0.48
4:A:666:ILE:HD12	4:A:667:GLY:N	2.26	0.48
4:A:886:ILE:HG13	4:A:943:LEU:CD1	2.43	0.48
5:B:309:GLN:O	5:B:312:GLU:HB3	2.13	0.48
5:B:1156:ASP:O	5:B:1157:ALA:O	2.32	0.48
7:D:16:LYS:H	7:D:16:LYS:HD3	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:19:PHE:HB3	4:A:1413:GLY:CA	2.43	0.48
4:A:1444:MET:HE1	9:F:135:ARG:HB2	1.95	0.48
11:H:44:VAL:HG13	11:H:48:PRO:HA	1.96	0.48
4:A:1076:ALA:HA	4:A:1079:MET:HE3	1.95	0.48
4:A:35:ILE:HD12	4:A:83:HIS:O	2.13	0.48
4:A:1279:ILE:HD11	4:A:1316:VAL:HG22	1.95	0.48
5:B:683:SER:O	5:B:687:GLU:HB2	2.14	0.48
15:L:52:GLY:O	15:L:53:HIS:C	2.51	0.48
4:A:898:ARG:O	4:A:1029:ARG:NH1	2.46	0.48
6:C:6:PRO:CB	6:C:25:VAL:HG12	2.41	0.48
12:I:50:THR:HG22	12:I:52:ILE:H	1.79	0.48
3:P:8:A:C2'	3:P:9:G:H5'	2.44	0.48
4:A:699:ALA:O	4:A:700:ASN:CB	2.61	0.48
5:B:1174:LYS:O	5:B:1176:ASN:N	2.47	0.48
5:B:314:LEU:O	5:B:317:CYS:HB3	2.14	0.48
4:A:1162:VAL:HG12	4:A:1162:VAL:O	2.14	0.48
5:B:261:ARG:HB3	5:B:261:ARG:NH1	2.29	0.48
14:K:7:PHE:HA	14:K:10:PHE:HE2	1.76	0.48
4:A:1120:LEU:N	4:A:1120:LEU:HD12	2.29	0.48
4:A:224:PHE:CE1	4:A:231:PRO:HG3	2.49	0.48
5:B:863:GLU:O	5:B:961:LEU:HD22	2.14	0.48
5:B:1183:LYS:CE	5:B:1183:LYS:N	2.76	0.48
7:D:151:PHE:CE2	10:G:89:GLY:HA2	2.49	0.48
4:A:1162:VAL:HG11	12:I:41:PRO:HG3	1.96	0.48
3:P:5:A:H2'	3:P:6:G:C8	2.49	0.48
4:A:939:ASP:OD2	4:A:1020:CYS:HA	2.14	0.48
5:B:280:ILE:CG2	5:B:285:ILE:HG13	2.43	0.48
4:A:622:VAL:HG13	4:A:622:VAL:O	2.14	0.48
11:H:40:LEU:CD1	11:H:123:MET:HB2	2.44	0.47
4:A:72:GLU:O	4:A:73:GLY:O	2.32	0.47
4:A:92:HIS:O	4:A:93:VAL:C	2.52	0.47
4:A:1094:VAL:HG12	4:A:1095:THR:N	2.29	0.47
5:B:806:THR:HG22	5:B:808:ALA:HB3	1.96	0.47
4:A:474:VAL:HG22	4:A:474:VAL:O	2.13	0.47
6:C:166:GLU:O	6:C:167:HIS:HB2	2.14	0.47
14:K:6:ARG:C	14:K:8:GLU:H	2.16	0.47
5:B:25:ILE:HG23	5:B:658:ILE:HD11	1.96	0.47
4:A:809:THR:O	4:A:813:PHE:N	2.37	0.47
4:A:218:ASP:HA	4:A:221:SER:OG	2.14	0.47
5:B:1183:LYS:HE3	5:B:1183:LYS:O	2.14	0.47
15:L:28:LYS:HG3	15:L:39:SER:OG	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:40:LEU:CD1	15:L:44:ASP:HB3	2.44	0.47
4:A:148:CYS:HB3	4:A:168:GLY:HA2	1.96	0.47
4:A:22:PHE:HB2	5:B:1211:ASN:ND2	2.28	0.47
11:H:118:PHE:N	11:H:118:PHE:CD1	2.82	0.47
6:C:112:ASN:HB2	6:C:114:TYR:CE1	2.49	0.47
4:A:445:ASN:HB2	4:A:455:MET:HG2	1.96	0.47
4:A:361:LEU:HD12	4:A:474:VAL:HB	1.96	0.47
11:H:4:THR:HG22	11:H:5:LEU:H	1.79	0.47
5:B:611:PRO:CB	5:B:685:LEU:HD11	2.41	0.47
5:B:190:TYR:CD2	13:J:62:ARG:HB3	2.49	0.47
4:A:1019:CYS:O	4:A:1022:LEU:N	2.47	0.47
11:H:135:LEU:HD13	11:H:137:GLN:NE2	2.28	0.47
10:G:66:GLY:O	10:G:67:SER:C	2.52	0.47
5:B:300:HIS:O	5:B:303:TYR:HE2	1.97	0.47
13:J:16:ASP:O	13:J:18:TRP:N	2.47	0.47
4:A:399:HIS:CB	4:A:400:PRO:CD	2.86	0.47
4:A:1316:VAL:HG12	4:A:1316:VAL:O	2.13	0.47
1:T:16:DG:H5'	4:A:1403:GLU:HG2	1.95	0.47
6:C:175:ALA:HB1	13:J:43:ARG:NH1	2.30	0.47
4:A:382:PRO:HD3	4:A:428:TYR:CD2	2.49	0.47
4:A:811:GLN:O	4:A:812:GLU:C	2.53	0.47
5:B:604:ARG:NH2	5:B:613:VAL:O	2.48	0.47
12:I:105:SER:O	12:I:106:CYS:HB3	2.14	0.47
4:A:335:ARG:NH1	5:B:1202:LEU:HD22	2.30	0.47
4:A:626:ASN:O	4:A:631:HIS:HD2	1.97	0.47
6:C:209:TYR:N	6:C:209:TYR:CD1	2.76	0.47
5:B:269:ILE:HG22	5:B:282:ILE:HG23	1.94	0.47
4:A:946:VAL:HG22	8:E:201:LYS:HD2	1.95	0.47
12:I:4:PHE:CD1	12:I:4:PHE:C	2.88	0.47
4:A:365:GLY:O	4:A:468:PHE:HA	2.13	0.47
10:G:138:THR:HG22	10:G:139:ILE:HG13	1.96	0.47
10:G:44:TYR:O	10:G:78:VAL:HA	2.13	0.47
5:B:796:LEU:HD11	5:B:821:GLN:NE2	2.29	0.47
5:B:840:ILE:HB	5:B:1011:ILE:HB	1.96	0.47
9:F:93:ILE:HD11	9:F:134:ILE:CD1	2.37	0.47
2:N:6:DA:O5'	2:N:6:DA:H2'	2.14	0.47
13:J:7:CYS:HA	13:J:49:MET:HE3	1.97	0.47
12:I:92:ARG:HG2	12:I:94:ASP:OD1	2.14	0.47
4:A:626:ASN:C	4:A:628:GLY:H	2.16	0.47
7:D:176:GLU:O	7:D:178:ALA:N	2.48	0.47
5:B:90:ILE:CD1	5:B:432:MET:SD	3.02	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:23:ASN:C	13:J:25:LEU:N	2.66	0.47
7:D:34:GLN:C	7:D:36:LYS:N	2.67	0.47
4:A:1030:ARG:NH1	4:A:1035:TYR:OH	2.48	0.47
5:B:293:PRO:HG2	5:B:296:GLU:CB	2.44	0.47
4:A:1409:LEU:HD13	5:B:1207:LEU:CD2	2.43	0.47
4:A:1220:PHE:CE2	4:A:1263:ILE:HG23	2.49	0.47
8:E:43:LYS:O	8:E:45:LYS:N	2.45	0.47
4:A:996:ASN:C	4:A:998:LEU:HD12	2.35	0.47
6:C:52:GLU:CD	6:C:154:LYS:HD2	2.34	0.47
8:E:19:VAL:HG11	8:E:80:VAL:HG11	1.96	0.47
5:B:29:ASP:HB3	5:B:658:ILE:CD1	2.44	0.47
4:A:1436:ILE:O	4:A:1437:GLY:C	2.51	0.47
5:B:401:PHE:HB2	5:B:517:THR:OG1	2.14	0.47
7:D:191:ALA:O	7:D:193:THR:N	2.47	0.47
12:I:80:SER:CB	12:I:103:CYS:SG	3.02	0.47
5:B:167:ILE:O	5:B:167:ILE:HG22	2.15	0.47
15:L:38:LEU:HD11	15:L:49:LYS:HE2	1.95	0.47
4:A:961:ARG:HG2	4:A:965:GLN:HE21	1.79	0.47
12:I:49:ILE:HG22	12:I:49:ILE:O	2.13	0.47
4:A:1261:LYS:O	4:A:1264:GLU:HB3	2.13	0.47
5:B:781:PHE:HE2	5:B:793:ALA:HB1	1.79	0.47
4:A:466:SER:CA	14:K:2:ASN:HD22	2.28	0.47
1:T:20:DC:H2"	1:T:21:DT:C5'	2.44	0.47
4:A:853:ASP:OD1	4:A:855:THR:N	2.47	0.47
5:B:847:ASP:C	5:B:849:GLY:N	2.67	0.47
5:B:37:PHE:CE2	5:B:542:MET:HA	2.50	0.47
5:B:680:THR:O	5:B:684:LEU:CD1	2.63	0.47
4:A:24:PRO:HD2	4:A:233:TRP:NE1	2.29	0.47
4:A:444:PHE:HB2	4:A:458:HIS:HD2	1.80	0.47
4:A:873:MET:C	4:A:1058:VAL:CG2	2.83	0.47
4:A:404:TYR:HB2	4:A:433:GLU:HB2	1.97	0.47
7:D:19:GLU:O	7:D:21:GLU:N	2.48	0.47
5:B:575:PRO:HG2	5:B:576:ASP:H	1.78	0.47
12:I:83:ASN:HA	12:I:102:VAL:O	2.14	0.47
4:A:623:GLY:C	4:A:625:SER:H	2.17	0.47
4:A:738:LYS:HB2	4:A:740:LEU:HG	1.96	0.47
10:G:101:VAL:CG1	10:G:102:GLN:N	2.77	0.47
10:G:1:MET:HG2	10:G:85:GLU:OE1	2.14	0.47
5:B:857:ARG:HD2	5:B:945:GLU:OE1	2.15	0.47
4:A:1389:PHE:CZ	4:A:1402:PHE:CE2	3.02	0.47
6:C:174:ALA:HA	13:J:10:CYS:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:899:VAL:CG2	4:A:908:LEU:HD21	2.45	0.47
4:A:808:LEU:HD23	4:A:813:PHE:CA	2.40	0.47
4:A:23:SER:O	4:A:25:GLU:N	2.47	0.47
4:A:1364:ASN:HD22	4:A:1365:TYR:N	2.13	0.47
5:B:953:LEU:O	5:B:953:LEU:HD23	2.14	0.47
4:A:591:PHE:HA	4:A:595:THR:CG2	2.44	0.47
4:A:1373:ASP:CA	4:A:1376:THR:HG22	2.44	0.47
4:A:310:GLY:O	4:A:312:PRO:HD2	2.14	0.47
5:B:465:ASN:N	5:B:465:ASN:ND2	2.63	0.47
6:C:105:GLY:O	6:C:149:LYS:O	2.32	0.47
4:A:993:LEU:HD23	4:A:1022:LEU:HD21	1.95	0.47
4:A:947:PHE:CD2	4:A:954:TRP:CZ2	3.02	0.47
4:A:15:LYS:HD3	5:B:1220:ARG:HH21	1.80	0.47
4:A:1280:GLU:O	4:A:1282:VAL:HG23	2.15	0.47
5:B:909:ASP:OD1	5:B:909:ASP:N	2.47	0.47
4:A:244:PRO:CB	4:A:245:PRO:HD3	2.45	0.47
5:B:824:ILE:O	5:B:824:ILE:HG22	2.14	0.47
4:A:547:LEU:HD22	14:K:58:PHE:HD1	1.76	0.47
14:K:57:LEU:HD12	14:K:77:THR:O	2.15	0.47
9:F:82:THR:CG2	9:F:84:TYR:H	2.18	0.47
12:I:106:CYS:O	12:I:107:SER:CB	2.62	0.47
4:A:340:LEU:HD13	4:A:1429:ILE:HG23	1.97	0.47
5:B:970:THR:HG22	5:B:971:THR:N	2.30	0.47
5:B:435:THR:C	5:B:437:GLU:N	2.66	0.47
15:L:38:LEU:CD1	15:L:49:LYS:HE2	2.45	0.47
11:H:100:THR:CG2	11:H:101:ALA:N	2.76	0.47
10:G:125:SER:OG	10:G:128:PRO:HA	2.14	0.47
5:B:376:PHE:CE2	5:B:569:TYR:HD2	2.33	0.47
4:A:472:LEU:O	4:A:475:THR:HB	2.15	0.47
5:B:798:TYR:CD2	5:B:798:TYR:N	2.82	0.47
6:C:69:LEU:N	6:C:69:LEU:CD1	2.78	0.47
5:B:29:ASP:CG	5:B:658:ILE:HD13	2.35	0.47
4:A:1315:GLU:C	4:A:1317:MET:H	2.18	0.47
4:A:528:LEU:HD23	4:A:751:SER:HA	1.96	0.47
4:A:1205:LYS:O	4:A:1206:ASP:C	2.54	0.47
6:C:46:ILE:HG23	6:C:157:CYS:HB3	1.96	0.47
4:A:14:VAL:HG21	5:B:1216:LEU:CD1	2.44	0.47
4:A:384:ASN:O	4:A:386:ASP:N	2.47	0.47
4:A:377:PRO:HD3	4:A:493:GLN:OE1	2.14	0.47
7:D:24:ALA:C	7:D:26:THR:H	2.18	0.47
5:B:360:PHE:CD2	5:B:360:PHE:C	2.88	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:351:THR:CB	5:B:1103:ILE:HD12	2.44	0.47
5:B:1007:VAL:CG2	5:B:1008:PRO:HD2	2.45	0.47
5:B:844:SER:O	5:B:847:ASP:HB2	2.14	0.47
8:E:94:LYS:HG3	8:E:98:ILE:HD11	1.97	0.47
5:B:1160:VAL:CG1	5:B:1161:HIS:N	2.78	0.47
4:A:871:ASP:OD2	4:A:873:MET:HB2	2.15	0.47
5:B:1201:LYS:HE2	5:B:1205:GLN:CD	2.35	0.47
15:L:40:LEU:HB3	15:L:41:SER:H	1.52	0.47
8:E:157:SER:C	8:E:159:ASP:N	2.68	0.47
4:A:1362:TYR:CD1	4:A:1363:VAL:N	2.83	0.47
4:A:618:GLU:O	4:A:621:THR:N	2.36	0.47
11:H:11:GLN:HA	11:H:53:ASP:O	2.15	0.47
5:B:118:ARG:HH11	5:B:204:ILE:HD11	1.80	0.47
5:B:986:GLN:OE1	5:B:986:GLN:HA	2.13	0.47
4:A:737:LEU:HA	4:A:737:LEU:HD23	1.69	0.47
4:A:247:ARG:HG3	4:A:247:ARG:HH11	1.81	0.46
4:A:1438:THR:HG22	9:F:92:ARG:HD2	1.97	0.46
4:A:862:ASN:HA	8:E:174:GLN:HB3	1.97	0.46
4:A:252:PHE:O	4:A:253:ASN:CB	2.63	0.46
6:C:77:ILE:C	6:C:79:GLN:H	2.18	0.46
8:E:94:LYS:HG3	8:E:98:ILE:CD1	2.45	0.46
4:A:757:ASN:HA	5:B:1021:MET:SD	2.55	0.46
8:E:90:VAL:O	8:E:90:VAL:HG22	2.15	0.46
12:I:8:ARG:CG	12:I:34:TYR:HE1	2.26	0.46
11:H:24:CYS:HB2	11:H:44:VAL:HG21	1.96	0.46
5:B:90:ILE:HD11	5:B:432:MET:SD	2.55	0.46
5:B:1138:MET:HA	5:B:1138:MET:CE	2.45	0.46
5:B:293:PRO:CG	5:B:296:GLU:OE1	2.63	0.46
12:I:5:ARG:HG2	12:I:6:PHE:O	2.15	0.46
8:E:164:LEU:HD11	8:E:211:TYR:CE1	2.50	0.46
5:B:230:ALA:N	5:B:231:PRO:HD2	2.30	0.46
4:A:596:THR:C	4:A:598:LEU:N	2.69	0.46
10:G:79:PHE:HE2	10:G:105:PRO:CG	2.28	0.46
4:A:469:ARG:HB3	4:A:469:ARG:HH11	1.80	0.46
5:B:616:ILE:CD1	5:B:616:ILE:N	2.76	0.46
5:B:38:PHE:CD1	5:B:811:TYR:CD2	3.04	0.46
4:A:1029:ARG:HG3	4:A:1029:ARG:HH11	1.80	0.46
5:B:181:LEU:HD22	5:B:189:LEU:CD2	2.45	0.46
5:B:957:ASN:O	5:B:958:GLN:C	2.53	0.46
4:A:1280:GLU:O	4:A:1281:ARG:C	2.53	0.46
10:G:87:VAL:HG21	10:G:103:VAL:HG11	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:388:CYS:O	5:B:391:ASP:N	2.43	0.46
5:B:40:GLU:HG2	5:B:40:GLU:O	2.14	0.46
4:A:315:LEU:HD13	5:B:471:LYS:HB3	1.97	0.46
4:A:500:GLU:OE2	4:A:1438:THR:HG21	2.15	0.46
5:B:1142:GLY:C	5:B:1144:ALA:H	2.18	0.46
6:C:43:THR:CG2	6:C:44:LEU:N	2.64	0.46
6:C:66:ARG:CZ	13:J:2:ILE:HG21	2.44	0.46
5:B:43:LEU:HD11	5:B:811:TYR:O	2.15	0.46
4:A:332:LYS:H	4:A:337:ARG:HB3	1.79	0.46
1:T:11:DT:C2'	1:T:12:DA:H5'	2.46	0.46
13:J:48:ARG:C	13:J:48:ARG:HD2	2.35	0.46
5:B:1001:PHE:CE2	6:C:34:ARG:CZ	2.99	0.46
4:A:665:GLY:O	4:A:667:GLY:N	2.48	0.46
8:E:29:PHE:O	8:E:30:ILE:HG13	2.15	0.46
5:B:603:LEU:HB3	5:B:609:ILE:CG1	2.46	0.46
5:B:121:ASN:OD1	5:B:963:PHE:HZ	1.99	0.46
5:B:1034:VAL:HG21	5:B:1055:ILE:HG23	1.96	0.46
5:B:94:LYS:HG2	5:B:95:ILE:H	1.78	0.46
4:A:1072:ILE:HD11	4:A:1368:MET:HG2	1.97	0.46
4:A:349:ALA:C	5:B:1128:LEU:HD11	2.35	0.46
5:B:212:LEU:HD12	5:B:409:ALA:HB1	1.98	0.46
4:A:726:ARG:O	4:A:729:ALA:HB3	2.14	0.46
4:A:629:LEU:O	4:A:633:VAL:HG23	2.15	0.46
5:B:664:THR:HG23	5:B:678:GLU:N	2.29	0.46
6:C:69:LEU:H	6:C:69:LEU:CD1	2.28	0.46
5:B:580:VAL:HG13	5:B:624:LEU:HB3	1.97	0.46
5:B:593:PRO:O	5:B:594:ALA:C	2.53	0.46
6:C:6:PRO:HB3	6:C:25:VAL:CG1	2.41	0.46
5:B:1125:ASP:O	5:B:1126:GLY:O	2.34	0.46
12:I:29:CYS:SG	12:I:31:THR:HB	2.56	0.46
5:B:1167:GLY:H	5:B:1217:TYR:HE1	1.64	0.46
8:E:85:GLU:O	8:E:88:VAL:HG23	2.15	0.46
4:A:971:PHE:HE2	4:A:1040:GLN:HG2	1.81	0.46
4:A:713:SER:O	4:A:717:ASN:ND2	2.49	0.46
6:C:27:LEU:O	6:C:30:ALA:N	2.49	0.46
4:A:854:ASN:HB2	4:A:1000:LEU:HD21	1.96	0.46
4:A:253:ASN:HB3	5:B:935:ARG:NH2	2.31	0.46
5:B:1166:CYS:O	5:B:1166:CYS:SG	2.74	0.46
5:B:29:ASP:HB3	5:B:658:ILE:HD13	1.98	0.46
4:A:528:LEU:HD23	4:A:751:SER:CA	2.46	0.46
6:C:18:VAL:HG23	6:C:240:VAL:HB	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:189:THR:HG22	6:C:190:ASP:N	2.31	0.46
5:B:871:THR:HG22	5:B:872:GLU:N	2.30	0.46
4:A:264:PHE:O	4:A:267:ALA:HB3	2.15	0.46
9:F:75:PRO:O	9:F:77:ASP:O	2.32	0.46
5:B:641:GLU:HA	5:B:641:GLU:OE1	2.15	0.46
4:A:210:ILE:O	4:A:214:ILE:HG13	2.14	0.46
4:A:65:LEU:O	4:A:66:LYS:C	2.53	0.46
4:A:1000:LEU:HD23	4:A:1000:LEU:HA	1.81	0.46
5:B:797:TYR:O	13:J:1:MET:HG2	2.15	0.46
5:B:555:ILE:HD11	5:B:587:HIS:CE1	2.51	0.46
11:H:4:THR:O	11:H:5:LEU:HD23	2.16	0.46
5:B:31:TRP:HA	5:B:31:TRP:CE3	2.50	0.46
5:B:102:VAL:O	5:B:109:THR:HA	2.16	0.46
5:B:1034:VAL:O	5:B:1037:LEU:N	2.45	0.46
4:A:1349:TYR:N	4:A:1372:VAL:HG21	2.31	0.46
4:A:608:ILE:HD12	4:A:613:ILE:CD1	2.45	0.46
5:B:283:VAL:O	5:B:286:PHE:N	2.49	0.46
4:A:512:VAL:HA	4:A:519:PRO:HA	1.97	0.46
4:A:206:GLU:O	4:A:210:ILE:HG13	2.16	0.46
4:A:65:LEU:O	4:A:66:LYS:O	2.34	0.46
7:D:156:ASP:C	7:D:158:GLU:H	2.19	0.46
8:E:93:MET:SD	8:E:97:VAL:HG23	2.55	0.46
5:B:903:VAL:O	5:B:948:ILE:HG23	2.16	0.46
6:C:77:ILE:CG2	6:C:161:LYS:HE3	2.45	0.46
11:H:128:ASN:O	11:H:128:ASN:OD1	2.34	0.46
5:B:39:ARG:NH2	5:B:665:GLU:CD	2.69	0.46
4:A:1437:GLY:CA	9:F:88:TYR:CD2	2.99	0.46
4:A:265:LYS:HE2	4:A:322:VAL:HG11	1.98	0.46
4:A:218:ASP:O	4:A:219:PHE:C	2.53	0.46
5:B:361:LEU:HD11	5:B:377:PHE:CD2	2.50	0.46
6:C:125:MET:HB2	6:C:127:ARG:HH21	1.81	0.46
14:K:107:THR:O	14:K:111:LEU:HG	2.16	0.46
5:B:165:VAL:HG11	5:B:448:ILE:CD1	2.46	0.46
4:A:75:ASN:O	4:A:76:GLU:HB3	2.15	0.46
4:A:1239:ARG:HB3	4:A:1239:ARG:NH1	2.31	0.46
7:D:27:LEU:HD13	7:D:173:HIS:CD2	2.50	0.46
4:A:416:ARG:HG3	4:A:417:TYR:CE2	2.51	0.46
7:D:7:THR:HB	10:G:42:PHE:HZ	1.77	0.46
8:E:55:ARG:C	8:E:57:MET:N	2.69	0.46
8:E:46:TYR:CD2	8:E:58:MET:HG2	2.51	0.46
4:A:806:ARG:NH1	5:B:729:ILE:HG13	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:185:CYS:HB2	7:D:211:LEU:HD22	1.96	0.46
4:A:738:LYS:C	4:A:740:LEU:H	2.19	0.46
4:A:556:TRP:CZ3	4:A:558:GLY:HA2	2.51	0.46
11:H:138:GLU:O	11:H:139:ASN:C	2.53	0.46
4:A:351:THR:HB	5:B:1103:ILE:HD11	1.97	0.46
4:A:61:ILE:CG2	4:A:62:ASP:H	2.22	0.46
8:E:20:LYS:NZ	8:E:60:PHE:HE1	2.13	0.46
12:I:69:PRO:HG2	12:I:85:PHE:CD2	2.50	0.46
5:B:980:PHE:HE2	5:B:1094:ARG:HB2	1.81	0.46
5:B:758:PHE:HB2	5:B:1024:ALA:HB1	1.98	0.46
7:D:153:ARG:HB3	7:D:154:PHE:CD1	2.51	0.46
5:B:227:LYS:HB2	5:B:395:GLN:OE1	2.16	0.46
4:A:909:ASP:O	4:A:911:SER:N	2.49	0.46
5:B:893:LEU:HD22	5:B:897:GLY:C	2.36	0.46
5:B:883:LEU:O	5:B:885:MET:N	2.49	0.46
5:B:825:VAL:HG21	5:B:1092:TYR:HE1	1.80	0.46
5:B:780:VAL:HG21	13:J:56:LEU:CD1	2.46	0.46
5:B:555:ILE:HG22	5:B:556:THR:N	2.31	0.46
4:A:10:PRO:HD2	5:B:1191:ILE:O	2.16	0.46
4:A:960:ILE:CA	4:A:963:ILE:HG22	2.41	0.46
5:B:591:ARG:O	5:B:593:PRO:HD3	2.16	0.46
14:K:55:LYS:HB3	14:K:81:TYR:CE1	2.51	0.46
4:A:711:ARG:O	4:A:714:PHE:HB3	2.15	0.46
5:B:975:GLN:HG2	5:B:976:ILE:N	2.31	0.46
4:A:346:ASP:CG	5:B:1108:ARG:HA	2.36	0.46
4:A:683:ILE:HG21	4:A:801:GLU:CG	2.45	0.46
5:B:221:ASN:OD1	5:B:242:SER:HA	2.16	0.46
4:A:298:PHE:HD2	4:A:299:HIS:N	2.13	0.46
12:I:12:ASN:HB3	12:I:13:MET:H	1.55	0.46
5:B:412:LEU:HB3	5:B:466:TRP:CZ2	2.51	0.46
5:B:228:LYS:O	5:B:229:ALA:O	2.34	0.46
4:A:259:GLU:OE1	4:A:263:THR:HG21	2.16	0.46
7:D:138:ASN:OD1	7:D:141:LEU:HB2	2.15	0.46
4:A:128:ILE:O	4:A:134:ARG:HG3	2.16	0.46
10:G:1:MET:CE	10:G:1:MET:O	2.64	0.45
4:A:92:HIS:O	4:A:95:PHE:N	2.46	0.45
4:A:254:GLU:HB2	5:B:935:ARG:HH12	1.80	0.45
5:B:520:GLY:HA2	5:B:748:ILE:HG22	1.98	0.45
2:N:1:DC:H1'	2:N:2:DA:H5'	1.98	0.45
2:N:3:DA:H1'	2:N:4:DG:H5'	1.97	0.45
12:I:80:SER:OG	12:I:105:SER:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:863:GLU:OE1	5:B:962:LYS:HD2	2.16	0.45
5:B:764:SER:HB3	5:B:765:PRO:CD	2.46	0.45
5:B:118:ARG:CG	5:B:204:ILE:HD13	2.46	0.45
11:H:31:THR:O	11:H:31:THR:HG22	2.16	0.45
4:A:252:PHE:O	4:A:256:GLN:NE2	2.49	0.45
4:A:254:GLU:HB2	5:B:935:ARG:HH22	1.81	0.45
4:A:474:VAL:C	4:A:477:PRO:HD2	2.35	0.45
4:A:573:SER:O	4:A:576:GLN:HB2	2.14	0.45
5:B:745:PRO:C	5:B:747:MET:N	2.69	0.45
5:B:778:MET:HE1	5:B:1094:ARG:HD3	1.95	0.45
5:B:1040:ASN:O	5:B:1042:GLY:N	2.50	0.45
4:A:340:LEU:CD2	5:B:1199:ALA:HB3	2.47	0.45
7:D:12:ARG:O	7:D:14:ARG:HG3	2.16	0.45
5:B:324:ILE:CG2	5:B:325:GLN:N	2.79	0.45
5:B:240:ILE:HG22	5:B:254:LEU:HB3	1.98	0.45
4:A:1195:LEU:HD11	4:A:1267:MET:CE	2.45	0.45
4:A:1397:LEU:HB2	4:A:1426:GLU:OE1	2.16	0.45
5:B:126:SER:CB	5:B:172:ILE:HD11	2.45	0.45
4:A:464:PRO:O	4:A:465:TYR:O	2.35	0.45
5:B:1162:ILE:HD11	5:B:1194:ILE:CD1	2.43	0.45
5:B:1161:HIS:NE2	5:B:1175:LEU:HD21	2.31	0.45
2:N:2:DA:H2"	2:N:3:DA:OP2	2.15	0.45
5:B:1004:GLU:HB2	5:B:1006:ILE:HG13	1.97	0.45
5:B:593:PRO:HG2	5:B:617:ARG:CZ	2.45	0.45
5:B:521:LEU:HB3	5:B:633:VAL:CG1	2.42	0.45
4:A:347:PHE:H	5:B:1107:ALA:HA	1.80	0.45
14:K:12:LEU:HD12	14:K:12:LEU:N	2.29	0.45
4:A:913:LEU:HD21	4:A:915:SER:OG	2.15	0.45
10:G:30:LEU:HD22	10:G:72:VAL:HG11	1.97	0.45
4:A:577:ILE:O	4:A:579:SER:N	2.48	0.45
8:E:55:ARG:C	8:E:57:MET:H	2.19	0.45
4:A:203:SER:OG	4:A:206:GLU:HB2	2.17	0.45
5:B:750:GLY:O	5:B:751:VAL:C	2.54	0.45
4:A:1095:THR:HG21	4:A:1103:GLU:OE1	2.16	0.45
1:T:18:DC:H5'	4:A:832:ALA:O	2.17	0.45
4:A:399:HIS:O	4:A:401:GLY:N	2.49	0.45
4:A:1323:ASP:C	4:A:1325:THR:N	2.70	0.45
5:B:32:ALA:O	5:B:35:SER:HB2	2.16	0.45
5:B:39:ARG:HG2	5:B:39:ARG:NH1	2.31	0.45
11:H:95:TYR:CE2	11:H:97:MET:HG3	2.52	0.45
4:A:650:GLN:HB3	4:A:654:ASN:HD21	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:898:ARG:HB2	4:A:933:TYR:CE1	2.52	0.45
5:B:1202:LEU:O	5:B:1206:GLU:HG3	2.16	0.45
13:J:19:GLU:O	13:J:23:ASN:HB2	2.16	0.45
10:G:132:SER:HB3	10:G:135:ASP:HB2	1.97	0.45
4:A:1438:THR:CB	5:B:1144:ALA:HB3	2.27	0.45
8:E:22:MET:CE	8:E:26:ARG:HE	2.30	0.45
5:B:844:SER:O	5:B:847:ASP:N	2.46	0.45
14:K:31:VAL:CG1	14:K:32:VAL:N	2.80	0.45
14:K:58:PHE:CE2	14:K:74:ARG:NE	2.76	0.45
12:I:32:CYS:SG	12:I:33:SER:N	2.89	0.45
10:G:108:VAL:HG13	10:G:159:ALA:O	2.17	0.45
6:C:252:GLN:CG	14:K:95:ILE:HG23	2.46	0.45
4:A:552:TRP:NE1	14:K:62:LYS:HB3	2.31	0.45
7:D:29:LEU:O	7:D:30:GLY:C	2.52	0.45
4:A:73:GLY:O	4:A:75:ASN:N	2.50	0.45
1:T:23:DC:H2''	1:T:24:DT:O5'	2.16	0.45
10:G:45:ILE:HD13	10:G:78:VAL:HG13	1.98	0.45
6:C:76:ASP:OD2	6:C:128:ASN:N	2.48	0.45
6:C:143:LEU:HD21	6:C:146:LYS:CE	2.47	0.45
5:B:1160:VAL:HG12	5:B:1161:HIS:N	2.32	0.45
14:K:53:ASP:HB3	14:K:56:VAL:CG2	2.35	0.45
4:A:666:ILE:HD12	4:A:666:ILE:N	2.32	0.45
5:B:189:LEU:HD12	5:B:196:PRO:HA	1.99	0.45
5:B:53:GLN:HG2	5:B:547:VAL:CG2	2.38	0.45
14:K:88:LYS:O	14:K:91:CYS:HB2	2.17	0.45
4:A:313:GLN:O	4:A:314:ALA:HB3	2.16	0.45
7:D:195:ILE:CG2	7:D:198:LEU:HG	2.46	0.45
5:B:449:ASN:O	5:B:451:LYS:N	2.50	0.45
5:B:212:LEU:HD12	5:B:409:ALA:CB	2.47	0.45
4:A:889:SER:HB3	4:A:1297:GLU:HG2	1.98	0.45
5:B:131:ASP:HA	5:B:164:LYS:HB3	1.97	0.45
8:E:145:THR:HG21	8:E:187:TYR:CE2	2.51	0.45
4:A:341:MET:CE	4:A:843:LYS:HZ1	2.30	0.45
14:K:53:ASP:C	14:K:55:LYS:N	2.70	0.45
5:B:1096:ARG:HA	5:B:1098:MET:HE2	1.99	0.45
5:B:311:LEU:O	5:B:312:GLU:C	2.55	0.45
9:F:73:ALA:HA	9:F:143:PHE:CE1	2.52	0.45
10:G:143:ILE:CG2	10:G:144:ARG:H	2.29	0.45
4:A:1146:VAL:HG11	4:A:1207:LEU:CD1	2.47	0.45
5:B:282:ILE:CD1	5:B:382:ILE:HD13	2.47	0.45
12:I:82:GLU:O	12:I:104:LEU:HG	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:107:SER:O	6:C:109:SER:N	2.47	0.45
5:B:315:LYS:HE3	12:I:4:PHE:CD2	2.52	0.45
3:P:5:A:H2'	3:P:6:G:H8	1.82	0.45
4:A:1355:VAL:O	4:A:1355:VAL:HG12	2.17	0.45
4:A:1404:GLU:HB2	4:A:1408:ILE:HG13	1.98	0.45
4:A:320:ARG:HH21	4:A:323:LYS:HZ1	1.65	0.45
12:I:69:PRO:HG2	12:I:85:PHE:CE2	2.52	0.45
5:B:979:LYS:HG2	5:B:1095:LEU:HD13	1.99	0.45
5:B:1038:SER:C	5:B:1040:ASN:N	2.70	0.45
4:A:146:MET:CA	4:A:171:GLN:HB2	2.47	0.45
15:L:36:SER:O	15:L:37:LYS:C	2.55	0.45
4:A:1299:VAL:CG1	4:A:1300:LYS:H	2.28	0.45
4:A:1226:VAL:HG12	4:A:1227:ILE:N	2.32	0.45
4:A:28:ARG:O	4:A:29:ALA:C	2.55	0.45
5:B:466:TRP:O	5:B:468:GLU:N	2.48	0.45
5:B:270:LYS:HA	5:B:281:PRO:HA	1.99	0.45
15:L:43:THR:O	15:L:43:THR:HG22	2.15	0.45
5:B:512:ARG:HG2	5:B:512:ARG:HH11	1.82	0.45
4:A:445:ASN:HA	4:A:478:TYR:CE2	2.52	0.45
6:C:179:GLU:CG	6:C:180:TYR:N	2.78	0.45
5:B:828:ALA:O	5:B:834:ASN:ND2	2.48	0.45
13:J:12:LYS:O	13:J:14:VAL:CG2	2.59	0.45
4:A:871:ASP:OD1	4:A:1366:ARG:NH2	2.49	0.45
12:I:58:VAL:HG12	12:I:58:VAL:O	2.16	0.45
4:A:683:ILE:HD13	4:A:801:GLU:CG	2.47	0.45
6:C:259:LEU:HD21	14:K:92:ASN:CG	2.38	0.45
4:A:1394:THR:CG2	4:A:1398:MET:SD	3.04	0.45
6:C:226:ASP:O	6:C:227:THR:CB	2.61	0.45
6:C:183:TRP:CZ2	6:C:207:CYS:HB3	2.51	0.45
4:A:936:LEU:O	4:A:939:ASP:HB2	2.17	0.45
14:K:17:SER:O	14:K:18:LYS:C	2.54	0.45
5:B:436:VAL:O	5:B:436:VAL:HG12	2.17	0.45
5:B:882:THR:O	5:B:883:LEU:HB2	2.16	0.45
10:G:7:LEU:CD1	10:G:45:ILE:HD11	2.47	0.45
5:B:1007:VAL:HG22	5:B:1008:PRO:HD2	1.98	0.45
4:A:1224:LEU:HD11	4:A:1240:CYS:HB2	1.99	0.45
5:B:519:TRP:HE1	5:B:635:ARG:NH2	2.15	0.45
14:K:56:VAL:HA	14:K:77:THR:HG22	1.98	0.45
6:C:31:ASN:O	6:C:32:SER:C	2.55	0.45
8:E:24:LYS:HG3	8:E:25:ASP:N	2.32	0.45
8:E:133:GLU:HB3	8:E:135:PHE:HE1	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:1096:ARG:O	5:B:1097:HIS:CG	2.70	0.45
6:C:29:MET:CE	14:K:98:LEU:HG	2.47	0.45
5:B:284:ILE:HG23	5:B:324:ILE:CD1	2.47	0.45
11:H:82:PRO:C	11:H:84:ALA:H	2.15	0.45
4:A:34:LYS:N	4:A:34:LYS:CD	2.80	0.45
4:A:1299:VAL:CG1	4:A:1300:LYS:N	2.78	0.45
4:A:1152:ILE:HG22	4:A:1192:LEU:O	2.17	0.45
5:B:281:PRO:O	5:B:283:VAL:N	2.50	0.45
5:B:1151:LEU:N	5:B:1151:LEU:CD1	2.80	0.45
4:A:1170:ILE:HG22	4:A:1174:PHE:HE1	1.82	0.45
5:B:797:TYR:HE1	5:B:854:LEU:CD2	2.30	0.44
5:B:563:MET:HE2	5:B:587:HIS:C	2.37	0.44
11:H:91:ASP:C	11:H:93:TYR:N	2.70	0.44
4:A:774:ARG:H	4:A:774:ARG:HG2	1.49	0.44
4:A:1120:LEU:H	4:A:1120:LEU:HD13	1.82	0.44
13:J:64:ASN:CB	13:J:65:PRO:HD3	2.44	0.44
4:A:963:ILE:HD13	4:A:1049:ILE:CG1	2.46	0.44
5:B:550:ASP:OD1	5:B:551:PRO:HD2	2.17	0.44
4:A:231:PRO:C	4:A:233:TRP:H	2.20	0.44
5:B:558:LEU:O	5:B:561:TRP:N	2.49	0.44
4:A:106:VAL:HG13	4:A:112:LYS:H	1.82	0.44
8:E:114:ASN:O	8:E:115:ASN:CB	2.63	0.44
5:B:695:ALA:O	5:B:698:GLU:HB3	2.17	0.44
4:A:788:SER:O	4:A:789:LYS:O	2.35	0.44
10:G:152:SER:O	10:G:153:GLN:HB2	2.17	0.44
5:B:799:PRO:CB	5:B:818:PRO:HG2	2.47	0.44
7:D:195:ILE:O	7:D:198:LEU:HG	2.17	0.44
6:C:27:LEU:O	6:C:28:ALA:C	2.56	0.44
9:F:128:LYS:HD3	9:F:149:GLU:O	2.17	0.44
4:A:920:LEU:HD23	4:A:920:LEU:C	2.37	0.44
11:H:116:TYR:HE2	11:H:140:ALA:HB1	1.82	0.44
7:D:48:ILE:HG21	10:G:4:ILE:HD12	1.99	0.44
11:H:130:ARG:HB3	11:H:133:ASN:HB2	1.99	0.44
11:H:91:ASP:O	11:H:93:TYR:N	2.47	0.44
4:A:568:PRO:HG2	4:A:569:LYS:H	1.83	0.44
8:E:21:GLU:O	8:E:24:LYS:HG2	2.17	0.44
4:A:23:SER:O	4:A:26:GLU:N	2.50	0.44
14:K:93:SER:O	14:K:97:LYS:HG3	2.17	0.44
5:B:596:LEU:O	5:B:600:LEU:HG	2.17	0.44
5:B:600:LEU:O	5:B:609:ILE:HD12	2.17	0.44
6:C:239:PRO:O	6:C:241:ASP:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:157:ASP:C	4:A:159:THR:N	2.70	0.44
7:D:151:PHE:N	7:D:151:PHE:HD1	2.15	0.44
4:A:994:GLN:HA	4:A:997:LEU:HG	1.99	0.44
4:A:1428:VAL:HG22	5:B:1147:LEU:HD21	1.98	0.44
4:A:1433:MET:CE	10:G:63:PRO:HB2	2.47	0.44
5:B:1177:HIS:O	5:B:1179:GLN:N	2.51	0.44
4:A:35:ILE:HA	4:A:52:GLY:O	2.17	0.44
4:A:53:LEU:CD2	4:A:54:ASN:HD22	2.30	0.44
1:T:24:DT:OP2	5:B:942:ARG:NH2	2.50	0.44
4:A:353:ILE:HB	4:A:470:LEU:CD2	2.47	0.44
8:E:61:GLN:HG2	8:E:62:ALA:N	2.32	0.44
5:B:840:ILE:CG2	5:B:994:TYR:HD1	2.30	0.44
5:B:995:ARG:HH12	6:C:165:LYS:HG2	1.82	0.44
4:A:138:ILE:HD12	4:A:222:LEU:HD23	1.98	0.44
5:B:952:VAL:HG12	5:B:953:LEU:N	2.33	0.44
6:C:238:ILE:HD11	6:C:246:ARG:NH1	2.32	0.44
4:A:114:LEU:HD13	4:A:171:GLN:OE1	2.17	0.44
6:C:26:ASP:O	6:C:27:LEU:C	2.56	0.44
14:K:103:THR:O	14:K:105:PHE:N	2.50	0.44
5:B:527:THR:OG1	5:B:528:PRO:HD2	2.18	0.44
4:A:373:THR:HG21	5:B:1105:ALA:HB3	1.98	0.44
5:B:1030:LEU:HD12	5:B:1030:LEU:HA	1.83	0.44
5:B:882:THR:HG21	5:B:935:ARG:HA	2.00	0.44
4:A:472:LEU:O	4:A:475:THR:CG2	2.65	0.44
4:A:784:LEU:HB3	4:A:785:PRO:HD2	1.98	0.44
4:A:1130:GLN:HA	4:A:1133:LEU:HD12	2.00	0.44
14:K:57:LEU:N	14:K:76:GLN:O	2.50	0.44
14:K:49:GLU:OE2	14:K:97:LYS:HE3	2.16	0.44
4:A:1100:ARG:NH2	4:A:1351:GLU:CG	2.76	0.44
6:C:208:GLU:C	6:C:210:GLU:H	2.21	0.44
4:A:648:ASN:O	4:A:649:ILE:C	2.55	0.44
4:A:108:MET:O	4:A:109:HIS:HB2	2.18	0.44
4:A:1162:VAL:CG1	12:I:41:PRO:HG3	2.48	0.44
6:C:193:TYR:C	6:C:193:TYR:CD1	2.90	0.44
5:B:846:ILE:HG23	5:B:974:PRO:CG	2.46	0.44
5:B:615:MET:HA	5:B:625:LYS:O	2.18	0.44
4:A:1277:GLU:C	4:A:1279:ILE:H	2.20	0.44
5:B:519:TRP:C	5:B:519:TRP:CD1	2.91	0.44
4:A:341:MET:CE	5:B:1135:ARG:NH1	2.80	0.44
2:N:4:DG:H1'	2:N:5:DT:H5'	1.99	0.44
13:J:36:LEU:HB2	13:J:47:ARG:NH1	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1068:ALA:HA	4:A:1367:HIS:ND1	2.32	0.44
4:A:563:PRO:HG3	4:A:572:TRP:CE2	2.52	0.44
4:A:412:ARG:NH2	5:B:1108:ARG:NH2	2.65	0.44
6:C:61:GLU:HA	6:C:64:ALA:HB3	2.00	0.44
11:H:81:PRO:HB2	11:H:82:PRO:CD	2.44	0.44
5:B:810:GLU:HA	5:B:815:ARG:NH1	2.29	0.44
4:A:1148:ILE:O	12:I:48:LEU:N	2.46	0.44
8:E:48:ASP:CG	8:E:49:SER:N	2.71	0.44
8:E:55:ARG:NH1	8:E:113:GLN:NE2	2.66	0.44
4:A:262:LEU:C	4:A:264:PHE:H	2.21	0.44
7:D:29:LEU:HD22	10:G:82:PHE:CE2	2.53	0.44
14:K:68:PHE:HB3	14:K:70:ARG:NH1	2.32	0.44
14:K:24:ASP:OD1	14:K:26:LYS:N	2.51	0.44
10:G:48:VAL:HG13	10:G:74:TYR:HD1	1.82	0.44
4:A:464:PRO:HG2	4:A:465:TYR:CD1	2.51	0.44
5:B:36:ALA:HA	5:B:39:ARG:HD2	1.99	0.44
8:E:138:ALA:HA	8:E:141:VAL:HG23	2.00	0.44
12:I:78:CYS:O	12:I:80:SER:N	2.51	0.44
7:D:153:ARG:HG2	7:D:218:GLU:HG3	1.99	0.44
5:B:1216:LEU:C	5:B:1217:TYR:HD1	2.21	0.44
5:B:402:GLY:HA2	5:B:695:ALA:HB3	1.99	0.44
4:A:1450:LEU:CG	4:A:1450:LEU:O	2.65	0.44
5:B:842:ASN:HB3	5:B:1009:ASP:HA	2.00	0.44
4:A:1260:LEU:CG	4:A:1260:LEU:O	2.64	0.44
5:B:615:MET:C	5:B:616:ILE:HD12	2.36	0.44
5:B:661:LEU:C	5:B:663:ALA:H	2.20	0.44
5:B:745:PRO:C	5:B:747:MET:H	2.21	0.44
2:N:1:DC:H2"	2:N:2:DA:OP2	2.16	0.44
4:A:456:MET:HB3	4:A:507:VAL:HG22	2.00	0.44
5:B:23:ALA:HB1	5:B:24:PRO:CD	2.42	0.44
5:B:244:LEU:HD13	5:B:247:GLY:O	2.18	0.44
5:B:203:PHE:HB3	5:B:205:ILE:CD1	2.48	0.44
5:B:278:GLN:HG2	5:B:279:ASP:N	2.26	0.44
7:D:51:ASN:O	7:D:54:GLU:HB3	2.18	0.44
4:A:1265:ASN:O	4:A:1267:MET:N	2.51	0.44
4:A:1385:THR:HG22	4:A:1386:ARG:H	1.82	0.44
7:D:156:ASP:C	7:D:158:GLU:N	2.71	0.44
6:C:200:GLU:O	6:C:202:PRO:HD3	2.18	0.44
10:G:101:VAL:HG12	10:G:102:GLN:N	2.33	0.44
4:A:56:PRO:O	4:A:57:ARG:CG	2.57	0.44
4:A:903:ASN:ND2	4:A:905:ASP:H	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:844:ALA:C	4:A:845:LEU:HD23	2.38	0.44
14:K:59:ALA:HA	14:K:74:ARG:O	2.17	0.44
14:K:78:THR:O	14:K:81:TYR:HB3	2.18	0.44
4:A:1118:VAL:CG2	4:A:1306:LEU:HB2	2.45	0.44
4:A:808:LEU:CD2	4:A:813:PHE:HA	2.45	0.44
8:E:180:ARG:NH2	8:E:192:ARG:HD2	2.32	0.44
4:A:626:ASN:O	4:A:628:GLY:N	2.50	0.44
4:A:14:VAL:CG2	5:B:1216:LEU:HD12	2.46	0.44
15:L:28:LYS:CB	15:L:39:SER:HA	2.47	0.44
5:B:525:ALA:O	5:B:768:THR:HA	2.17	0.44
4:A:1191:TRP:CE3	4:A:1191:TRP:HA	2.53	0.44
4:A:1289:ARG:HD2	4:A:1303:GLU:OE2	2.18	0.44
7:D:50:LEU:HD13	7:D:55:ALA:CB	2.48	0.44
4:A:834:THR:HG21	4:A:1077:THR:OG1	2.18	0.44
4:A:1105:LEU:HD22	4:A:1384:VAL:HG21	1.99	0.44
6:C:62:PHE:O	6:C:66:ARG:HG3	2.18	0.44
5:B:552:MET:C	5:B:554:ILE:H	2.22	0.44
5:B:37:PHE:HE1	5:B:41:LYS:HG3	1.78	0.44
4:A:845:LEU:HB3	4:A:848:ILE:HD12	2.00	0.44
14:K:58:PHE:HB3	14:K:76:GLN:HE21	1.83	0.44
4:A:1313:LEU:HD23	4:A:1338:VAL:HB	2.00	0.44
4:A:23:SER:O	4:A:24:PRO:C	2.53	0.44
5:B:196:PRO:HG2	5:B:197:PHE:H	1.82	0.44
5:B:981:ALA:HB3	5:B:1095:LEU:HD21	1.99	0.44
4:A:345:VAL:CG1	5:B:1130:PHE:HB2	2.48	0.44
6:C:241:ASP:OD1	6:C:242:GLN:N	2.48	0.44
4:A:343:LYS:CE	5:B:1156:ASP:OD2	2.66	0.44
7:D:18:VAL:O	7:D:18:VAL:HG23	2.18	0.44
4:A:1293:SER:OG	4:A:1295:THR:CG2	2.66	0.44
5:B:222:ILE:HG22	5:B:223:VAL:N	2.32	0.44
5:B:361:LEU:HD11	5:B:377:PHE:CE2	2.52	0.44
8:E:55:ARG:HB2	8:E:84:ASP:OD2	2.18	0.44
4:A:130:ASP:HB3	4:A:133:LYS:HB2	2.00	0.44
5:B:314:LEU:O	5:B:318:VAL:HG23	2.18	0.44
5:B:123:THR:OG1	5:B:458:LYS:HE2	2.18	0.44
6:C:121:VAL:O	6:C:121:VAL:HG12	2.17	0.44
4:A:576:GLN:HG3	11:H:119:GLY:HA3	2.00	0.43
4:A:836:TYR:CZ	4:A:840:ARG:HD2	2.53	0.43
4:A:224:PHE:HD2	4:A:229:SER:O	2.00	0.43
4:A:418:SER:O	4:A:420:ARG:N	2.51	0.43
4:A:1429:ILE:O	5:B:1197:PRO:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1339:LEU:HD13	8:E:147:HIS:CD2	2.52	0.43
5:B:1147:LEU:CD2	5:B:1151:LEU:HD22	2.48	0.43
11:H:116:TYR:O	11:H:122:LEU:HA	2.17	0.43
8:E:207:ARG:CB	8:E:207:ARG:NH1	2.81	0.43
5:B:840:ILE:HD13	5:B:994:TYR:HE1	1.83	0.43
4:A:1434:ALA:O	4:A:1436:ILE:N	2.50	0.43
4:A:427:GLN:HB2	4:A:430:TRP:CE2	2.53	0.43
4:A:666:ILE:N	5:B:1026:LEU:HD13	2.33	0.43
5:B:1072:MET:HE3	5:B:1085:ILE:HD13	1.99	0.43
5:B:1110:PRO:HG2	5:B:1119:VAL:HG22	2.00	0.43
4:A:504:LEU:HD11	9:F:91:ALA:CB	2.48	0.43
12:I:8:ARG:HB2	12:I:9:ASP:OD1	2.18	0.43
4:A:1444:MET:O	9:F:133:VAL:N	2.51	0.43
14:K:87:LEU:O	14:K:88:LYS:C	2.56	0.43
15:L:49:LYS:O	15:L:50:ASP:HB3	2.17	0.43
4:A:768:GLN:NE2	4:A:816:HIS:HD1	2.16	0.43
4:A:996:ASN:O	4:A:998:LEU:HD12	2.17	0.43
4:A:552:TRP:HE1	14:K:62:LYS:HB3	1.83	0.43
11:H:100:THR:HG22	11:H:101:ALA:H	1.81	0.43
4:A:270:LEU:O	4:A:270:LEU:HD12	2.18	0.43
5:B:806:THR:C	5:B:808:ALA:N	2.69	0.43
6:C:114:TYR:HB2	6:C:116:LYS:HG2	2.01	0.43
4:A:1120:LEU:O	4:A:1323:ASP:HB2	2.18	0.43
5:B:38:PHE:HD1	5:B:811:TYR:CD2	2.36	0.43
5:B:681:TRP:HA	5:B:684:LEU:HD13	2.00	0.43
4:A:427:GLN:O	4:A:428:TYR:C	2.56	0.43
4:A:886:ILE:HG13	4:A:943:LEU:HD12	1.99	0.43
5:B:558:LEU:O	5:B:560:GLU:N	2.50	0.43
4:A:396:PRO:HG3	4:A:416:ARG:HB3	1.99	0.43
4:A:412:ARG:HH22	5:B:1108:ARG:NH2	2.16	0.43
5:B:333:PHE:O	5:B:334:ILE:CG1	2.66	0.43
7:D:134:THR:CG2	7:D:135:GLY:H	2.29	0.43
5:B:166:PHE:C	5:B:167:ILE:HG13	2.39	0.43
9:F:79:ARG:NH2	9:F:150:GLU:OE1	2.39	0.43
4:A:490:HIS:HB3	5:B:1150:ARG:NH1	2.32	0.43
8:E:102:GLU:O	8:E:104:ASN:N	2.51	0.43
8:E:81:GLU:HG2	8:E:82:PHE:N	2.33	0.43
10:G:21:ARG:HD3	10:G:21:ARG:HA	1.68	0.43
7:D:139:LYS:HB2	7:D:139:LYS:HE2	1.88	0.43
4:A:54:ASN:HB3	4:A:247:ARG:NH1	2.31	0.43
8:E:28:TYR:CD1	8:E:78:LEU:HD13	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:K:65:HIS:CG	14:K:66:PRO:HD2	2.53	0.43
5:B:992:ILE:HD11	14:K:66:PRO:HB2	1.99	0.43
11:H:4:THR:HG22	11:H:5:LEU:N	2.33	0.43
11:H:95:TYR:HE2	11:H:97:MET:CG	2.31	0.43
15:L:55:ILE:O	15:L:56:LEU:CB	2.64	0.43
8:E:171:LYS:HD3	8:E:171:LYS:N	2.33	0.43
4:A:680:THR:HA	4:A:683:ILE:CD1	2.48	0.43
5:B:284:ILE:HD13	5:B:333:PHE:CD2	2.43	0.43
10:G:115:MET:HB2	10:G:116:PRO:CD	2.47	0.43
4:A:115:LEU:HB2	4:A:122:MET:CE	2.49	0.43
5:B:129:PHE:HE2	5:B:166:PHE:CD1	2.36	0.43
4:A:1227:ILE:CG2	4:A:1228:TRP:N	2.81	0.43
4:A:108:MET:HB3	4:A:210:ILE:HD13	2.00	0.43
5:B:785:TYR:CD1	5:B:786:ASN:N	2.86	0.43
4:A:814:PHE:O	4:A:817:ALA:HB3	2.19	0.43
5:B:882:THR:O	5:B:883:LEU:CB	2.67	0.43
5:B:582:VAL:HG12	5:B:587:HIS:NE2	2.33	0.43
5:B:34:ILE:O	5:B:37:PHE:N	2.52	0.43
1:T:12:DA:C2'	1:T:13:DC:H5'	2.49	0.43
9:F:99:LEU:O	9:F:103:MET:HG2	2.19	0.43
4:A:78:PRO:HA	5:B:1201:LYS:NZ	2.33	0.43
4:A:548:ASN:OD1	14:K:60:ALA:HB1	2.18	0.43
4:A:1209:MET:HE1	4:A:1236:LEU:HB3	2.00	0.43
5:B:1147:LEU:HD23	5:B:1151:LEU:HD22	2.00	0.43
4:A:68:GLN:C	4:A:70:CYS:N	2.68	0.43
4:A:853:ASP:O	4:A:854:ASN:CB	2.62	0.43
4:A:963:ILE:HD13	4:A:1049:ILE:HG12	2.01	0.43
5:B:520:GLY:CA	5:B:748:ILE:HG22	2.48	0.43
1:T:12:DA:H2''	1:T:13:DC:H5'	2.00	0.43
4:A:709:THR:CG2	4:A:711:ARG:HB2	2.49	0.43
5:B:393:LYS:HA	5:B:393:LYS:CE	2.45	0.43
4:A:1206:ASP:C	4:A:1274:ARG:NH1	2.71	0.43
4:A:1042:PHE:CE2	4:A:1046:LEU:HD11	2.53	0.43
4:A:1114:PRO:HG2	4:A:1115:SER:H	1.82	0.43
5:B:280:ILE:HG21	5:B:285:ILE:HG13	2.00	0.43
5:B:785:TYR:C	5:B:785:TYR:CD1	2.91	0.43
13:J:31:ASP:O	13:J:32:GLU:C	2.57	0.43
15:L:61:THR:HG22	15:L:62:LYS:N	2.33	0.43
7:D:48:ILE:CG2	10:G:4:ILE:HB	2.39	0.43
5:B:97:VAL:HG12	5:B:178:ASN:ND2	2.32	0.43
4:A:399:HIS:NE2	4:A:462:VAL:HG11	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:37:PHE:HE2	5:B:542:MET:HA	1.84	0.43
5:B:1034:VAL:O	5:B:1036:ALA:N	2.51	0.43
4:A:1394:THR:HG22	4:A:1395:GLY:H	1.83	0.43
4:A:29:ALA:HB1	5:B:1184:GLY:HA3	2.01	0.43
5:B:1115:THR:HG22	5:B:1117:GLN:HG3	2.01	0.43
4:A:596:THR:C	4:A:598:LEU:H	2.22	0.43
10:G:80:LYS:CD	10:G:80:LYS:N	2.78	0.43
5:B:879:ARG:HA	5:B:879:ARG:HD3	1.81	0.43
4:A:535:THR:HG21	4:A:616:VAL:CA	2.33	0.43
8:E:28:TYR:CE1	8:E:78:LEU:CD1	3.02	0.43
5:B:826:ALA:HB2	5:B:1008:PRO:HB3	1.99	0.43
4:A:1435:PRO:O	4:A:1436:ILE:HG13	2.19	0.43
9:F:84:TYR:CD1	9:F:84:TYR:N	2.87	0.43
8:E:177:ARG:O	8:E:212:ARG:CD	2.66	0.43
5:B:308:TRP:CD1	5:B:308:TRP:N	2.85	0.43
4:A:1102:LYS:O	4:A:1106:ASN:ND2	2.51	0.43
6:C:107:SER:C	6:C:109:SER:N	2.72	0.43
4:A:600:PRO:C	4:A:602:ASP:N	2.72	0.43
5:B:259:TYR:HD1	5:B:259:TYR:H	1.67	0.43
11:H:10:PHE:N	11:H:10:PHE:CD1	2.87	0.43
4:A:116:ASP:C	4:A:118:HIS:N	2.70	0.43
10:G:110:VAL:HG22	10:G:161:GLY:O	2.19	0.43
4:A:415:LEU:HA	4:A:415:LEU:HD23	1.83	0.43
4:A:91:PHE:HB2	4:A:297:GLN:HE22	1.84	0.43
4:A:466:SER:HB2	5:B:1099:VAL:CG1	2.49	0.43
4:A:1017:LEU:O	4:A:1017:LEU:HD12	2.18	0.43
4:A:47:ARG:HH12	4:A:254:GLU:CG	2.31	0.43
4:A:475:THR:CG2	4:A:476:SER:N	2.67	0.43
13:J:1:MET:H1	13:J:56:LEU:HB2	1.83	0.43
13:J:57:ILE:CA	13:J:60:PHE:HD2	2.24	0.43
11:H:93:TYR:N	11:H:93:TYR:CD1	2.87	0.43
6:C:47:ASP:CA	15:L:69:ALA:CB	2.93	0.43
9:F:89:GLU:HB3	9:F:134:ILE:HD11	2.01	0.43
5:B:848:ARG:NH1	13:J:8:PHE:O	2.52	0.43
4:A:709:THR:HB	4:A:712:GLU:H	1.84	0.43
9:F:82:THR:HA	9:F:83:PRO:HD3	1.87	0.43
5:B:814:PHE:C	5:B:816:GLU:N	2.73	0.43
4:A:850:VAL:HG21	4:A:1058:VAL:HG11	2.01	0.43
5:B:125:SER:CA	5:B:171:PRO:HA	2.42	0.43
12:I:98:VAL:HG12	12:I:99:LEU:N	2.33	0.43
5:B:761:HIS:HB2	5:B:1024:ALA:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:1196:ILE:HD12	5:B:1200:ALA:HB3	2.00	0.43
4:A:106:VAL:CG1	4:A:112:LYS:N	2.82	0.43
5:B:95:ILE:HG13	5:B:130:VAL:CG2	2.47	0.43
5:B:763:GLN:O	5:B:765:PRO:N	2.52	0.43
7:D:4:SER:C	7:D:5:THR:OG1	2.56	0.43
5:B:872:GLU:OE2	5:B:914:LYS:HE2	2.18	0.43
4:A:89:PRO:C	4:A:204:THR:HG21	2.39	0.43
6:C:22:LEU:HD13	6:C:230:MET:HE1	2.00	0.43
5:B:1187:ASN:O	5:B:1188:LYS:CB	2.66	0.43
5:B:508:LEU:O	5:B:509:ALA:HB2	2.19	0.43
5:B:918:ILE:HD12	5:B:935:ARG:HD3	2.01	0.43
6:C:65:HIS:O	6:C:69:LEU:HD13	2.19	0.43
5:B:542:MET:HB3	5:B:636:PRO:CD	2.48	0.43
4:A:1402:PHE:CD1	4:A:1403:GLU:HG3	2.54	0.43
4:A:1434:ALA:HA	4:A:1435:PRO:HD3	1.82	0.43
15:L:46:VAL:CG1	15:L:56:LEU:HD12	2.48	0.43
4:A:12:ARG:NE	5:B:1192:TYR:HE2	2.17	0.43
6:C:16:ASP:C	6:C:17:ASN:ND2	2.71	0.43
9:F:77:ASP:C	9:F:79:ARG:N	2.72	0.43
5:B:236:HIS:CE1	5:B:389:ALA:HA	2.54	0.43
5:B:100:PRO:HD2	5:B:180:TYR:HE1	1.81	0.42
5:B:840:ILE:HG21	5:B:994:TYR:HD1	1.84	0.42
11:H:127:GLY:HA3	11:H:130:ARG:HH22	1.83	0.42
15:L:46:VAL:HG13	15:L:56:LEU:HD12	1.99	0.42
4:A:899:VAL:HG22	4:A:908:LEU:HD21	2.00	0.42
4:A:61:ILE:O	4:A:63:ARG:N	2.52	0.42
5:B:1081:LEU:O	5:B:1082:MET:C	2.57	0.42
6:C:191:TYR:HD2	6:C:201:TRP:CD1	2.37	0.42
8:E:60:PHE:CD2	8:E:60:PHE:C	2.91	0.42
5:B:603:LEU:HB3	5:B:609:ILE:HG13	2.01	0.42
4:A:340:LEU:HD21	5:B:1199:ALA:HB3	2.01	0.42
5:B:522:VAL:HG12	5:B:523:CYS:N	2.34	0.42
4:A:1225:PHE:CE2	4:A:1227:ILE:HD11	2.53	0.42
5:B:56:ASP:HB2	5:B:57:TYR:HD1	1.84	0.42
4:A:1006:ILE:HD11	8:E:163:GLU:HG3	2.00	0.42
14:K:8:GLU:O	14:K:37:LYS:HD2	2.20	0.42
5:B:1162:ILE:HG22	5:B:1163:CYS:N	2.33	0.42
5:B:542:MET:CG	5:B:747:MET:HB3	2.46	0.42
4:A:843:LYS:HA	4:A:843:LYS:HD3	1.75	0.42
5:B:549:THR:HG22	5:B:550:ASP:N	2.23	0.42
5:B:189:LEU:O	5:B:192:LEU:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:1107:ALA:O	5:B:1108:ARG:O	2.36	0.42
6:C:213:PRO:O	6:C:214:ASN:CB	2.65	0.42
4:A:1010:ALA:O	4:A:1013:ASP:HB2	2.19	0.42
4:A:830:LYS:HG2	4:A:1098:VAL:HG21	2.01	0.42
5:B:1084:GLN:OE1	6:C:189:THR:HG22	2.18	0.42
8:E:147:HIS:CD2	8:E:149:LEU:H	2.36	0.42
12:I:13:MET:O	12:I:14:LEU:HD23	2.19	0.42
4:A:1191:TRP:HD1	4:A:1256:GLU:HB2	1.83	0.42
4:A:110:CYS:HB3	4:A:167:CYS:SG	2.59	0.42
4:A:1261:LYS:HA	4:A:1264:GLU:HB3	2.00	0.42
7:D:192:LYS:HE3	7:D:204:ASP:OD1	2.19	0.42
5:B:496:ARG:NH1	5:B:539:LEU:HB2	2.33	0.42
4:A:557:ASP:O	4:A:559:VAL:HG23	2.19	0.42
4:A:964:ILE:O	4:A:967:ALA:HB3	2.19	0.42
5:B:100:PRO:HD3	5:B:172:ILE:HD12	2.00	0.42
4:A:215:SER:HB3	4:A:218:ASP:OD2	2.19	0.42
4:A:1214:GLU:OE1	4:A:1214:GLU:HA	2.19	0.42
5:B:860:MET:HG2	5:B:861:ASP:H	1.84	0.42
5:B:1202:LEU:HD22	5:B:1206:GLU:CD	2.40	0.42
4:A:914:GLU:HB2	4:A:979:SER:O	2.18	0.42
5:B:240:ILE:CD1	5:B:377:PHE:HE2	2.32	0.42
5:B:129:PHE:HE2	5:B:166:PHE:HD1	1.67	0.42
7:D:63:LEU:O	7:D:129:LEU:HD11	2.20	0.42
4:A:1074:GLU:H	4:A:1075:PRO:HD2	1.82	0.42
4:A:806:ARG:HD3	5:B:728:ARG:HA	2.01	0.42
4:A:1111:MET:HE2	4:A:1330:ASN:OD1	2.19	0.42
6:C:138:GLU:OE1	6:C:138:GLU:N	2.48	0.42
4:A:932:GLU:O	4:A:935:GLN:HB3	2.20	0.42
4:A:391:LEU:O	4:A:394:ASN:HB2	2.20	0.42
10:G:79:PHE:HZ	10:G:106:MET:CE	2.33	0.42
4:A:573:SER:O	4:A:574:GLY:C	2.57	0.42
6:C:66:ARG:NH2	13:J:5:VAL:CG2	2.81	0.42
13:J:63:TYR:O	13:J:64:ASN:HB2	2.18	0.42
5:B:37:PHE:C	5:B:37:PHE:CD1	2.92	0.42
5:B:822:ASN:O	13:J:48:ARG:NH1	2.52	0.42
5:B:848:ARG:HD2	13:J:7:CYS:O	2.19	0.42
12:I:74:GLU:HA	12:I:80:SER:O	2.19	0.42
11:H:145:ARG:O	11:H:146:ARG:HB2	2.19	0.42
8:E:164:LEU:HD21	8:E:211:TYR:CG	2.54	0.42
4:A:452:LYS:HE3	5:B:1141:HIS:ND1	2.34	0.42
7:D:122:GLU:HA	7:D:125:SER:OG	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:I:56:ALA:O	12:I:57:GLY:O	2.37	0.42
4:A:1107:VAL:HG12	4:A:1107:VAL:O	2.19	0.42
7:D:47:LEU:CD1	10:G:3:PHE:CD2	3.02	0.42
4:A:302:THR:CG2	4:A:303:TYR:N	2.81	0.42
1:T:24:DT:OP1	5:B:857:ARG:NH2	2.52	0.42
4:A:47:ARG:HH12	4:A:254:GLU:HG2	1.84	0.42
5:B:180:TYR:N	5:B:180:TYR:CD1	2.86	0.42
6:C:160:LYS:O	6:C:161:LYS:O	2.37	0.42
11:H:55:LEU:HD22	11:H:144:ILE:HG21	1.98	0.42
5:B:742:GLU:O	5:B:743:ILE:C	2.58	0.42
4:A:899:VAL:CG2	4:A:1029:ARG:HG2	2.49	0.42
8:E:16:PHE:HZ	8:E:20:LYS:HE2	1.74	0.42
9:F:72:LYS:O	9:F:73:ALA:CB	2.67	0.42
11:H:81:PRO:HB3	11:H:82:PRO:HD2	1.99	0.42
14:K:63:VAL:O	14:K:63:VAL:CG2	2.63	0.42
5:B:199:MET:N	5:B:199:MET:SD	2.76	0.42
5:B:424:LEU:HD22	5:B:453:ILE:HD11	2.00	0.42
4:A:961:ARG:O	4:A:965:GLN:HG3	2.18	0.42
4:A:344:ARG:NE	5:B:1120:GLU:HB2	2.35	0.42
14:K:109:TRP:O	14:K:112:GLN:HB2	2.19	0.42
14:K:18:LYS:NZ	14:K:38:GLU:HG2	2.34	0.42
4:A:241:VAL:HA	4:A:242:PRO:HD2	1.83	0.42
4:A:84:ILE:HD11	4:A:270:LEU:HD13	2.02	0.42
5:B:806:THR:O	5:B:809:MET:HG3	2.19	0.42
4:A:857:ARG:CZ	9:F:139:PRO:HG3	2.49	0.42
4:A:534:LEU:HG	4:A:534:LEU:O	2.19	0.42
4:A:574:GLY:O	4:A:575:LYS:C	2.58	0.42
5:B:831:SER:HB3	5:B:994:TYR:OH	2.20	0.42
2:N:5:DT:H6	2:N:5:DT:H2'	1.53	0.42
6:C:133:ILE:CD1	6:C:237:SER:CA	2.94	0.42
4:A:664:THR:CG2	4:A:665:GLY:N	2.83	0.42
5:B:112:LEU:HD21	5:B:117:ALA:HB2	2.02	0.42
5:B:197:PHE:HZ	5:B:816:GLU:HG2	1.85	0.42
5:B:776:GLN:O	5:B:1095:LEU:HA	2.19	0.42
5:B:1110:PRO:O	5:B:1119:VAL:HG13	2.20	0.42
5:B:121:ASN:HD22	5:B:207:GLY:HA3	1.84	0.42
5:B:498:THR:HB	5:B:537:LYS:O	2.20	0.42
4:A:1444:MET:HE3	4:A:1444:MET:HB2	1.86	0.42
8:E:124:VAL:HG13	8:E:132:ILE:CD1	2.50	0.42
10:G:99:PHE:CZ	10:G:143:ILE:HD13	2.54	0.42
15:L:34:CYS:O	15:L:36:SER:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:763:GLN:O	5:B:764:SER:C	2.58	0.42
4:A:1036:ARG:HH11	4:A:1036:ARG:HG2	1.85	0.42
4:A:577:ILE:O	4:A:578:LEU:C	2.55	0.42
12:I:4:PHE:HD1	12:I:4:PHE:C	2.22	0.42
7:D:161:GLY:O	7:D:165:GLN:HG3	2.20	0.42
13:J:41:LEU:HD23	13:J:41:LEU:N	2.34	0.42
7:D:47:LEU:CD1	7:D:48:ILE:N	2.81	0.42
6:C:235:VAL:HG21	13:J:6:ARG:NH2	2.35	0.42
5:B:661:LEU:C	5:B:663:ALA:N	2.73	0.42
2:N:3:DA:H1'	2:N:4:DG:C8	2.55	0.42
4:A:793:SER:HB2	4:A:794:PRO:HD2	2.01	0.42
8:E:136:ASN:OD1	8:E:138:ALA:N	2.53	0.42
4:A:872:GLY:O	4:A:1058:VAL:HG23	2.20	0.42
6:C:259:LEU:HD12	6:C:259:LEU:HA	1.93	0.42
4:A:207:ILE:O	4:A:211:PHE:HD1	2.02	0.42
4:A:1197:LEU:HD11	4:A:1238:ILE:HD11	2.01	0.42
14:K:43:GLY:HA2	14:K:71:PHE:CZ	2.55	0.42
4:A:33:ALA:O	4:A:83:HIS:HD2	2.02	0.42
5:B:579:ARG:HD2	5:B:586:TRP:CZ2	2.55	0.42
6:C:44:LEU:HD21	6:C:159:ALA:CB	2.50	0.42
14:K:65:HIS:HD2	14:K:67:PHE:HB2	1.84	0.42
5:B:563:MET:HE2	5:B:587:HIS:O	2.19	0.42
4:A:1120:LEU:HD23	4:A:1124:HIS:O	2.19	0.42
4:A:341:MET:HE1	5:B:1135:ARG:NH1	2.34	0.42
13:J:47:ARG:HG2	13:J:47:ARG:NH1	2.31	0.42
4:A:901:LEU:HD13	4:A:919:ILE:HG23	2.02	0.42
4:A:1364:ASN:C	4:A:1364:ASN:ND2	2.73	0.42
9:F:72:LYS:O	9:F:73:ALA:HB3	2.20	0.42
4:A:683:ILE:HD13	4:A:801:GLU:HG3	2.02	0.42
6:C:104:PHE:HD2	6:C:105:GLY:H	1.67	0.42
12:I:13:MET:HE2	12:I:14:LEU:H	1.84	0.42
5:B:468:GLU:HB3	5:B:469:GLN:H	1.70	0.42
5:B:469:GLN:HB2	5:B:470:LYS:H	1.52	0.42
14:K:83:PRO:O	14:K:84:LYS:C	2.58	0.42
6:C:80:LEU:HD11	6:C:95:CYS:C	2.40	0.42
5:B:889:THR:HG22	5:B:891:ASP:H	1.84	0.42
5:B:903:VAL:CG1	5:B:904:ARG:N	2.83	0.42
5:B:169:ARG:HB2	5:B:454:THR:CG2	2.33	0.42
6:C:112:ASN:CB	6:C:114:TYR:CE1	3.02	0.42
13:J:3:VAL:CG2	13:J:18:TRP:CG	3.01	0.42
4:A:399:HIS:CG	4:A:400:PRO:N	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:234:ILE:HG21	5:B:237:VAL:CG2	2.50	0.42
11:H:113:ALA:HB1	11:H:125:LEU:O	2.20	0.42
4:A:525:GLN:HG3	5:B:836:GLU:HG2	2.02	0.42
6:C:248:ILE:HG13	6:C:248:ILE:H	1.65	0.42
9:F:97:ARG:HA	9:F:97:ARG:HD2	1.79	0.42
4:A:1007:ILE:C	4:A:1009:ASN:H	2.24	0.42
5:B:1216:LEU:O	5:B:1217:TYR:HD1	2.01	0.42
12:I:2:THR:HG22	12:I:2:THR:O	2.20	0.42
4:A:883:LEU:CD2	4:A:1021:LEU:HB2	2.50	0.42
4:A:1173:HIS:C	4:A:1174:PHE:CD1	2.93	0.42
6:C:80:LEU:HD11	6:C:95:CYS:CA	2.49	0.42
4:A:434:ARG:HE	4:A:437:MET:HG3	1.85	0.42
11:H:33:GLN:C	11:H:35:GLN:H	2.22	0.42
6:C:56:THR:HG22	6:C:58:LEU:HD23	2.01	0.42
4:A:91:PHE:HB3	4:A:96:ILE:HG12	2.02	0.42
8:E:22:MET:HB2	8:E:187:TYR:CE1	2.55	0.42
5:B:376:PHE:HE2	5:B:569:TYR:HD2	1.68	0.42
4:A:1120:LEU:O	4:A:1323:ASP:N	2.52	0.42
12:I:92:ARG:HB3	12:I:95:THR:OG1	2.19	0.42
4:A:407:ARG:HB3	4:A:430:TRP:NE1	2.34	0.42
4:A:418:SER:C	4:A:420:ARG:N	2.72	0.42
4:A:433:GLU:OE1	5:B:1108:ARG:NH1	2.53	0.42
5:B:956:THR:HG22	5:B:957:ASN:N	2.35	0.42
4:A:1346:ALA:CB	8:E:149:LEU:HD13	2.50	0.42
4:A:600:PRO:O	4:A:602:ASP:N	2.52	0.42
7:D:195:ILE:HG22	7:D:195:ILE:O	2.20	0.42
12:I:59:VAL:C	12:I:61:ASP:N	2.73	0.42
4:A:353:ILE:HG21	4:A:487:MET:HG3	2.01	0.41
4:A:463:ILE:HB	4:A:464:PRO:HD2	2.01	0.41
14:K:6:ARG:HD3	14:K:6:ARG:HA	1.94	0.41
4:A:1127:ASP:O	4:A:1130:GLN:HB3	2.20	0.41
5:B:39:ARG:NH2	5:B:665:GLU:CG	2.83	0.41
5:B:581:PHE:HA	5:B:585:VAL:O	2.19	0.41
4:A:49:LYS:HZ2	4:A:60:SER:HA	1.84	0.41
4:A:249:SER:O	4:A:250:ILE:CG1	2.60	0.41
5:B:603:LEU:HA	5:B:603:LEU:HD22	1.87	0.41
12:I:50:THR:HG22	12:I:51:ASN:N	2.35	0.41
4:A:590:ARG:HD2	4:A:605:MET:CB	2.50	0.41
7:D:16:LYS:O	7:D:16:LYS:HG2	2.20	0.41
6:C:187:LYS:HG3	6:C:219:PHE:CE1	2.54	0.41
9:F:79:ARG:HG3	9:F:144:GLU:OE1	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1385:THR:C	4:A:1387:HIS:N	2.72	0.41
5:B:1177:HIS:C	5:B:1179:GLN:H	2.24	0.41
14:K:68:PHE:N	14:K:68:PHE:CD2	2.85	0.41
4:A:639:PRO:HG2	4:A:640:GLN:H	1.84	0.41
4:A:59:GLY:HA2	4:A:67:CYS:SG	2.61	0.41
5:B:807:ARG:HG2	5:B:1045:SER:HG	1.83	0.41
4:A:886:ILE:CD1	4:A:943:LEU:HB3	2.42	0.41
5:B:558:LEU:C	5:B:560:GLU:N	2.74	0.41
8:E:192:ARG:HG3	8:E:192:ARG:NH1	2.34	0.41
6:C:236:GLY:C	6:C:238:ILE:N	2.71	0.41
5:B:1202:LEU:O	5:B:1203:LEU:C	2.57	0.41
4:A:730:GLY:C	4:A:732:LEU:N	2.73	0.41
4:A:606:LEU:O	4:A:613:ILE:HB	2.20	0.41
9:F:147:SER:OG	9:F:150:GLU:HG3	2.20	0.41
5:B:412:LEU:HB3	5:B:466:TRP:HZ2	1.85	0.41
5:B:286:PHE:O	5:B:289:LEU:HB2	2.20	0.41
5:B:331:LEU:HD12	5:B:331:LEU:N	2.35	0.41
4:A:715:GLU:O	4:A:717:ASN:N	2.53	0.41
10:G:79:PHE:CE2	10:G:105:PRO:HG2	2.53	0.41
4:A:858:ASN:ND2	4:A:860:LEU:N	2.59	0.41
8:E:62:ALA:HB3	8:E:78:LEU:HD22	2.01	0.41
4:A:1138:ILE:CG2	4:A:1316:VAL:HG13	2.51	0.41
5:B:542:MET:HE1	5:B:743:ILE:HG21	2.01	0.41
4:A:836:TYR:OH	4:A:1403:GLU:OE2	2.35	0.41
11:H:42:ILE:CG2	11:H:43:ASN:N	2.82	0.41
4:A:1283:VAL:CG1	4:A:1284:MET:N	2.77	0.41
8:E:117:THR:O	8:E:120:ALA:HB3	2.20	0.41
4:A:867:ILE:CG2	4:A:872:GLY:N	2.84	0.41
5:B:1097:HIS:H	5:B:1098:MET:CE	2.31	0.41
5:B:1119:VAL:HG23	5:B:1126:GLY:HA2	2.02	0.41
5:B:298:LEU:CD2	5:B:298:LEU:N	2.83	0.41
4:A:106:VAL:HA	4:A:114:LEU:HD21	2.03	0.41
15:L:28:LYS:HB2	15:L:39:SER:HB2	2.02	0.41
15:L:40:LEU:HA	15:L:40:LEU:HD23	1.91	0.41
6:C:104:PHE:HD2	6:C:105:GLY:N	2.19	0.41
10:G:96:GLN:HB3	10:G:121:PHE:CE2	2.55	0.41
4:A:1409:LEU:HA	4:A:1409:LEU:HD23	1.92	0.41
4:A:996:ASN:HA	4:A:998:LEU:HD12	2.02	0.41
6:C:58:LEU:N	6:C:58:LEU:CD2	2.83	0.41
5:B:1169:MET:CE	5:B:1204:PHE:HB2	2.50	0.41
10:G:111:THR:HB	10:G:114:LEU:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:635:ARG:HH11	4:A:635:ARG:HA	1.85	0.41
4:A:208:LEU:HD23	4:A:208:LEU:C	2.40	0.41
5:B:172:ILE:HG22	5:B:173:MET:H	1.84	0.41
6:C:145:CYS:HA	13:J:2:ILE:CD1	2.43	0.41
4:A:775:ILE:HG21	4:A:783:THR:HG23	2.02	0.41
5:B:405:ARG:NH2	5:B:632:ARG:HD3	2.35	0.41
4:A:6:TYR:CD1	4:A:7:SER:N	2.88	0.41
9:F:88:TYR:N	9:F:88:TYR:CD1	2.88	0.41
5:B:801:LYS:O	13:J:52:THR:CG2	2.60	0.41
5:B:824:ILE:HG12	13:J:48:ARG:NH1	2.36	0.41
4:A:567:LYS:CD	11:H:95:TYR:HA	2.50	0.41
4:A:711:ARG:HH11	12:I:95:THR:HB	1.85	0.41
5:B:604:ARG:O	5:B:607:GLY:N	2.54	0.41
6:C:242:GLN:C	6:C:244:VAL:H	2.24	0.41
6:C:243:VAL:HG12	6:C:243:VAL:O	2.20	0.41
5:B:1182:CYS:C	5:B:1183:LYS:HE3	2.41	0.41
4:A:1007:ILE:C	4:A:1009:ASN:N	2.73	0.41
15:L:65:VAL:HG23	15:L:65:VAL:O	2.21	0.41
10:G:26:LEU:O	10:G:27:LYS:C	2.59	0.41
4:A:996:ASN:HB3	4:A:1050:GLU:OE2	2.20	0.41
5:B:1147:LEU:O	5:B:1148:LYS:C	2.57	0.41
4:A:516:SER:O	4:A:517:ASN:C	2.58	0.41
4:A:986:ILE:O	4:A:990:VAL:HG23	2.19	0.41
11:H:100:THR:HG1	11:H:138:GLU:HG3	1.84	0.41
4:A:53:LEU:O	4:A:54:ASN:C	2.59	0.41
4:A:54:ASN:HA	4:A:58:LEU:HD12	2.03	0.41
4:A:472:LEU:O	4:A:475:THR:CB	2.69	0.41
5:B:211:VAL:HG23	5:B:483:LEU:HB2	2.02	0.41
6:C:175:ALA:HB2	13:J:10:CYS:HB2	2.03	0.41
14:K:31:VAL:O	14:K:74:ARG:HA	2.21	0.41
15:L:55:ILE:H	15:L:55:ILE:HG12	1.41	0.41
10:G:15:PRO:O	10:G:16:SER:C	2.59	0.41
8:E:24:LYS:HB2	8:E:24:LYS:HE3	1.77	0.41
5:B:401:PHE:HD2	5:B:521:LEU:HD12	1.85	0.41
4:A:683:ILE:O	4:A:686:ALA:N	2.53	0.41
10:G:145:VAL:CG1	10:G:146:LYS:H	2.32	0.41
6:C:131:HIS:HA	6:C:132:PRO:HD3	1.93	0.41
6:C:17:ASN:N	6:C:240:VAL:HG11	2.35	0.41
6:C:100:THR:CG2	6:C:101:LEU:N	2.83	0.41
5:B:1084:GLN:CD	5:B:1084:GLN:N	2.74	0.41
4:A:1362:TYR:HD1	4:A:1363:VAL:N	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:865:LYS:NZ	5:B:869:SER:HA	2.35	0.41
5:B:605:ARG:NH1	5:B:639:ILE:HD13	2.35	0.41
5:B:618:ASP:OD1	5:B:621:GLU:HB3	2.20	0.41
5:B:218:SER:O	5:B:219:ALA:O	2.38	0.41
5:B:726:ALA:O	5:B:727:LYS:O	2.39	0.41
10:G:126:ASN:HA	10:G:126:ASN:HD22	1.54	0.41
6:C:229:TYR:CD1	6:C:229:TYR:N	2.87	0.41
5:B:843:GLN:N	5:B:994:TYR:O	2.37	0.41
14:K:5:ASP:O	14:K:6:ARG:C	2.58	0.41
4:A:438:ASP:OD1	4:A:462:VAL:HG23	2.21	0.41
5:B:616:ILE:HG13	5:B:697:GLU:HA	2.02	0.41
4:A:1138:ILE:HG21	4:A:1316:VAL:HG13	2.03	0.41
5:B:34:ILE:O	5:B:35:SER:C	2.59	0.41
10:G:14:HIS:HD2	10:G:16:SER:CB	2.33	0.41
4:A:224:PHE:CD2	4:A:231:PRO:HG3	2.56	0.41
4:A:1212:VAL:O	4:A:1216:ILE:HG13	2.19	0.41
5:B:862:GLN:HG2	5:B:963:PHE:CD1	2.42	0.41
6:C:242:GLN:C	6:C:244:VAL:N	2.72	0.41
5:B:770:GLN:HG2	5:B:983:ARG:O	2.20	0.41
4:A:973:ILE:HD11	4:A:1038:THR:HG23	2.03	0.41
4:A:42:ASP:HB3	4:A:45:GLN:CA	2.51	0.41
6:C:254:LYS:HB3	6:C:254:LYS:HE2	1.89	0.41
4:A:971:PHE:N	4:A:971:PHE:CD1	2.88	0.41
4:A:243:PRO:CB	4:A:244:PRO:HD2	2.50	0.41
4:A:302:THR:HG22	4:A:303:TYR:N	2.35	0.41
4:A:52:GLY:O	4:A:56:PRO:HG2	2.21	0.41
4:A:53:LEU:CD2	4:A:54:ASN:N	2.64	0.41
1:T:19:DC:H2''	1:T:20:DC:H5'	2.02	0.41
6:C:167:HIS:HD2	6:C:168:ALA:H	1.69	0.41
4:A:1127:ASP:HB3	4:A:1130:GLN:HB2	1.95	0.41
4:A:845:LEU:O	4:A:846:GLU:C	2.59	0.41
4:A:1315:GLU:C	4:A:1317:MET:N	2.73	0.41
4:A:1365:TYR:O	4:A:1367:HIS:N	2.54	0.41
4:A:404:TYR:CD2	4:A:414:ASP:HA	2.56	0.41
8:E:124:VAL:CG1	8:E:132:ILE:HB	2.47	0.41
4:A:298:PHE:O	4:A:299:HIS:C	2.59	0.41
5:B:313:MET:O	5:B:316:PRO:HG2	2.20	0.41
5:B:466:TRP:HA	5:B:466:TRP:CE3	2.54	0.41
8:E:163:GLU:O	8:E:164:LEU:C	2.58	0.41
4:A:1385:THR:C	4:A:1387:HIS:H	2.23	0.41
15:L:43:THR:C	15:L:45:ALA:H	2.22	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:383:ASN:O	5:B:384:ARG:C	2.58	0.41
1:T:15:DT:H73	16:T:67:CPT:N1	2.35	0.41
10:G:1:MET:HG2	10:G:85:GLU:CD	2.41	0.41
4:A:860:LEU:CB	4:A:862:ASN:OD1	2.69	0.41
5:B:172:ILE:CG2	5:B:173:MET:H	2.34	0.41
4:A:360:GLU:O	4:A:361:LEU:C	2.57	0.41
4:A:361:LEU:CD1	4:A:474:VAL:HB	2.51	0.41
4:A:1423:GLY:O	4:A:1424:VAL:C	2.59	0.41
14:K:55:LYS:CB	14:K:81:TYR:CE1	3.04	0.41
4:A:316:GLN:HB2	4:A:322:VAL:HG23	2.02	0.41
6:C:179:GLU:CG	6:C:180:TYR:H	2.28	0.41
4:A:224:PHE:CD2	4:A:231:PRO:HD3	2.56	0.41
4:A:1364:ASN:O	4:A:1366:ARG:HG3	2.21	0.41
7:D:173:HIS:NE2	7:D:201:LYS:NZ	2.69	0.41
4:A:1409:LEU:O	4:A:1412:ALA:HB3	2.20	0.41
4:A:1273:LEU:CD1	4:A:1273:LEU:N	2.83	0.41
5:B:1079:LYS:N	6:C:27:LEU:HD21	2.36	0.41
7:D:138:ASN:C	7:D:140:ASP:N	2.74	0.41
4:A:1405:THR:HB	4:A:1406:VAL:H	1.58	0.41
11:H:118:PHE:O	11:H:120:GLY:N	2.53	0.41
4:A:58:LEU:HD13	4:A:243:PRO:HA	2.02	0.41
4:A:71:GLN:O	4:A:73:GLY:N	2.50	0.41
4:A:252:PHE:HB2	4:A:256:GLN:CD	2.40	0.41
5:B:830:TYR:O	5:B:831:SER:C	2.59	0.41
6:C:69:LEU:HD12	6:C:69:LEU:H	1.85	0.41
11:H:143:LEU:N	11:H:143:LEU:HD12	2.36	0.41
5:B:26:THR:O	5:B:29:ASP:HB2	2.21	0.41
5:B:1002:THR:O	5:B:1003:ALA:C	2.59	0.41
4:A:567:LYS:CB	4:A:568:PRO:HD2	2.50	0.41
4:A:322:VAL:HG12	4:A:322:VAL:O	2.21	0.41
7:D:53:SER:H	7:D:148:LEU:CD2	2.34	0.41
12:I:85:PHE:HD1	12:I:99:LEU:HD13	1.83	0.41
5:B:979:LYS:HG2	5:B:1095:LEU:CD1	2.50	0.41
5:B:1106:ARG:HG3	5:B:1107:ALA:N	2.35	0.41
5:B:334:ILE:O	5:B:334:ILE:HG22	2.21	0.41
8:E:124:VAL:N	8:E:125:PRO:HD2	2.35	0.41
4:A:1348:LEU:HG	4:A:1372:VAL:HG23	2.01	0.41
12:I:62:ILE:CG1	12:I:62:ILE:O	2.66	0.41
5:B:526:GLU:CG	5:B:538:ASN:HD22	2.31	0.41
8:E:157:SER:C	8:E:159:ASP:H	2.23	0.41
4:A:838:GLN:O	4:A:842:VAL:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:154:VAL:HG12	10:G:155:SER:N	2.36	0.41
4:A:43:GLU:O	4:A:44:THR:CB	2.68	0.41
4:A:42:ASP:HB3	4:A:45:GLN:N	2.33	0.41
5:B:431:TYR:CD2	5:B:447:ALA:HB2	2.56	0.41
4:A:1072:ILE:O	4:A:1075:PRO:HG2	2.21	0.41
5:B:729:ILE:HG22	5:B:729:ILE:O	2.21	0.41
4:A:512:VAL:O	4:A:512:VAL:HG12	2.21	0.41
4:A:935:GLN:O	4:A:938:LYS:N	2.54	0.41
14:K:68:PHE:HB3	14:K:70:ARG:HH11	1.84	0.41
8:E:102:GLU:C	8:E:104:ASN:N	2.71	0.41
7:D:192:LYS:HB3	7:D:192:LYS:HZ2	1.85	0.41
4:A:818:MET:HA	5:B:514:LEU:HB3	2.02	0.41
5:B:255:GLN:HB2	5:B:272:THR:HB	2.01	0.41
5:B:977:GLY:HA3	5:B:1099:VAL:CG2	2.50	0.41
5:B:806:THR:HG21	5:B:808:ALA:HB3	2.02	0.41
4:A:860:LEU:HB3	4:A:862:ASN:OD1	2.21	0.41
5:B:878:GLN:O	5:B:879:ARG:C	2.58	0.41
5:B:615:MET:O	5:B:697:GLU:HG3	2.20	0.41
4:A:1119:TYR:O	4:A:1120:LEU:O	2.39	0.41
10:G:22:MET:C	10:G:24:GLN:N	2.74	0.41
4:A:666:ILE:HD11	5:B:1086:PHE:HE1	1.86	0.41
5:B:170:LEU:HA	5:B:171:PRO:HD2	1.89	0.41
5:B:777:ALA:HA	5:B:1095:LEU:HA	2.02	0.41
4:A:412:ARG:NH2	5:B:1108:ARG:NH1	2.69	0.41
12:I:54:GLU:OE2	12:I:118:ARG:CZ	2.69	0.41
4:A:1443:VAL:C	4:A:1444:MET:HG3	2.40	0.41
5:B:329:THR:O	5:B:332:ASP:HB3	2.20	0.41
10:G:99:PHE:CD1	10:G:99:PHE:C	2.95	0.41
4:A:1347:ALA:O	4:A:1348:LEU:C	2.59	0.41
5:B:465:ASN:ND2	5:B:477:ALA:HB2	2.35	0.41
4:A:388:LEU:HD22	4:A:432:VAL:HB	2.02	0.41
8:E:55:ARG:O	8:E:57:MET:N	2.53	0.41
4:A:971:PHE:O	4:A:972:HIS:C	2.59	0.41
5:B:212:LEU:HD13	5:B:409:ALA:HA	2.03	0.41
5:B:895:ASP:C	5:B:897:GLY:H	2.24	0.41
5:B:877:PRO:C	5:B:878:GLN:HG3	2.42	0.40
6:C:167:HIS:CE1	15:L:70:ARG:HA	2.57	0.40
11:H:127:GLY:O	11:H:128:ASN:CB	2.69	0.40
11:H:5:LEU:N	11:H:60:ALA:HB2	2.37	0.40
1:T:11:DT:H1'	1:T:12:DA:H5'	2.02	0.40
4:A:901:LEU:HD22	4:A:919:ILE:HG22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:1001:PHE:HD2	6:C:34:ARG:NH2	2.17	0.40
4:A:1242:VAL:O	4:A:1243:VAL:HB	2.21	0.40
4:A:335:ARG:O	4:A:336:ILE:C	2.60	0.40
14:K:46:ILE:O	14:K:46:ILE:HG22	2.21	0.40
6:C:217:ASP:HA	6:C:218:PRO:HD3	1.89	0.40
6:C:186:LEU:HB3	6:C:188:HIS:CD2	2.56	0.40
5:B:258:LEU:O	5:B:258:LEU:CG	2.67	0.40
4:A:522:GLY:HA2	4:A:630:ILE:CD1	2.51	0.40
5:B:174:LEU:HD22	5:B:202:TYR:CE1	2.56	0.40
5:B:174:LEU:HD21	5:B:204:ILE:HD11	2.03	0.40
7:D:158:GLU:O	7:D:161:GLY:N	2.51	0.40
6:C:80:LEU:CD1	6:C:95:CYS:HA	2.51	0.40
13:J:59:LYS:H	13:J:59:LYS:HG2	1.72	0.40
10:G:79:PHE:CE2	10:G:105:PRO:CG	3.03	0.40
4:A:486:GLU:O	4:A:487:MET:HG2	2.21	0.40
5:B:552:MET:C	5:B:554:ILE:N	2.74	0.40
2:N:3:DA:C1'	2:N:4:DG:H5'	2.52	0.40
5:B:758:PHE:O	5:B:760:ASP:N	2.54	0.40
5:B:129:PHE:CE2	5:B:166:PHE:HD1	2.39	0.40
7:D:63:LEU:HA	7:D:63:LEU:HD22	1.66	0.40
4:A:781:ASP:O	4:A:782:ARG:HB3	2.21	0.40
4:A:42:ASP:HB3	4:A:45:GLN:HA	2.03	0.40
6:C:54:ASN:HB2	6:C:153:LEU:CD1	2.52	0.40
15:L:25:ALA:O	15:L:26:THR:CB	2.69	0.40
4:A:1237:ILE:HG22	4:A:1238:ILE:N	2.36	0.40
8:E:191:LYS:O	8:E:193:GLY:N	2.55	0.40
6:C:59:ALA:O	6:C:62:PHE:CB	2.69	0.40
13:J:1:MET:H2	13:J:57:ILE:H	1.65	0.40
5:B:616:ILE:CG1	5:B:697:GLU:HA	2.51	0.40
11:H:9:ILE:HA	11:H:55:LEU:O	2.21	0.40
4:A:18:GLN:H	5:B:1215:ARG:HB2	1.86	0.40
4:A:7:SER:CB	5:B:1193:GLN:NE2	2.83	0.40
5:B:33:VAL:O	5:B:36:ALA:HB3	2.22	0.40
4:A:1434:ALA:CB	4:A:1436:ILE:HD12	2.52	0.40
2:N:5:DT:H1'	2:N:6:DA:H5'	2.03	0.40
4:A:711:ARG:O	4:A:714:PHE:N	2.51	0.40
4:A:1317:MET:HE1	4:A:1338:VAL:HG11	2.02	0.40
4:A:219:PHE:CD2	4:A:231:PRO:HD2	2.56	0.40
5:B:858:SER:HA	5:B:966:VAL:O	2.22	0.40
9:F:77:ASP:O	9:F:79:ARG:N	2.54	0.40
5:B:610:ASN:C	5:B:612:GLU:H	2.25	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:325:ILE:HG22	5:B:1210:MET:HE1	2.02	0.40
4:A:935:GLN:O	4:A:936:LEU:C	2.59	0.40
6:C:52:GLU:HB3	6:C:154:LYS:HB2	2.03	0.40
7:D:29:LEU:N	7:D:29:LEU:HD23	2.35	0.40
4:A:964:ILE:O	4:A:967:ALA:N	2.55	0.40
6:C:204:SER:C	6:C:206:ASN:N	2.73	0.40
4:A:1215:ARG:HG2	4:A:1215:ARG:HH11	1.87	0.40
4:A:853:ASP:C	4:A:853:ASP:OD1	2.60	0.40
4:A:535:THR:CG2	4:A:575:LYS:HE2	2.50	0.40
5:B:839:MET:CE	5:B:1010:LEU:HD21	2.42	0.40
5:B:797:TYR:HE1	5:B:854:LEU:HD21	1.86	0.40
5:B:796:LEU:HD12	5:B:797:TYR:N	2.37	0.40
13:J:52:THR:HG22	13:J:52:THR:O	2.20	0.40
4:A:863:VAL:HG11	4:A:866:PHE:CE2	2.56	0.40
5:B:205:ILE:N	5:B:205:ILE:CD1	2.84	0.40
9:F:154:ASP:HB3	9:F:155:LEU:H	1.67	0.40
12:I:34:TYR:HE2	12:I:36:GLU:HB3	1.86	0.40
4:A:289:ILE:C	4:A:291:GLU:N	2.74	0.40
6:C:67:LEU:HD11	6:C:155:LEU:HD13	2.02	0.40
5:B:766:ARG:HD3	5:B:766:ARG:HA	1.91	0.40
10:G:119:LEU:HD13	10:G:132:SER:HB2	2.03	0.40
5:B:294:ASP:C	5:B:296:GLU:H	2.22	0.40
4:A:693:VAL:HA	4:A:696:GLU:HB3	2.03	0.40
5:B:118:ARG:HG2	5:B:204:ILE:HD13	2.03	0.40
5:B:895:ASP:C	5:B:897:GLY:N	2.74	0.40
7:D:159:THR:O	7:D:163:VAL:HG23	2.21	0.40
5:B:564:GLU:HA	5:B:565:PRO:HD2	1.93	0.40
5:B:1060:ARG:HA	5:B:1060:ARG:HD2	1.74	0.40
4:A:57:ARG:O	4:A:68:GLN:NE2	2.42	0.40
4:A:95:PHE:O	4:A:96:ILE:C	2.59	0.40
5:B:126:SER:HB3	5:B:172:ILE:CD1	2.51	0.40
4:A:534:LEU:CD1	4:A:541:ILE:HD11	2.51	0.40
4:A:463:ILE:HD13	4:A:469:ARG:HG3	2.00	0.40
6:C:62:PHE:O	6:C:65:HIS:HB3	2.22	0.40
6:C:165:LYS:O	14:K:6:ARG:NH1	2.53	0.40
4:A:783:THR:HG21	4:A:815:PHE:CE2	2.56	0.40
5:B:1163:CYS:HB3	5:B:1166:CYS:O	2.22	0.40
13:J:36:LEU:HD12	13:J:47:ARG:HH12	1.82	0.40
4:A:709:THR:HG22	4:A:711:ARG:N	2.18	0.40
4:A:1313:LEU:HD23	4:A:1338:VAL:CB	2.52	0.40
8:E:120:ALA:O	8:E:122:LYS:N	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:1110:PRO:HG2	5:B:1119:VAL:CG2	2.51	0.40
5:B:203:PHE:N	5:B:203:PHE:CD1	2.89	0.40
5:B:308:TRP:HA	5:B:311:LEU:HD12	2.03	0.40
4:A:1377:THR:O	4:A:1378:GLN:C	2.59	0.40
5:B:1035:ALA:HB1	5:B:1040:ASN:O	2.21	0.40
4:A:103:CYS:C	4:A:105:CYS:N	2.75	0.40
4:A:1121:GLU:O	4:A:1122:PRO:C	2.59	0.40
4:A:804:TYR:OH	5:B:763:GLN:HA	2.21	0.40
4:A:878:ILE:HG23	4:A:956:LEU:N	2.36	0.40
12:I:13:MET:HG3	12:I:14:LEU:N	2.37	0.40
4:A:551:TYR:CE2	14:K:62:LYS:HE2	2.57	0.40
5:B:889:THR:CG2	5:B:891:ASP:OD2	2.69	0.40
4:A:986:ILE:HG22	4:A:987:VAL:N	2.37	0.40
4:A:1215:ARG:HG2	4:A:1215:ARG:NH1	2.37	0.40
6:C:89:GLU:O	6:C:90:ASP:HB3	2.21	0.40
8:E:63:ASN:HA	8:E:64:PRO:HD3	1.78	0.40
4:A:431:LYS:HE3	4:A:431:LYS:HB2	1.95	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	
4	A	1406/1733 (81%)	988 (70%)	277 (20%)	141 (10%)	1	13
5	B	1090/1224 (89%)	754 (69%)	217 (20%)	119 (11%)	0	11
6	C	264/318 (83%)	181 (69%)	50 (19%)	33 (12%)	0	8
7	D	173/221 (78%)	125 (72%)	28 (16%)	20 (12%)	0	9
8	E	212/215 (99%)	157 (74%)	38 (18%)	17 (8%)	1	19
9	F	82/155 (53%)	62 (76%)	15 (18%)	5 (6%)	2	27
10	G	169/171 (99%)	131 (78%)	30 (18%)	8 (5%)	3	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	H	129/146 (88%)	90 (70%)	19 (15%)	20 (16%)	0	5
12	I	117/122 (96%)	84 (72%)	23 (20%)	10 (8%)	1	17
13	J	63/70 (90%)	36 (57%)	15 (24%)	12 (19%)	0	3
14	K	112/120 (93%)	86 (77%)	20 (18%)	6 (5%)	2	30
15	L	44/70 (63%)	17 (39%)	14 (32%)	13 (30%)	0	0
All	All	3861/4565 (85%)	2711 (70%)	746 (19%)	404 (10%)	1	11

All (404) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	42	ASP
4	A	44	THR
4	A	48	ALA
4	A	54	ASN
4	A	55	ASP
4	A	57	ARG
4	A	62	ASP
4	A	66	LYS
4	A	67	CYS
4	A	73	GLY
4	A	74	MET
4	A	93	VAL
4	A	154	SER
4	A	223	GLY
4	A	250	ILE
4	A	253	ASN
4	A	255	SER
4	A	286	HIS
4	A	311	GLN
4	A	312	PRO
4	A	318	SER
4	A	322	VAL
4	A	332	LYS
4	A	335	ARG
4	A	336	ILE
4	A	385	ILE
4	A	423	ASP
4	A	536	LEU
4	A	567	LYS
4	A	597	LEU

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Mol	Chain	Res	Type
4	A	626	ASN
4	A	780	VAL
4	A	789	LYS
4	A	968	GLN
4	A	1002	GLY
4	A	1036	ARG
4	A	1115	SER
4	A	1120	LEU
4	A	1122	PRO
4	A	1223	ASP
4	A	1314	SER
4	A	1365	TYR
4	A	1366	ARG
4	A	1378	GLN
4	A	1405	THR
5	B	21	GLU
5	B	45	SER
5	B	108	VAL
5	B	206	ASN
5	B	219	ALA
5	B	229	ALA
5	B	258	LEU
5	B	259	TYR
5	B	266	ALA
5	B	334	ILE
5	B	367	LEU
5	B	401	PHE
5	B	474	SER
5	B	509	ALA
5	B	643	ASP
5	B	709	ASP
5	B	727	LYS
5	B	731	VAL
5	B	751	VAL
5	B	764	SER
5	B	943	SER
5	B	951	GLN
5	B	958	GLN
5	B	1046	PRO
5	B	1069	PHE
5	B	1097	HIS
5	B	1100	ASP

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Mol	Chain	Res	Type
5	B	1108	ARG
5	B	1156	ASP
5	B	1157	ALA
5	B	1171	VAL
5	B	1175	LEU
5	B	1178	ASN
5	B	1181	GLU
5	B	1182	CYS
5	B	1183	LYS
5	B	1188	LYS
6	C	87	PHE
6	C	141	GLY
6	C	149	LYS
6	C	161	LYS
6	C	173	ALA
6	C	184	ASN
6	C	209	TYR
6	C	214	ASN
6	C	215	GLU
7	D	5	THR
7	D	8	PHE
7	D	19	GLU
7	D	20	GLU
7	D	21	GLU
7	D	52	LEU
7	D	131	GLU
7	D	192	LYS
7	D	199	ASN
8	E	44	ALA
8	E	130	ALA
8	E	192	ARG
8	E	206	GLY
10	G	62	LEU
10	G	63	PRO
10	G	118	ASP
10	G	139	ILE
11	H	108	SER
11	H	128	ASN
12	I	3	THR
12	I	9	ASP
12	I	47	GLU
13	J	2	ILE

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Mol	Chain	Res	Type
13	J	6	ARG
13	J	17	LYS
13	J	29	GLU
13	J	32	GLU
13	J	55	ASP
13	J	64	ASN
14	K	7	PHE
15	L	35	SER
15	L	50	ASP
15	L	53	HIS
15	L	60	ARG
4	A	58	LEU
4	A	59	GLY
4	A	69	THR
4	A	76	GLU
4	A	113	LEU
4	A	117	GLU
4	A	205	GLU
4	A	226	GLU
4	A	263	THR
4	A	283	GLY
4	A	410	GLY
4	A	465	TYR
4	A	517	ASN
4	A	543	LEU
4	A	601	LYS
4	A	609	ASP
4	A	619	LYS
4	A	661	GLY
4	A	666	ILE
4	A	716	ASP
4	A	731	ARG
4	A	775	ILE
4	A	847	ASP
4	A	875	ALA
4	A	986	ILE
4	A	1124	HIS
4	A	1212	VAL
4	A	1221	LYS
4	A	1255	GLU
5	B	58	THR
5	B	67	SER

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Mol	Chain	Res	Type
5	B	68	THR
5	B	260	GLY
5	B	282	ILE
5	B	328	GLU
5	B	369	GLY
5	B	394	ASP
5	B	450	ALA
5	B	467	GLY
5	B	470	LYS
5	B	477	ALA
5	B	591	ARG
5	B	605	ARG
5	B	613	VAL
5	B	712	PRO
5	B	792	MET
5	B	867	GLY
5	B	884	ARG
5	B	907	GLY
5	B	1003	ALA
5	B	1041	GLU
5	B	1103	ILE
5	B	1126	GLY
5	B	1131	GLY
5	B	1155	SER
5	B	1167	GLY
5	B	1186	ASP
6	C	78	GLU
6	C	84	ARG
6	C	108	GLU
6	C	110	THR
6	C	156	THR
6	C	175	ALA
6	C	216	GLY
6	C	231	ASN
7	D	9	GLN
7	D	53	SER
7	D	177	VAL
8	E	73	PRO
8	E	74	ASP
8	E	106	GLN
8	E	121	MET
8	E	174	GLN

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Mol	Chain	Res	Type
9	F	73	ALA
9	F	81	THR
9	F	154	ASP
10	G	167	TYR
11	H	59	ILE
11	H	62	SER
11	H	81	PRO
11	H	82	PRO
11	H	84	ALA
11	H	90	ALA
11	H	140	ALA
12	I	11	ASN
12	I	57	GLY
12	I	79	HIS
12	I	91	ARG
12	I	106	CYS
13	J	28	ASP
14	K	15	GLY
14	K	104	ASN
15	L	43	THR
15	L	54	ARG
4	A	4	GLN
4	A	232	GLU
4	A	298	PHE
4	A	321	PRO
4	A	331	GLY
4	A	399	HIS
4	A	418	SER
4	A	846	GLU
4	A	854	ASN
4	A	871	ASP
4	A	1016	THR
4	A	1324	PRO
4	A	1335	ILE
4	A	1377	THR
4	A	1393	ASN
4	A	1402	PHE
5	B	46	GLN
5	B	184	ALA
5	B	193	LYS
5	B	257	LYS
5	B	460	ALA

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Mol	Chain	Res	Type
5	B	559	SER
5	B	641	GLU
5	B	708	GLU
5	B	711	GLU
5	B	738	PHE
5	B	746	SER
5	B	754	SER
5	B	878	GLN
5	B	879	ARG
5	B	881	ASN
5	B	942	ARG
5	B	1016	ALA
5	B	1035	ALA
5	B	1143	ALA
6	C	90	ASP
6	C	153	LEU
6	C	212	PRO
6	C	213	PRO
6	C	240	VAL
7	D	6	SER
7	D	218	GLU
8	E	43	LYS
8	E	45	LYS
8	E	59	SER
8	E	103	LYS
8	E	115	ASN
9	F	112	GLU
10	G	35	GLU
11	H	32	THR
11	H	109	LYS
12	I	107	SER
13	J	27	GLU
14	K	111	LEU
15	L	44	ASP
15	L	55	ILE
15	L	59	ALA
4	A	45	GLN
4	A	70	CYS
4	A	128	ILE
4	A	169	ASN
4	A	219	PHE
4	A	400	PRO

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Mol	Chain	Res	Type
4	A	424	ILE
4	A	592	ASP
4	A	852	TYR
4	A	916	GLY
4	A	958	VAL
4	A	1126	ALA
4	A	1229	SER
4	A	1281	ARG
4	A	1302	PRO
4	A	1438	THR
5	B	65	GLU
5	B	171	PRO
5	B	333	PHE
5	B	365	THR
5	B	409	ALA
5	B	478	GLY
5	B	480	SER
5	B	869	SER
5	B	909	ASP
5	B	1017	ILE
6	C	60	ASP
6	C	132	PRO
6	C	167	HIS
6	C	208	GLU
6	C	217	ASP
7	D	13	ARG
8	E	76	GLY
10	G	154	VAL
11	H	17	PRO
11	H	60	ALA
11	H	77	ARG
11	H	92	ASP
11	H	139	ASN
12	I	95	THR
13	J	24	LEU
13	J	33	GLY
14	K	29	ASN
15	L	64	LEU
4	A	61	ILE
4	A	84	ILE
4	A	245	PRO
4	A	544	ASP

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Mol	Chain	Res	Type
4	A	591	PHE
4	A	599	SER
4	A	782	ARG
4	A	910	PRO
4	A	920	LEU
4	A	1114	PRO
4	A	1116	LEU
4	A	1128	GLN
4	A	1165	GLU
4	A	1242	VAL
4	A	1297	GLU
4	A	1300	LYS
5	B	24	PRO
5	B	28	GLU
5	B	114	PRO
5	B	115	GLN
5	B	262	GLU
5	B	295	GLY
5	B	309	GLN
5	B	346	GLU
5	B	362	PRO
5	B	421	PHE
5	B	436	VAL
5	B	551	PRO
5	B	565	PRO
5	B	978	ASP
5	B	1045	SER
6	C	142	VAL
6	C	148	ARG
7	D	15	LEU
7	D	31	GLN
7	D	174	PRO
8	E	104	ASN
9	F	104	ASN
11	H	52	GLN
14	K	4	PRO
15	L	40	LEU
4	A	5	GLN
4	A	111	GLY
4	A	419	LYS
4	A	492	PRO
4	A	598	LEU

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Mol	Chain	Res	Type
4	A	753	GLY
4	A	1071	SER
5	B	283	VAL
5	B	611	PRO
5	B	688	GLY
5	B	1011	ILE
6	C	195	GLN
7	D	16	LYS
11	H	12	VAL
11	H	83	GLN
15	L	26	THR
15	L	56	LEU
4	A	568	PRO
4	A	600	PRO
4	A	627	GLY
4	A	1341	ILE
5	B	575	PRO
7	D	202	ILE
10	G	20	PRO
4	A	244	PRO
4	A	1435	PRO
5	B	818	PRO
6	C	51	VAL
6	C	139	GLY
13	J	14	VAL
4	A	196	GLU
4	A	284	ALA
4	A	1031	VAL
4	A	1164	PRO
5	B	511	PRO
5	B	1214	PRO
6	C	6	PRO
8	E	38	PRO
4	A	357	PRO
4	A	765	VAL
5	B	658	ILE
5	B	901	PRO
11	H	44	VAL

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	
4	A	1239/1520 (82%)	1124 (91%)	115 (9%)	11	47
5	B	962/1061 (91%)	887 (92%)	75 (8%)	16	55
6	C	234/274 (85%)	211 (90%)	23 (10%)	10	44
7	D	159/200 (80%)	129 (81%)	30 (19%)	2	14
8	E	196/197 (100%)	190 (97%)	6 (3%)	47	80
9	F	74/137 (54%)	65 (88%)	9 (12%)	6	34
10	G	152/152 (100%)	139 (91%)	13 (9%)	13	51
11	H	117/128 (91%)	112 (96%)	5 (4%)	35	74
12	I	113/116 (97%)	104 (92%)	9 (8%)	15	54
13	J	60/65 (92%)	56 (93%)	4 (7%)	20	62
14	K	99/102 (97%)	89 (90%)	10 (10%)	9	43
15	L	40/57 (70%)	36 (90%)	4 (10%)	9	43
All	All	3445/4009 (86%)	3142 (91%)	303 (9%)	12	50

All (303) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	2	VAL
4	A	34	LYS
4	A	37	PHE
4	A	38	PRO
4	A	62	ASP
4	A	68	GLN
4	A	83	HIS
4	A	93	VAL
4	A	100	LYS
4	A	108	MET
4	A	122	MET
4	A	200	ARG
4	A	215	SER
4	A	221	SER

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Mol	Chain	Res	Type
4	A	270	LEU
4	A	302	THR
4	A	312	PRO
4	A	320	ARG
4	A	321	PRO
4	A	326	ARG
4	A	335	ARG
4	A	345	VAL
4	A	354	SER
4	A	381	THR
4	A	396	PRO
4	A	406	ILE
4	A	407	ARG
4	A	408	ASP
4	A	412	ARG
4	A	418	SER
4	A	442	VAL
4	A	443	LEU
4	A	445	ASN
4	A	449	SER
4	A	450	LEU
4	A	451	HIS
4	A	460	VAL
4	A	462	VAL
4	A	469	ARG
4	A	470	LEU
4	A	487	MET
4	A	493	GLN
4	A	503	GLN
4	A	512	VAL
4	A	515	GLN
4	A	518	LYS
4	A	560	ILE
4	A	562	THR
4	A	584	ASN
4	A	590	ARG
4	A	618	GLU
4	A	626	ASN
4	A	635	ARG
4	A	659	HIS
4	A	666	ILE
4	A	670	ILE

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Mol	Chain	Res	Type
4	A	692	ASP
4	A	711	ARG
4	A	727	ASP
4	A	739	ASP
4	A	768	GLN
4	A	774	ARG
4	A	779	PHE
4	A	821	ARG
4	A	834	THR
4	A	858	ASN
4	A	871	ASP
4	A	873	MET
4	A	903	ASN
4	A	907	THR
4	A	929	LEU
4	A	939	ASP
4	A	940	ARG
4	A	942	PHE
4	A	969	GLN
4	A	992	ASP
4	A	1001	ARG
4	A	1017	LEU
4	A	1029	ARG
4	A	1035	TYR
4	A	1037	LEU
4	A	1067	LEU
4	A	1110	ASN
4	A	1111	MET
4	A	1116	LEU
4	A	1120	LEU
4	A	1122	PRO
4	A	1127	ASP
4	A	1138	ILE
4	A	1146	VAL
4	A	1152	ILE
4	A	1155	ASP
4	A	1173	HIS
4	A	1187	GLN
4	A	1206	ASP
4	A	1240	CYS
4	A	1264	GLU
4	A	1271	ILE

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Mol	Chain	Res	Type
4	A	1291	VAL
4	A	1295	THR
4	A	1298	TYR
4	A	1329	THR
4	A	1332	PHE
4	A	1333	ILE
4	A	1359	ASP
4	A	1364	ASN
4	A	1372	VAL
4	A	1386	ARG
4	A	1389	PHE
4	A	1405	THR
4	A	1415	SER
4	A	1432	GLN
4	A	1442	ASP
4	A	1443	VAL
4	A	1445	ILE
5	B	30	SER
5	B	37	PHE
5	B	46	GLN
5	B	57	TYR
5	B	61	ASP
5	B	175	ARG
5	B	188	ASP
5	B	194	GLU
5	B	199	MET
5	B	217	ARG
5	B	223	VAL
5	B	250	PHE
5	B	261	ARG
5	B	268	THR
5	B	298	LEU
5	B	365	THR
5	B	371	GLU
5	B	393	LYS
5	B	399	ASP
5	B	401	PHE
5	B	427	ASP
5	B	429	PHE
5	B	463	THR
5	B	465	ASN
5	B	466	TRP

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Mol	Chain	Res	Type
5	B	485	ARG
5	B	498	THR
5	B	502	ILE
5	B	516	ASN
5	B	557	PHE
5	B	582	VAL
5	B	593	PRO
5	B	603	LEU
5	B	615	MET
5	B	628	THR
5	B	644	GLU
5	B	682	SER
5	B	724	ASP
5	B	737	THR
5	B	742	GLU
5	B	748	ILE
5	B	755	ILE
5	B	787	VAL
5	B	811	TYR
5	B	830	TYR
5	B	835	GLN
5	B	839	MET
5	B	878	GLN
5	B	894	ASP
5	B	901	PRO
5	B	909	ASP
5	B	939	THR
5	B	953	LEU
5	B	957	ASN
5	B	978	ASP
5	B	999	MET
5	B	1002	THR
5	B	1006	ILE
5	B	1022	THR
5	B	1047	PHE
5	B	1084	GLN
5	B	1087	PHE
5	B	1095	LEU
5	B	1099	VAL
5	B	1108	ARG
5	B	1112	GLN
5	B	1122	ARG

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Mol	Chain	Res	Type
5	B	1129	ARG
5	B	1138	MET
5	B	1159	ARG
5	B	1170	THR
5	B	1176	ASN
5	B	1183	LYS
5	B	1202	LEU
5	B	1216	LEU
6	C	22	LEU
6	C	35	ARG
6	C	56	THR
6	C	58	LEU
6	C	60	ASP
6	C	62	PHE
6	C	74	SER
6	C	77	ILE
6	C	89	GLU
6	C	91	HIS
6	C	104	PHE
6	C	128	ASN
6	C	129	ILE
6	C	140	ASN
6	C	147	LEU
6	C	163	ILE
6	C	166	GLU
6	C	193	TYR
6	C	209	TYR
6	C	214	ASN
6	C	240	VAL
6	C	251	LEU
6	C	266	ASP
7	D	5	THR
7	D	8	PHE
7	D	11	ARG
7	D	12	ARG
7	D	13	ARG
7	D	15	LEU
7	D	16	LYS
7	D	17	LYS
7	D	19	GLU
7	D	22	GLU
7	D	47	LEU

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Mol	Chain	Res	Type
7	D	50	LEU
7	D	63	LEU
7	D	70	PHE
7	D	126	ILE
7	D	137	ASN
7	D	139	LYS
7	D	148	LEU
7	D	149	THR
7	D	151	PHE
7	D	152	SER
7	D	170	THR
7	D	174	PRO
7	D	182	SER
7	D	187	THR
7	D	192	LYS
7	D	193	THR
7	D	202	ILE
7	D	206	GLU
7	D	221	TYR
8	E	60	PHE
8	E	74	ASP
8	E	104	ASN
8	E	114	ASN
8	E	132	ILE
8	E	153	HIS
9	F	79	ARG
9	F	81	THR
9	F	90	ARG
9	F	99	LEU
9	F	111	LEU
9	F	122	MET
9	F	143	PHE
9	F	148	VAL
9	F	153	VAL
10	G	1	MET
10	G	13	LEU
10	G	21	ARG
10	G	45	ILE
10	G	52	ASP
10	G	74	TYR
10	G	78	VAL
10	G	79	PHE

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Mol	Chain	Res	Type
10	G	80	LYS
10	G	87	VAL
10	G	88	ASP
10	G	126	ASN
10	G	171	ILE
11	H	86	ASP
11	H	95	TYR
11	H	102	TYR
11	H	130	ARG
11	H	134	ASN
12	I	4	PHE
12	I	9	ASP
12	I	15	TYR
12	I	34	TYR
12	I	75	CYS
12	I	85	PHE
12	I	86	PHE
12	I	100	PHE
12	I	101	PHE
13	J	16	ASP
13	J	44	TYR
13	J	46	CYS
13	J	48	ARG
14	K	1	MET
14	K	5	ASP
14	K	10	PHE
14	K	25	THR
14	K	41	THR
14	K	47	ARG
14	K	50	LEU
14	K	61	TYR
14	K	78	THR
14	K	114	LEU
15	L	27	LEU
15	L	54	ARG
15	L	55	ILE
15	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
4	A	54	ASN

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Mol	Chain	Res	Type
4	A	92	HIS
4	A	225	ASN
4	A	299	HIS
4	A	339	ASN
4	A	435	HIS
4	A	447	GLN
4	A	451	HIS
4	A	493	GLN
4	A	503	GLN
4	A	517	ASN
4	A	631	HIS
4	A	654	ASN
4	A	736	ASN
4	A	741	ASN
4	A	757	ASN
4	A	768	GLN
4	A	786	HIS
4	A	858	ASN
4	A	903	ASN
4	A	926	GLN
4	A	965	GLN
4	A	994	GLN
4	A	1106	ASN
4	A	1130	GLN
4	A	1140	HIS
4	A	1173	HIS
4	A	1364	ASN
5	B	121	ASN
5	B	178	ASN
5	B	215	GLN
5	B	236	HIS
5	B	350	GLN
5	B	363	HIS
5	B	366	GLN
5	B	465	ASN
5	B	484	ASN
5	B	513	GLN
5	B	515	HIS
5	B	516	ASN
5	B	518	HIS
5	B	538	ASN
5	B	734	HIS

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Mol	Chain	Res	Type
5	B	744	HIS
5	B	763	GLN
5	B	821	GLN
5	B	842	ASN
5	B	957	ASN
5	B	1015	HIS
5	B	1065	GLN
5	B	1076	HIS
5	B	1117	GLN
5	B	1161	HIS
5	B	1179	GLN
5	B	1193	GLN
5	B	1211	ASN
6	C	17	ASN
6	C	24	ASN
6	C	73	GLN
6	C	79	GLN
6	C	112	ASN
6	C	123	ASN
6	C	167	HIS
6	C	252	GLN
7	D	9	GLN
7	D	39	ASN
7	D	40	HIS
7	D	74	GLN
7	D	137	ASN
7	D	143	ASN
7	D	179	GLN
8	E	8	ASN
8	E	32	GLN
8	E	101	GLN
8	E	104	ASN
8	E	113	GLN
8	E	114	ASN
8	E	143	ASN
8	E	147	HIS
10	G	14	HIS
10	G	53	ASN
10	G	97	HIS
10	G	122	ASN
10	G	126	ASN
11	H	131	ASN

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Mol	Chain	Res	Type
11	H	137	GLN
12	I	12	ASN
12	I	60	GLN
12	I	89	GLN
12	I	90	GLN
13	J	64	ASN
14	K	44	ASN
14	K	65	HIS
14	K	76	GLN
14	K	89	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	P	9/10 (90%)	1 (11%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	P	3	U

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 9 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length

(or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
16	CPT	T	67	1	0,2,4	0.00	-	0,1,6	0.00	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
16	CPT	T	67	1	-	0/0/0/0	0/0/0/0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	T	67	CPT	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	T	17/17 (100%)	-0.39	0 100 100	110, 139, 169, 175	0
2	N	7/7 (100%)	0.40	0 100 100	148, 156, 169, 171	0
3	P	10/10 (100%)	-0.21	0 100 100	118, 128, 165, 172	0
4	A	1416/1733 (81%)	-0.29	8 (0%) 90 82	44, 103, 161, 199	0
5	B	1108/1224 (90%)	-0.23	14 (1%) 79 65	47, 116, 176, 199	0
6	C	266/318 (83%)	-0.37	0 100 100	64, 100, 144, 162	0
7	D	177/221 (80%)	-0.17	2 (1%) 82 69	70, 120, 177, 190	0
8	E	214/215 (99%)	-0.21	2 (0%) 85 74	79, 144, 185, 197	0
9	F	84/155 (54%)	-0.51	0 100 100	53, 81, 115, 132	0
10	G	171/171 (100%)	-0.28	0 100 100	82, 103, 141, 150	0
11	H	133/146 (91%)	0.18	3 (2%) 64 48	119, 149, 180, 188	0
12	I	119/122 (97%)	-0.08	2 (1%) 73 58	94, 150, 183, 199	0
13	J	65/70 (92%)	-0.57	0 100 100	71, 96, 131, 140	0
14	K	114/120 (95%)	-0.37	0 100 100	64, 101, 130, 149	0
15	L	46/70 (65%)	-0.09	0 100 100	96, 154, 172, 178	0
All	All	3947/4599 (85%)	-0.26	31 (0%) 87 77	44, 111, 175, 199	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	A	1176	LEU	10.4
4	A	1175	SER	5.1
5	B	471	LYS	4.8
4	A	1455	PRO	3.7
5	B	470	LYS	3.6
11	H	140	ALA	3.1
4	A	257	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
5	B	883	LEU	2.8
5	B	508	LEU	2.7
5	B	882	THR	2.7
4	A	255	SER	2.7
5	B	734	HIS	2.6
5	B	919	SER	2.6
5	B	133	LYS	2.5
8	E	51	GLY	2.4
12	I	119	THR	2.3
4	A	251	SER	2.3
11	H	107	VAL	2.3
7	D	8	PHE	2.2
12	I	120	GLN	2.2
4	A	1092	LYS	2.1
5	B	92	PHE	2.1
5	B	715	ALA	2.1
5	B	472	ALA	2.1
11	H	113	ALA	2.1
5	B	871	THR	2.1
5	B	732	SER	2.1
7	D	9	GLN	2.0
8	E	44	ALA	2.0
4	A	253	ASN	2.0
5	B	733	HIS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
17	ZN	B	1307	1/1	0.99	0.19	-0.08	71,71,71,71	0
17	ZN	J	101	1/1	0.99	0.22	-0.22	68,68,68,68	0
17	ZN	I	203	1/1	0.99	0.14	-0.24	113,113,113,113	0
17	ZN	C	319	1/1	0.99	0.14	-0.28	60,60,60,60	0
17	ZN	L	105	1/1	0.99	0.10	-1.15	127,127,127,127	0
17	ZN	I	204	1/1	0.99	0.07	-1.32	196,196,196,196	0
17	ZN	A	1735	1/1	1.00	0.12	-1.37	65,65,65,65	0
17	ZN	A	1734	1/1	0.98	0.09	-2.80	108,108,108,108	0
18	MG	A	1736	1/1	0.97	0.21	-	58,58,58,58	0
16	CPT	T	67	3/5	0.96	0.23	-	131,131,131,132	0

6.5 Other polymers [i](#)

There are no such residues in this entry.