



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:54 AM UTC

PDB ID : 2B8K / pdb_00002b8k
Title : 12-subunit RNA Polymerase II
Authors : Meyer, P.A.; Ye, P.; Zhang, M.; Suh, M.H.; Fu, J.
Deposited on : 2005-10-07
Resolution : 4.15 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

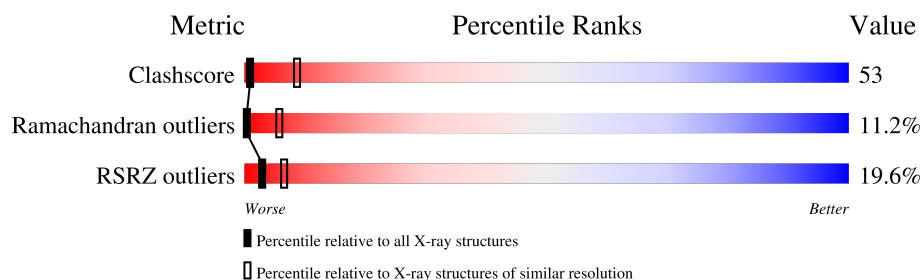
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.15 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))
Clashscore	190562	1019 (4.48-3.84)
Ramachandran outliers	187476	1035 (4.50-3.82)
RSRZ outliers	180081	1074 (4.50-3.82)

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

Mol	Chain	Length	Quality of chain
1	A	1733	
2	B	1224	
3	C	318	
4	D	221	
5	E	215	
6	F	155	
7	G	215	
8	H	146	

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Mol	Chain	Length	Quality of chain
9	I	122	37% 36% 49% 12% .
10	J	70	11% 20% 51% 21% 7%
11	K	120	13% 38% 52% . . .
12	L	70	31% 14% 33% 19% 34%

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 31040 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called DNA-directed RNA polymerase II largest subunit.

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

- Molecule 2 is a protein called DNA-directed RNA polymerase II 140 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1114	Total	C	N	O	S	0	0	0
			8800	5573	1540	1633	54			

- Molecule 3 is a protein called DNA-directed RNA polymerase II 45 kDa polypeptide.

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

- Molecule 4 is a protein called DNA-directed RNA polymerase II 32 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	182	Total	C	N	O	S	0	0	0
			1373	851	243	277	2			

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III 27 kDa polypeptide.

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

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III 23 kDa polypeptide.

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

- Molecule 7 is a protein called DNA-directed RNA polymerase II 19 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	171	Total	C	N	O	S	0	0	0
			1339	861	222	248	8			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	172	SER	-	expression tag	UNP P34087
G	173	HIS	-	expression tag	UNP P34087
G	174	GLU	-	expression tag	UNP P34087
G	175	LYS	-	expression tag	UNP P34087
G	176	ARG	-	expression tag	UNP P34087
G	177	ARG	-	expression tag	UNP P34087
G	178	TRP	-	expression tag	UNP P34087
G	179	LYS	-	expression tag	UNP P34087
G	180	LYS	-	expression tag	UNP P34087
G	181	ASN	-	expression tag	UNP P34087
G	182	PHE	-	expression tag	UNP P34087
G	183	ILE	-	expression tag	UNP P34087
G	184	ALA	-	expression tag	UNP P34087
G	185	VAL	-	expression tag	UNP P34087
G	186	SER	-	expression tag	UNP P34087
G	187	ALA	-	expression tag	UNP P34087
G	188	ALA	-	expression tag	UNP P34087
G	189	ASN	-	expression tag	UNP P34087
G	190	ARG	-	expression tag	UNP P34087
G	191	PHE	-	expression tag	UNP P34087
G	192	LYS	-	expression tag	UNP P34087
G	193	LYS	-	expression tag	UNP P34087
G	194	ILE	-	expression tag	UNP P34087
G	195	SER	-	expression tag	UNP P34087
G	196	SER	-	expression tag	UNP P34087
G	197	SER	-	expression tag	UNP P34087
G	198	GLY	-	expression tag	UNP P34087
G	199	ALA	-	expression tag	UNP P34087
G	200	LEU	-	expression tag	UNP P34087
G	201	ASP	-	expression tag	UNP P34087
G	202	TYR	-	expression tag	UNP P34087

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Chain	Residue	Modelled	Actual	Comment	Reference
G	203	ASP	-	expression tag	UNP P34087
G	204	ILE	-	expression tag	UNP P34087
G	205	PRO	-	expression tag	UNP P34087
G	206	THR	-	expression tag	UNP P34087
G	207	THR	-	expression tag	UNP P34087
G	208	ALA	-	expression tag	UNP P34087
G	209	SER	-	expression tag	UNP P34087
G	210	GLU	-	expression tag	UNP P34087
G	211	ASN	-	expression tag	UNP P34087
G	212	LEU	-	expression tag	UNP P34087
G	213	TYR	-	expression tag	UNP P34087
G	214	PHE	-	expression tag	UNP P34087
G	215	GLN	-	expression tag	UNP P34087

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III 14.5 kDa polypeptide.

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

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

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

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

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

- Molecule 11 is a protein called DNA-directed RNA polymerase II 13.6 kDa polypeptide.

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

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III 7.7 kDa polypeptide.

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

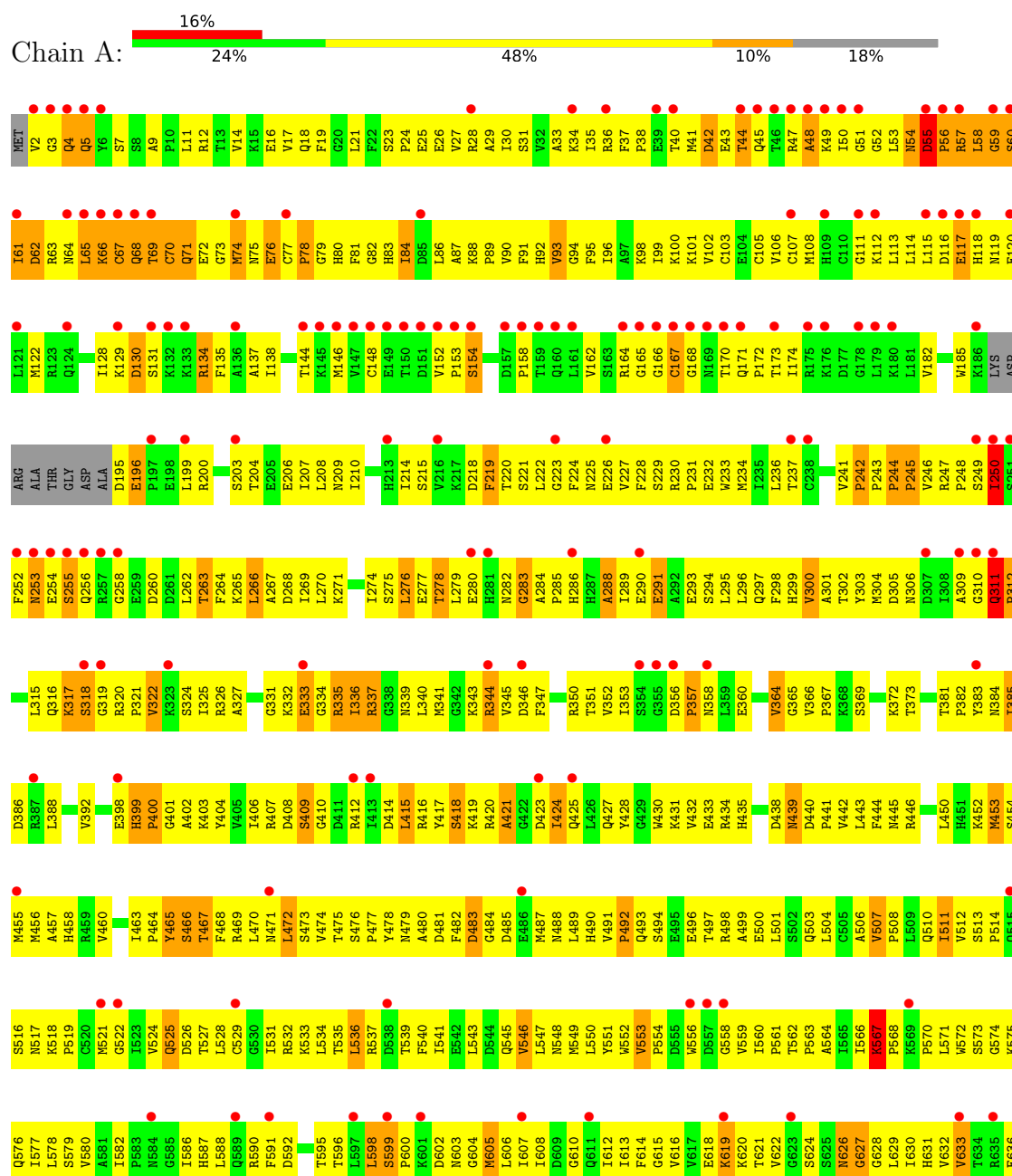
- Molecule 13 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

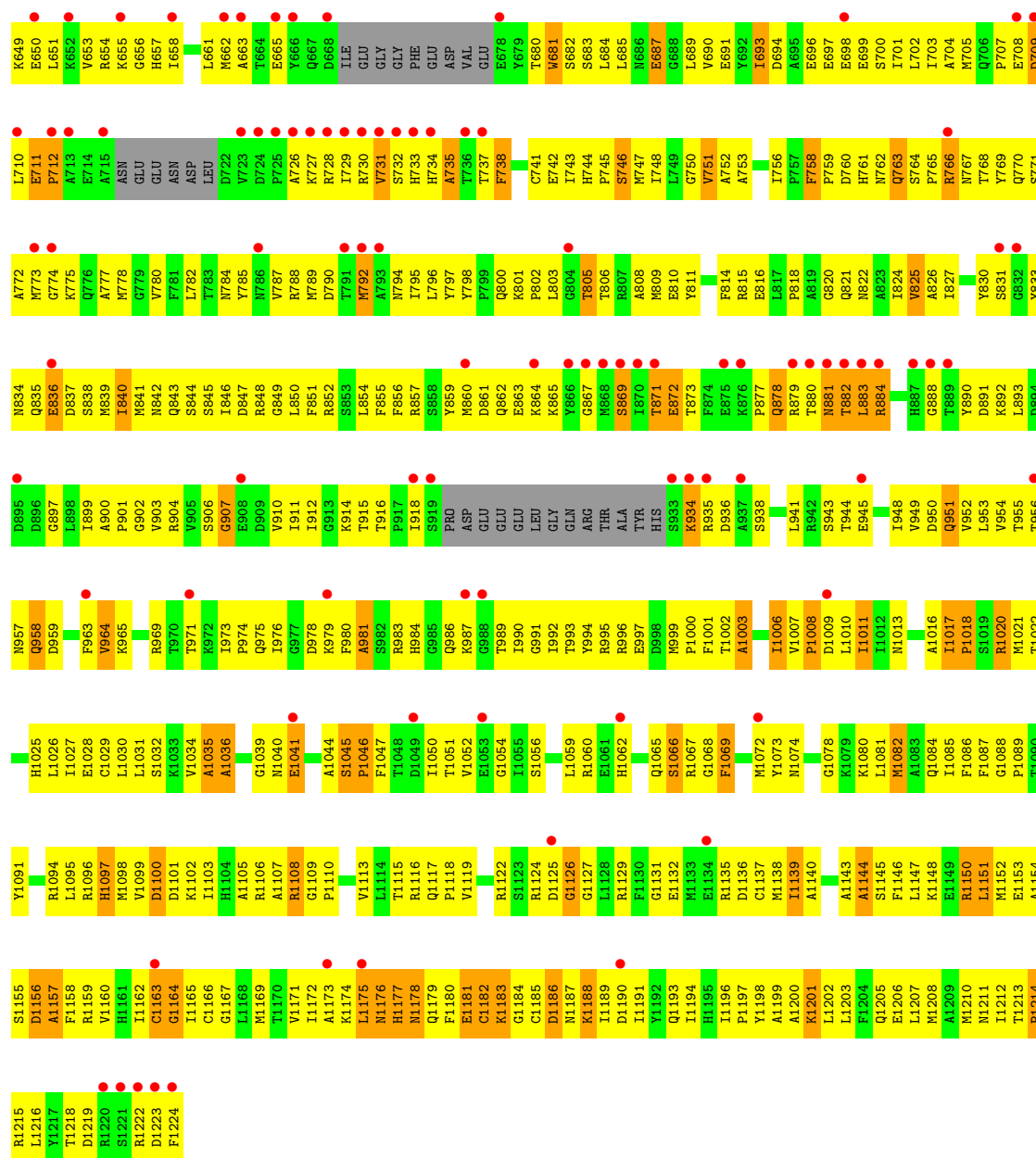
3 Residue-property plots

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

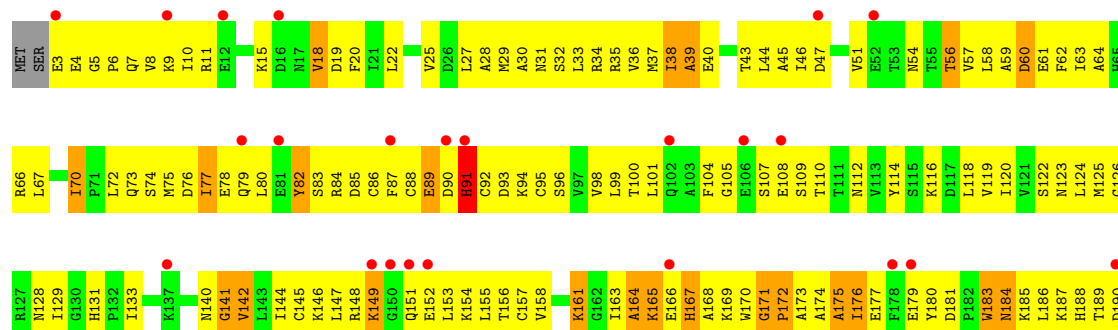
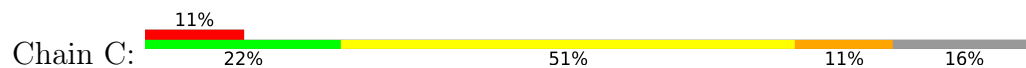
- Molecule 1: DNA-directed RNA polymerase II largest subunit

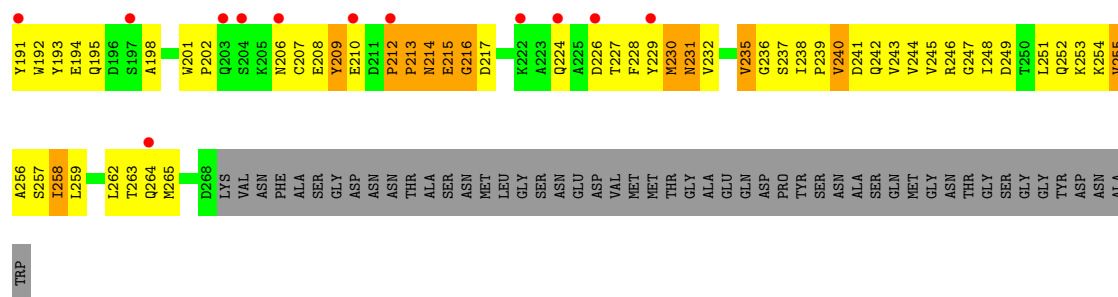


LEU	S1415	K1350	D1288	K1221	R1159	G1097	R1036	H972	T904	R840	A776	K708	K637
VAL	A1416	E1351	R1289	N1222	S1160	V1098	L1037	I973	D905	L841	F777	T709	
ASN	E1417	D1223	K1290	D1223	T1161	P1099	T1038	H906	H906	D974	F778	L710	L645
ALA	E1418	L1224	V1162	L1224	V1162	R1100	K1039	H975	T907	K843	F779	R711	F646
ASP	V1355		P1292	P1292	P1163	L1101	Q1040	T976	D908	L845	D781	S713	G647
LEU	D1420	V1226	P1293	V1226	P1164	K1102	A1041	K977	D909	L846	R782	S714	N648
ASP	C1421	I1227	P1294	I1227	E1165	E1103	F1042	P978	P910	E846	T783	F714	I649
VAL	R1422	W1228		W1228	D1166	I1104	D1043	S979	S911	D847	T784		Q650
LYS	G1423	S1229	E1297	S1229	E1167	L1105	M1044	S879	L912	D980	L784	V718	Q650
ASP	V1424	D1230	V1298	D1230	E1168	M1106	M1044	R981	L913	P785	V719	V719	K651
GLU	S1425	D1231	V1299	D1231	E1168	V1107	V1045	L981	E914	M849	H786	R720	V652
LEU	E1426	K1300						T982					V653
MET													N654
LEU													F655
PHE													
PRO	I1429	E1303	E1303	D1233	Q1171	A1108	N1048	I983	F918	Y852	S787	L722	
SER	L1430	V1304	V1304	E1234	L1172	K1109	K984	D853	D853	N854	F788	L722	L658
PRO	G1431	V1305	V1305	E1235	H1173	N1110	E1050	D985	I919	N854	K789	V725	L659
LEU	M1432	A1369	A1369	L1236	F1174	M1111	Q1052	I986	G921	T855	D791	A724	N660
VAL	Q1433	L1370	L1370	L1237	S1175	K1112	F1053	V987	D922	R857	D791	A725	
ASP	A1434	L1371	L1371	I1238	L1176	T1113	L1054	V990	L923	N858	P794	K728	G661
SER	P1435	V1372	T1308	C1240	ASP	S1115	R1055		K924	S859	E795	A729	F662
GLY	A1436	D1373	D1309	G1240	GLU	T1117	S1056		L925	L860	S796	G730	S663
ASN	G1437	V1374	G1310	R1241	GLU	L1118	V1057		Q926	L860	T797	R731	T664
ASP	T1438	M1375	V1312	V1242	ALA	Y1119	V1058		N996	N862	G798	L732	G665
ASP	G1439	L1376	L1313	V1243	GLU	Y1118	H1059		L928	N863	F799	A733	I666
ALA	A1440	T1377	S1314	ARG	GLN	L1120	P1060		L929	I864	V800	E734	G667
MET	F1441	Q1378	E1315	PRO	SER	E1121	Q1061			Q865	E801	V735	D668
ALA		G1379	V1316	LYS	PHE	F1222	E1062		E832	F866	N802	N736	T689
GLY		L1381	M1317	SER	ASP	G1123	M1063		Y933	S803	I867	L737	I670
GLY		L1382	T1318	LEU	ASP	H1124	G1002		K934	Y868	Y804	K738	A671
PHE		L1385	V1319	ALA	S1189	A1126	Q1003		Q835	G869	L805	D739	D672
THR		R1386	P1320	THR	P1190	D1127	L1006		L936	E870	G807	L740	G673
ALA	L1460	R1387	G1321	GLU	V1191	Q1128	I1006		V937	D871	N741	V747	P674
TYR	V1451	F1388	I1322	GLU	L1192	E1129	I1007		K838	G872	L808	V742	T675
GLY	K1452	F1389	P1323	A1264	L1193	Q1130	Q1008		D939	M873	H815	V743	T682
ALA	M1453	E1265	P1324	E1265	R1194	K1131	A874		R940	D874	H816	K744	I683
ALA	M1454	E1266	T1325	E1266	L1195	K1132	N1071		N818	A875	A817	S751	E685
ASP	P1455	D1267	R1326	D1267	E1196	L1133	G1073		F942	A876	Q819	G753	A696
ASP		D1267	I1327	D1267	L1197	I1134	E1074		L943	H877	G819	S754	K687
TYR		K1261	Y1328	K1261	L1198	R1135	P1075		F947	I878	G820	F755	K688
GLY		K1262	T1329	K1262		S1136	A1013		V948	K880	R621	V756	K689
GLY		E1263	M1330	E1263	A1201	A1137	T1077		D948	K881	H816	N757	V693
THR		E1264	S1331	E1264	M1202	I1138	T1078		G950	S882	N818	G762	T694
SER		T1265	F1332	T1265	N1203	E1139	M1079			L883	Q819	A763	K695
PRO		T1266	I1333	T1266	D1204	H1140	T1080		W854	D884	G820	C764	Q696
PHE		M1267	D1334	M1267	K1205	T1141	L1081			T885	G820	V765	A699
GLY		L1268	I1335	L1268	D1206	T1142	ASN		P957	I886	E822	G766	N700
TYR		E1269	E1337	E1269	L1207	L1143	THR			G887	G923	Q767	L701
GLY		T1272	V1338	T1272	T1208	T1147	PHE			G888	L824	Q768	
GLY		L1273	G1340	L1273	G1210	I1148	ALA		I960	F593	R825	Q768	A704
ALA		R1274	E1341	R1274	Q1211	A1149	GLY		R961	E894	D826	Q768	A705
VAL		G1275	V1212	G1275	V1212	S1150	VAL		R962	K895	T627	I774	A706
THR			G1213		G1213	E1151	ALA		I963	R896	A828	R774	H706
SER			E1214		E1214	I1152	ALA		I964	Y897	V829		G707
PRO			R1215		R1215	R1029	ALA		Q965	K830	C764		
GLY			L1216		L1216	R1030	SER		N966	R898	T631		
PHE			K1217		K1217	D1155	K1092		A967	D900	Y836		
GLY			T1218		T1218	P1156	V1094		Q968	L901	I837		
VAL			T1219		T1219	D1157	E1094		Q969	L902	T970		
SER			F1220		F1220	P1158	S1096			N903	R839		

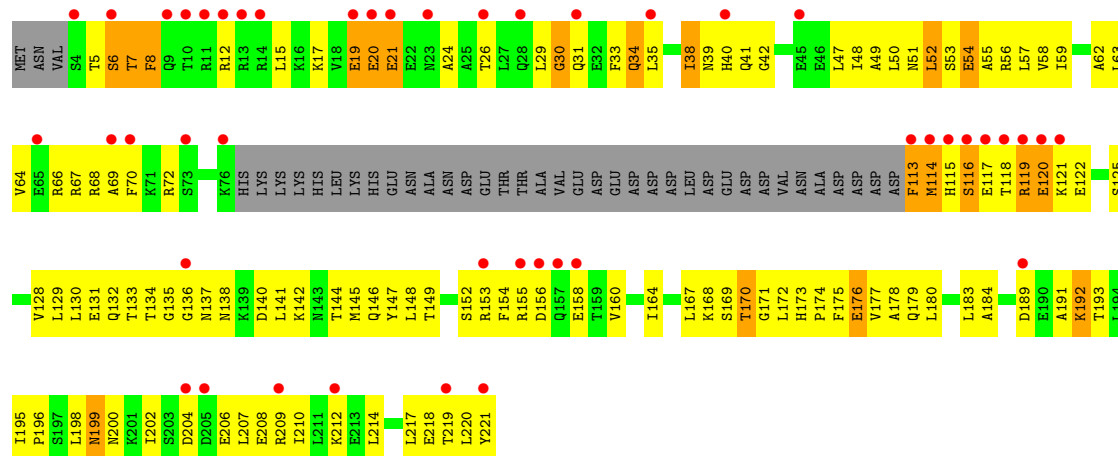


● Molecule 3: DNA-directed RNA polymerase II 45 kDa polypeptide

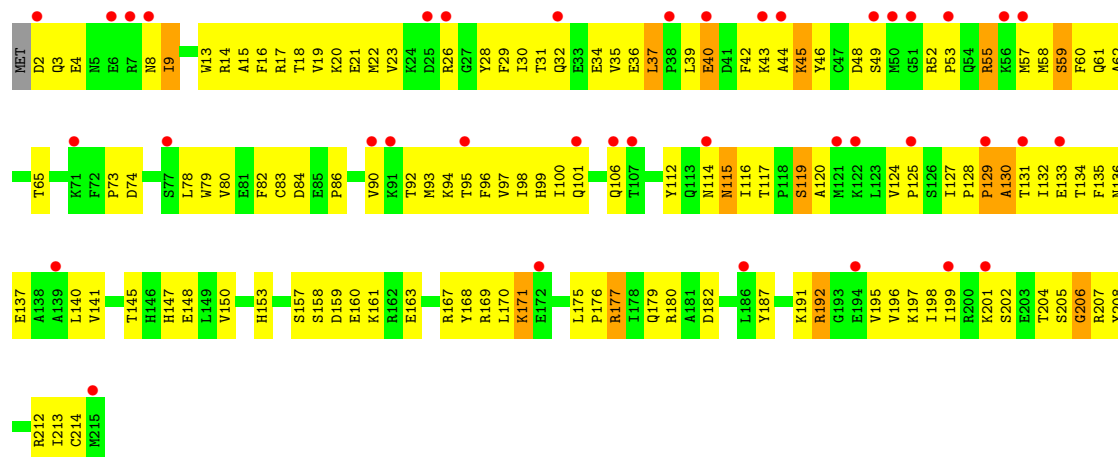




• Molecule 4: DNA-directed RNA polymerase II 32 kDa polypeptide

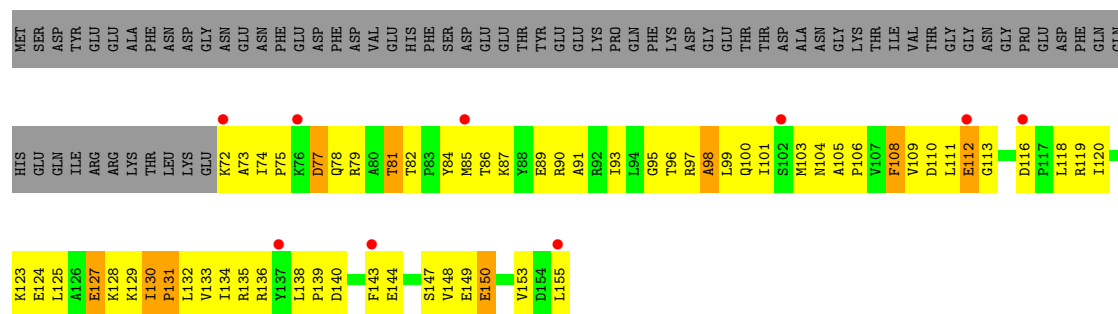


• Molecule 5: DNA-directed RNA polymerases I, II, and III 27 kDa polypeptide

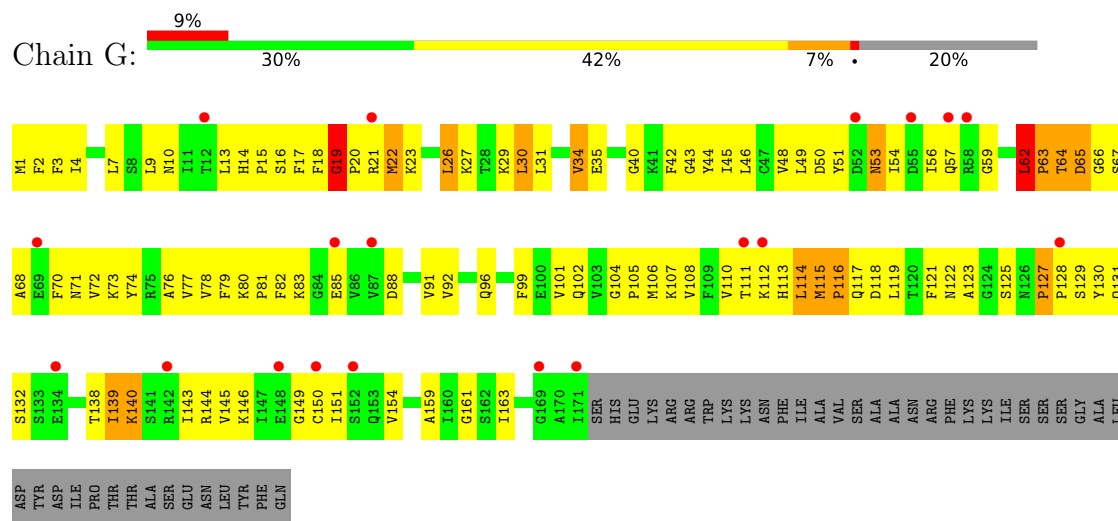


• Molecule 6: DNA-directed RNA polymerases I, II, and III 23 kDa polypeptide

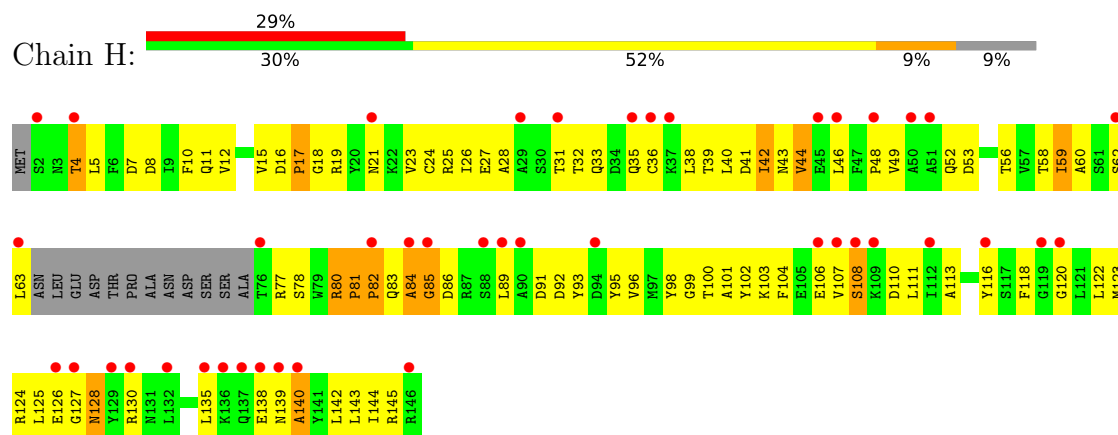




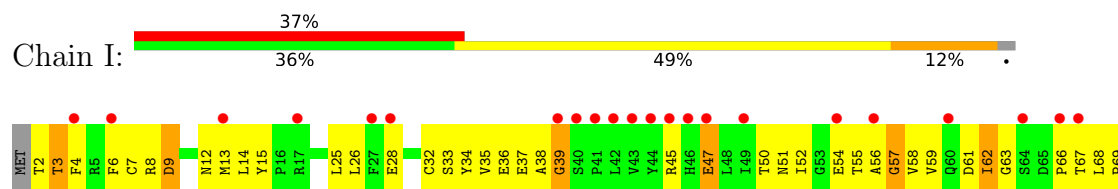
• Molecule 7: DNA-directed RNA polymerase II 19 kDa polypeptide

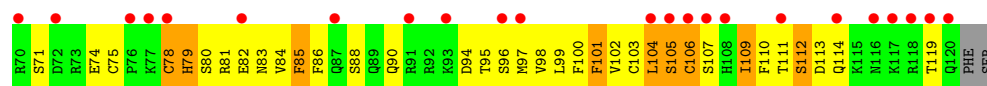


• Molecule 8: DNA-directed RNA polymerases I, II, and III 14.5 kDa polypeptide

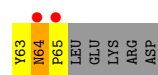
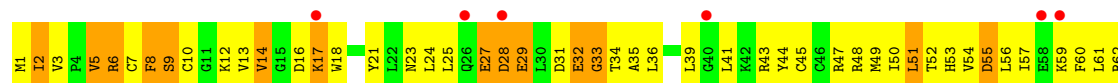
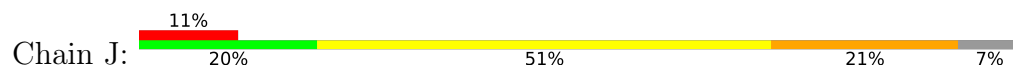


• Molecule 9: DNA-directed RNA polymerase II subunit 9

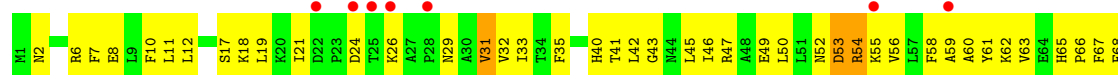




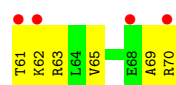
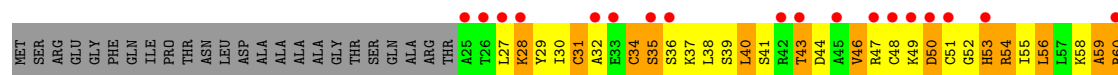
- Molecule 10: DNA-directed RNA polymerases I/II/III subunit 10



- Molecule 11: DNA-directed RNA polymerase II 13.6 kDa polypeptide



- Molecule 12: DNA-directed RNA polymerases I, II, and III 7.7 kDa polypeptide



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	220.69Å 394.33Å 281.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	158.11 – 4.15 158.11 – 4.15	Depositor EDS
% Data completeness (in resolution range)	(Not available) (158.11-4.15) 83.4 (158.11-4.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.20 (at 4.15Å)	Xtriage
Refinement program		Depositor
R, R_{free}	0.387 , (Not available) (Not available) , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	118.6	Xtriage
Anisotropy	0.584	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 176.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.023 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.023 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	31040	wwPDB-VP
Average B, all atoms (Å ²)	169.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.01% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.61	6/11339 (0.1%)	1.14	102/15334 (0.7%)
2	B	0.69	18/8971 (0.2%)	1.32	94/12103 (0.8%)
3	C	0.62	0/2133	1.13	14/2891 (0.5%)
4	D	0.64	2/1382 (0.1%)	1.25	18/1862 (1.0%)
5	E	0.48	0/1788	0.99	9/2406 (0.4%)
6	F	0.67	0/691	1.21	10/933 (1.1%)
7	G	0.61	0/1367	1.13	15/1844 (0.8%)
8	H	0.46	0/1086	1.02	7/1470 (0.5%)
9	I	0.77	1/989 (0.1%)	1.33	11/1331 (0.8%)
10	J	0.61	0/541	1.12	2/727 (0.3%)
11	K	0.58	1/938 (0.1%)	1.03	3/1267 (0.2%)
12	L	0.68	0/365	1.07	2/485 (0.4%)
All	All	0.63	28/31590 (0.1%)	1.19	287/42653 (0.7%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
2	B	1	10
3	C	0	1
9	I	0	1
All	All	1	14

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	I	39	GLY	C-N	-15.97	0.84	1.33
2	B	442	PHE	C-N	-14.02	1.14	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	446	LEU	N-CA	-12.46	1.30	1.46
2	B	439	ALA	C-N	12.33	1.51	1.33
2	B	444	MET	C-N	11.91	1.44	1.32
2	B	475	SER	C-N	10.57	1.48	1.33
2	B	405	ARG	C-N	-9.72	1.21	1.33
1	A	807	GLY	C-N	-9.56	1.20	1.33
1	A	1274	ARG	C-N	-8.52	1.21	1.32
2	B	476	ARG	C-N	-8.15	1.22	1.33
1	A	1141	THR	C-N	-8.01	1.21	1.33
4	D	119	ARG	CA-C	-7.37	1.43	1.52
2	B	445	LYS	N-CA	7.12	1.52	1.46
2	B	446	LEU	CA-CB	-6.54	1.42	1.53
2	B	466	TRP	C-N	-6.45	1.24	1.33
2	B	444	MET	CA-C	6.44	1.60	1.52
1	A	876	ALA	C-N	6.36	1.41	1.33
2	B	1150	ARG	C-N	6.26	1.42	1.34
2	B	439	ALA	N-CA	6.21	1.53	1.46
2	B	217	ARG	C-N	-5.83	1.25	1.33
2	B	471	LYS	C-N	-5.65	1.25	1.33
2	B	445	LYS	CA-C	5.49	1.56	1.53
1	A	999	VAL	CA-CB	-5.44	1.50	1.55
11	K	114	LEU	C-N	-5.35	1.25	1.33
2	B	474	SER	C-N	5.28	1.41	1.33
4	D	119	ARG	N-CA	-5.22	1.39	1.45
2	B	438	GLU	C-N	-5.13	1.26	1.33
1	A	250	ILE	CA-CB	5.09	1.61	1.54

All (287) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	475	SER	CB-CA-C	-49.05	12.82	110.42
9	I	39	GLY	O-C-N	-22.34	93.66	122.70
2	B	442	PHE	CA-C-N	20.73	161.13	121.54
2	B	442	PHE	C-N-CA	20.73	161.13	121.54
2	B	476	ARG	CA-C-N	-19.64	84.02	121.54
2	B	476	ARG	C-N-CA	-19.64	84.02	121.54
2	B	445	LYS	CA-C-N	-19.35	84.58	121.54
2	B	445	LYS	C-N-CA	-19.35	84.58	121.54
2	B	445	LYS	N-CA-C	18.16	126.19	108.75
2	B	471	LYS	CA-C-N	17.30	154.59	121.54
2	B	471	LYS	C-N-CA	17.30	154.59	121.54
2	B	439	ALA	N-CA-CB	-14.61	87.01	111.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1185	CYS	N-CA-C	-13.65	96.59	113.38
2	B	439	ALA	CA-C-O	-13.48	104.65	119.34
4	D	54	GLU	N-CA-C	-13.31	97.54	114.04
1	A	452	LYS	N-CA-C	-13.17	96.98	111.07
1	A	1274	ARG	CA-C-N	-11.99	104.54	121.56
1	A	1274	ARG	C-N-CA	-11.99	104.54	121.56
2	B	446	LEU	N-CA-CB	-11.71	90.70	110.49
2	B	444	MET	CA-C-N	11.37	135.29	123.13
2	B	444	MET	C-N-CA	11.37	135.29	123.13
2	B	438	GLU	CA-C-O	-10.85	102.36	120.80
4	D	26	THR	N-CA-C	-10.62	97.97	112.94
2	B	438	GLU	CB-CA-C	-10.23	90.65	110.10
1	A	344	ARG	N-CA-C	-9.77	97.36	110.55
2	B	475	SER	N-CA-CB	9.71	126.90	110.49
9	I	104	LEU	N-CA-C	-9.62	100.29	112.90
2	B	442	PHE	O-C-N	-9.47	109.99	122.59
1	A	1274	ARG	O-C-N	9.24	137.03	122.99
2	B	446	LEU	CA-CB-CG	-9.20	84.09	116.30
3	C	258	ILE	N-CA-C	-8.87	104.18	111.81
2	B	476	ARG	N-CA-C	8.77	129.48	110.80
1	A	567	LYS	CA-C-N	-8.69	108.98	119.84
1	A	567	LYS	C-N-CA	-8.69	108.98	119.84
4	D	120	GLU	N-CA-C	-8.64	92.39	110.80
6	F	127	GLU	N-CA-C	-8.62	102.08	112.59
7	G	62	LEU	CA-C-N	-8.51	109.20	119.84
7	G	62	LEU	C-N-CA	-8.51	109.20	119.84
4	D	171	GLY	N-CA-C	-8.46	103.64	115.32
3	C	39	ALA	N-CA-C	8.39	123.65	113.41
4	D	7	THR	N-CA-C	8.24	124.88	107.67
1	A	1261	LYS	N-CA-C	-8.22	105.25	114.62
2	B	405	ARG	O-C-N	-8.18	113.18	123.24
1	A	320	ARG	CA-C-N	8.01	129.86	119.84
1	A	320	ARG	C-N-CA	8.01	129.86	119.84
1	A	582	ILE	CA-C-N	7.97	127.90	119.85
1	A	582	ILE	C-N-CA	7.97	127.90	119.85
2	B	446	LEU	N-CA-C	-7.83	94.12	110.80
2	B	438	GLU	CA-C-N	-7.83	109.63	122.08
2	B	438	GLU	C-N-CA	-7.83	109.63	122.08
3	C	38	ILE	N-CA-C	7.81	117.92	110.42
1	A	982	THR	N-CA-C	-7.72	99.61	110.50
1	A	1141	THR	CA-C-N	-7.64	109.65	122.64
1	A	1141	THR	C-N-CA	-7.64	109.65	122.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	G	30	LEU	N-CA-C	-7.64	102.64	110.97
1	A	466	SER	N-CA-C	7.62	122.32	112.26
1	A	1262	LYS	N-CA-C	-7.62	102.98	111.82
1	A	928	LEU	N-CA-C	-7.58	102.71	110.97
1	A	288	ALA	N-CA-C	-7.56	101.94	113.89
2	B	395	GLN	N-CA-C	-7.54	100.58	110.53
1	A	1422	ARG	N-CA-C	-7.48	103.72	114.12
1	A	564	ALA	N-CA-C	-7.48	103.06	111.14
3	C	40	GLU	N-CA-C	7.36	121.57	112.59
8	H	80	ARG	CA-C-N	7.32	127.92	120.38
8	H	80	ARG	C-N-CA	7.32	127.92	120.38
2	B	1020	ARG	N-CA-C	-7.30	103.40	111.36
2	B	1052	VAL	N-CA-C	-7.29	103.75	110.82
2	B	476	ARG	O-C-N	-7.24	112.96	122.59
6	F	130	ILE	CA-C-N	7.17	128.81	119.84
6	F	130	ILE	C-N-CA	7.17	128.81	119.84
1	A	454	SER	N-CA-C	-7.14	104.44	113.01
1	A	1141	THR	O-C-N	7.14	132.54	123.12
1	A	440	ASP	N-CA-C	-7.13	100.66	109.65
7	G	22	MET	N-CA-C	-7.10	103.24	112.68
1	A	729	ALA	N-CA-C	-7.08	103.64	111.36
1	A	293	GLU	N-CA-C	-7.08	104.67	113.38
2	B	476	ARG	CA-C-O	-7.07	110.41	120.51
1	A	337	ARG	N-CA-C	7.05	119.05	111.36
5	E	171	LYS	N-CA-C	-7.03	99.52	110.42
4	D	72	ARG	N-CA-C	-7.02	104.68	113.18
1	A	266	LEU	N-CA-C	-6.99	102.88	111.40
2	B	681	TRP	N-CA-C	-6.98	100.88	111.56
4	D	55	ALA	N-CA-C	-6.97	103.12	111.69
2	B	882	THR	N-CA-C	6.95	119.49	111.02
2	B	296	GLU	N-CA-C	-6.91	103.52	112.23
1	A	539	THR	N-CA-C	6.90	119.37	108.67
4	D	38	ILE	N-CA-C	6.89	117.82	108.17
1	A	1403	GLU	N-CA-C	6.87	125.44	110.80
1	A	950	GLY	N-CA-C	-6.85	105.61	115.27
1	A	425	GLN	N-CA-C	-6.84	98.06	109.07
1	A	1291	VAL	CA-C-N	6.84	128.38	119.84
1	A	1291	VAL	C-N-CA	6.84	128.38	119.84
1	A	291	GLU	N-CA-C	-6.80	105.27	113.97
7	G	129	SER	N-CA-C	6.79	118.11	108.74
2	B	1151	LEU	N-CA-C	6.72	119.44	111.71
4	D	34	GLN	N-CA-C	-6.72	101.86	110.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1311	VAL	N-CA-C	6.71	118.79	107.18
1	A	738	LYS	N-CA-C	6.67	119.17	110.43
9	I	112	SER	N-CA-C	-6.66	103.47	112.26
6	F	77	ASP	N-CA-C	-6.61	100.19	110.17
2	B	66	ASP	N-CA-C	-6.61	104.53	112.59
2	B	208	SER	N-CA-C	6.61	119.81	110.50
1	A	472	LEU	N-CA-C	6.60	118.27	111.14
10	J	10	CYS	CA-CB-SG	6.59	129.56	114.40
1	A	30	ILE	N-CA-C	6.55	117.24	110.36
1	A	453	MET	N-CA-C	6.52	120.69	112.87
1	A	1436	ILE	O-C-N	-6.49	115.57	123.03
1	A	1138	ILE	CB-CA-C	-6.48	106.20	111.71
1	A	227	VAL	N-CA-C	6.48	117.38	111.81
2	B	872	GLU	N-CA-C	-6.48	102.17	110.53
2	B	445	LYS	CB-CA-C	-6.48	107.01	116.53
2	B	292	ILE	N-CA-C	6.47	122.85	108.88
2	B	1173	ALA	N-CA-C	6.46	118.45	109.15
2	B	535	LEU	N-CA-C	-6.45	105.54	113.41
1	A	1434	ALA	CA-C-N	6.42	127.87	119.84
1	A	1434	ALA	C-N-CA	6.42	127.87	119.84
4	D	173	HIS	CA-C-N	6.42	127.86	119.84
4	D	173	HIS	C-N-CA	6.42	127.86	119.84
1	A	1010	ALA	N-CA-C	-6.42	104.33	111.71
1	A	158	PRO	N-CA-C	-6.41	106.15	114.03
3	C	165	LYS	N-CA-C	-6.40	102.83	112.04
1	A	360	GLU	N-CA-C	-6.37	102.57	110.41
2	B	363	HIS	N-CA-C	-6.32	101.62	110.35
2	B	1009	ASP	N-CA-C	-6.32	106.11	113.88
1	A	242	PRO	CA-C-N	6.30	126.87	120.38
1	A	242	PRO	C-N-CA	6.30	126.87	120.38
1	A	311	GLN	N-CA-C	6.27	123.66	109.81
1	A	689	LYS	N-CA-C	-6.26	104.90	112.54
2	B	444	MET	N-CA-C	6.21	118.88	108.02
1	A	1413	GLY	N-CA-C	-6.20	106.97	114.66
5	E	9	ILE	N-CA-C	-6.20	105.78	111.67
4	D	8	PHE	N-CA-C	6.19	123.99	110.80
2	B	471	LYS	O-C-N	6.18	129.45	122.22
1	A	511	ILE	N-CA-C	6.15	117.64	110.62
1	A	998	LEU	N-CA-C	6.15	119.53	109.76
5	E	32	GLN	N-CA-C	-6.13	105.29	112.89
1	A	199	LEU	N-CA-C	6.12	118.26	108.41
12	L	31	CYS	N-CA-C	-6.05	100.88	109.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	398	GLU	N-CA-C	-6.04	102.98	110.41
9	I	109	ILE	N-CA-C	6.03	115.04	106.53
7	G	64	THR	N-CA-C	-6.02	105.85	113.43
8	H	4	THR	N-CA-C	-6.01	100.20	109.52
2	B	112	LEU	N-CA-C	6.01	119.37	110.48
2	B	475	SER	CA-C-N	6.00	133.01	121.54
2	B	475	SER	C-N-CA	6.00	133.01	121.54
2	B	555	ILE	N-CA-C	-5.99	105.01	110.82
1	A	1275	GLY	N-CA-C	5.98	118.69	110.56
1	A	1445	ILE	CB-CA-C	-5.97	104.18	111.88
1	A	56	PRO	N-CA-C	-5.94	100.23	112.47
2	B	1201	LYS	N-CA-C	-5.91	103.81	111.02
2	B	805	THR	N-CA-C	5.91	117.19	108.86
9	I	79	HIS	N-CA-C	5.89	119.77	112.47
1	A	415	LEU	N-CA-C	5.88	119.28	111.75
2	B	1177	HIS	N-CA-C	-5.88	106.34	112.93
1	A	424	ILE	N-CA-C	5.87	121.56	109.34
2	B	1078	GLY	N-CA-C	-5.86	106.90	115.63
2	B	687	GLU	N-CA-C	-5.85	104.81	112.41
9	I	81	ARG	N-CA-C	5.83	118.34	110.88
11	K	8	GLU	N-CA-C	-5.82	106.41	112.93
2	B	1163	CYS	N-CA-C	-5.81	100.23	109.59
2	B	471	LYS	CA-C-O	5.79	126.64	120.10
1	A	1021	LEU	N-CA-C	-5.79	104.88	111.07
4	D	170	THR	N-CA-C	5.79	117.67	111.36
1	A	562	THR	CA-C-N	5.78	127.07	119.84
1	A	562	THR	C-N-CA	5.78	127.07	119.84
10	J	5	VAL	N-CA-C	-5.78	102.13	109.58
2	B	1045	SER	CA-C-N	5.76	127.04	119.84
2	B	1045	SER	C-N-CA	5.76	127.04	119.84
9	I	105	SER	N-CA-C	5.75	120.07	112.25
4	D	113	PHE	CA-C-N	5.74	132.50	121.54
4	D	113	PHE	C-N-CA	5.74	132.50	121.54
1	A	663	SER	N-CA-C	5.74	115.41	107.73
5	E	177	ARG	N-CA-C	5.72	119.01	110.14
2	B	428	ILE	N-CA-C	-5.71	103.95	111.09
4	D	114	MET	N-CA-C	5.71	122.97	110.80
1	A	1098	VAL	CB-CA-C	-5.71	108.27	113.70
1	A	346	ASP	O-C-N	5.71	129.46	122.84
3	C	183	TRP	N-CA-C	-5.68	97.93	107.99
2	B	840	ILE	N-CA-C	-5.68	99.56	107.80
1	A	1444	MET	N-CA-C	5.66	118.29	109.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	173	THR	N-CA-C	-5.65	103.07	110.53
2	B	1129	ARG	N-CA-C	5.65	119.45	109.96
9	I	85	PHE	N-CA-C	5.64	118.77	110.59
1	A	683	ILE	N-CA-C	-5.64	105.35	110.82
2	B	934	LYS	N-CA-C	5.63	118.44	108.24
8	H	16	ASP	N-CA-C	5.61	119.42	107.91
5	E	65	THR	N-CA-C	-5.61	102.18	110.48
1	A	467	THR	N-CA-C	5.61	118.60	109.24
4	D	176	GLU	N-CA-C	-5.61	104.56	111.40
2	B	1164	GLY	N-CA-C	-5.60	107.98	115.32
6	F	105	ALA	N-CA-C	-5.60	101.99	110.39
6	F	120	ILE	N-CA-C	-5.59	105.08	110.72
7	G	2	PHE	N-CA-C	-5.59	102.62	110.50
2	B	558	LEU	N-CA-C	5.57	117.04	110.97
2	B	1036	ALA	N-CA-C	-5.55	105.63	112.90
2	B	763	GLN	N-CA-C	-5.55	101.83	110.10
1	A	513	SER	CA-C-N	5.54	125.24	119.64
1	A	513	SER	C-N-CA	5.54	125.24	119.64
2	B	609	ILE	N-CA-C	-5.54	99.77	107.80
3	C	96	SER	N-CA-C	5.54	117.49	109.07
1	A	710	LEU	N-CA-C	-5.53	105.35	111.71
2	B	378	LEU	N-CA-C	-5.53	105.16	112.34
1	A	637	LYS	N-CA-C	5.44	117.29	111.36
1	A	553	VAL	CA-C-N	5.44	125.11	119.56
1	A	553	VAL	C-N-CA	5.44	125.11	119.56
2	B	1139	ILE	N-CA-C	-5.43	105.24	110.72
1	A	778	GLY	N-CA-C	-5.41	105.85	112.77
5	E	119	SER	N-CA-C	-5.41	105.82	112.90
2	B	1213	THR	N-CA-C	5.39	117.24	109.04
8	H	42	ILE	N-CA-C	5.38	115.45	108.35
1	A	507	VAL	CB-CA-C	-5.38	108.59	113.70
8	H	85	GLY	N-CA-C	-5.37	108.44	114.40
2	B	213	ILE	N-CA-C	5.37	117.03	108.87
2	B	616	ILE	N-CA-C	5.36	115.84	108.12
7	G	65	ASP	N-CA-C	-5.35	102.25	109.95
11	K	31	VAL	N-CA-C	5.35	116.40	108.65
2	B	650	GLU	N-CA-C	5.34	116.64	108.52
4	D	119	ARG	CA-C-O	5.32	127.12	121.11
7	G	114	LEU	N-CA-C	-5.32	106.46	113.17
1	A	55	ASP	N-CA-C	5.32	121.57	109.81
2	B	1008	PRO	N-CA-C	5.31	119.04	111.13
7	G	140	LYS	N-CA-C	5.30	119.38	113.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	12	VAL	N-CA-C	5.30	115.22	108.12
1	A	999	VAL	N-CA-C	-5.29	106.51	111.48
6	F	153	VAL	N-CA-C	5.29	113.99	106.53
1	A	60	SER	N-CA-C	5.26	114.98	108.19
1	A	1299	VAL	N-CA-C	5.26	117.63	108.95
2	B	217	ARG	O-C-N	-5.26	117.43	123.42
2	B	1066	SER	N-CA-C	5.24	119.30	113.01
3	C	91	HIS	N-CA-C	5.24	121.96	110.80
6	F	112	GLU	N-CA-C	-5.23	106.15	113.37
7	G	40	GLY	N-CA-C	-5.23	108.18	114.66
1	A	67	CYS	N-CA-C	-5.22	99.67	110.80
9	I	101	PHE	CA-C-N	-5.22	115.93	123.03
9	I	101	PHE	C-N-CA	-5.22	115.93	123.03
1	A	1102	LYS	N-CA-C	-5.22	105.49	111.07
9	I	119	THR	N-CA-C	-5.21	107.30	113.97
1	A	229	SER	N-CA-C	5.20	115.90	107.32
2	B	628	THR	N-CA-C	-5.19	107.60	114.04
1	A	685	GLU	N-CA-C	-5.19	105.80	111.82
1	A	294	SER	N-CA-C	-5.18	105.32	111.69
11	K	19	LEU	N-CA-C	5.17	118.02	109.85
2	B	944	THR	N-CA-C	5.17	117.71	111.40
2	B	606	LYS	N-CA-C	-5.16	107.64	114.04
1	A	346	ASP	CA-C-N	-5.16	115.20	122.63
1	A	346	ASP	C-N-CA	-5.16	115.20	122.63
7	G	19	GLY	CA-C-N	5.16	126.28	119.84
7	G	19	GLY	C-N-CA	5.16	126.28	119.84
1	A	990	VAL	N-CA-C	-5.15	105.36	110.62
3	C	148	ARG	N-CA-C	5.15	121.77	110.80
1	A	1333	ILE	N-CA-C	-5.15	104.95	110.36
1	A	227	VAL	CB-CA-C	-5.14	105.64	111.55
2	B	964	VAL	N-CA-C	5.14	115.68	108.17
3	C	193	TYR	N-CA-C	5.13	115.06	108.34
3	C	38	ILE	CB-CA-C	-5.13	105.41	111.97
2	B	981	ALA	N-CA-C	5.12	116.31	108.52
6	F	108	PHE	N-CA-C	5.12	119.24	113.15
2	B	424	LEU	N-CA-C	-5.11	104.69	112.04
2	B	526	GLU	N-CA-C	5.10	116.97	107.99
2	B	1113	VAL	CB-CA-C	-5.10	106.40	111.30
2	B	825	VAL	N-CA-C	5.09	115.97	110.21
5	E	52	ARG	CA-C-N	5.09	125.25	119.90
5	E	52	ARG	C-N-CA	5.09	125.25	119.90
2	B	99	LYS	CA-C-N	5.09	126.20	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	99	LYS	C-N-CA	5.09	126.20	119.84
5	E	55	ARG	N-CA-C	5.09	116.52	111.07
2	B	774	GLY	N-CA-C	-5.08	108.77	114.40
2	B	871	THR	N-CA-C	5.07	117.71	109.24
2	B	361	LEU	CA-C-N	5.07	126.18	119.84
2	B	361	LEU	C-N-CA	5.07	126.18	119.84
3	C	235	VAL	N-CA-C	-5.07	106.74	111.45
1	A	222	LEU	N-CA-C	-5.06	102.27	110.32
1	A	1310	GLY	N-CA-C	-5.06	102.16	110.56
7	G	127	PRO	CA-C-N	5.06	125.06	119.90
7	G	127	PRO	C-N-CA	5.06	125.06	119.90
1	A	237	THR	N-CA-C	-5.06	108.85	114.62
2	B	277	LYS	N-CA-C	5.05	117.52	111.71
3	C	70	ILE	CA-C-N	5.05	124.96	119.76
3	C	70	ILE	C-N-CA	5.05	124.96	119.76
1	A	491	VAL	CA-C-N	5.04	126.14	119.84
1	A	491	VAL	C-N-CA	5.04	126.14	119.84
1	A	1391	ARG	N-CA-C	-5.04	108.17	114.56
6	F	98	ALA	N-CA-C	-5.02	105.50	110.97
2	B	693	ILE	N-CA-C	5.02	114.99	107.51
12	L	34	CYS	N-CA-C	-5.01	107.32	112.93
1	A	134	ARG	N-CA-C	-5.01	107.00	113.01
1	A	1399	ARG	N-CA-C	-5.01	106.43	112.54

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	475	SER	CA

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	303	TYR	Sidechain
1	A	807	GLY	Mainchain
2	B	217	ARG	Mainchain
2	B	405	ARG	Mainchain
2	B	438	GLU	Peptide
2	B	439	ALA	Peptide,Mainchain
2	B	442	PHE	Peptide
2	B	445	LYS	Peptide
2	B	474	SER	Peptide,Mainchain
2	B	475	SER	Mainchain

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Mol	Chain	Res	Type	Group
3	C	82	TYR	Sidechain
9	I	39	GLY	Mainchain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	11140	0	11219	1288	0
2	B	8800	0	8778	1032	0
3	C	2095	0	2053	255	0
4	D	1373	0	1312	154	0
5	E	1752	0	1776	160	0
6	F	679	0	701	97	0
7	G	1339	0	1357	153	0
8	H	1068	0	1040	109	0
9	I	971	0	929	101	0
10	J	532	0	542	103	0
11	K	920	0	929	92	0
12	L	363	0	387	47	0
13	A	2	0	0	0	0
13	B	1	0	0	0	0
13	C	1	0	0	0	0
13	I	2	0	0	0	0
13	J	1	0	0	0	0
13	L	1	0	0	0	0
All	All	31040	0	31023	3309	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 (3309) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:469:GLN:CA	2:B:474:SER:CB	1.80	1.51
4:D:119:ARG:N	4:D:121:LYS:HB2	1.46	1.30
4:D:113:PHE:CB	4:D:156:ASP:OD1	1.78	1.30

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:118:THR:HA	4:D:121:LYS:CB	1.64	1.27
2:B:435:THR:CG2	2:B:439:ALA:HB2	1.63	1.26
1:A:315:LEU:HD11	2:B:472:ALA:O	1.40	1.22
1:A:77:CYS:O	1:A:78:PRO:O	1.65	1.13
10:J:5:VAL:HG12	10:J:6:ARG:HG3	1.30	1.12
4:D:118:THR:HA	4:D:121:LYS:HB3	1.32	1.11
1:A:768:GLN:HG2	1:A:816:HIS:HA	1.22	1.09
7:G:138:THR:HG22	7:G:139:ILE:H	1.12	1.09
2:B:435:THR:HG21	2:B:439:ALA:CB	1.83	1.08
1:A:53:LEU:HD23	1:A:54:ASN:N	1.69	1.08
1:A:315:LEU:CD1	2:B:472:ALA:O	2.00	1.07
1:A:541:ILE:HD13	1:A:549:MET:HE1	1.33	1.07
2:B:273:LEU:HB2	2:B:276:ILE:HD12	1.37	1.07
4:D:40:HIS:HB3	7:G:73:LYS:NZ	1.70	1.07
2:B:469:GLN:N	2:B:474:SER:CB	2.18	1.06
1:A:798:GLY:HA2	1:A:815:PHE:CD1	1.92	1.04
4:D:118:THR:C	4:D:121:LYS:HB2	1.81	1.04
8:H:100:THR:HG23	8:H:138:GLU:HA	1.37	1.04
1:A:768:GLN:CG	1:A:816:HIS:HA	1.87	1.03
1:A:254:GLU:HB2	2:B:935:ARG:HH12	1.24	1.03
4:D:118:THR:CA	4:D:121:LYS:CB	2.37	1.03
4:D:48:ILE:HG21	7:G:4:ILE:HB	1.40	1.02
1:A:855:THR:HG21	1:A:857:ARG:HE	1.22	1.01
1:A:1161:THR:HG22	1:A:1163:ILE:H	1.23	1.01
6:F:93:ILE:HD11	6:F:134:ILE:HD11	1.42	1.01
4:D:118:THR:HA	4:D:121:LYS:HB2	1.41	1.01
4:D:118:THR:CA	4:D:121:LYS:HB2	1.91	1.00
7:G:15:PRO:HA	7:G:18:PHE:CD1	1.96	0.99
2:B:23:ALA:HB1	2:B:24:PRO:HD2	1.45	0.98
2:B:46:GLN:HG3	2:B:47:GLN:H	1.28	0.98
2:B:65:GLU:HG3	2:B:66:ASP:H	1.27	0.98
1:A:53:LEU:HD23	1:A:54:ASN:H	1.26	0.98
2:B:549:THR:HG22	2:B:550:ASP:H	1.24	0.98
1:A:779:PHE:HE1	1:A:785:PRO:HD3	1.28	0.97
2:B:806:THR:HG22	2:B:808:ALA:H	1.27	0.97
2:B:189:LEU:HA	2:B:192:LEU:HD12	1.45	0.97
7:G:7:LEU:HB2	7:G:74:TYR:CE2	2.00	0.96
4:D:117:GLU:H	4:D:155:ARG:HH12	1.07	0.96
2:B:800:GLN:HB3	10:J:52:THR:HG21	1.46	0.96
1:A:77:CYS:O	1:A:77:CYS:SG	2.24	0.95
1:A:754:SER:H	1:A:757:ASN:HD22	1.11	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:47:LEU:HD13	4:D:48:ILE:H	1.31	0.95
3:C:142:VAL:H	10:J:16:ASP:HB3	1.31	0.95
1:A:563:PRO:HG3	1:A:572:TRP:CZ2	2.00	0.94
1:A:1329:THR:HG22	1:A:1331:SER:H	1.30	0.94
3:C:166:GLU:HG3	11:K:10:PHE:HZ	1.31	0.94
1:A:963:ILE:HD11	1:A:1048:ASN:HB3	1.50	0.94
2:B:824:ILE:HG22	2:B:1087:PHE:HE2	1.31	0.93
9:I:85:PHE:H	9:I:85:PHE:HD2	1.06	0.93
11:K:47:ARG:HB3	11:K:47:ARG:HH11	1.32	0.93
1:A:84:ILE:HD11	1:A:270:LEU:HD13	1.51	0.93
4:D:119:ARG:H	4:D:121:LYS:HB2	1.25	0.92
1:A:768:GLN:HG2	1:A:816:HIS:CA	1.98	0.92
9:I:34:TYR:HD2	9:I:35:VAL:N	1.67	0.92
3:C:39:ALA:HA	3:C:164:ALA:HB3	1.47	0.92
1:A:709:THR:HG22	1:A:711:ARG:H	1.32	0.92
1:A:55:ASP:C	1:A:57:ARG:H	1.72	0.92
1:A:901:LEU:H	1:A:926:GLN:NE2	1.67	0.92
8:H:4:THR:HA	8:H:60:ALA:HB2	1.51	0.92
6:F:81:THR:HG21	6:F:136:ARG:HD3	1.52	0.92
2:B:999:MET:HA	2:B:999:MET:HE3	1.52	0.91
1:A:567:LYS:HB3	8:H:96:VAL:H	1.35	0.91
3:C:47:ASP:HA	12:L:69:ALA:HB3	1.50	0.90
4:D:134:THR:HG22	4:D:136:GLY:H	1.36	0.90
1:A:567:LYS:HD3	8:H:95:TYR:CD2	2.06	0.90
9:I:7:CYS:HB3	9:I:14:LEU:HD21	1.53	0.90
1:A:40:THR:HG22	1:A:41:MET:HG3	1.52	0.90
2:B:1224:PHE:HE2	5:E:171:LYS:HG3	1.37	0.90
1:A:399:HIS:HB3	1:A:400:PRO:HD3	1.51	0.90
2:B:1072:MET:HE3	2:B:1085:ILE:HB	1.54	0.90
4:D:118:THR:C	4:D:121:LYS:CB	2.46	0.89
1:A:1017:LEU:HB2	5:E:206:GLY:H	1.38	0.89
5:E:180:ARG:HH21	5:E:192:ARG:HB2	1.38	0.89
2:B:515:HIS:H	2:B:518:HIS:HD2	1.19	0.89
2:B:1072:MET:CE	2:B:1085:ILE:HB	2.03	0.89
2:B:212:LEU:HD23	2:B:480:SER:HB2	1.55	0.88
10:J:3:VAL:HG21	10:J:18:TRP:HB2	1.54	0.88
11:K:65:HIS:HD2	11:K:67:PHE:H	1.21	0.88
9:I:34:TYR:CD2	9:I:35:VAL:N	2.42	0.88
1:A:1242:VAL:HG12	1:A:1243:VAL:H	1.38	0.88
4:D:118:THR:CA	4:D:121:LYS:HB3	2.01	0.88
2:B:1201:LYS:HE2	2:B:1205:GLN:OE1	1.72	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:567:LYS:CG	1:A:568:PRO:HD2	2.04	0.87
3:C:44:LEU:HB2	3:C:77:ILE:HD11	1.53	0.87
3:C:57:VAL:HG11	10:J:60:PHE:HB3	1.57	0.87
2:B:98:THR:O	2:B:126:SER:HB2	1.73	0.87
1:A:524:VAL:HG12	1:A:525:GLN:H	1.37	0.87
10:J:16:ASP:OD1	10:J:17:LYS:HD2	1.75	0.87
2:B:806:THR:N	2:B:809:MET:HE3	1.89	0.86
2:B:800:GLN:HB3	10:J:52:THR:CG2	2.04	0.86
8:H:81:PRO:HB2	8:H:82:PRO:HD2	1.56	0.86
1:A:560:ILE:HG13	8:H:78:SER:HB2	1.56	0.86
3:C:33:LEU:HG	3:C:37:MET:HE2	1.56	0.86
1:A:254:GLU:HB2	2:B:935:ARG:NH1	1.90	0.86
2:B:168:GLY:H	2:B:450:ALA:HB1	1.38	0.86
4:D:40:HIS:HB3	7:G:73:LYS:HZ1	1.39	0.86
7:G:1:MET:SD	7:G:79:PHE:CD1	2.69	0.86
4:D:119:ARG:N	4:D:121:LYS:CB	2.36	0.86
4:D:144:THR:O	4:D:148:LEU:HB2	1.75	0.86
2:B:233:PRO:HG2	2:B:234:ILE:HD12	1.58	0.86
2:B:435:THR:HG21	2:B:439:ALA:HB2	0.88	0.86
1:A:1189:SER:O	1:A:1241:ARG:HD3	1.75	0.86
1:A:1094:VAL:HG13	1:A:1113:THR:HG21	1.58	0.85
3:C:164:ALA:HA	3:C:167:HIS:O	1.76	0.85
1:A:903:ASN:HD22	1:A:904:THR:N	1.73	0.85
9:I:75:CYS:SG	9:I:79:HIS:N	2.49	0.85
7:G:138:THR:HG22	7:G:139:ILE:N	1.92	0.85
10:J:57:ILE:HA	10:J:60:PHE:HD2	1.41	0.85
1:A:70:CYS:O	1:A:72:GLU:HG2	1.76	0.85
1:A:351:THR:HB	2:B:1103:ILE:HD12	1.59	0.85
2:B:465:ASN:HD22	2:B:465:ASN:N	1.73	0.85
1:A:56:PRO:O	1:A:57:ARG:HG3	1.75	0.84
1:A:1445:ILE:H	1:A:1445:ILE:HD12	1.39	0.84
2:B:363:HIS:O	2:B:364:ILE:HB	1.77	0.84
7:G:1:MET:SD	7:G:79:PHE:HD1	2.00	0.84
1:A:79:GLY:HA3	1:A:243:PRO:CG	2.08	0.84
2:B:483:LEU:HD11	2:B:491:THR:HG23	1.58	0.84
4:D:130:LEU:C	4:D:132:GLN:H	1.86	0.84
5:E:94:LYS:HE2	5:E:98:ILE:HD11	1.57	0.84
1:A:598:LEU:HA	8:H:122:LEU:HD13	1.59	0.84
3:C:20:PHE:HE1	3:C:22:LEU:HD12	1.42	0.84
5:E:19:VAL:O	5:E:23:VAL:HG23	1.78	0.84
2:B:705:MET:H	2:B:710:LEU:HD12	1.42	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:589:VAL:HG12	2:B:590:HIS:H	1.40	0.83
1:A:779:PHE:CE1	1:A:785:PRO:HD3	2.13	0.83
1:A:1444:MET:HE1	6:F:135:ARG:HB2	1.58	0.83
2:B:435:THR:CG2	2:B:439:ALA:CB	2.47	0.83
2:B:1096:ARG:O	2:B:1097:HIS:HB2	1.79	0.83
3:C:47:ASP:HA	12:L:69:ALA:CB	2.06	0.83
3:C:232:VAL:HG21	3:C:244:VAL:HG22	1.58	0.83
10:J:64:ASN:HB3	10:J:65:PRO:CD	2.08	0.83
2:B:882:THR:HG22	2:B:884:ARG:H	1.44	0.83
1:A:567:LYS:HG3	1:A:568:PRO:HD2	1.60	0.83
7:G:13:LEU:HD21	7:G:17:PHE:HB2	1.61	0.83
1:A:1332:PHE:H	1:A:1332:PHE:HD2	1.26	0.83
2:B:515:HIS:HD2	2:B:517:THR:H	1.27	0.83
2:B:37:PHE:CE1	2:B:41:LYS:HG3	2.13	0.83
2:B:955:THR:HG23	12:L:54:ARG:O	1.78	0.83
1:A:335:ARG:NH1	2:B:1202:LEU:HD13	1.94	0.83
1:A:1329:THR:HG22	1:A:1331:SER:N	1.93	0.82
2:B:401:PHE:HA	2:B:404:LYS:HG3	1.61	0.82
8:H:23:VAL:HG22	8:H:43:ASN:HA	1.61	0.82
7:G:34:VAL:HG12	7:G:45:ILE:HG21	1.61	0.82
2:B:577:ALA:HB1	2:B:589:VAL:HG11	1.62	0.82
2:B:842:ASN:ND2	2:B:845:SER:H	1.77	0.82
2:B:282:ILE:HD12	2:B:382:ILE:HD13	1.60	0.82
3:C:43:THR:HG22	3:C:44:LEU:N	1.93	0.82
3:C:66:ARG:NH2	10:J:5:VAL:HG23	1.94	0.82
7:G:128:PRO:O	7:G:138:THR:HG23	1.78	0.82
2:B:847:ASP:HB3	3:C:167:HIS:NE2	1.95	0.82
3:C:262:LEU:HD11	11:K:87:LEU:HD23	1.62	0.82
1:A:605:MET:HE2	1:A:607:ILE:HG13	1.61	0.82
3:C:98:VAL:C	3:C:99:LEU:HD23	2.05	0.82
3:C:213:PRO:O	3:C:214:ASN:HB2	1.76	0.82
1:A:438:ASP:O	1:A:439:ASN:HB2	1.78	0.81
5:E:22:MET:HE3	5:E:26:ARG:HE	1.45	0.81
1:A:534:LEU:O	1:A:574:GLY:HA3	1.81	0.81
2:B:1007:VAL:HG22	2:B:1008:PRO:HD2	1.61	0.81
8:H:40:LEU:HD13	8:H:123:MET:HB2	1.60	0.81
1:A:353:ILE:HD13	1:A:487:MET:HE2	1.63	0.81
1:A:1155:ASP:OD2	1:A:1161:THR:HG23	1.80	0.81
4:D:170:THR:CG2	4:D:172:LEU:HG	2.11	0.81
1:A:868:TYR:CE1	1:A:1064:VAL:HG11	2.15	0.81
4:D:118:THR:O	4:D:122:GLU:N	2.13	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:886:ILE:HD11	1:A:943:LEU:HB3	1.62	0.81
2:B:778:MET:HE1	2:B:1094:ARG:HD3	1.63	0.81
3:C:56:THR:HG22	3:C:57:VAL:H	1.46	0.81
1:A:254:GLU:HG3	2:B:935:ARG:HH22	1.45	0.81
1:A:249:SER:O	1:A:250:ILE:HG13	1.81	0.80
1:A:340:LEU:HD13	1:A:1429:ILE:HG23	1.61	0.80
2:B:1163:CYS:SG	2:B:1165:ILE:HB	2.21	0.80
1:A:93:VAL:HG13	1:A:301:ALA:HB1	1.62	0.80
2:B:918:ILE:HB	2:B:935:ARG:HD2	1.62	0.80
2:B:102:VAL:HG23	2:B:112:LEU:HB2	1.62	0.80
1:A:709:THR:HG23	9:I:94:ASP:HA	1.63	0.80
2:B:35:SER:HA	2:B:811:TYR:HE2	1.45	0.80
2:B:1162:ILE:HG22	2:B:1163:CYS:H	1.47	0.80
3:C:212:PRO:HB3	3:C:213:PRO:HD2	1.63	0.80
1:A:741:ASN:HD22	1:A:744:LYS:H	1.26	0.80
1:A:1118:VAL:HG12	1:A:1327:ILE:HG13	1.63	0.79
1:A:356:ASP:HB2	1:A:469:ARG:NH1	1.97	0.79
1:A:670:ILE:HG23	1:A:805:LEU:HD21	1.63	0.79
2:B:25:ILE:HD11	2:B:653:VAL:O	1.82	0.79
8:H:42:ILE:HG23	8:H:95:TYR:HE1	1.47	0.79
3:C:22:LEU:HD13	3:C:230:MET:HE3	1.64	0.79
10:J:14:VAL:CG1	10:J:50:ILE:HD11	2.12	0.79
8:H:102:TYR:OH	8:H:122:LEU:HD22	1.82	0.79
11:K:113:THR:O	11:K:114:LEU:HB2	1.81	0.79
4:D:153:ARG:NH2	4:D:184:ALA:HA	1.98	0.79
1:A:67:CYS:O	1:A:70:CYS:HB3	1.82	0.79
1:A:285:PRO:HG2	1:A:288:ALA:HB3	1.64	0.79
1:A:1422:ARG:HH22	2:B:1224:PHE:C	1.90	0.79
2:B:1065:GLN:HE21	2:B:1067:ARG:H	1.29	0.79
10:J:64:ASN:HB3	10:J:65:PRO:HD3	1.64	0.79
1:A:503:GLN:HE21	6:F:90:ARG:HH21	1.28	0.79
5:E:135:PHE:HD2	5:E:140:LEU:HD21	1.45	0.79
2:B:611:PRO:HB3	2:B:685:LEU:HD11	1.64	0.78
5:E:29:PHE:O	5:E:30:ILE:HG13	1.82	0.78
1:A:858:ASN:ND2	1:A:860:LEU:H	1.81	0.78
1:A:335:ARG:HA	1:A:339:ASN:HB2	1.64	0.78
1:A:1329:THR:H	1:A:1335:ILE:HD11	1.49	0.78
3:C:32:SER:O	3:C:36:VAL:HG23	1.82	0.78
2:B:120:ARG:HG2	2:B:955:THR:HG21	1.65	0.78
7:G:23:LYS:HG3	7:G:56:ILE:HD11	1.64	0.78
11:K:45:LEU:HG	11:K:94:ILE:HD13	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:34:TYR:HE2	9:I:36:GLU:HB3	1.49	0.78
1:A:76:GLU:HG3	1:A:76:GLU:O	1.81	0.78
1:A:1336:MET:HE3	1:A:1381:LEU:HG	1.65	0.78
2:B:361:LEU:HD21	2:B:377:PHE:CD2	2.19	0.78
1:A:1341:ILE:HG23	1:A:1342:GLU:N	1.98	0.77
2:B:200:GLY:HA2	2:B:202:TYR:CE2	2.19	0.77
1:A:388:LEU:O	1:A:392:VAL:HG23	1.85	0.77
1:A:1341:ILE:HD12	1:A:1379:GLY:O	1.85	0.77
2:B:613:VAL:HG13	2:B:627:PHE:O	1.85	0.77
1:A:340:LEU:HD21	2:B:1200:ALA:N	1.99	0.77
2:B:778:MET:HE2	2:B:1094:ARG:HG2	1.67	0.77
2:B:579:ARG:HB2	2:B:586:TRP:NE1	2.00	0.77
1:A:1116:LEU:N	1:A:1308:THR:HG22	2.00	0.77
2:B:37:PHE:CD1	2:B:41:LYS:HG3	2.20	0.77
2:B:879:ARG:HH11	2:B:883:LEU:HD22	1.50	0.77
5:E:117:THR:HG22	5:E:119:SER:H	1.50	0.77
1:A:855:THR:HG21	1:A:857:ARG:NE	1.97	0.77
1:A:855:THR:HG23	1:A:857:ARG:HG3	1.67	0.77
7:G:81:PRO:HG3	7:G:106:MET:SD	2.25	0.77
1:A:590:ARG:HG3	1:A:590:ARG:NH1	2.00	0.77
2:B:1159:ARG:HD3	2:B:1193:GLN:HG3	1.64	0.77
3:C:43:THR:HG22	3:C:44:LEU:H	1.48	0.77
3:C:77:ILE:HG23	3:C:161:LYS:HE3	1.67	0.77
11:K:21:ILE:HG12	11:K:33:ILE:HG12	1.67	0.77
5:E:175:LEU:HD23	5:E:176:PRO:HD2	1.66	0.76
1:A:445:ASN:HB2	1:A:455:MET:HG2	1.67	0.76
1:A:588:LEU:O	1:A:606:LEU:HA	1.85	0.76
6:F:111:LEU:C	6:F:113:GLY:H	1.90	0.76
1:A:798:GLY:HA2	1:A:815:PHE:HD1	1.43	0.76
2:B:1065:GLN:HE21	2:B:1066:SER:N	1.82	0.76
1:A:590:ARG:HG3	1:A:590:ARG:HH11	1.51	0.76
2:B:859:TYR:OH	2:B:941:LEU:HD12	1.86	0.76
1:A:858:ASN:C	1:A:858:ASN:HD22	1.94	0.76
2:B:999:MET:HG3	2:B:1000:PRO:HD2	1.68	0.76
2:B:446:LEU:O	2:B:447:ALA:CB	2.34	0.76
4:D:66:ARG:HD2	4:D:133:THR:HB	1.68	0.76
2:B:53:GLN:HG2	2:B:547:VAL:HG22	1.67	0.76
5:E:192:ARG:HH11	5:E:192:ARG:HG3	1.51	0.76
1:A:87:ALA:HB3	1:A:276:LEU:HD23	1.67	0.76
2:B:763:GLN:HG2	2:B:765:PRO:HD2	1.66	0.76
2:B:801:LYS:O	10:J:52:THR:HG23	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:806:THR:H	2:B:809:MET:HE3	1.50	0.76
1:A:265:LYS:HZ3	1:A:322:VAL:HG13	1.49	0.75
1:A:768:GLN:NE2	1:A:816:HIS:ND1	2.35	0.75
7:G:43:GLY:HA3	7:G:80:LYS:HB3	1.68	0.75
11:K:46:ILE:O	11:K:50:LEU:HB2	1.85	0.75
2:B:1034:VAL:HG12	2:B:1035:ALA:N	1.98	0.75
1:A:23:SER:HB3	1:A:233:TRP:CZ2	2.21	0.75
1:A:528:LEU:O	1:A:531:ILE:HG22	1.86	0.75
2:B:899:ILE:HD11	2:B:911:ILE:HA	1.68	0.75
1:A:356:ASP:HB2	1:A:469:ARG:HH11	1.50	0.75
2:B:408:LEU:HG	2:B:409:ALA:H	1.52	0.75
2:B:1165:ILE:HD13	4:D:17:LYS:CB	2.17	0.75
2:B:172:ILE:HD13	2:B:178:ASN:HB3	1.69	0.75
4:D:40:HIS:HB3	7:G:73:LYS:HZ3	1.47	0.75
2:B:642:ASP:HB3	2:B:649:LYS:CD	2.17	0.75
2:B:863:GLU:OE2	2:B:873:THR:HA	1.85	0.75
2:B:955:THR:HG22	2:B:956:THR:N	2.00	0.75
2:B:953:LEU:HD21	2:B:965:LYS:HB2	1.68	0.75
1:A:23:SER:HB3	1:A:233:TRP:CE2	2.21	0.75
1:A:1409:LEU:HD13	2:B:1207:LEU:HD21	1.67	0.75
2:B:521:LEU:HD22	2:B:633:VAL:HG12	1.68	0.75
5:E:90:VAL:HG23	5:E:120:ALA:HA	1.69	0.75
8:H:59:ILE:HG22	8:H:60:ALA:N	2.02	0.74
1:A:244:PRO:HB2	1:A:245:PRO:HD3	1.69	0.74
1:A:836:TYR:CE2	1:A:840:ARG:HD2	2.22	0.74
1:A:91:PHE:HB2	1:A:297:GLN:NE2	2.01	0.74
1:A:590:ARG:NH2	1:A:620:LYS:HB3	2.01	0.74
2:B:1069:PHE:H	2:B:1069:PHE:HD1	1.34	0.74
2:B:37:PHE:HE2	2:B:542:MET:HA	1.52	0.74
7:G:115:MET:HB3	7:G:116:PRO:HD2	1.69	0.74
1:A:164:ARG:HG3	1:A:165:GLY:H	1.52	0.74
2:B:806:THR:HG22	2:B:808:ALA:N	2.03	0.74
2:B:978:ASP:OD2	2:B:1098:MET:HG2	1.88	0.74
2:B:1065:GLN:NE2	2:B:1067:ARG:H	1.84	0.74
7:G:15:PRO:HA	7:G:18:PHE:CE1	2.22	0.74
1:A:68:GLN:C	1:A:70:CYS:H	1.95	0.74
1:A:351:THR:HB	2:B:1103:ILE:CD1	2.18	0.74
2:B:955:THR:HG22	2:B:956:THR:H	1.53	0.74
5:E:198:ILE:HD11	5:E:212:ARG:HG3	1.69	0.74
1:A:754:SER:H	1:A:757:ASN:ND2	1.86	0.74
1:A:87:ALA:CB	1:A:276:LEU:HD23	2.18	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:535:THR:HG21	1:A:616:VAL:HA	1.70	0.73
1:A:1450:LEU:O	1:A:1450:LEU:HG	1.88	0.73
4:D:47:LEU:HD13	4:D:48:ILE:N	2.03	0.73
1:A:1114:PRO:O	1:A:1115:SER:O	2.06	0.73
1:A:1312:ASN:O	1:A:1316:VAL:HG23	1.88	0.73
2:B:580:VAL:HG22	2:B:624:LEU:HB3	1.69	0.73
5:E:2:ASP:O	5:E:3:GLN:HG2	1.87	0.73
11:K:65:HIS:CD2	11:K:67:PHE:H	2.05	0.73
1:A:1323:ASP:OD1	1:A:1325:THR:HB	1.88	0.73
2:B:871:THR:HG22	2:B:872:GLU:O	1.88	0.73
1:A:567:LYS:NZ	8:H:46:LEU:HB2	2.03	0.73
1:A:800:VAL:HG22	1:A:812:GLU:HB3	1.70	0.73
5:E:16:PHE:CZ	5:E:20:LYS:HE2	2.24	0.73
8:H:81:PRO:CB	8:H:82:PRO:HD2	2.19	0.73
12:L:30:ILE:O	12:L:56:LEU:HA	1.89	0.73
1:A:1402:PHE:CE1	1:A:1403:GLU:HG3	2.23	0.73
1:A:164:ARG:HG3	1:A:165:GLY:N	2.04	0.73
2:B:847:ASP:HB3	3:C:167:HIS:CD2	2.24	0.73
1:A:1445:ILE:HD12	1:A:1445:ILE:N	2.04	0.73
4:D:130:LEU:O	4:D:132:GLN:N	2.22	0.73
12:L:48:CYS:HB3	12:L:51:CYS:O	1.88	0.73
2:B:378:LEU:HD12	2:B:378:LEU:O	1.88	0.73
2:B:766:ARG:HH22	2:B:1020:ARG:HH11	1.37	0.73
3:C:263:THR:C	3:C:265:MET:H	1.97	0.73
8:H:36:CYS:HA	8:H:126:GLU:O	1.89	0.73
10:J:5:VAL:HG12	10:J:6:ARG:CG	2.15	0.73
1:A:1420:ASP:HB3	1:A:1422:ARG:HG3	1.71	0.72
2:B:1183:LYS:N	2:B:1183:LYS:HE3	2.03	0.72
3:C:166:GLU:HG3	11:K:10:PHE:CZ	2.21	0.72
1:A:1424:VAL:HG11	2:B:1139:ILE:HD13	1.69	0.72
2:B:616:ILE:HG13	2:B:697:GLU:HG3	1.70	0.72
10:J:36:LEU:HD12	10:J:47:ARG:NH1	2.04	0.72
12:L:32:ALA:HB3	12:L:55:ILE:HD12	1.72	0.72
2:B:745:PRO:O	2:B:748:ILE:HG12	1.89	0.72
1:A:1121:GLU:HG2	1:A:1122:PRO:HD2	1.72	0.72
2:B:401:PHE:HD2	2:B:521:LEU:HD12	1.54	0.72
2:B:701:ILE:HD11	2:B:703:ILE:HD11	1.72	0.72
6:F:138:LEU:HB3	6:F:139:PRO:HD2	1.72	0.72
1:A:1437:GLY:O	1:A:1439:GLY:N	2.23	0.72
2:B:642:ASP:O	2:B:644:GLU:N	2.22	0.72
1:A:1076:ALA:HA	1:A:1079:MET:HE2	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:335:ARG:HH12	2:B:1202:LEU:HD13	1.54	0.72
2:B:400:HIS:ND1	2:B:517:THR:HG21	2.05	0.72
2:B:1115:THR:HG22	2:B:1117:GLN:HG3	1.71	0.72
2:B:1138:MET:HE2	2:B:1146:PHE:HD2	1.54	0.72
1:A:741:ASN:HD21	1:A:743:VAL:HB	1.54	0.72
5:E:213:ILE:HG12	5:E:214:CYS:H	1.54	0.72
8:H:59:ILE:HG22	8:H:60:ALA:H	1.54	0.72
1:A:321:PRO:O	1:A:322:VAL:HB	1.88	0.71
1:A:899:VAL:HB	1:A:929:LEU:CD1	2.20	0.71
1:A:1004:ASN:ND2	5:E:167:ARG:HD2	2.05	0.71
2:B:411:PRO:O	2:B:414:ALA:HB3	1.88	0.71
3:C:175:ALA:O	3:C:176:ILE:HG13	1.90	0.71
2:B:365:THR:HG23	2:B:367:LEU:H	1.54	0.71
3:C:73:GLN:HB3	3:C:131:HIS:H	1.55	0.71
1:A:1239:ARG:HH22	1:A:1241:ARG:NH2	1.88	0.71
1:A:1332:PHE:HD2	1:A:1332:PHE:N	1.86	0.71
2:B:594:ALA:HA	2:B:617:ARG:NH1	2.05	0.71
1:A:853:ASP:OD1	1:A:855:THR:HB	1.89	0.71
2:B:39:ARG:NH2	2:B:665:GLU:HG2	2.04	0.71
2:B:516:ASN:HD22	2:B:516:ASN:N	1.87	0.71
1:A:69:THR:C	1:A:71:GLN:H	1.98	0.71
1:A:808:LEU:HD23	1:A:813:PHE:HA	1.71	0.71
2:B:227:LYS:HB2	2:B:395:GLN:OE1	1.90	0.71
1:A:230:ARG:H	1:A:233:TRP:HE3	1.34	0.71
1:A:504:LEU:HD11	6:F:91:ALA:HB1	1.73	0.71
1:A:1329:THR:CG2	1:A:1331:SER:H	2.03	0.71
1:A:91:PHE:HB2	1:A:297:GLN:HE22	1.54	0.71
2:B:770:GLN:CD	2:B:983:ARG:HA	2.16	0.71
4:D:5:THR:O	4:D:6:SER:O	2.07	0.71
5:E:202:SER:OG	5:E:204:THR:HG22	1.88	0.71
2:B:1182:CYS:O	2:B:1182:CYS:SG	2.48	0.71
4:D:176:GLU:C	4:D:178:ALA:H	1.98	0.71
2:B:603:LEU:HD13	2:B:608:ASP:HB2	1.72	0.71
1:A:441:PRO:HD2	1:A:498:ARG:NH2	2.06	0.70
1:A:567:LYS:CD	1:A:568:PRO:HD2	2.20	0.70
9:I:71:SER:OG	9:I:83:ASN:HB2	1.91	0.70
11:K:47:ARG:HB3	11:K:47:ARG:NH1	2.04	0.70
11:K:50:LEU:HD11	11:K:75:ILE:HD13	1.73	0.70
1:A:92:HIS:O	1:A:94:GLY:N	2.24	0.70
1:A:475:THR:HG23	1:A:476:SER:N	2.05	0.70
1:A:913:LEU:HD12	1:A:914:GLU:N	2.05	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:393:LYS:HA	2:B:393:LYS:HE3	1.74	0.70
2:B:557:PHE:C	2:B:557:PHE:CD2	2.68	0.70
1:A:75:ASN:O	1:A:76:GLU:HB3	1.91	0.70
1:A:384:ASN:OD1	1:A:388:LEU:HD12	1.91	0.70
1:A:463:ILE:HD12	1:A:469:ARG:HD2	1.73	0.70
5:E:179:GLN:HB2	5:E:182:ASP:HB2	1.73	0.70
2:B:65:GLU:HG3	2:B:66:ASP:N	2.05	0.70
2:B:549:THR:HG22	2:B:550:ASP:N	2.05	0.70
2:B:830:TYR:CE2	2:B:1000:PRO:HD3	2.27	0.70
2:B:1006:ILE:HD13	10:J:44:TYR:CE2	2.27	0.70
2:B:1099:VAL:O	2:B:1101:ASP:N	2.24	0.70
1:A:302:THR:HA	1:A:305:ASP:O	1.91	0.70
1:A:794:PRO:HG2	1:A:795:GLU:OE2	1.92	0.70
1:A:567:LYS:HB3	8:H:96:VAL:N	2.05	0.70
2:B:766:ARG:NH2	2:B:1020:ARG:HH11	1.90	0.70
2:B:1182:CYS:C	2:B:1183:LYS:HE3	2.16	0.70
1:A:1424:VAL:HG13	1:A:1436:ILE:HD11	1.74	0.70
3:C:167:HIS:CE1	12:L:70:ARG:HB3	2.27	0.70
7:G:80:LYS:HD3	7:G:80:LYS:N	2.06	0.70
1:A:225:ASN:HD22	1:A:228:PHE:H	1.39	0.70
1:A:466:SER:O	2:B:1103:ILE:HD11	1.92	0.70
1:A:1239:ARG:HH22	1:A:1241:ARG:HH22	1.40	0.70
2:B:737:THR:HG21	9:I:66:PRO:HA	1.74	0.70
2:B:770:GLN:OE1	2:B:983:ARG:HA	1.92	0.70
2:B:847:ASP:C	2:B:849:GLY:H	1.98	0.70
1:A:666:ILE:HD12	1:A:667:GLY:H	1.57	0.69
2:B:333:PHE:O	2:B:334:ILE:HG13	1.92	0.69
2:B:708:GLU:O	2:B:710:LEU:N	2.25	0.69
4:D:33:PHE:CE1	7:G:80:LYS:HE3	2.27	0.69
5:E:22:MET:HE3	5:E:26:ARG:NE	2.06	0.69
1:A:901:LEU:HD22	1:A:919:ILE:CG2	2.22	0.69
2:B:579:ARG:HB2	2:B:586:TRP:HE1	1.56	0.69
2:B:642:ASP:HB3	2:B:649:LYS:CG	2.21	0.69
3:C:20:PHE:CE1	3:C:22:LEU:HD12	2.25	0.69
8:H:113:ALA:HB2	8:H:126:GLU:HG3	1.72	0.69
1:A:1308:THR:HG23	1:A:1309:ASP:N	2.06	0.69
2:B:446:LEU:O	2:B:447:ALA:HB3	1.92	0.69
2:B:728:ARG:HH12	2:B:1047:PHE:HB3	1.57	0.69
4:D:170:THR:HG21	4:D:172:LEU:HG	1.73	0.69
5:E:48:ASP:CG	5:E:49:SER:H	1.99	0.69
8:H:40:LEU:HD22	8:H:123:MET:HE3	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:GLY:HA3	1:A:243:PRO:HG2	1.74	0.69
1:A:746:MET:HE3	2:B:1018:PRO:HG2	1.73	0.69
1:A:901:LEU:HG	1:A:926:GLN:HE21	1.57	0.69
2:B:593:PRO:HG2	2:B:617:ARG:NH2	2.06	0.69
2:B:953:LEU:HD23	2:B:953:LEU:O	1.92	0.69
7:G:138:THR:CG2	7:G:139:ILE:H	1.96	0.69
1:A:14:VAL:HG21	2:B:1216:LEU:HD13	1.74	0.69
1:A:1438:THR:HB	2:B:1144:ALA:HB3	1.74	0.69
2:B:1099:VAL:CG1	2:B:1100:ASP:N	2.56	0.69
2:B:1159:ARG:HB3	2:B:1159:ARG:NH1	2.06	0.69
3:C:184:ASN:ND2	3:C:187:LYS:HA	2.07	0.69
1:A:248:PRO:O	1:A:260:ASP:HB2	1.93	0.69
1:A:1139:GLU:O	1:A:1274:ARG:O	2.08	0.69
2:B:654:ARG:H	2:B:657:HIS:HD2	1.38	0.69
2:B:707:PRO:O	2:B:711:GLU:HG3	1.93	0.69
2:B:1017:ILE:HB	2:B:1018:PRO:HD3	1.74	0.69
3:C:45:ALA:HA	3:C:72:LEU:HD12	1.75	0.69
1:A:107:CYS:N	1:A:114:LEU:HD21	2.08	0.69
1:A:254:GLU:CG	2:B:935:ARG:HH22	2.06	0.69
1:A:856:THR:HB	1:A:865:GLN:HB2	1.75	0.69
2:B:211:VAL:O	2:B:480:SER:HA	1.91	0.69
2:B:1065:GLN:HE21	2:B:1067:ARG:N	1.91	0.69
4:D:29:LEU:HD22	7:G:82:PHE:CE2	2.28	0.69
1:A:254:GLU:CB	2:B:935:ARG:HH12	2.03	0.69
1:A:55:ASP:CG	1:A:55:ASP:O	2.32	0.69
1:A:106:VAL:HG13	1:A:112:LYS:O	1.93	0.69
1:A:384:ASN:CG	1:A:388:LEU:HD12	2.17	0.69
1:A:675:THR:O	1:A:679:ILE:HG13	1.93	0.69
1:A:844:ALA:C	1:A:845:LEU:HD23	2.17	0.69
2:B:1197:PRO:HG2	2:B:1200:ALA:CB	2.22	0.69
3:C:172:PRO:O	3:C:235:VAL:HG23	1.93	0.69
4:D:40:HIS:CB	7:G:73:LYS:HZ3	2.06	0.69
7:G:18:PHE:HA	7:G:22:MET:CE	2.22	0.69
1:A:1291:VAL:HG13	1:A:1292:PRO:HD2	1.74	0.68
2:B:217:ARG:HD2	2:B:217:ARG:C	2.18	0.68
2:B:351:TYR:CE1	2:B:355:ILE:HD11	2.28	0.68
2:B:642:ASP:HB3	2:B:649:LYS:HG3	1.74	0.68
2:B:778:MET:CE	2:B:1094:ARG:HD3	2.22	0.68
2:B:975:GLN:HG2	2:B:976:ILE:H	1.56	0.68
7:G:14:HIS:CD2	7:G:16:SER:HB2	2.27	0.68
1:A:427:GLN:HG3	1:A:430:TRP:CZ2	2.28	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:46:GLN:HG3	2:B:47:GLN:N	2.07	0.68
8:H:4:THR:HA	8:H:60:ALA:CB	2.22	0.68
2:B:95:ILE:HG13	2:B:130:VAL:HG22	1.75	0.68
4:D:48:ILE:CG2	7:G:4:ILE:HB	2.19	0.68
10:J:1:MET:H2	10:J:56:LEU:N	1.91	0.68
12:L:38:LEU:O	12:L:39:SER:HB3	1.93	0.68
1:A:152:VAL:CG1	1:A:153:PRO:HD2	2.24	0.68
1:A:903:ASN:HD22	1:A:903:ASN:C	1.97	0.68
1:A:1002:GLY:HA3	1:A:1007:ILE:HG21	1.75	0.68
2:B:1169:MET:HE1	2:B:1201:LYS:HA	1.74	0.68
5:E:124:VAL:HG13	5:E:132:ILE:HB	1.74	0.68
1:A:19:PHE:O	1:A:1416:ALA:HA	1.93	0.68
2:B:1087:PHE:HD2	2:B:1088:GLY:N	1.90	0.68
11:K:31:VAL:HG12	11:K:32:VAL:N	2.08	0.68
1:A:115:LEU:HB2	1:A:122:MET:HE2	1.76	0.68
1:A:337:ARG:HD3	2:B:1132:GLU:OE1	1.94	0.68
6:F:97:ARG:O	6:F:101:ILE:HG13	1.93	0.68
1:A:78:PRO:HA	2:B:1201:LYS:NZ	2.08	0.68
1:A:979:SER:OG	1:A:981:LEU:HG	1.94	0.68
1:A:1120:LEU:O	1:A:1323:ASP:HB2	1.93	0.68
2:B:615:MET:HB3	2:B:626:ILE:HG12	1.76	0.68
3:C:114:TYR:HB3	3:C:140:ASN:O	1.93	0.68
4:D:34:GLN:O	4:D:47:LEU:HD23	1.94	0.68
5:E:22:MET:HE3	5:E:26:ARG:HH21	1.59	0.68
6:F:125:LEU:HG	6:F:125:LEU:O	1.94	0.68
8:H:89:LEU:C	8:H:91:ASP:H	2.02	0.68
8:H:93:TYR:HB3	8:H:144:ILE:O	1.93	0.68
2:B:635:ARG:NH2	2:B:742:GLU:OE2	2.26	0.68
7:G:1:MET:HE1	7:G:80:LYS:H	1.59	0.68
1:A:54:ASN:HB3	1:A:247:ARG:HH12	1.59	0.68
1:A:809:THR:OG1	1:A:812:GLU:HG3	1.94	0.68
2:B:1197:PRO:HG2	2:B:1200:ALA:HB2	1.76	0.68
5:E:135:PHE:HB3	5:E:140:LEU:HD11	1.74	0.68
8:H:126:GLU:C	8:H:130:ARG:HH22	2.02	0.68
9:I:101:PHE:N	9:I:101:PHE:CD1	2.61	0.68
1:A:311:GLN:HB3	1:A:312:PRO:HD3	1.76	0.67
2:B:370:PHE:HE2	2:B:373:ARG:HH11	1.42	0.67
6:F:86:THR:OG1	6:F:89:GLU:HG3	1.93	0.67
9:I:13:MET:HG3	9:I:14:LEU:N	2.09	0.67
1:A:84:ILE:O	1:A:84:ILE:HG23	1.95	0.67
1:A:351:THR:HG22	2:B:1103:ILE:HA	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:385:ILE:HG22	1:A:386:ASP:N	2.09	0.67
2:B:521:LEU:HB3	2:B:633:VAL:HG11	1.75	0.67
4:D:117:GLU:N	4:D:155:ARG:HH12	1.87	0.67
6:F:90:ARG:HD3	6:F:155:LEU:CD1	2.24	0.67
7:G:14:HIS:ND1	7:G:15:PRO:HD2	2.09	0.67
1:A:55:ASP:C	1:A:57:ARG:N	2.41	0.67
2:B:1073:TYR:CE2	2:B:1080:LYS:HG2	2.29	0.67
3:C:18:VAL:HG12	3:C:18:VAL:O	1.94	0.67
1:A:107:CYS:H	1:A:114:LEU:HD21	1.57	0.67
1:A:388:LEU:HD22	1:A:432:VAL:HG21	1.76	0.67
1:A:866:PHE:O	1:A:867:ILE:HG13	1.94	0.67
7:G:18:PHE:HA	7:G:22:MET:HE2	1.76	0.67
1:A:1394:THR:HG21	1:A:1398:MET:SD	2.35	0.67
2:B:515:HIS:CD2	2:B:517:THR:H	2.11	0.67
3:C:179:GLU:HG2	3:C:180:TYR:N	2.08	0.67
4:D:117:GLU:H	4:D:155:ARG:NH1	1.87	0.67
1:A:35:ILE:HG22	1:A:35:ILE:O	1.94	0.67
1:A:344:ARG:HD2	2:B:1118:PRO:O	1.95	0.67
1:A:450:LEU:HD12	1:A:450:LEU:N	2.09	0.67
1:A:869:GLY:O	5:E:204:THR:HG21	1.95	0.67
1:A:902:LEU:HG	1:A:926:GLN:HG3	1.76	0.67
1:A:981:LEU:HD21	1:A:1038:THR:C	2.19	0.67
1:A:1007:ILE:C	1:A:1009:ASN:H	2.02	0.67
1:A:986:ILE:HG22	1:A:987:VAL:N	2.10	0.67
1:A:1424:VAL:HG13	1:A:1436:ILE:CD1	2.24	0.67
2:B:36:ALA:HA	2:B:39:ARG:HD2	1.76	0.67
2:B:112:LEU:HD12	2:B:113:TYR:H	1.58	0.67
2:B:831:SER:HB3	2:B:994:TYR:OH	1.95	0.67
2:B:1002:THR:HG23	2:B:1006:ILE:HG13	1.77	0.67
6:F:82:THR:HG22	6:F:84:TYR:H	1.58	0.67
6:F:97:ARG:HD3	6:F:130:ILE:HG23	1.77	0.67
7:G:30:LEU:HD13	7:G:72:VAL:HG11	1.77	0.67
7:G:143:ILE:HG22	7:G:144:ARG:N	2.09	0.67
1:A:804:TYR:OH	1:A:816:HIS:NE2	2.28	0.67
2:B:1162:ILE:HG22	2:B:1163:CYS:N	2.09	0.67
3:C:43:THR:CG2	3:C:44:LEU:H	2.08	0.67
3:C:67:LEU:HD11	3:C:155:LEU:CD1	2.25	0.67
4:D:156:ASP:C	4:D:158:GLU:H	2.03	0.67
2:B:995:ARG:HH12	3:C:165:LYS:HG2	1.59	0.67
2:B:996:ARG:NH1	3:C:38:ILE:HG23	2.10	0.67
1:A:23:SER:HA	1:A:233:TRP:CD1	2.30	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:824:ILE:CG2	2:B:1087:PHE:HE2	2.08	0.67
2:B:839:MET:HG3	2:B:1010:LEU:HD11	1.77	0.67
2:B:980:PHE:CE2	2:B:1094:ARG:HG3	2.30	0.67
4:D:122:GLU:HA	4:D:125:SER:OG	1.95	0.67
7:G:1:MET:HE1	7:G:80:LYS:N	2.10	0.67
1:A:1227:ILE:HG22	1:A:1228:TRP:N	2.10	0.66
2:B:378:LEU:O	2:B:382:ILE:HG13	1.95	0.66
4:D:53:SER:HB3	4:D:152:SER:CB	2.25	0.66
9:I:50:THR:HG22	9:I:52:ILE:H	1.59	0.66
1:A:775:ILE:HG23	1:A:818:MET:HE1	1.77	0.66
2:B:192:LEU:O	2:B:193:LYS:HB2	1.94	0.66
2:B:569:TYR:CE1	2:B:589:VAL:HG21	2.30	0.66
9:I:111:THR:HG22	9:I:112:SER:N	2.09	0.66
1:A:63:ARG:HA	1:A:74:MET:SD	2.34	0.66
1:A:75:ASN:O	1:A:76:GLU:CB	2.43	0.66
1:A:979:SER:OG	1:A:980:ASP:N	2.28	0.66
2:B:1223:ASP:O	2:B:1224:PHE:HB2	1.94	0.66
10:J:53:HIS:C	10:J:53:HIS:CD2	2.73	0.66
12:L:40:LEU:HD13	12:L:44:ASP:HB3	1.77	0.66
1:A:353:ILE:CD1	1:A:487:MET:HE2	2.26	0.66
3:C:238:ILE:CG2	3:C:242:GLN:HB2	2.25	0.66
6:F:90:ARG:HG3	6:F:91:ALA:N	2.11	0.66
2:B:852:ARG:HH22	12:L:70:ARG:C	2.04	0.66
3:C:66:ARG:HH21	10:J:5:VAL:HG23	1.60	0.66
3:C:177:GLU:HB2	3:C:231:ASN:HB3	1.78	0.66
9:I:34:TYR:CE2	9:I:36:GLU:HB3	2.30	0.66
1:A:875:ALA:HA	1:A:878:ILE:HD12	1.77	0.66
2:B:465:ASN:HD22	2:B:465:ASN:H	1.43	0.66
2:B:563:MET:HE3	2:B:580:VAL:HB	1.77	0.66
2:B:902:GLY:O	12:L:65:VAL:HG11	1.95	0.66
2:B:1159:ARG:HB3	2:B:1159:ARG:HH11	1.61	0.66
3:C:189:THR:HG22	3:C:190:ASP:H	1.59	0.66
1:A:1115:SER:O	1:A:1116:LEU:HB3	1.96	0.66
3:C:189:THR:HG22	3:C:190:ASP:N	2.11	0.66
1:A:319:GLY:HA3	2:B:472:ALA:HB3	1.78	0.66
1:A:372:LYS:HA	1:A:435:HIS:ND1	2.11	0.66
2:B:1001:PHE:CE1	2:B:1073:TYR:HB2	2.31	0.66
5:E:15:ALA:O	5:E:19:VAL:HG23	1.94	0.66
5:E:46:TYR:CD2	5:E:58:MET:HG2	2.31	0.66
7:G:1:MET:SD	7:G:1:MET:C	2.78	0.66
1:A:399:HIS:O	1:A:401:GLY:N	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1107:VAL:HG12	1:A:1107:VAL:O	1.96	0.66
2:B:39:ARG:HH21	2:B:665:GLU:HG2	1.59	0.66
3:C:186:LEU:HD21	3:C:224:GLN:O	1.95	0.66
8:H:81:PRO:CB	8:H:82:PRO:CD	2.73	0.66
2:B:199:MET:HE2	2:B:492:LEU:HD23	1.75	0.66
2:B:1202:LEU:O	2:B:1206:GLU:HG3	1.96	0.66
7:G:7:LEU:HD11	7:G:45:ILE:HD11	1.78	0.66
1:A:341:MET:HE1	2:B:1135:ARG:NH1	2.10	0.65
1:A:843:LYS:HD3	1:A:846:GLU:OE2	1.95	0.65
1:A:1441:PHE:CZ	6:F:89:GLU:HA	2.31	0.65
2:B:247:GLY:H	2:B:418:LYS:HZ1	1.43	0.65
2:B:642:ASP:HA	2:B:649:LYS:HA	1.77	0.65
2:B:1045:SER:O	2:B:1046:PRO:O	2.14	0.65
3:C:43:THR:CG2	3:C:44:LEU:N	2.59	0.65
7:G:34:VAL:CG1	7:G:45:ILE:HG21	2.26	0.65
9:I:52:ILE:HG13	9:I:52:ILE:O	1.95	0.65
1:A:1161:THR:HG22	1:A:1163:ILE:N	2.04	0.65
2:B:999:MET:HA	2:B:999:MET:CE	2.25	0.65
4:D:176:GLU:O	4:D:178:ALA:N	2.26	0.65
9:I:102:VAL:HG12	9:I:103:CYS:N	2.12	0.65
10:J:1:MET:HE2	10:J:60:PHE:CE2	2.31	0.65
1:A:332:LYS:HG3	1:A:333:GLU:HG2	1.79	0.65
1:A:1293:SER:OG	1:A:1294:PRO:HD2	1.97	0.65
2:B:880:THR:O	2:B:881:ASN:HB2	1.96	0.65
3:C:152:GLU:OE2	3:C:154:LYS:HE3	1.95	0.65
3:C:179:GLU:HG2	3:C:180:TYR:H	1.61	0.65
12:L:58:LYS:O	12:L:58:LYS:HG2	1.96	0.65
5:E:84:ASP:O	5:E:86:PRO:HD3	1.96	0.65
5:E:157:SER:C	5:E:159:ASP:H	2.03	0.65
8:H:56:THR:HB	8:H:145:ARG:HG2	1.78	0.65
1:A:23:SER:HA	1:A:233:TRP:NE1	2.12	0.65
1:A:77:CYS:O	1:A:78:PRO:C	2.40	0.65
2:B:758:PHE:CE2	2:B:1044:ALA:HA	2.32	0.65
2:B:857:ARG:HD2	2:B:945:GLU:OE1	1.96	0.65
2:B:952:VAL:HG12	2:B:953:LEU:H	1.61	0.65
2:B:975:GLN:O	2:B:990:ILE:HD12	1.97	0.65
2:B:1172:ILE:HG22	2:B:1172:ILE:O	1.96	0.65
1:A:442:VAL:HB	1:A:489:LEU:HD11	1.77	0.65
1:A:743:VAL:O	1:A:747:VAL:HG23	1.97	0.65
2:B:1007:VAL:CG2	2:B:1008:PRO:HD2	2.26	0.65
3:C:183:TRP:CZ2	3:C:207:CYS:HB3	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:601:ARG:O	2:B:605:ARG:HG3	1.97	0.65
2:B:604:ARG:NH2	2:B:613:VAL:O	2.29	0.65
8:H:38:LEU:HD12	8:H:124:ARG:O	1.96	0.65
12:L:39:SER:O	12:L:40:LEU:HG	1.97	0.65
1:A:535:THR:HG23	1:A:575:LYS:HE2	1.79	0.65
2:B:118:ARG:HH22	2:B:194:GLU:CD	2.04	0.65
2:B:622:LYS:HE2	9:I:59:VAL:HG22	1.79	0.65
5:E:157:SER:OG	5:E:160:GLU:HG3	1.97	0.65
6:F:111:LEU:HD12	6:F:111:LEU:N	2.12	0.65
7:G:91:VAL:HB	7:G:139:ILE:O	1.95	0.65
9:I:51:ASN:O	9:I:54:GLU:HG3	1.96	0.65
1:A:18:GLN:HB2	2:B:1215:ARG:HB2	1.77	0.65
1:A:1348:LEU:HG	1:A:1372:VAL:HG23	1.78	0.65
2:B:705:MET:HA	2:B:705:MET:HE3	1.78	0.65
1:A:69:THR:O	1:A:71:GLN:N	2.29	0.65
1:A:295:LEU:O	1:A:298:PHE:HB3	1.97	0.65
1:A:541:ILE:HG22	1:A:546:VAL:HG23	1.79	0.65
2:B:731:VAL:HG12	2:B:732:SER:H	1.62	0.65
2:B:798:TYR:HE2	3:C:62:PHE:CE2	2.15	0.65
2:B:850:LEU:HD12	2:B:851:PHE:H	1.62	0.65
5:E:124:VAL:HG13	5:E:132:ILE:HD12	1.79	0.65
10:J:57:ILE:HA	10:J:60:PHE:CD2	2.30	0.65
1:A:547:LEU:HD22	11:K:58:PHE:CD1	2.32	0.64
2:B:798:TYR:HE2	3:C:62:PHE:CZ	2.14	0.64
3:C:147:LEU:HB2	3:C:151:GLN:HB2	1.78	0.64
4:D:118:THR:O	4:D:122:GLU:HB2	1.97	0.64
5:E:22:MET:CE	5:E:26:ARG:HH21	2.11	0.64
1:A:315:LEU:HD13	2:B:472:ALA:O	1.92	0.64
2:B:1224:PHE:CE2	5:E:171:LYS:HG3	2.28	0.64
8:H:123:MET:HE1	8:H:142:LEU:HD11	1.78	0.64
1:A:567:LYS:HE3	8:H:46:LEU:HD12	1.78	0.64
2:B:653:VAL:CG2	2:B:689:LEU:HB3	2.27	0.64
2:B:899:ILE:CD1	2:B:911:ILE:HA	2.27	0.64
6:F:135:ARG:HD3	6:F:143:PHE:CD2	2.32	0.64
7:G:51:TYR:C	7:G:51:TYR:CD2	2.75	0.64
1:A:2:VAL:HG21	2:B:1158:PHE:N	2.11	0.64
1:A:88:LYS:HE3	1:A:280:GLU:OE2	1.97	0.64
2:B:842:ASN:HD22	2:B:845:SER:CB	2.11	0.64
2:B:1051:THR:HB	2:B:1054:GLY:H	1.60	0.64
1:A:1348:LEU:HG	1:A:1372:VAL:CG2	2.27	0.64
3:C:165:LYS:O	11:K:6:ARG:NH1	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:176:PRO:O	5:E:212:ARG:HA	1.96	0.64
5:E:213:ILE:HG12	5:E:214:CYS:N	2.12	0.64
1:A:1039:LYS:HG3	1:A:1043:ASP:OD2	1.98	0.64
2:B:704:ALA:HB3	2:B:741:CYS:SG	2.37	0.64
2:B:1056:SER:HB3	2:B:1066:SER:HB2	1.78	0.64
2:B:1085:ILE:N	2:B:1085:ILE:HD12	2.12	0.64
6:F:111:LEU:C	6:F:113:GLY:N	2.56	0.64
6:F:119:ARG:HH11	6:F:119:ARG:HG3	1.61	0.64
7:G:59:GLY:HA3	7:G:70:PHE:CD2	2.33	0.64
1:A:154:SER:HB3	1:A:162:VAL:HG21	1.79	0.64
1:A:672:ASP:HB2	1:A:736:ASN:OD1	1.98	0.64
3:C:123:ASN:HD22	3:C:125:MET:HG2	1.60	0.64
4:D:56:ARG:HA	4:D:148:LEU:HD13	1.79	0.64
1:A:665:GLY:HA2	2:B:1026:LEU:HD21	1.78	0.64
1:A:897:TYR:HD2	1:A:936:LEU:HD13	1.62	0.64
1:A:1193:LEU:HD12	1:A:1194:ARG:N	2.13	0.64
2:B:197:PHE:CZ	2:B:816:GLU:HG2	2.32	0.64
2:B:229:ALA:HB1	2:B:231:PRO:HD2	1.79	0.64
2:B:357:GLN:O	2:B:366:GLN:HA	1.97	0.64
2:B:710:LEU:HA	2:B:733:HIS:HB3	1.79	0.64
3:C:99:LEU:HA	3:C:119:VAL:O	1.98	0.64
1:A:404:TYR:HB2	1:A:433:GLU:HB2	1.80	0.63
1:A:500:GLU:OE2	2:B:1145:SER:HB2	1.98	0.63
1:A:590:ARG:HH21	1:A:620:LYS:HB3	1.61	0.63
9:I:2:THR:O	9:I:3:THR:C	2.39	0.63
1:A:47:ARG:HH12	1:A:254:GLU:HG2	1.63	0.63
2:B:860:MET:HG2	2:B:861:ASP:N	2.14	0.63
6:F:86:THR:HG23	6:F:89:GLU:OE1	1.98	0.63
7:G:9:LEU:HD12	7:G:10:ASN:H	1.63	0.63
8:H:91:ASP:C	8:H:93:TYR:H	2.05	0.63
9:I:101:PHE:HD1	9:I:101:PHE:H	1.46	0.63
11:K:53:ASP:HB3	11:K:56:VAL:HG23	1.79	0.63
1:A:50:ILE:C	1:A:52:GLY:H	2.06	0.63
1:A:1261:LYS:O	1:A:1264:GLU:HB3	1.99	0.63
3:C:66:ARG:NH1	10:J:2:ILE:HG21	2.13	0.63
10:J:47:ARG:HG2	10:J:47:ARG:HH11	1.64	0.63
12:L:31:CYS:HB3	12:L:35:SER:N	2.13	0.63
1:A:401:GLY:C	1:A:435:HIS:HD2	2.06	0.63
1:A:646:PHE:O	1:A:650:GLN:HG3	1.99	0.63
1:A:1341:ILE:CG2	1:A:1342:GLU:N	2.62	0.63
4:D:50:LEU:HD11	7:G:4:ILE:HD11	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:384:ASN:O	1:A:385:ILE:C	2.41	0.63
1:A:866:PHE:C	1:A:867:ILE:HG13	2.22	0.63
1:A:886:ILE:HG22	1:A:887:GLY:N	2.13	0.63
1:A:1121:GLU:CG	1:A:1122:PRO:HD2	2.29	0.63
1:A:1341:ILE:HG23	1:A:1342:GLU:H	1.61	0.63
1:A:1436:ILE:O	1:A:1437:GLY:C	2.42	0.63
3:C:168:ALA:O	3:C:170:TRP:N	2.30	0.63
8:H:99:GLY:N	8:H:118:PHE:HD2	1.97	0.63
1:A:720:ARG:O	1:A:724:GLU:HB2	1.97	0.63
1:A:1206:ASP:HB3	1:A:1274:ARG:HH12	1.64	0.63
2:B:580:VAL:HG22	2:B:624:LEU:CB	2.27	0.63
2:B:824:ILE:HG22	2:B:1087:PHE:CE2	2.23	0.63
2:B:1065:GLN:NE2	2:B:1066:SER:N	2.47	0.63
2:B:1138:MET:HE2	2:B:1146:PHE:CD2	2.33	0.63
9:I:8:ARG:CG	9:I:34:TYR:HE1	2.12	0.63
10:J:23:ASN:C	10:J:25:LEU:H	2.05	0.63
1:A:899:VAL:HB	1:A:929:LEU:HD11	1.80	0.63
1:A:1191:TRP:CD1	1:A:1256:GLU:HB2	2.33	0.63
2:B:879:ARG:NH1	2:B:883:LEU:HD22	2.13	0.63
3:C:212:PRO:CB	3:C:213:PRO:HD2	2.29	0.63
5:E:78:LEU:HD23	5:E:78:LEU:C	2.24	0.63
11:K:49:GLU:HG3	11:K:94:ILE:CG1	2.29	0.63
12:L:32:ALA:HB3	12:L:55:ILE:CD1	2.27	0.63
2:B:63:ILE:O	2:B:67:SER:HB3	1.98	0.63
2:B:862:GLN:HG2	2:B:963:PHE:HD1	1.63	0.63
4:D:56:ARG:HB2	4:D:148:LEU:HD22	1.80	0.63
1:A:366:VAL:HG21	1:A:460:VAL:HG22	1.81	0.63
1:A:670:ILE:HG23	1:A:805:LEU:CD2	2.28	0.63
1:A:1224:LEU:HD12	1:A:1241:ARG:O	1.98	0.63
2:B:1165:ILE:HG22	2:B:1166:CYS:N	2.13	0.63
1:A:524:VAL:HG12	1:A:525:GLN:N	2.12	0.62
2:B:437:GLU:CA	2:B:438:GLU:N	2.62	0.62
4:D:191:ALA:O	4:D:193:THR:N	2.32	0.62
6:F:93:ILE:HD11	6:F:134:ILE:CD1	2.26	0.62
7:G:110:VAL:HG22	7:G:161:GLY:O	1.97	0.62
11:K:49:GLU:HG3	11:K:94:ILE:HG12	1.80	0.62
1:A:255:SER:OG	2:B:918:ILE:HG23	1.99	0.62
1:A:1027:ALA:O	1:A:1031:VAL:HG23	1.99	0.62
2:B:23:ALA:HB1	2:B:24:PRO:CD	2.26	0.62
2:B:399:ASP:O	2:B:515:HIS:CG	2.52	0.62
2:B:906:SER:O	2:B:941:LEU:HD23	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:31:ASN:O	3:C:32:SER:C	2.42	0.62
7:G:23:LYS:HG3	7:G:56:ILE:CD1	2.29	0.62
9:I:6:PHE:HB3	9:I:12:ASN:O	1.99	0.62
1:A:714:PHE:HB2	9:I:97:MET:HE1	1.81	0.62
1:A:1021:LEU:O	1:A:1024:SER:HB3	1.99	0.62
1:A:1120:LEU:HD12	1:A:1120:LEU:N	2.15	0.62
1:A:1325:THR:O	5:E:148:GLU:HB2	1.99	0.62
2:B:1180:PHE:HB3	2:B:1191:ILE:HD12	1.80	0.62
6:F:89:GLU:OE2	6:F:134:ILE:HG21	1.99	0.62
1:A:135:PHE:C	1:A:137:ALA:H	2.06	0.62
1:A:1332:PHE:N	1:A:1332:PHE:CD2	2.58	0.62
1:A:1454:MET:O	1:A:1454:MET:HG3	1.98	0.62
2:B:121:ASN:HA	2:B:207:GLY:CA	2.29	0.62
1:A:134:ARG:O	1:A:134:ARG:HG2	1.99	0.62
1:A:722:LEU:O	1:A:725:ALA:HB3	1.99	0.62
1:A:4:GLN:O	1:A:5:GLN:O	2.17	0.62
1:A:114:LEU:HD13	1:A:171:GLN:OE1	1.99	0.62
2:B:365:THR:HG23	2:B:367:LEU:HG	1.82	0.62
2:B:465:ASN:N	2:B:465:ASN:ND2	2.45	0.62
1:A:1074:GLU:HB3	1:A:1075:PRO:CD	2.30	0.62
2:B:1099:VAL:C	2:B:1101:ASP:H	2.07	0.62
6:F:111:LEU:HD12	6:F:111:LEU:H	1.65	0.62
1:A:49:LYS:HE2	1:A:61:ILE:HD12	1.81	0.62
1:A:129:LYS:O	1:A:130:ASP:HB2	1.99	0.62
1:A:382:PRO:HB3	1:A:428:TYR:HE2	1.65	0.62
1:A:467:THR:O	1:A:469:ARG:HG3	2.00	0.62
1:A:503:GLN:HE21	6:F:90:ARG:NH2	1.96	0.62
1:A:591:PHE:HA	1:A:595:THR:HG21	1.80	0.62
1:A:1349:TYR:CE1	1:A:1368:MET:HE3	2.34	0.62
2:B:43:LEU:HD11	2:B:811:TYR:O	1.99	0.62
2:B:953:LEU:CD2	2:B:965:LYS:HB2	2.28	0.62
1:A:289:ILE:C	1:A:291:GLU:H	2.07	0.62
1:A:590:ARG:HB3	1:A:605:MET:N	2.15	0.62
1:A:774:ARG:O	1:A:775:ILE:C	2.43	0.62
2:B:97:VAL:HG12	2:B:178:ASN:HD21	1.64	0.62
2:B:212:LEU:CD2	2:B:480:SER:HB2	2.29	0.62
2:B:247:GLY:H	2:B:418:LYS:NZ	1.98	0.62
2:B:604:ARG:NH1	2:B:691:GLU:OE2	2.31	0.62
8:H:98:TYR:C	8:H:118:PHE:HD2	2.08	0.62
1:A:407:ARG:HG2	1:A:430:TRP:CH2	2.35	0.62
2:B:217:ARG:HE	2:B:405:ARG:HB2	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:515:HIS:H	2:B:518:HIS:CD2	2.10	0.62
2:B:615:MET:C	2:B:616:ILE:HD12	2.25	0.62
4:D:54:GLU:O	4:D:58:VAL:HG23	1.99	0.62
5:E:207:ARG:CB	5:E:207:ARG:HH11	2.13	0.62
2:B:205:ILE:O	2:B:207:GLY:N	2.32	0.61
2:B:549:THR:H	2:B:628:THR:HG23	1.65	0.61
3:C:238:ILE:HG23	3:C:242:GLN:HB2	1.81	0.61
11:K:47:ARG:HH11	11:K:47:ARG:CB	2.11	0.61
1:A:1197:LEU:HD12	1:A:1209:MET:HE1	1.82	0.61
3:C:146:LYS:C	3:C:147:LEU:HD23	2.26	0.61
4:D:198:LEU:O	4:D:200:ASN:N	2.33	0.61
5:E:22:MET:HE3	5:E:26:ARG:NH2	2.15	0.61
7:G:74:TYR:H	7:G:74:TYR:HD2	1.46	0.61
1:A:475:THR:CG2	1:A:476:SER:N	2.63	0.61
2:B:314:LEU:O	2:B:317:CYS:HB3	2.00	0.61
11:K:21:ILE:HG23	11:K:31:VAL:HG11	1.82	0.61
1:A:2:VAL:HG21	2:B:1157:ALA:C	2.25	0.61
2:B:1152:MET:CE	2:B:1157:ALA:HA	2.29	0.61
5:E:78:LEU:HD23	5:E:79:TRP:N	2.15	0.61
9:I:111:THR:HG22	9:I:112:SER:H	1.65	0.61
10:J:12:LYS:O	10:J:14:VAL:HG23	2.00	0.61
1:A:783:THR:HG21	1:A:815:PHE:CE2	2.35	0.61
2:B:401:PHE:HB2	2:B:517:THR:OG1	2.01	0.61
2:B:606:LYS:HD2	2:B:608:ASP:OD2	2.01	0.61
3:C:244:VAL:O	3:C:248:ILE:HG13	2.00	0.61
5:E:23:VAL:HG13	5:E:78:LEU:HD13	1.80	0.61
1:A:481:ASP:OD1	1:A:485:ASP:OD2	2.18	0.61
1:A:738:LYS:HB2	1:A:740:LEU:HG	1.83	0.61
2:B:134:LYS:NZ	2:B:444:MET:N	2.40	0.61
1:A:90:VAL:HG13	1:A:297:GLN:HA	1.82	0.61
1:A:224:PHE:CE2	1:A:231:PRO:HG3	2.36	0.61
8:H:100:THR:OG1	8:H:138:GLU:HG3	2.00	0.61
1:A:144:THR:O	1:A:146:MET:HG3	2.01	0.61
2:B:542:MET:HE2	2:B:743:ILE:HG13	1.83	0.61
2:B:882:THR:HG22	2:B:884:ARG:N	2.13	0.61
1:A:69:THR:C	1:A:71:GLN:N	2.55	0.61
1:A:119:ASN:O	1:A:122:MET:HB3	2.01	0.61
1:A:265:LYS:NZ	1:A:322:VAL:HG22	2.15	0.61
2:B:171:PRO:HD2	2:B:457:LEU:HD13	1.82	0.61
2:B:822:ASN:O	10:J:48:ARG:NH1	2.34	0.61
8:H:83:GLN:C	8:H:85:GLY:H	2.08	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:36:SER:O	12:L:37:LYS:C	2.44	0.61
1:A:412:ARG:NH2	2:B:1108:ARG:NH1	2.48	0.61
1:A:907:THR:CG2	1:A:908:LEU:N	2.63	0.61
1:A:1291:VAL:HG13	1:A:1292:PRO:CD	2.31	0.61
4:D:192:LYS:HZ3	4:D:199:ASN:HA	1.66	0.61
9:I:26:LEU:HD23	9:I:37:GLU:HA	1.83	0.61
9:I:105:SER:O	9:I:106:CYS:HB3	2.01	0.61
1:A:71:GLN:C	1:A:73:GLY:H	2.09	0.60
1:A:1345:ARG:HG3	1:A:1376:THR:HG21	1.83	0.60
2:B:197:PHE:HZ	2:B:816:GLU:HG2	1.65	0.60
2:B:1115:THR:O	2:B:1116:ARG:HB2	2.01	0.60
1:A:867:ILE:HD12	5:E:208:TYR:HE1	1.65	0.60
1:A:1063:MET:HG3	1:A:1436:ILE:HG23	1.82	0.60
2:B:745:PRO:O	2:B:747:MET:N	2.33	0.60
2:B:745:PRO:C	2:B:747:MET:H	2.09	0.60
2:B:949:VAL:HG12	2:B:950:ASP:N	2.15	0.60
4:D:144:THR:HG21	7:G:46:LEU:HD13	1.83	0.60
1:A:108:MET:SD	1:A:210:ILE:HD13	2.41	0.60
1:A:384:ASN:O	1:A:386:ASP:N	2.34	0.60
1:A:1299:VAL:HG12	1:A:1300:LYS:N	2.15	0.60
2:B:542:MET:HE3	2:B:636:PRO:HG3	1.83	0.60
2:B:731:VAL:HG12	2:B:732:SER:N	2.16	0.60
2:B:1001:PHE:CE2	3:C:34:ARG:CZ	2.83	0.60
2:B:1034:VAL:C	2:B:1036:ALA:H	2.09	0.60
3:C:208:GLU:O	3:C:210:GLU:N	2.35	0.60
4:D:56:ARG:HD3	4:D:149:THR:HA	1.82	0.60
1:A:152:VAL:HG12	1:A:153:PRO:HD2	1.83	0.60
1:A:613:ILE:O	1:A:614:PHE:HB3	2.01	0.60
4:D:220:LEU:O	4:D:221:TYR:HD1	1.85	0.60
12:L:31:CYS:SG	12:L:34:CYS:N	2.69	0.60
1:A:590:ARG:O	1:A:591:PHE:HB2	2.01	0.60
2:B:361:LEU:HD21	2:B:377:PHE:HD2	1.66	0.60
2:B:642:ASP:HB3	2:B:649:LYS:HD2	1.82	0.60
2:B:744:HIS:CG	2:B:745:PRO:HD2	2.37	0.60
4:D:68:ARG:C	4:D:70:PHE:H	2.09	0.60
1:A:416:ARG:C	1:A:417:TYR:HD2	2.09	0.60
1:A:590:ARG:HD2	1:A:605:MET:HB3	1.81	0.60
2:B:622:LYS:CE	9:I:59:VAL:HG22	2.32	0.60
2:B:121:ASN:HA	2:B:207:GLY:HA2	1.81	0.60
2:B:787:VAL:O	2:B:787:VAL:HG12	2.02	0.60
5:E:94:LYS:CE	5:E:98:ILE:HD11	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:122:ASN:ND2	7:G:125:SER:HB3	2.16	0.60
9:I:62:ILE:O	9:I:62:ILE:HG12	2.01	0.60
1:A:325:ILE:HG21	2:B:1210:MET:HG3	1.84	0.60
1:A:774:ARG:NH2	1:A:797:LYS:HB2	2.17	0.60
2:B:373:ARG:HG3	2:B:566:LEU:HD23	1.84	0.60
2:B:980:PHE:HE2	2:B:1094:ARG:CG	2.14	0.60
9:I:85:PHE:HD1	9:I:99:LEU:HD13	1.67	0.60
11:K:60:ALA:O	11:K:73:LEU:HD12	2.01	0.60
11:K:65:HIS:HD2	11:K:67:PHE:N	1.98	0.60
1:A:78:PRO:HA	2:B:1201:LYS:HZ2	1.67	0.60
1:A:666:ILE:HD11	2:B:1067:ARG:O	2.02	0.60
2:B:287:ARG:NH1	2:B:324:ILE:O	2.34	0.60
9:I:85:PHE:CD2	9:I:85:PHE:N	2.60	0.60
1:A:399:HIS:CB	1:A:400:PRO:HD3	2.28	0.60
2:B:859:TYR:CZ	2:B:941:LEU:HD12	2.37	0.60
2:B:1099:VAL:HG12	2:B:1100:ASP:N	2.17	0.60
3:C:238:ILE:HG22	3:C:243:VAL:HG23	1.83	0.60
5:E:29:PHE:C	5:E:30:ILE:HG13	2.26	0.60
7:G:14:HIS:HD2	7:G:16:SER:HB2	1.66	0.60
7:G:17:PHE:C	7:G:19:GLY:H	2.10	0.60
1:A:146:MET:HA	1:A:171:GLN:HB2	1.83	0.59
1:A:353:ILE:HG21	1:A:487:MET:HE3	1.84	0.59
2:B:469:GLN:CA	2:B:474:SER:CA	2.76	0.59
12:L:60:ARG:HG2	12:L:61:THR:H	1.67	0.59
1:A:265:LYS:NZ	1:A:322:VAL:HG13	2.17	0.59
1:A:913:LEU:HD12	1:A:914:GLU:H	1.66	0.59
1:A:1097:GLY:O	1:A:1100:ARG:HB3	2.01	0.59
1:A:1105:LEU:HD22	1:A:1384:VAL:HG21	1.83	0.59
1:A:1313:LEU:O	1:A:1315:GLU:N	2.35	0.59
2:B:955:THR:CG2	2:B:956:THR:H	2.15	0.59
2:B:1180:PHE:O	2:B:1181:GLU:O	2.20	0.59
3:C:66:ARG:NH1	3:C:144:ILE:O	2.35	0.59
7:G:3:PHE:CD1	7:G:80:LYS:NZ	2.70	0.59
1:A:728:LYS:O	1:A:732:LEU:HG	2.01	0.59
1:A:853:ASP:OD1	1:A:855:THR:CB	2.51	0.59
1:A:1059:HIS:ND1	6:F:86:THR:HA	2.17	0.59
1:A:1341:ILE:CG2	1:A:1342:GLU:H	2.15	0.59
2:B:172:ILE:HD13	2:B:178:ASN:CB	2.32	0.59
2:B:205:ILE:N	2:B:205:ILE:HD12	2.17	0.59
2:B:980:PHE:HD2	2:B:1094:ARG:HA	1.67	0.59
1:A:98:LYS:O	1:A:99:ILE:C	2.45	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:782:ARG:NH2	2:B:699:GLU:O	2.34	0.59
1:A:1116:LEU:HG	1:A:1308:THR:HB	1.83	0.59
1:A:1430:LEU:HB2	1:A:1432:GLN:HG3	1.85	0.59
2:B:265:SER:O	2:B:266:ALA:HB3	2.02	0.59
2:B:758:PHE:CE1	2:B:1027:ILE:HG22	2.37	0.59
3:C:254:LYS:O	3:C:256:ALA:N	2.35	0.59
3:C:22:LEU:HD13	3:C:230:MET:CE	2.32	0.59
9:I:102:VAL:CG1	9:I:103:CYS:N	2.65	0.59
12:L:27:LEU:O	12:L:28:LYS:HG2	2.03	0.59
1:A:971:PHE:CE2	1:A:1040:GLN:HG2	2.37	0.59
2:B:834:ASN:HB3	2:B:840:ILE:HG13	1.84	0.59
3:C:45:ALA:HA	3:C:72:LEU:CD1	2.31	0.59
4:D:202:ILE:HG21	4:D:207:LEU:HB2	1.82	0.59
11:K:10:PHE:N	11:K:10:PHE:CD2	2.71	0.59
11:K:61:TYR:C	11:K:61:TYR:CD2	2.78	0.59
1:A:12:ARG:HD2	2:B:1218:THR:HB	1.83	0.59
1:A:107:CYS:SG	1:A:171:GLN:HG2	2.42	0.59
1:A:262:LEU:C	1:A:264:PHE:H	2.11	0.59
1:A:1155:ASP:OD1	1:A:1161:THR:HA	2.03	0.59
2:B:29:ASP:HB3	2:B:658:ILE:HD13	1.83	0.59
2:B:310:MET:O	2:B:313:MET:HB2	2.02	0.59
4:D:33:PHE:CZ	7:G:80:LYS:HE3	2.38	0.59
6:F:77:ASP:C	6:F:79:ARG:H	2.10	0.59
12:L:43:THR:HG22	12:L:43:THR:O	2.02	0.59
1:A:472:LEU:HD11	2:B:835:GLN:NE2	2.17	0.59
2:B:460:ALA:HB1	2:B:466:TRP:CZ3	2.38	0.59
3:C:124:LEU:O	3:C:125:MET:HB2	2.01	0.59
5:E:35:VAL:C	5:E:37:LEU:H	2.09	0.59
8:H:17:PRO:HB3	8:H:24:CYS:SG	2.43	0.59
11:K:63:VAL:HG23	11:K:63:VAL:O	2.03	0.59
1:A:50:ILE:O	1:A:52:GLY:N	2.28	0.59
2:B:1031:LEU:HD23	2:B:1044:ALA:HB2	1.85	0.59
2:B:1099:VAL:HG12	2:B:1100:ASP:H	1.67	0.59
5:E:131:THR:HG21	5:E:191:LYS:NZ	2.18	0.59
1:A:195:ASP:O	1:A:196:GLU:HB3	2.03	0.59
1:A:1015:VAL:HG12	1:A:1019:CYS:SG	2.42	0.59
1:A:1140:HIS:CE1	1:A:1272:THR:HG23	2.38	0.59
2:B:640:VAL:O	2:B:641:GLU:C	2.46	0.59
5:E:198:ILE:CD1	5:E:212:ARG:HG3	2.32	0.59
7:G:106:MET:CG	7:G:107:LYS:N	2.66	0.59
7:G:119:LEU:HD12	7:G:131:GLN:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:44:VAL:O	8:H:44:VAL:HG12	2.03	0.59
10:J:14:VAL:O	10:J:14:VAL:HG12	2.03	0.59
1:A:518:LYS:HE2	1:A:624:SER:O	2.02	0.58
1:A:1063:MET:CG	1:A:1436:ILE:HG23	2.33	0.58
1:A:1166:ASP:OD2	1:A:1239:ARG:HD2	2.03	0.58
2:B:616:ILE:HD12	2:B:616:ILE:N	2.18	0.58
3:C:35:ARG:NH1	11:K:41:THR:OG1	2.35	0.58
1:A:185:TRP:CZ3	1:A:200:ARG:HG2	2.37	0.58
1:A:549:MET:SD	1:A:577:ILE:HD11	2.43	0.58
2:B:557:PHE:C	2:B:557:PHE:HD2	2.09	0.58
2:B:811:TYR:N	2:B:811:TYR:CD1	2.71	0.58
4:D:156:ASP:C	4:D:158:GLU:N	2.60	0.58
11:K:65:HIS:CD2	11:K:67:PHE:HB2	2.38	0.58
12:L:53:HIS:O	12:L:55:ILE:HG12	2.04	0.58
1:A:311:GLN:O	1:A:312:PRO:C	2.47	0.58
1:A:472:LEU:O	1:A:475:THR:HB	2.03	0.58
1:A:658:LEU:HD23	1:A:659:HIS:CE1	2.38	0.58
1:A:783:THR:HG21	1:A:815:PHE:CZ	2.38	0.58
2:B:516:ASN:N	2:B:516:ASN:ND2	2.51	0.58
2:B:737:THR:CG2	9:I:66:PRO:HA	2.33	0.58
2:B:955:THR:CG2	2:B:956:THR:N	2.67	0.58
3:C:254:LYS:O	3:C:258:ILE:HD13	2.04	0.58
4:D:128:VAL:O	4:D:132:GLN:HG3	2.03	0.58
4:D:153:ARG:HH22	4:D:184:ALA:HA	1.68	0.58
1:A:407:ARG:HB3	1:A:430:TRP:CE2	2.38	0.58
1:A:868:TYR:HD2	1:A:1058:VAL:HG21	1.68	0.58
5:E:39:LEU:O	5:E:42:PHE:HB3	2.02	0.58
9:I:55:THR:HG21	9:I:109:ILE:HD13	1.84	0.58
1:A:503:GLN:C	1:A:504:LEU:HD12	2.29	0.58
1:A:998:LEU:H	1:A:998:LEU:HD12	1.69	0.58
1:A:1115:SER:C	1:A:1308:THR:HG22	2.28	0.58
1:A:1164:PRO:HG2	1:A:1165:GLU:H	1.69	0.58
2:B:359:GLU:O	2:B:362:PRO:HD3	2.04	0.58
2:B:840:ILE:HB	2:B:1011:ILE:HB	1.84	0.58
3:C:241:ASP:O	3:C:245:VAL:HG23	2.03	0.58
4:D:134:THR:CG2	4:D:135:GLY:N	2.66	0.58
9:I:8:ARG:HG3	9:I:34:TYR:CE1	2.38	0.58
10:J:44:TYR:HA	10:J:47:ARG:HB2	1.85	0.58
11:K:12:LEU:H	11:K:12:LEU:HD12	1.68	0.58
1:A:469:ARG:NH2	2:B:991:GLY:O	2.36	0.58
2:B:118:ARG:HH11	2:B:204:ILE:HD11	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:616:ILE:CG1	2:B:697:GLU:HA	2.33	0.58
2:B:847:ASP:C	2:B:849:GLY:N	2.61	0.58
3:C:235:VAL:HG13	10:J:13:VAL:CG2	2.34	0.58
3:C:263:THR:C	3:C:265:MET:N	2.61	0.58
4:D:130:LEU:HD22	4:D:134:THR:OG1	2.03	0.58
8:H:143:LEU:HD12	8:H:143:LEU:N	2.19	0.58
11:K:58:PHE:HB3	11:K:76:GLN:HB3	1.84	0.58
1:A:446:ARG:HD3	1:A:480:ALA:HB2	1.86	0.58
1:A:560:ILE:HG13	8:H:78:SER:CB	2.32	0.58
1:A:605:MET:HE3	1:A:606:LEU:H	1.68	0.58
1:A:965:GLN:O	1:A:968:GLN:HB2	2.04	0.58
2:B:604:ARG:HH22	2:B:614:SER:HA	1.69	0.58
2:B:705:MET:N	2:B:710:LEU:HD12	2.16	0.58
5:E:14:ARG:HH21	5:E:141:VAL:CG1	2.17	0.58
6:F:109:VAL:HG11	6:F:123:LYS:HG2	1.85	0.58
1:A:35:ILE:HA	1:A:52:GLY:O	2.04	0.58
1:A:665:GLY:O	1:A:667:GLY:N	2.37	0.58
1:A:1385:THR:HG22	1:A:1386:ARG:N	2.18	0.58
4:D:40:HIS:CB	7:G:73:LYS:NZ	2.55	0.58
1:A:11:LEU:HB2	2:B:1193:GLN:OE1	2.04	0.58
1:A:63:ARG:HA	1:A:74:MET:CE	2.33	0.58
1:A:278:THR:O	1:A:282:ASN:HB2	2.04	0.58
1:A:1116:LEU:HD11	1:A:1118:VAL:HG13	1.86	0.58
2:B:196:PRO:HG2	2:B:197:PHE:H	1.68	0.58
2:B:1001:PHE:HE2	3:C:34:ARG:CZ	2.17	0.58
1:A:471:ASN:OD1	1:A:472:LEU:N	2.36	0.58
1:A:545:GLN:O	1:A:546:VAL:C	2.46	0.58
2:B:224:GLN:O	2:B:238:ALA:HA	2.04	0.58
2:B:899:ILE:HD11	2:B:910:VAL:O	2.04	0.58
2:B:1102:LYS:O	2:B:1103:ILE:C	2.47	0.58
4:D:191:ALA:C	4:D:193:THR:H	2.11	0.58
7:G:7:LEU:CD1	7:G:45:ILE:HD11	2.33	0.58
8:H:18:GLY:O	8:H:19:ARG:HB2	2.04	0.58
9:I:61:ASP:C	9:I:63:GLY:H	2.12	0.58
1:A:2:VAL:HG21	2:B:1158:PHE:CA	2.34	0.57
1:A:1035:TYR:O	1:A:1037:LEU:N	2.37	0.57
1:A:1323:ASP:C	1:A:1325:THR:H	2.12	0.57
1:A:1327:ILE:HG22	5:E:147:HIS:HE1	1.69	0.57
1:A:1444:MET:O	6:F:132:LEU:HA	2.04	0.57
2:B:54:PHE:HA	2:B:58:THR:HB	1.86	0.57
2:B:838:SER:HB2	2:B:989:THR:O	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:51:ASN:O	4:D:54:GLU:HB3	2.04	0.57
5:E:90:VAL:HA	5:E:120:ALA:HB2	1.85	0.57
6:F:99:LEU:HD12	6:F:99:LEU:O	2.04	0.57
1:A:503:GLN:NE2	6:F:90:ARG:HH21	2.00	0.57
1:A:598:LEU:O	1:A:599:SER:C	2.47	0.57
1:A:698:GLN:HA	9:I:97:MET:O	2.04	0.57
1:A:1030:ARG:NH1	1:A:1035:TYR:OH	2.37	0.57
1:A:1400:CYS:SG	1:A:1409:LEU:HG	2.44	0.57
2:B:102:VAL:CG2	2:B:112:LEU:HD22	2.34	0.57
2:B:850:LEU:HD12	2:B:851:PHE:N	2.19	0.57
2:B:911:ILE:HD11	2:B:941:LEU:HD13	1.86	0.57
5:E:157:SER:C	5:E:159:ASP:N	2.60	0.57
5:E:180:ARG:HH21	5:E:192:ARG:CB	2.15	0.57
7:G:3:PHE:CE1	7:G:80:LYS:HE2	2.39	0.57
9:I:14:LEU:HA	9:I:28:GLU:O	2.04	0.57
1:A:262:LEU:O	1:A:264:PHE:N	2.37	0.57
1:A:310:GLY:O	1:A:312:PRO:HD2	2.03	0.57
1:A:401:GLY:C	1:A:435:HIS:CD2	2.82	0.57
1:A:532:ARG:HH22	1:A:745:GLN:HG2	1.67	0.57
1:A:658:LEU:HD13	2:B:831:SER:HA	1.86	0.57
1:A:863:VAL:HG11	1:A:866:PHE:CD2	2.40	0.57
2:B:283:VAL:O	2:B:286:PHE:N	2.37	0.57
2:B:825:VAL:CG1	2:B:826:ALA:N	2.67	0.57
10:J:3:VAL:HA	10:J:53:HIS:CE1	2.39	0.57
1:A:49:LYS:HZ1	1:A:61:ILE:N	2.02	0.57
1:A:1051:ALA:O	1:A:1055:ARG:HG3	2.04	0.57
2:B:180:TYR:HD1	2:B:180:TYR:H	1.51	0.57
2:B:244:LEU:HD21	2:B:366:GLN:NE2	2.20	0.57
3:C:36:VAL:HG21	3:C:251:LEU:HD22	1.86	0.57
1:A:1007:ILE:C	1:A:1009:ASN:N	2.62	0.57
2:B:833:TYR:N	2:B:833:TYR:CD1	2.73	0.57
6:F:103:MET:O	6:F:104:ASN:HB2	2.03	0.57
9:I:55:THR:CG2	9:I:58:VAL:HG21	2.34	0.57
1:A:61:ILE:O	1:A:63:ARG:N	2.38	0.57
1:A:81:PHE:CZ	2:B:1208:MET:HE2	2.39	0.57
2:B:117:ALA:HA	2:B:122:LEU:HD12	1.85	0.57
2:B:435:THR:HG23	2:B:439:ALA:CB	2.33	0.57
10:J:3:VAL:HG21	10:J:18:TRP:CB	2.31	0.57
1:A:265:LYS:HE2	1:A:322:VAL:CG1	2.35	0.57
1:A:1074:GLU:HB3	1:A:1075:PRO:HD3	1.87	0.57
1:A:1198:ASP:O	1:A:1202:MET:HG2	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1362:TYR:CD1	1:A:1363:VAL:N	2.73	0.57
1:A:1364:ASN:HD22	1:A:1365:TYR:N	2.02	0.57
2:B:258:LEU:HG	2:B:258:LEU:O	2.05	0.57
2:B:364:ILE:HG12	2:B:585:VAL:HG13	1.86	0.57
2:B:785:TYR:CD1	2:B:785:TYR:C	2.82	0.57
6:F:75:PRO:O	6:F:77:ASP:O	2.23	0.57
11:K:90:ALA:O	11:K:94:ILE:HG13	2.04	0.57
1:A:382:PRO:HD3	1:A:428:TYR:CD2	2.40	0.57
2:B:35:SER:O	2:B:39:ARG:HG3	2.05	0.57
3:C:27:LEU:O	3:C:28:ALA:C	2.47	0.57
10:J:14:VAL:HG12	10:J:50:ILE:HD11	1.86	0.57
1:A:321:PRO:O	1:A:322:VAL:CB	2.53	0.57
1:A:356:ASP:OD2	11:K:65:HIS:HE1	1.88	0.57
1:A:714:PHE:O	1:A:718:VAL:HG23	2.05	0.57
3:C:76:ASP:O	3:C:79:GLN:HG2	2.05	0.57
4:D:59:ILE:HG21	4:D:145:MET:SD	2.45	0.57
8:H:99:GLY:N	8:H:118:PHE:CD2	2.72	0.57
1:A:714:PHE:CB	9:I:97:MET:HE1	2.35	0.57
1:A:853:ASP:O	1:A:854:ASN:HB2	2.04	0.57
1:A:958:VAL:O	1:A:958:VAL:HG12	2.05	0.57
1:A:1396:ALA:O	1:A:1398:MET:N	2.38	0.57
2:B:351:TYR:O	2:B:355:ILE:HG13	2.05	0.57
2:B:957:ASN:O	2:B:959:ASP:N	2.37	0.57
4:D:189:ASP:O	4:D:193:THR:HB	2.05	0.57
7:G:1:MET:O	7:G:3:PHE:CE1	2.58	0.57
7:G:26:LEU:O	7:G:27:LYS:C	2.48	0.57
11:K:82:ASP:OD1	11:K:84:LYS:N	2.38	0.57
1:A:590:ARG:HH11	1:A:590:ARG:CG	2.18	0.56
1:A:632:VAL:O	1:A:633:VAL:C	2.48	0.56
2:B:44:VAL:O	2:B:45:SER:C	2.48	0.56
2:B:46:GLN:CG	2:B:47:GLN:H	2.10	0.56
2:B:114:PRO:O	2:B:116:GLU:N	2.38	0.56
2:B:949:VAL:HG12	2:B:950:ASP:H	1.70	0.56
2:B:952:VAL:HG12	2:B:953:LEU:N	2.20	0.56
5:E:114:ASN:O	5:E:115:ASN:HB3	2.03	0.56
7:G:35:GLU:OE2	7:G:48:VAL:HG23	2.05	0.56
1:A:47:ARG:HH12	1:A:254:GLU:CG	2.18	0.56
1:A:64:ASN:O	1:A:65:LEU:C	2.48	0.56
1:A:244:PRO:CB	1:A:245:PRO:HD3	2.34	0.56
1:A:311:GLN:HB3	1:A:312:PRO:CD	2.33	0.56
1:A:1127:ASP:HB3	1:A:1130:GLN:CB	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1214:GLU:O	1:A:1218:GLN:HG2	2.05	0.56
2:B:205:ILE:N	2:B:205:ILE:CD1	2.68	0.56
2:B:311:LEU:O	2:B:312:GLU:C	2.48	0.56
2:B:1103:ILE:O	2:B:1122:ARG:NH1	2.38	0.56
2:B:1196:ILE:HB	2:B:1197:PRO:HD2	1.86	0.56
3:C:239:PRO:HB2	3:C:241:ASP:OD1	2.05	0.56
6:F:81:THR:HG21	6:F:136:ARG:CD	2.32	0.56
7:G:1:MET:HG3	7:G:85:GLU:OE2	2.05	0.56
12:L:47:ARG:HH11	12:L:47:ARG:HG3	1.70	0.56
1:A:21:LEU:HG	1:A:1413:GLY:O	2.06	0.56
1:A:67:CYS:O	1:A:68:GLN:HB2	2.04	0.56
1:A:79:GLY:HA3	1:A:243:PRO:HG3	1.86	0.56
1:A:108:MET:SD	1:A:108:MET:N	2.79	0.56
1:A:252:PHE:O	1:A:256:GLN:NE2	2.39	0.56
1:A:265:LYS:N	1:A:265:LYS:HD2	2.20	0.56
1:A:299:HIS:C	1:A:301:ALA:H	2.11	0.56
1:A:490:HIS:HB3	2:B:1150:ARG:NH1	2.20	0.56
1:A:663:SER:OG	1:A:664:THR:N	2.36	0.56
1:A:940:ARG:HG2	1:A:940:ARG:HH11	1.71	0.56
1:A:1418:LEU:HD23	2:B:1222:ARG:HD2	1.86	0.56
2:B:190:TYR:CE2	10:J:62:ARG:HB3	2.40	0.56
2:B:805:THR:HA	2:B:809:MET:HE1	1.86	0.56
3:C:60:ASP:OD2	12:L:60:ARG:NH2	2.39	0.56
3:C:76:ASP:O	3:C:77:ILE:C	2.48	0.56
6:F:90:ARG:HD3	6:F:155:LEU:HD11	1.87	0.56
6:F:109:VAL:HG12	6:F:110:ASP:N	2.20	0.56
6:F:130:ILE:O	6:F:148:VAL:HG21	2.06	0.56
7:G:1:MET:SD	7:G:1:MET:O	2.63	0.56
9:I:74:GLU:HA	9:I:80:SER:O	2.06	0.56
10:J:1:MET:N	10:J:56:LEU:N	2.53	0.56
10:J:27:GLU:C	10:J:29:GLU:H	2.13	0.56
1:A:1283:VAL:HG12	1:A:1284:MET:N	2.21	0.56
2:B:882:THR:HB	2:B:934:LYS:O	2.05	0.56
3:C:56:THR:HG22	3:C:57:VAL:N	2.16	0.56
12:L:40:LEU:HD22	12:L:44:ASP:CG	2.31	0.56
1:A:23:SER:O	1:A:24:PRO:C	2.48	0.56
1:A:492:PRO:O	1:A:493:GLN:NE2	2.38	0.56
1:A:567:LYS:CG	1:A:568:PRO:CD	2.79	0.56
1:A:852:TYR:CE2	1:A:1060:PRO:HB2	2.40	0.56
1:A:877:HIS:C	1:A:878:ILE:HG13	2.29	0.56
2:B:35:SER:HA	2:B:811:TYR:CE2	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:579:ARG:HG2	2:B:579:ARG:HH11	1.69	0.56
2:B:997:GLU:CD	2:B:997:GLU:H	2.13	0.56
5:E:93:MET:SD	5:E:97:VAL:HG23	2.46	0.56
7:G:99:PHE:HZ	7:G:163:ILE:HD13	1.70	0.56
8:H:116:TYR:HB2	8:H:123:MET:HB3	1.86	0.56
1:A:475:THR:CG2	1:A:476:SER:H	2.19	0.56
1:A:586:ILE:HG22	1:A:587:HIS:N	2.21	0.56
1:A:666:ILE:CD1	1:A:667:GLY:H	2.18	0.56
1:A:836:TYR:CD2	1:A:840:ARG:HD2	2.40	0.56
1:A:858:ASN:ND2	1:A:858:ASN:C	2.59	0.56
1:A:907:THR:HG22	1:A:908:LEU:N	2.20	0.56
1:A:1010:ALA:HA	1:A:1013:ASP:OD2	2.06	0.56
1:A:1029:ARG:HH11	1:A:1029:ARG:HG3	1.70	0.56
2:B:549:THR:CG2	2:B:550:ASP:H	2.06	0.56
2:B:877:PRO:C	2:B:878:GLN:HG3	2.31	0.56
2:B:980:PHE:CD2	2:B:1094:ARG:HA	2.40	0.56
5:E:3:GLN:HG3	5:E:4:GLU:N	2.21	0.56
7:G:7:LEU:O	7:G:73:LYS:HD2	2.05	0.56
9:I:68:LEU:HB3	9:I:84:VAL:HG23	1.87	0.56
10:J:53:HIS:CD2	10:J:54:VAL:N	2.74	0.56
1:A:817:ALA:O	1:A:818:MET:C	2.48	0.56
1:A:1157:ASP:C	1:A:1159:ARG:H	2.14	0.56
2:B:295:GLY:H	2:B:298:LEU:HD23	1.70	0.56
2:B:1001:PHE:CE2	3:C:34:ARG:NE	2.73	0.56
2:B:1162:ILE:HD11	2:B:1194:ILE:HD13	1.87	0.56
5:E:192:ARG:HG3	5:E:192:ARG:NH1	2.21	0.56
7:G:51:TYR:O	7:G:54:ILE:HG13	2.06	0.56
9:I:25:LEU:HB3	9:I:38:ALA:HB2	1.88	0.56
1:A:722:LEU:HD22	1:A:799:PHE:CD1	2.41	0.56
1:A:857:ARG:HD3	1:A:861:GLY:O	2.06	0.56
1:A:873:MET:HE3	1:A:957:PRO:HG3	1.87	0.56
1:A:899:VAL:HB	1:A:929:LEU:HD12	1.87	0.56
2:B:604:ARG:NH2	2:B:614:SER:HA	2.21	0.56
2:B:705:MET:H	2:B:710:LEU:CD1	2.14	0.56
3:C:174:ALA:O	3:C:175:ALA:HB2	2.05	0.56
1:A:3:GLY:O	1:A:4:GLN:HB2	2.06	0.56
1:A:35:ILE:HG22	1:A:84:ILE:HD12	1.86	0.56
1:A:269:ILE:HG12	1:A:299:HIS:HB3	1.88	0.56
1:A:482:PHE:C	1:A:484:GLY:H	2.13	0.56
1:A:666:ILE:HD12	1:A:666:ILE:N	2.21	0.56
1:A:844:ALA:O	1:A:845:LEU:HD23	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:855:THR:CG2	1:A:857:ARG:HE	2.07	0.56
1:A:897:TYR:CD2	1:A:936:LEU:HD13	2.40	0.56
1:A:1299:VAL:HG12	1:A:1300:LYS:H	1.71	0.56
2:B:637:LEU:HD12	2:B:693:ILE:HD12	1.88	0.56
3:C:51:VAL:HG22	3:C:155:LEU:HD22	1.88	0.56
4:D:64:VAL:C	4:D:66:ARG:H	2.14	0.56
7:G:111:THR:HB	7:G:114:LEU:HB2	1.88	0.56
1:A:427:GLN:HB2	1:A:430:TRP:CD1	2.41	0.56
1:A:547:LEU:HD22	11:K:58:PHE:CE1	2.41	0.56
2:B:308:TRP:CH2	9:I:45:ARG:HG2	2.41	0.56
2:B:984:HIS:CG	2:B:1025:HIS:HB2	2.41	0.56
3:C:252:GLN:HG3	11:K:95:ILE:HG23	1.87	0.56
8:H:81:PRO:HB2	8:H:82:PRO:CD	2.30	0.56
1:A:49:LYS:NZ	1:A:61:ILE:HG13	2.22	0.55
1:A:268:ASP:HB3	1:A:299:HIS:ND1	2.21	0.55
2:B:129:PHE:HA	2:B:165:VAL:O	2.06	0.55
2:B:710:LEU:O	2:B:711:GLU:HG2	2.06	0.55
5:E:23:VAL:O	5:E:28:TYR:HB2	2.07	0.55
7:G:56:ILE:O	7:G:57:GLN:HB2	2.06	0.55
1:A:60:SER:C	1:A:61:ILE:HG13	2.30	0.55
1:A:845:LEU:O	1:A:846:GLU:C	2.49	0.55
2:B:29:ASP:HB3	2:B:658:ILE:CD1	2.36	0.55
2:B:527:THR:OG1	2:B:528:PRO:HD2	2.06	0.55
2:B:843:GLN:O	2:B:846:ILE:HB	2.07	0.55
5:E:197:LYS:HE2	5:E:199:ILE:HD11	1.87	0.55
7:G:88:ASP:HB3	7:G:144:ARG:HA	1.88	0.55
7:G:150:CYS:C	7:G:151:ILE:HG13	2.31	0.55
8:H:123:MET:HE1	8:H:142:LEU:CD1	2.36	0.55
1:A:114:LEU:O	1:A:115:LEU:HG	2.07	0.55
1:A:845:LEU:HB3	1:A:848:ILE:HD12	1.88	0.55
1:A:963:ILE:HD13	1:A:1049:ILE:HG12	1.87	0.55
1:A:1279:ILE:HD11	1:A:1316:VAL:HG21	1.88	0.55
6:F:90:ARG:HD3	6:F:155:LEU:HD12	1.88	0.55
1:A:207:ILE:O	1:A:208:LEU:C	2.48	0.55
1:A:265:LYS:HD2	1:A:265:LYS:H	1.72	0.55
1:A:903:ASN:C	1:A:903:ASN:ND2	2.64	0.55
1:A:1242:VAL:O	1:A:1243:VAL:HB	2.07	0.55
1:A:1438:THR:HB	2:B:1144:ALA:CB	2.37	0.55
2:B:195:CYS:SG	2:B:197:PHE:HB2	2.47	0.55
3:C:215:GLU:O	3:C:216:GLY:C	2.50	0.55
8:H:95:TYR:HB3	8:H:144:ILE:HB	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:268:ASP:HB3	1:A:299:HIS:CE1	2.41	0.55
1:A:458:HIS:CE1	1:A:507:VAL:HG21	2.41	0.55
1:A:730:GLY:O	1:A:732:LEU:N	2.40	0.55
2:B:763:GLN:HG2	2:B:765:PRO:CD	2.35	0.55
2:B:865:LYS:NZ	2:B:869:SER:HA	2.22	0.55
4:D:52:LEU:HD21	4:D:147:TYR:HE2	1.70	0.55
1:A:873:MET:C	1:A:1058:VAL:CG2	2.80	0.55
1:A:1017:LEU:CB	5:E:205:SER:HA	2.37	0.55
1:A:1373:ASP:HA	1:A:1376:THR:HG22	1.89	0.55
3:C:5:GLY:O	3:C:7:GLN:HG3	2.06	0.55
6:F:118:LEU:HD12	6:F:118:LEU:O	2.07	0.55
7:G:145:VAL:HG12	7:G:146:LYS:N	2.21	0.55
11:K:21:ILE:HG23	11:K:31:VAL:CG1	2.36	0.55
1:A:504:LEU:HD12	1:A:504:LEU:N	2.21	0.55
1:A:840:ARG:O	1:A:841:LEU:C	2.47	0.55
1:A:1032:LEU:O	1:A:1036:ARG:HD3	2.07	0.55
1:A:1279:ILE:HD11	1:A:1316:VAL:CG2	2.37	0.55
2:B:223:VAL:HG11	2:B:381:MET:HG2	1.88	0.55
2:B:526:GLU:OE2	2:B:752:ALA:HB2	2.06	0.55
2:B:746:SER:HB2	2:B:1046:PRO:HG2	1.89	0.55
2:B:773:MET:C	2:B:775:LYS:H	2.13	0.55
2:B:1165:ILE:CD1	4:D:17:LYS:CB	2.85	0.55
3:C:254:LYS:C	3:C:256:ALA:H	2.15	0.55
7:G:117:GLN:C	7:G:119:LEU:H	2.15	0.55
8:H:89:LEU:HB3	8:H:91:ASP:OD1	2.07	0.55
10:J:44:TYR:HA	10:J:47:ARG:CB	2.37	0.55
1:A:166:GLY:O	1:A:167:CYS:SG	2.65	0.55
1:A:567:LYS:CB	1:A:568:PRO:CD	2.85	0.55
1:A:1409:LEU:HD13	2:B:1207:LEU:CD2	2.36	0.55
2:B:57:TYR:CD1	2:B:57:TYR:N	2.74	0.55
2:B:199:MET:N	2:B:199:MET:SD	2.79	0.55
2:B:360:PHE:C	2:B:360:PHE:CD2	2.85	0.55
2:B:971:THR:OG1	3:C:61:GLU:HG3	2.07	0.55
3:C:168:ALA:C	3:C:170:TRP:N	2.64	0.55
8:H:84:ALA:C	8:H:86:ASP:H	2.15	0.55
1:A:185:TRP:HZ3	1:A:200:ARG:HG2	1.71	0.55
1:A:353:ILE:HG21	1:A:487:MET:CE	2.37	0.55
1:A:548:ASN:HA	11:K:60:ALA:HB1	1.89	0.55
2:B:38:PHE:HD1	2:B:811:TYR:CD2	2.24	0.55
2:B:97:VAL:HG12	2:B:178:ASN:ND2	2.22	0.55
2:B:324:ILE:HD13	2:B:330:ALA:HA	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:806:THR:HA	2:B:1045:SER:OG	2.07	0.55
3:C:39:ALA:CA	3:C:164:ALA:HB3	2.28	0.55
5:E:128:PRO:HA	5:E:129:PRO:C	2.32	0.55
7:G:125:SER:OG	7:G:128:PRO:HA	2.07	0.55
8:H:100:THR:HG22	8:H:101:ALA:N	2.21	0.55
1:A:56:PRO:O	1:A:57:ARG:CG	2.51	0.55
1:A:658:LEU:HD23	1:A:659:HIS:HE1	1.72	0.55
1:A:1227:ILE:HG22	1:A:1228:TRP:H	1.70	0.55
2:B:114:PRO:HG2	2:B:115:GLN:H	1.71	0.55
2:B:235:SER:C	2:B:236:HIS:HD2	2.14	0.55
2:B:603:LEU:HB3	2:B:609:ILE:CD1	2.37	0.55
2:B:696:GLU:O	2:B:699:GLU:HB2	2.07	0.55
2:B:893:LEU:HD11	2:B:910:VAL:HG11	1.88	0.55
2:B:1115:THR:CG2	2:B:1117:GLN:HG3	2.36	0.55
6:F:96:THR:O	6:F:100:GLN:HG3	2.07	0.55
11:K:12:LEU:HD12	11:K:12:LEU:N	2.21	0.55
1:A:341:MET:HE1	2:B:1135:ARG:HH12	1.69	0.54
2:B:95:ILE:CG1	2:B:130:VAL:HG22	2.37	0.54
2:B:254:LEU:HD23	2:B:381:MET:HE1	1.90	0.54
2:B:492:LEU:O	2:B:495:LEU:N	2.40	0.54
2:B:493:SER:HA	2:B:751:VAL:HG21	1.90	0.54
2:B:558:LEU:C	2:B:560:GLU:H	2.15	0.54
2:B:1082:MET:O	3:C:189:THR:HG23	2.07	0.54
3:C:31:ASN:OD1	3:C:34:ARG:NH1	2.40	0.54
7:G:27:LYS:O	7:G:30:LEU:HB3	2.07	0.54
10:J:1:MET:HE2	10:J:60:PHE:CZ	2.42	0.54
1:A:68:GLN:C	1:A:70:CYS:N	2.65	0.54
1:A:800:VAL:CG1	1:A:808:LEU:HG	2.38	0.54
1:A:1220:PHE:O	1:A:1221:LYS:HB2	2.08	0.54
1:A:1451:VAL:C	1:A:1453:TYR:H	2.16	0.54
7:G:81:PRO:HB3	7:G:106:MET:HE1	1.88	0.54
1:A:50:ILE:C	1:A:52:GLY:N	2.64	0.54
1:A:90:VAL:HG12	1:A:91:PHE:N	2.22	0.54
1:A:350:ARG:HB2	1:A:488:ASN:OD1	2.07	0.54
1:A:598:LEU:HD22	8:H:25:ARG:NH1	2.22	0.54
1:A:873:MET:HG2	1:A:957:PRO:HB3	1.89	0.54
1:A:1372:VAL:O	1:A:1376:THR:HG22	2.08	0.54
2:B:125:SER:HA	2:B:171:PRO:HA	1.89	0.54
2:B:1040:ASN:O	2:B:1041:GLU:C	2.50	0.54
9:I:82:GLU:HB3	9:I:104:LEU:HD12	1.90	0.54
9:I:99:LEU:C	9:I:100:PHE:HD1	2.16	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:399:HIS:HB3	1:A:400:PRO:CD	2.30	0.54
1:A:666:ILE:H	2:B:1026:LEU:HD22	1.72	0.54
1:A:896:ARG:NH2	1:A:1030:ARG:NH2	2.55	0.54
2:B:552:MET:C	2:B:554:ILE:H	2.15	0.54
2:B:1034:VAL:CG1	2:B:1035:ALA:N	2.67	0.54
2:B:1152:MET:HE3	2:B:1157:ALA:HA	1.90	0.54
11:K:47:ARG:HD3	11:K:59:ALA:O	2.08	0.54
1:A:265:LYS:CE	1:A:322:VAL:HG13	2.37	0.54
1:A:316:GLN:O	1:A:317:LYS:C	2.50	0.54
1:A:829:VAL:C	1:A:831:THR:H	2.14	0.54
1:A:842:VAL:HG11	2:B:1136:ASP:OD2	2.07	0.54
1:A:939:ASP:O	1:A:943:LEU:HG	2.07	0.54
4:D:24:ALA:HA	7:G:83:LYS:O	2.08	0.54
11:K:47:ARG:O	11:K:47:ARG:HD2	2.08	0.54
1:A:464:PRO:HG2	1:A:465:TYR:HD1	1.73	0.54
2:B:1180:PHE:HB3	2:B:1191:ILE:CD1	2.38	0.54
3:C:18:VAL:HG23	3:C:240:VAL:HB	1.90	0.54
5:E:46:TYR:CE2	5:E:58:MET:HA	2.43	0.54
8:H:41:ASP:OD2	8:H:122:LEU:N	2.41	0.54
1:A:416:ARG:C	1:A:417:TYR:CD2	2.85	0.54
2:B:582:VAL:HG23	2:B:626:ILE:HB	1.89	0.54
2:B:980:PHE:HE1	2:B:990:ILE:HD11	1.73	0.54
4:D:51:ASN:O	4:D:52:LEU:O	2.25	0.54
1:A:694:THR:O	1:A:698:GLN:HG3	2.08	0.54
1:A:738:LYS:C	1:A:740:LEU:H	2.15	0.54
1:A:1118:VAL:O	1:A:1305:VAL:HG13	2.08	0.54
2:B:235:SER:OG	2:B:236:HIS:CD2	2.61	0.54
2:B:872:GLU:HA	2:B:915:THR:O	2.08	0.54
3:C:8:VAL:HG12	3:C:9:LYS:N	2.23	0.54
3:C:168:ALA:C	3:C:170:TRP:H	2.16	0.54
3:C:226:ASP:O	3:C:227:THR:HB	2.07	0.54
1:A:960:ILE:O	1:A:961:ARG:C	2.50	0.54
2:B:53:GLN:HG2	2:B:547:VAL:CG2	2.35	0.54
2:B:315:LYS:N	2:B:316:PRO:HD2	2.23	0.54
2:B:880:THR:HB	2:B:934:LYS:HD2	1.90	0.54
3:C:18:VAL:CG2	3:C:240:VAL:HB	2.37	0.54
3:C:166:GLU:O	3:C:167:HIS:HB2	2.08	0.54
3:C:258:ILE:HD12	3:C:258:ILE:N	2.22	0.54
1:A:364:VAL:O	1:A:364:VAL:HG13	2.08	0.54
1:A:381:THR:HG23	1:A:383:TYR:H	1.73	0.54
1:A:417:TYR:CD2	1:A:417:TYR:N	2.75	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:32:CYS:SG	9:I:33:SER:N	2.81	0.54
1:A:93:VAL:CG1	1:A:301:ALA:HB1	2.37	0.53
1:A:567:LYS:HB2	1:A:568:PRO:CD	2.39	0.53
2:B:465:ASN:H	2:B:465:ASN:ND2	2.04	0.53
3:C:98:VAL:O	3:C:99:LEU:HD23	2.08	0.53
4:D:153:ARG:C	4:D:154:PHE:CD1	2.86	0.53
11:K:50:LEU:HD11	11:K:75:ILE:CD1	2.36	0.53
1:A:265:LYS:HZ1	1:A:322:VAL:HG22	1.72	0.53
1:A:341:MET:HE2	1:A:843:LYS:HZ1	1.74	0.53
1:A:847:ASP:OD1	1:A:848:ILE:HG13	2.08	0.53
1:A:1017:LEU:HB3	5:E:205:SER:HA	1.89	0.53
1:A:1195:LEU:HD11	1:A:1267:MET:HE1	1.91	0.53
1:A:1364:ASN:O	1:A:1365:TYR:C	2.50	0.53
1:A:1369:ALA:O	1:A:1370:LEU:C	2.51	0.53
2:B:39:ARG:HG2	2:B:39:ARG:HH11	1.72	0.53
2:B:579:ARG:N	2:B:589:VAL:HG13	2.22	0.53
2:B:1074:ASN:HB2	2:B:1081:LEU:HD21	1.90	0.53
3:C:107:SER:C	3:C:109:SER:H	2.16	0.53
4:D:56:ARG:HD2	4:D:149:THR:OG1	2.08	0.53
5:E:207:ARG:HH11	5:E:207:ARG:HB3	1.72	0.53
10:J:43:ARG:HG3	10:J:45:CYS:SG	2.47	0.53
1:A:1053:PHE:C	1:A:1055:ARG:H	2.15	0.53
2:B:777:ALA:HA	2:B:1095:LEU:HA	1.90	0.53
2:B:841:MET:SD	2:B:846:ILE:HD11	2.49	0.53
2:B:865:LYS:HZ2	2:B:869:SER:HA	1.74	0.53
1:A:528:LEU:HD23	1:A:751:SER:HA	1.91	0.53
1:A:886:ILE:HD11	1:A:943:LEU:CB	2.35	0.53
1:A:1004:ASN:OD1	1:A:1005:GLU:N	2.42	0.53
2:B:213:ILE:HD12	2:B:497:ARG:HB3	1.90	0.53
2:B:234:ILE:HD12	2:B:234:ILE:N	2.23	0.53
2:B:1050:ILE:HG22	2:B:1051:THR:N	2.24	0.53
2:B:1068:GLY:O	2:B:1069:PHE:O	2.27	0.53
3:C:3:GLU:HG2	3:C:4:GLU:N	2.22	0.53
4:D:29:LEU:HD22	7:G:82:PHE:CD2	2.43	0.53
4:D:63:LEU:HD13	4:D:133:THR:OG1	2.09	0.53
4:D:202:ILE:CG2	4:D:207:LEU:HB2	2.38	0.53
5:E:9:ILE:HD11	5:E:53:PRO:HD3	1.90	0.53
5:E:90:VAL:O	5:E:90:VAL:HG22	2.08	0.53
10:J:44:TYR:HD2	10:J:44:TYR:N	2.07	0.53
1:A:244:PRO:O	1:A:247:ARG:N	2.41	0.53
1:A:546:VAL:O	1:A:550:LEU:HG	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:618:GLU:O	1:A:620:LYS:N	2.42	0.53
1:A:1377:THR:O	1:A:1379:GLY:N	2.41	0.53
2:B:281:PRO:O	2:B:283:VAL:N	2.41	0.53
2:B:615:MET:CB	2:B:626:ILE:HG12	2.39	0.53
2:B:803:LEU:CD1	2:B:1032:SER:HB3	2.38	0.53
3:C:235:VAL:HG13	10:J:13:VAL:HG23	1.89	0.53
4:D:137:ASN:C	4:D:137:ASN:HD22	2.17	0.53
5:E:78:LEU:HD21	5:E:80:VAL:HG23	1.89	0.53
9:I:13:MET:O	9:I:14:LEU:HD23	2.08	0.53
10:J:13:VAL:C	10:J:14:VAL:HG23	2.34	0.53
10:J:44:TYR:N	10:J:44:TYR:CD2	2.76	0.53
1:A:590:ARG:HB2	1:A:605:MET:HB3	1.90	0.53
1:A:874:ASP:N	1:A:1058:VAL:HG22	2.24	0.53
1:A:881:GLN:NE2	1:A:958:VAL:O	2.38	0.53
1:A:1007:ILE:O	1:A:1009:ASN:N	2.41	0.53
2:B:360:PHE:O	2:B:361:LEU:C	2.51	0.53
2:B:496:ARG:HB3	2:B:496:ARG:HH11	1.73	0.53
2:B:526:GLU:HG2	2:B:538:ASN:HD22	1.74	0.53
2:B:833:TYR:N	2:B:833:TYR:HD1	2.06	0.53
1:A:77:CYS:C	1:A:78:PRO:O	2.45	0.53
1:A:299:HIS:C	1:A:301:ALA:N	2.67	0.53
1:A:420:ARG:O	1:A:421:ALA:C	2.51	0.53
1:A:427:GLN:HG3	1:A:430:TRP:CE2	2.43	0.53
1:A:794:PRO:C	1:A:796:SER:H	2.15	0.53
1:A:817:ALA:O	1:A:819:GLY:N	2.41	0.53
1:A:1120:LEU:HD13	1:A:1304:TRP:O	2.09	0.53
2:B:455:SER:O	2:B:456:GLY:C	2.52	0.53
4:D:53:SER:HB3	4:D:152:SER:CA	2.38	0.53
5:E:55:ARG:HD2	5:E:83:CYS:O	2.08	0.53
7:G:1:MET:SD	7:G:79:PHE:CE1	3.02	0.53
1:A:306:ASN:HD21	1:A:322:VAL:HB	1.73	0.53
1:A:372:LYS:HA	1:A:435:HIS:HD1	1.73	0.53
1:A:814:PHE:O	1:A:817:ALA:HB3	2.08	0.53
1:A:852:TYR:CD2	1:A:1060:PRO:HB2	2.44	0.53
1:A:1094:VAL:HG12	1:A:1095:THR:N	2.24	0.53
2:B:872:GLU:CD	2:B:914:LYS:HE2	2.33	0.53
8:H:84:ALA:C	8:H:86:ASP:N	2.66	0.53
9:I:8:ARG:HG2	9:I:34:TYR:HE1	1.73	0.53
12:L:52:GLY:O	12:L:53:HIS:C	2.52	0.53
1:A:34:LYS:HB3	1:A:36:ARG:HE	1.73	0.53
1:A:43:GLU:O	1:A:44:THR:HB	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:THR:HG22	1:A:263:THR:O	2.09	0.53
1:A:366:VAL:CG2	1:A:460:VAL:HG22	2.39	0.53
1:A:577:ILE:C	1:A:579:SER:N	2.65	0.53
1:A:577:ILE:HA	1:A:580:VAL:HG23	1.91	0.53
1:A:605:MET:HE2	1:A:607:ILE:CG1	2.34	0.53
1:A:730:GLY:C	1:A:732:LEU:N	2.67	0.53
1:A:1365:TYR:O	1:A:1367:HIS:N	2.42	0.53
2:B:65:GLU:CG	2:B:66:ASP:H	2.12	0.53
2:B:798:TYR:CE2	3:C:62:PHE:CE2	2.97	0.53
2:B:879:ARG:HH11	2:B:883:LEU:CD2	2.20	0.53
9:I:50:THR:CG2	9:I:52:ILE:HG12	2.38	0.53
1:A:89:PRO:HB2	1:A:204:THR:HG22	1.91	0.53
1:A:90:VAL:CG1	1:A:297:GLN:HA	2.39	0.53
1:A:901:LEU:CG	1:A:926:GLN:HE21	2.22	0.53
2:B:39:ARG:HG2	2:B:39:ARG:NH1	2.23	0.53
2:B:459:TYR:C	2:B:459:TYR:CD2	2.86	0.53
2:B:483:LEU:HD11	2:B:491:THR:CG2	2.34	0.53
2:B:654:ARG:H	2:B:657:HIS:CD2	2.23	0.53
2:B:948:ILE:HG22	2:B:949:VAL:O	2.09	0.53
2:B:1107:ALA:O	2:B:1108:ARG:HG2	2.09	0.53
3:C:39:ALA:HA	3:C:164:ALA:CB	2.31	0.53
3:C:73:GLN:NE2	3:C:74:SER:H	2.06	0.53
4:D:116:SER:O	4:D:117:GLU:CB	2.57	0.53
6:F:101:ILE:HD11	6:F:124:GLU:OE1	2.09	0.53
10:J:44:TYR:HD2	10:J:44:TYR:H	1.55	0.53
1:A:92:HIS:HB3	1:A:95:PHE:HB2	1.89	0.52
1:A:241:VAL:HG13	1:A:266:LEU:HD13	1.91	0.52
1:A:325:ILE:HG22	2:B:1210:MET:HE2	1.92	0.52
1:A:534:LEU:O	1:A:534:LEU:HG	2.07	0.52
1:A:548:ASN:OD1	11:K:60:ALA:HB1	2.09	0.52
1:A:673:GLY:O	1:A:676:MET:HB2	2.09	0.52
1:A:730:GLY:C	1:A:732:LEU:H	2.18	0.52
2:B:383:ASN:O	2:B:384:ARG:C	2.53	0.52
2:B:1039:GLY:HA2	10:J:51:LEU:HD21	1.91	0.52
2:B:1208:MET:O	2:B:1211:ASN:N	2.40	0.52
3:C:147:LEU:HD12	3:C:151:GLN:O	2.09	0.52
5:E:22:MET:HE3	5:E:26:ARG:CZ	2.39	0.52
6:F:73:ALA:HA	6:F:143:PHE:CE1	2.43	0.52
8:H:138:GLU:O	8:H:139:ASN:C	2.52	0.52
12:L:34:CYS:O	12:L:35:SER:C	2.52	0.52
1:A:42:ASP:HB3	1:A:45:GLN:H	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:401:PHE:CD2	2:B:521:LEU:HD12	2.40	0.52
2:B:589:VAL:HG12	2:B:590:HIS:N	2.17	0.52
2:B:778:MET:HE2	2:B:1094:ARG:CG	2.37	0.52
8:H:127:GLY:O	8:H:128:ASN:HB2	2.10	0.52
1:A:18:GLN:O	2:B:1215:ARG:HG2	2.10	0.52
1:A:18:GLN:CB	2:B:1215:ARG:HB2	2.39	0.52
1:A:463:ILE:HB	1:A:464:PRO:HD2	1.91	0.52
1:A:744:LYS:HG2	1:A:748:MET:HE2	1.90	0.52
1:A:768:GLN:HG2	1:A:816:HIS:N	2.24	0.52
1:A:1322:ILE:O	1:A:1324:PRO:HD3	2.10	0.52
2:B:773:MET:C	2:B:775:LYS:N	2.65	0.52
2:B:1084:GLN:C	2:B:1085:ILE:HD12	2.35	0.52
3:C:254:LYS:C	3:C:256:ALA:N	2.67	0.52
6:F:140:ASP:C	6:F:140:ASP:OD1	2.52	0.52
10:J:3:VAL:HA	10:J:53:HIS:ND1	2.24	0.52
1:A:1343:ALA:HB2	5:E:150:VAL:HG22	1.92	0.52
2:B:57:TYR:N	2:B:57:TYR:HD1	2.08	0.52
2:B:189:LEU:O	2:B:192:LEU:N	2.28	0.52
4:D:33:PHE:CZ	7:G:80:LYS:CE	2.92	0.52
4:D:118:THR:O	4:D:122:GLU:CB	2.57	0.52
5:E:116:ILE:HG22	5:E:117:THR:N	2.23	0.52
5:E:161:LYS:C	5:E:163:GLU:N	2.68	0.52
1:A:1116:LEU:HB2	1:A:1329:THR:OG1	2.08	0.52
2:B:810:GLU:HB2	2:B:815:ARG:HH22	1.74	0.52
5:E:161:LYS:HD2	5:E:195:VAL:HG23	1.92	0.52
5:E:168:TYR:HB2	5:E:170:LEU:HG	1.90	0.52
6:F:81:THR:HB	6:F:136:ARG:HH11	1.75	0.52
10:J:23:ASN:C	10:J:25:LEU:N	2.64	0.52
1:A:353:ILE:HG21	1:A:487:MET:HG3	1.91	0.52
1:A:1208:THR:HG22	1:A:1210:GLY:H	1.75	0.52
1:A:1242:VAL:HG12	1:A:1243:VAL:N	2.17	0.52
6:F:109:VAL:HG13	6:F:127:GLU:OE1	2.09	0.52
1:A:92:HIS:O	1:A:95:PHE:N	2.34	0.52
1:A:231:PRO:C	1:A:233:TRP:H	2.18	0.52
2:B:750:GLY:O	2:B:751:VAL:C	2.53	0.52
5:E:161:LYS:C	5:E:163:GLU:H	2.17	0.52
7:G:1:MET:O	7:G:1:MET:HE2	2.10	0.52
7:G:79:PHE:CZ	7:G:106:MET:HE2	2.45	0.52
7:G:111:THR:HG22	7:G:113:HIS:H	1.74	0.52
8:H:31:THR:O	8:H:31:THR:HG22	2.10	0.52
1:A:84:ILE:HD11	1:A:270:LEU:CD1	2.34	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:504:LEU:HD11	6:F:91:ALA:CB	2.39	0.52
1:A:578:LEU:HD23	1:A:612:ILE:CD1	2.39	0.52
1:A:628:GLY:O	1:A:632:VAL:HG23	2.10	0.52
1:A:648:ASN:O	1:A:649:ILE:C	2.53	0.52
1:A:1327:ILE:HG22	5:E:147:HIS:CE1	2.45	0.52
2:B:1107:ALA:O	2:B:1108:ARG:O	2.28	0.52
3:C:239:PRO:O	3:C:241:ASP:N	2.43	0.52
7:G:26:LEU:O	7:G:29:LYS:N	2.43	0.52
8:H:4:THR:CA	8:H:60:ALA:HB2	2.34	0.52
9:I:100:PHE:N	9:I:100:PHE:CD1	2.78	0.52
1:A:40:THR:HG22	1:A:41:MET:CG	2.32	0.52
1:A:47:ARG:O	1:A:48:ALA:HB2	2.08	0.52
1:A:418:SER:O	1:A:420:ARG:N	2.43	0.52
1:A:630:ILE:HD13	1:A:646:PHE:CZ	2.45	0.52
1:A:1444:MET:CE	6:F:135:ARG:HB2	2.35	0.52
2:B:597:MET:HA	2:B:597:MET:HE3	1.91	0.52
2:B:1022:THR:HG23	2:B:1022:THR:O	2.10	0.52
2:B:1132:GLU:O	2:B:1135:ARG:HB3	2.09	0.52
4:D:47:LEU:HD11	7:G:3:PHE:CD2	2.45	0.52
5:E:55:ARG:C	5:E:57:MET:H	2.17	0.52
5:E:168:TYR:CB	5:E:170:LEU:HG	2.40	0.52
8:H:113:ALA:HB1	8:H:125:LEU:O	2.09	0.52
9:I:85:PHE:HD2	9:I:85:PHE:N	1.88	0.52
10:J:45:CYS:O	10:J:48:ARG:HG3	2.10	0.52
1:A:767:GLN:NE2	1:A:774:ARG:HB3	2.24	0.52
1:A:885:THR:O	1:A:940:ARG:HD2	2.10	0.52
1:A:1030:ARG:HG3	1:A:1034:GLU:OE2	2.09	0.52
1:A:1164:PRO:O	1:A:1166:ASP:N	2.43	0.52
2:B:333:PHE:C	2:B:334:ILE:HG13	2.34	0.52
2:B:555:ILE:HD11	2:B:587:HIS:CE1	2.44	0.52
6:F:130:ILE:O	6:F:148:VAL:CG2	2.58	0.52
8:H:139:ASN:O	8:H:140:ALA:HB2	2.08	0.52
9:I:55:THR:HG22	9:I:58:VAL:HG21	1.92	0.52
11:K:31:VAL:CG1	11:K:32:VAL:N	2.72	0.52
1:A:253:ASN:HB3	2:B:935:ARG:NH2	2.25	0.51
1:A:283:GLY:O	1:A:285:PRO:HD3	2.10	0.51
1:A:306:ASN:ND2	1:A:322:VAL:HB	2.24	0.51
1:A:335:ARG:O	1:A:336:ILE:C	2.52	0.51
1:A:1334:ASP:O	1:A:1336:MET:N	2.43	0.51
2:B:205:ILE:O	2:B:206:ASN:C	2.52	0.51
2:B:240:ILE:HG23	2:B:240:ILE:O	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1034:VAL:HG12	2:B:1035:ALA:H	1.75	0.51
3:C:181:ASP:OD2	3:C:185:LYS:N	2.41	0.51
8:H:59:ILE:O	8:H:60:ALA:HB3	2.10	0.51
1:A:277:GLU:C	1:A:279:LEU:H	2.17	0.51
1:A:901:LEU:HD22	1:A:919:ILE:HG21	1.92	0.51
2:B:377:PHE:C	2:B:379:GLY:N	2.62	0.51
2:B:616:ILE:HG13	2:B:697:GLU:HA	1.92	0.51
2:B:843:GLN:HB2	2:B:993:THR:HB	1.91	0.51
3:C:215:GLU:O	3:C:217:ASP:N	2.43	0.51
3:C:258:ILE:N	3:C:258:ILE:CD1	2.73	0.51
7:G:62:LEU:HB3	7:G:63:PRO:CD	2.39	0.51
8:H:82:PRO:C	8:H:84:ALA:H	2.17	0.51
12:L:34:CYS:SG	12:L:51:CYS:SG	3.08	0.51
1:A:55:ASP:N	1:A:56:PRO:HD3	2.24	0.51
1:A:854:ASN:HB3	1:A:1000:LEU:HD21	1.91	0.51
1:A:1336:MET:CE	1:A:1381:LEU:HG	2.39	0.51
2:B:900:ALA:HB3	12:L:61:THR:OG1	2.10	0.51
2:B:999:MET:HB3	2:B:1007:VAL:HG21	1.92	0.51
3:C:263:THR:O	3:C:265:MET:N	2.43	0.51
6:F:79:ARG:HG3	6:F:144:GLU:OE1	2.10	0.51
7:G:49:LEU:HG	7:G:76:ALA:HA	1.93	0.51
7:G:80:LYS:O	7:G:80:LYS:HG2	2.10	0.51
9:I:85:PHE:CD1	9:I:99:LEU:HD13	2.45	0.51
11:K:7:PHE:HA	11:K:10:PHE:CE2	2.45	0.51
1:A:93:VAL:HG22	1:A:301:ALA:HA	1.92	0.51
1:A:365:GLY:O	1:A:468:PHE:HA	2.11	0.51
1:A:525:GLN:CD	2:B:836:GLU:HG2	2.36	0.51
1:A:1127:ASP:HB3	1:A:1130:GLN:HB3	1.92	0.51
2:B:460:ALA:HB1	2:B:466:TRP:CE3	2.45	0.51
4:D:64:VAL:C	4:D:66:ARG:N	2.67	0.51
6:F:131:PRO:C	6:F:132:LEU:HD23	2.35	0.51
8:H:27:GLU:HA	8:H:38:LEU:O	2.11	0.51
8:H:40:LEU:CD1	8:H:123:MET:HB2	2.35	0.51
11:K:85:ASP:O	11:K:88:LYS:HB2	2.10	0.51
1:A:18:GLN:HB3	2:B:1215:ARG:HG3	1.91	0.51
1:A:134:ARG:O	1:A:138:ILE:HG13	2.11	0.51
1:A:262:LEU:C	1:A:264:PHE:N	2.66	0.51
1:A:757:ASN:HA	2:B:1021:MET:SD	2.50	0.51
1:A:901:LEU:HG	1:A:926:GLN:NE2	2.25	0.51
2:B:108:VAL:HG12	2:B:109:THR:H	1.74	0.51
2:B:240:ILE:CG2	2:B:254:LEU:HB3	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:637:LEU:O	2:B:690:VAL:HG13	2.10	0.51
2:B:843:GLN:O	2:B:844:SER:C	2.54	0.51
3:C:33:LEU:O	3:C:34:ARG:C	2.54	0.51
1:A:408:ASP:C	1:A:410:GLY:H	2.18	0.51
1:A:1063:MET:SD	1:A:1436:ILE:HG12	2.50	0.51
1:A:1161:THR:OG1	1:A:1239:ARG:NH2	2.44	0.51
1:A:1289:ARG:HD2	1:A:1303:GLU:OE2	2.10	0.51
2:B:204:ILE:C	2:B:205:ILE:HD12	2.36	0.51
2:B:300:HIS:CE1	2:B:376:PHE:CE1	2.99	0.51
4:D:118:THR:C	4:D:122:GLU:N	2.69	0.51
4:D:175:PHE:HZ	7:G:85:GLU:HG3	1.75	0.51
4:D:210:ILE:O	4:D:214:LEU:HG	2.10	0.51
1:A:58:LEU:HD22	1:A:80:HIS:O	2.11	0.51
1:A:68:GLN:O	1:A:70:CYS:N	2.43	0.51
1:A:89:PRO:C	1:A:204:THR:HG21	2.36	0.51
1:A:95:PHE:O	1:A:96:ILE:C	2.53	0.51
1:A:903:ASN:ND2	1:A:905:ASP:H	2.09	0.51
2:B:181:LEU:HD22	2:B:189:LEU:HD22	1.91	0.51
2:B:862:GLN:HG2	2:B:963:PHE:CD1	2.44	0.51
2:B:1174:LYS:O	2:B:1175:LEU:C	2.53	0.51
3:C:77:ILE:CG2	3:C:161:LYS:HE3	2.39	0.51
3:C:82:TYR:O	3:C:83:SER:C	2.54	0.51
6:F:77:ASP:C	6:F:79:ARG:N	2.67	0.51
7:G:117:GLN:O	7:G:119:LEU:N	2.43	0.51
1:A:605:MET:HE3	1:A:606:LEU:N	2.25	0.51
1:A:870:GLU:HB2	5:E:204:THR:HG21	1.92	0.51
1:A:979:SER:HG	1:A:981:LEU:HG	1.76	0.51
2:B:765:PRO:O	2:B:768:THR:N	2.44	0.51
3:C:145:CYS:HA	10:J:2:ILE:HD11	1.92	0.51
8:H:62:SER:O	8:H:63:LEU:C	2.54	0.51
1:A:26:GLU:O	1:A:27:VAL:C	2.54	0.51
1:A:231:PRO:HA	1:A:234:MET:HE2	1.92	0.51
1:A:382:PRO:HD3	1:A:428:TYR:CE2	2.45	0.51
1:A:608:ILE:HB	1:A:613:ILE:HD11	1.92	0.51
1:A:783:THR:HG22	1:A:784:LEU:HG	1.93	0.51
1:A:1305:VAL:HG12	1:A:1306:LEU:N	2.25	0.51
2:B:247:GLY:N	2:B:418:LYS:HZ1	2.07	0.51
2:B:284:ILE:HG12	2:B:324:ILE:HD12	1.92	0.51
2:B:521:LEU:HD13	2:B:633:VAL:HB	1.93	0.51
2:B:780:VAL:HG12	2:B:782:LEU:O	2.10	0.51
3:C:91:HIS:HD2	3:C:91:HIS:O	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:242:GLN:C	3:C:244:VAL:H	2.18	0.51
4:D:167:LEU:O	4:D:170:THR:OG1	2.23	0.51
5:E:14:ARG:HH21	5:E:141:VAL:HG12	1.73	0.51
1:A:367:PRO:HA	1:A:463:ILE:O	2.10	0.51
1:A:483:ASP:O	2:B:979:LYS:HE3	2.11	0.51
1:A:577:ILE:O	1:A:580:VAL:HG23	2.11	0.51
1:A:874:ASP:CA	1:A:1058:VAL:HG22	2.42	0.51
3:C:30:ALA:O	3:C:33:LEU:HB3	2.11	0.51
4:D:66:ARG:O	4:D:70:PHE:HB2	2.10	0.51
4:D:176:GLU:C	4:D:178:ALA:N	2.63	0.51
8:H:142:LEU:C	8:H:143:LEU:HD12	2.36	0.51
9:I:13:MET:HG3	9:I:14:LEU:H	1.75	0.51
1:A:37:PHE:N	1:A:37:PHE:CD1	2.79	0.50
1:A:265:LYS:HE2	1:A:322:VAL:HG13	1.93	0.50
1:A:325:ILE:CG2	2:B:1210:MET:HE2	2.42	0.50
1:A:823:GLY:O	1:A:825:ILE:N	2.44	0.50
1:A:1116:LEU:C	1:A:1116:LEU:HD12	2.36	0.50
1:A:1120:LEU:CD1	1:A:1120:LEU:H	2.24	0.50
2:B:63:ILE:HD12	2:B:421:PHE:CE2	2.46	0.50
2:B:230:ALA:N	2:B:231:PRO:HD2	2.25	0.50
2:B:511:PRO:O	2:B:512:ARG:C	2.54	0.50
2:B:728:ARG:NH1	2:B:1047:PHE:HB3	2.26	0.50
2:B:806:THR:CG2	2:B:808:ALA:HB3	2.41	0.50
2:B:1174:LYS:O	2:B:1176:ASN:HB2	2.11	0.50
2:B:1186:ASP:C	2:B:1186:ASP:OD1	2.54	0.50
6:F:99:LEU:HD12	6:F:99:LEU:C	2.36	0.50
1:A:24:PRO:HD2	1:A:233:TRP:CD1	2.46	0.50
1:A:115:LEU:CB	1:A:122:MET:HE2	2.41	0.50
2:B:179:CYS:SG	2:B:181:LEU:HB2	2.52	0.50
2:B:435:THR:CG2	2:B:437:GLU:HB2	2.42	0.50
3:C:6:PRO:HB3	3:C:25:VAL:HG12	1.92	0.50
7:G:13:LEU:CD2	7:G:17:PHE:HB2	2.39	0.50
11:K:69:ALA:O	11:K:70:ARG:HB3	2.10	0.50
1:A:58:LEU:O	1:A:59:GLY:O	2.30	0.50
1:A:244:PRO:CB	1:A:245:PRO:CD	2.89	0.50
1:A:356:ASP:O	1:A:358:ASN:N	2.42	0.50
1:A:388:LEU:HD22	1:A:432:VAL:CG2	2.41	0.50
1:A:567:LYS:HD3	8:H:95:TYR:CG	2.46	0.50
1:A:614:PHE:CD1	1:A:614:PHE:C	2.89	0.50
1:A:901:LEU:HD22	1:A:919:ILE:HG22	1.91	0.50
1:A:1265:ASN:C	1:A:1267:MET:N	2.67	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:893:LEU:HD22	2:B:897:GLY:C	2.36	0.50
2:B:1006:ILE:HD13	10:J:44:TYR:HE2	1.73	0.50
3:C:18:VAL:O	3:C:20:PHE:HD2	1.95	0.50
3:C:46:ILE:HG13	3:C:72:LEU:HD11	1.93	0.50
3:C:163:ILE:O	3:C:165:LYS:N	2.45	0.50
3:C:191:TYR:HD2	3:C:201:TRP:CD1	2.28	0.50
10:J:32:GLU:O	10:J:34:THR:N	2.44	0.50
10:J:53:HIS:HD2	10:J:54:VAL:N	2.08	0.50
1:A:414:ASP:OD1	1:A:416:ARG:HG3	2.11	0.50
1:A:567:LYS:HD2	1:A:568:PRO:HD2	1.92	0.50
1:A:921:GLY:O	1:A:922:ASP:C	2.53	0.50
1:A:982:THR:HB	1:A:985:ASP:H	1.76	0.50
1:A:1028:THR:O	1:A:1032:LEU:HD12	2.12	0.50
2:B:364:ILE:HG22	2:B:365:THR:N	2.26	0.50
2:B:603:LEU:HB3	2:B:609:ILE:HG13	1.92	0.50
2:B:653:VAL:HG23	2:B:689:LEU:HB3	1.93	0.50
2:B:953:LEU:HD23	2:B:965:LYS:H	1.76	0.50
2:B:984:HIS:CD2	2:B:1025:HIS:HB2	2.46	0.50
3:C:29:MET:HE2	11:K:98:LEU:CD2	2.42	0.50
4:D:192:LYS:HZ3	4:D:192:LYS:HB3	1.75	0.50
7:G:1:MET:O	7:G:3:PHE:CD1	2.64	0.50
1:A:116:ASP:O	1:A:118:HIS:N	2.45	0.50
1:A:215:SER:HB3	1:A:218:ASP:OD2	2.12	0.50
1:A:466:SER:HB3	2:B:1103:ILE:HG12	1.93	0.50
1:A:600:PRO:C	1:A:602:ASP:H	2.19	0.50
1:A:746:MET:CE	2:B:1018:PRO:HG2	2.40	0.50
1:A:809:THR:H	1:A:812:GLU:HB2	1.76	0.50
1:A:1280:GLU:O	1:A:1281:ARG:C	2.55	0.50
2:B:980:PHE:HE2	2:B:1094:ARG:CB	2.24	0.50
2:B:1039:GLY:HA2	10:J:51:LEU:CD2	2.42	0.50
2:B:1110:PRO:O	2:B:1119:VAL:HG13	2.11	0.50
3:C:90:ASP:O	3:C:91:HIS:CB	2.60	0.50
3:C:242:GLN:C	3:C:244:VAL:N	2.68	0.50
7:G:9:LEU:HG	7:G:10:ASN:N	2.27	0.50
8:H:27:GLU:HG2	8:H:39:THR:HG23	1.93	0.50
10:J:7:CYS:SG	10:J:49:MET:HE3	2.52	0.50
12:L:27:LEU:HD13	12:L:37:LYS:HE2	1.94	0.50
1:A:14:VAL:CG2	2:B:1216:LEU:HD13	2.40	0.50
1:A:443:LEU:O	1:A:489:LEU:HD12	2.12	0.50
1:A:507:VAL:HG13	1:A:521:MET:HE1	1.93	0.50
1:A:765:VAL:HG12	1:A:766:GLY:N	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1004:ASN:O	1:A:1008:GLN:HB2	2.12	0.50
1:A:1094:VAL:HG13	1:A:1113:THR:CG2	2.37	0.50
1:A:1410:PHE:HA	2:B:1212:ILE:CD1	2.41	0.50
2:B:642:ASP:CB	2:B:649:LYS:HA	2.41	0.50
2:B:1183:LYS:N	2:B:1183:LYS:CE	2.71	0.50
3:C:54:ASN:HB2	3:C:153:LEU:HD12	1.92	0.50
5:E:96:PHE:CZ	5:E:100:ILE:HD11	2.46	0.50
7:G:17:PHE:N	7:G:17:PHE:CD2	2.78	0.50
1:A:784:LEU:HB3	1:A:785:PRO:HD2	1.94	0.50
1:A:853:ASP:OD1	1:A:855:THR:N	2.43	0.50
1:A:868:TYR:CE1	1:A:1064:VAL:CG1	2.91	0.50
1:A:909:ASP:O	1:A:911:SER:N	2.45	0.50
2:B:496:ARG:NH1	2:B:539:LEU:HB2	2.27	0.50
2:B:745:PRO:C	2:B:747:MET:N	2.68	0.50
2:B:831:SER:CB	2:B:994:TYR:OH	2.60	0.50
3:C:98:VAL:HG23	3:C:122:SER:HB3	1.93	0.50
3:C:256:ALA:C	3:C:258:ILE:H	2.19	0.50
7:G:117:GLN:C	7:G:119:LEU:N	2.69	0.50
8:H:33:GLN:C	8:H:35:GLN:H	2.18	0.50
9:I:69:PRO:HG2	9:I:85:PHE:CD2	2.46	0.50
9:I:100:PHE:HD1	9:I:100:PHE:N	2.09	0.50
1:A:28:ARG:O	1:A:29:ALA:C	2.55	0.50
1:A:311:GLN:CB	1:A:312:PRO:HD3	2.42	0.50
1:A:326:ARG:HH22	1:A:1407:GLU:HG3	1.77	0.50
1:A:567:LYS:HB3	8:H:95:TYR:HA	1.93	0.50
1:A:996:ASN:O	1:A:998:LEU:HD12	2.10	0.50
2:B:785:TYR:C	2:B:787:VAL:H	2.19	0.50
2:B:973:ILE:HG23	2:B:974:PRO:HD2	1.93	0.50
2:B:1002:THR:HG21	2:B:1006:ILE:HD12	1.93	0.50
5:E:92:THR:O	5:E:95:THR:HB	2.11	0.50
9:I:50:THR:HG22	9:I:51:ASN:N	2.26	0.50
1:A:135:PHE:C	1:A:137:ALA:N	2.70	0.50
1:A:317:LYS:O	1:A:318:SER:CB	2.60	0.50
1:A:629:LEU:O	1:A:633:VAL:HG23	2.12	0.50
1:A:1377:THR:O	1:A:1378:GLN:C	2.54	0.50
2:B:327:ARG:O	2:B:331:LEU:HD13	2.11	0.50
2:B:466:TRP:CE3	2:B:466:TRP:HA	2.46	0.50
2:B:758:PHE:CE1	2:B:1027:ILE:CG2	2.95	0.50
2:B:1166:CYS:SG	2:B:1166:CYS:O	2.69	0.50
4:D:134:THR:HG22	4:D:135:GLY:N	2.27	0.50
6:F:116:ASP:C	6:F:116:ASP:OD1	2.55	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:80:LYS:O	7:G:82:PHE:CE1	2.65	0.50
9:I:102:VAL:CG1	9:I:103:CYS:H	2.24	0.50
1:A:218:ASP:HA	1:A:221:SER:OG	2.12	0.49
1:A:406:ILE:HG13	1:A:431:LYS:HB2	1.93	0.49
1:A:512:VAL:HA	1:A:519:PRO:HA	1.93	0.49
1:A:852:TYR:HA	1:A:1060:PRO:HB3	1.94	0.49
1:A:1319:VAL:HG13	1:A:1320:PRO:HD2	1.94	0.49
2:B:734:HIS:O	2:B:735:ALA:HB2	2.12	0.49
2:B:1084:GLN:OE1	3:C:189:THR:CG2	2.59	0.49
3:C:63:ILE:O	3:C:64:ALA:C	2.55	0.49
4:D:206:GLU:C	4:D:208:GLU:N	2.68	0.49
5:E:48:ASP:CG	5:E:49:SER:N	2.69	0.49
7:G:81:PRO:HA	7:G:85:GLU:OE1	2.12	0.49
8:H:102:TYR:N	8:H:102:TYR:CD2	2.80	0.49
9:I:4:PHE:HE1	9:I:6:PHE:HE2	1.58	0.49
10:J:27:GLU:O	10:J:29:GLU:N	2.45	0.49
2:B:102:VAL:HG22	2:B:112:LEU:HD22	1.94	0.49
2:B:370:PHE:HE2	2:B:373:ARG:NH1	2.08	0.49
2:B:437:GLU:CB	2:B:439:ALA:HA	2.42	0.49
2:B:882:THR:O	2:B:883:LEU:HB2	2.11	0.49
2:B:916:THR:O	2:B:935:ARG:HG3	2.12	0.49
2:B:1065:GLN:NE2	2:B:1067:ARG:N	2.54	0.49
2:B:1182:CYS:O	2:B:1183:LYS:C	2.54	0.49
4:D:56:ARG:NH2	4:D:57:LEU:HD21	2.26	0.49
1:A:545:GLN:O	1:A:548:ASN:N	2.46	0.49
1:A:984:LYS:O	1:A:985:ASP:C	2.54	0.49
1:A:1017:LEU:HB2	5:E:206:GLY:N	2.17	0.49
7:G:143:ILE:CG2	7:G:144:ARG:N	2.75	0.49
8:H:143:LEU:C	8:H:144:ILE:HG13	2.37	0.49
1:A:325:ILE:O	1:A:326:ARG:C	2.55	0.49
1:A:755:PHE:O	1:A:756:ILE:C	2.55	0.49
1:A:1209:MET:CE	1:A:1236:LEU:HB3	2.42	0.49
2:B:1174:LYS:O	2:B:1176:ASN:N	2.44	0.49
3:C:99:LEU:HD12	3:C:118:LEU:HD13	1.94	0.49
6:F:119:ARG:HG3	6:F:119:ARG:NH1	2.26	0.49
6:F:124:GLU:HB3	6:F:130:ILE:HG12	1.94	0.49
1:A:369:SER:CB	11:K:2:ASN:OD1	2.60	0.49
1:A:535:THR:CG2	1:A:616:VAL:HA	2.40	0.49
1:A:540:PHE:HB3	1:A:571:LEU:HD23	1.95	0.49
1:A:741:ASN:ND2	1:A:743:VAL:HB	2.24	0.49
1:A:763:ALA:O	1:A:803:SER:HB3	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1045:VAL:O	1:A:1049:ILE:HG13	2.13	0.49
1:A:1451:VAL:C	1:A:1453:TYR:N	2.70	0.49
2:B:38:PHE:CD1	2:B:811:TYR:CD2	3.01	0.49
2:B:401:PHE:N	2:B:517:THR:OG1	2.28	0.49
2:B:515:HIS:CD2	2:B:517:THR:HG23	2.48	0.49
2:B:542:MET:HE3	2:B:636:PRO:CG	2.42	0.49
2:B:661:LEU:C	2:B:663:ALA:H	2.19	0.49
1:A:61:ILE:HG22	1:A:62:ASP:H	1.78	0.49
1:A:62:ASP:HB3	1:A:64:ASN:ND2	2.28	0.49
1:A:243:PRO:O	1:A:244:PRO:C	2.56	0.49
1:A:351:THR:HG21	2:B:1103:ILE:HG13	1.95	0.49
1:A:357:PRO:HD2	2:B:833:TYR:CE1	2.47	0.49
1:A:849:MET:HE3	1:A:1061:GLY:O	2.13	0.49
1:A:1280:GLU:O	1:A:1281:ARG:O	2.30	0.49
2:B:616:ILE:HG12	2:B:697:GLU:HA	1.95	0.49
2:B:758:PHE:HE1	2:B:1027:ILE:HG22	1.77	0.49
2:B:794:ASN:C	2:B:795:ILE:HD12	2.37	0.49
4:D:135:GLY:C	4:D:137:ASN:H	2.21	0.49
12:L:48:CYS:SG	12:L:49:LYS:N	2.85	0.49
1:A:399:HIS:CG	1:A:400:PRO:N	2.78	0.49
1:A:1006:ILE:HD12	5:E:163:GLU:HG3	1.94	0.49
2:B:563:MET:HA	2:B:589:VAL:O	2.13	0.49
2:B:744:HIS:HD2	2:B:746:SER:OG	1.95	0.49
2:B:890:TYR:O	2:B:892:LYS:N	2.45	0.49
3:C:140:ASN:O	3:C:141:GLY:O	2.30	0.49
4:D:68:ARG:C	4:D:70:PHE:N	2.70	0.49
7:G:53:ASN:HD22	7:G:53:ASN:N	2.09	0.49
9:I:111:THR:HG22	9:I:113:ASP:N	2.27	0.49
12:L:49:LYS:O	12:L:50:ASP:CB	2.60	0.49
1:A:244:PRO:HG2	1:A:245:PRO:CD	2.43	0.49
1:A:877:HIS:O	1:A:878:ILE:CG1	2.60	0.49
1:A:1053:PHE:C	1:A:1055:ARG:N	2.70	0.49
1:A:1130:GLN:O	1:A:1134:ILE:HG13	2.12	0.49
2:B:361:LEU:N	2:B:362:PRO:CD	2.75	0.49
2:B:519:TRP:C	2:B:519:TRP:CD1	2.91	0.49
8:H:41:ASP:O	8:H:42:ILE:HG13	2.13	0.49
8:H:128:ASN:CG	8:H:128:ASN:O	2.54	0.49
1:A:38:PRO:HA	1:A:270:LEU:HD23	1.95	0.49
1:A:269:ILE:CG1	1:A:299:HIS:HB3	2.42	0.49
1:A:442:VAL:O	1:A:457:ALA:HA	2.12	0.49
1:A:857:ARG:NH1	6:F:139:PRO:HB2	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1073:GLY:O	1:A:1076:ALA:HB3	2.13	0.49
2:B:287:ARG:HG2	2:B:292:ILE:HA	1.93	0.49
2:B:903:VAL:HG12	2:B:904:ARG:N	2.28	0.49
3:C:77:ILE:C	3:C:79:GLN:H	2.20	0.49
4:D:138:ASN:OD1	4:D:141:LEU:HB2	2.13	0.49
6:F:89:GLU:HB3	6:F:134:ILE:HD13	1.95	0.49
8:H:99:GLY:HA3	8:H:118:PHE:HA	1.95	0.49
1:A:652:VAL:O	1:A:653:VAL:C	2.56	0.49
1:A:1001:ARG:O	1:A:1002:GLY:O	2.31	0.49
2:B:223:VAL:CG1	2:B:381:MET:HG2	2.42	0.49
2:B:308:TRP:CZ3	9:I:45:ARG:HB3	2.47	0.49
2:B:1001:PHE:CD1	2:B:1001:PHE:C	2.89	0.49
2:B:1081:LEU:O	2:B:1082:MET:C	2.55	0.49
3:C:77:ILE:O	3:C:79:GLN:N	2.46	0.49
3:C:243:VAL:O	3:C:243:VAL:HG12	2.11	0.49
4:D:115:HIS:CB	4:D:155:ARG:NH2	2.76	0.49
6:F:143:PHE:C	6:F:143:PHE:CD1	2.89	0.49
7:G:96:GLN:HA	7:G:121:PHE:CE2	2.48	0.49
1:A:40:THR:CG2	1:A:41:MET:HG3	2.36	0.48
1:A:605:MET:HE1	1:A:612:ILE:HG23	1.95	0.48
1:A:785:PRO:HG2	1:A:786:HIS:HD2	1.78	0.48
1:A:867:ILE:HD12	5:E:208:TYR:CE1	2.46	0.48
1:A:1005:GLU:O	1:A:1009:ASN:HB2	2.12	0.48
1:A:1349:TYR:HB2	1:A:1372:VAL:HG21	1.95	0.48
2:B:251:ILE:O	2:B:251:ILE:HG22	2.13	0.48
2:B:1087:PHE:HD2	2:B:1088:GLY:H	1.58	0.48
2:B:1187:ASN:OD1	2:B:1188:LYS:N	2.40	0.48
4:D:195:ILE:HG22	4:D:198:LEU:HG	1.95	0.48
5:E:202:SER:HB3	5:E:205:SER:O	2.13	0.48
7:G:1:MET:O	7:G:1:MET:CE	2.61	0.48
7:G:91:VAL:HG12	7:G:92:VAL:N	2.28	0.48
7:G:99:PHE:CE2	7:G:115:MET:HE2	2.49	0.48
1:A:16:GLU:HB3	1:A:1418:LEU:HD11	1.95	0.48
1:A:174:ILE:HG23	1:A:182:VAL:O	2.13	0.48
1:A:567:LYS:HZ2	8:H:46:LEU:HB2	1.78	0.48
1:A:981:LEU:CD2	1:A:1039:LYS:HA	2.42	0.48
1:A:1120:LEU:HD12	1:A:1120:LEU:H	1.78	0.48
2:B:125:SER:HA	2:B:172:ILE:H	1.78	0.48
2:B:839:MET:HE3	2:B:1010:LEU:HD11	1.93	0.48
5:E:29:PHE:O	5:E:30:ILE:CG1	2.59	0.48
7:G:15:PRO:O	7:G:16:SER:C	2.56	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:26:LEU:HD12	7:G:56:ILE:HD13	1.95	0.48
11:K:108:GLU:O	11:K:112:GLN:HG2	2.12	0.48
1:A:300:VAL:O	1:A:300:VAL:HG12	2.12	0.48
1:A:402:ALA:CB	1:A:434:ARG:HA	2.43	0.48
1:A:1369:ALA:O	1:A:1373:ASP:OD2	2.31	0.48
1:A:1388:GLY:O	1:A:1390:ASN:N	2.46	0.48
2:B:472:ALA:HB1	2:B:473:MET:HA	1.95	0.48
2:B:523:CYS:SG	2:B:524:PRO:HD2	2.54	0.48
2:B:550:ASP:OD1	2:B:551:PRO:HD2	2.13	0.48
2:B:642:ASP:CA	2:B:649:LYS:HA	2.41	0.48
2:B:800:GLN:HB3	10:J:52:THR:HG22	1.92	0.48
3:C:11:ARG:HD3	3:C:209:TYR:CE2	2.48	0.48
10:J:32:GLU:O	10:J:35:ALA:N	2.47	0.48
1:A:311:GLN:CB	1:A:312:PRO:CD	2.91	0.48
1:A:626:ASN:C	1:A:628:GLY:H	2.21	0.48
1:A:683:ILE:HD13	1:A:801:GLU:HG3	1.95	0.48
2:B:164:LYS:HZ3	2:B:443:ASN:CA	2.26	0.48
2:B:189:LEU:O	2:B:192:LEU:HB2	2.13	0.48
2:B:1178:ASN:O	2:B:1179:GLN:C	2.56	0.48
3:C:47:ASP:CA	12:L:69:ALA:CB	2.87	0.48
3:C:66:ARG:NH2	10:J:3:VAL:O	2.45	0.48
5:E:153:HIS:HB3	5:E:196:VAL:HG11	1.94	0.48
8:H:91:ASP:O	8:H:93:TYR:N	2.46	0.48
12:L:46:VAL:CG1	12:L:56:LEU:HD12	2.43	0.48
1:A:41:MET:O	1:A:42:ASP:C	2.56	0.48
1:A:244:PRO:O	1:A:246:VAL:N	2.46	0.48
1:A:340:LEU:HD13	1:A:1429:ILE:CG2	2.38	0.48
1:A:872:GLY:O	1:A:1058:VAL:HG23	2.14	0.48
1:A:1209:MET:HE1	1:A:1236:LEU:HB3	1.94	0.48
1:A:1342:GLU:CG	5:E:198:ILE:HD13	2.43	0.48
2:B:387:LEU:O	2:B:392:ARG:HB2	2.14	0.48
2:B:552:MET:C	2:B:554:ILE:N	2.72	0.48
3:C:112:ASN:HD22	3:C:112:ASN:N	2.12	0.48
4:D:192:LYS:HB3	4:D:192:LYS:NZ	2.28	0.48
5:E:22:MET:CE	5:E:26:ARG:NH2	2.74	0.48
1:A:299:HIS:O	1:A:301:ALA:N	2.46	0.48
1:A:898:ARG:HB2	1:A:933:TYR:CE1	2.49	0.48
1:A:1120:LEU:N	1:A:1120:LEU:CD1	2.76	0.48
2:B:1034:VAL:O	2:B:1036:ALA:N	2.46	0.48
2:B:1197:PRO:HG2	2:B:1200:ALA:HB3	1.92	0.48
3:C:25:VAL:HG23	3:C:228:PHE:CE1	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:105:GLY:O	3:C:149:LYS:O	2.32	0.48
4:D:138:ASN:C	4:D:140:ASP:N	2.70	0.48
6:F:127:GLU:O	6:F:129:LYS:HG3	2.14	0.48
10:J:16:ASP:OD1	10:J:17:LYS:N	2.43	0.48
10:J:48:ARG:HD2	10:J:49:MET:N	2.29	0.48
1:A:254:GLU:O	1:A:256:GLN:N	2.47	0.48
1:A:326:ARG:HG2	1:A:327:ALA:N	2.29	0.48
1:A:399:HIS:CB	1:A:400:PRO:CD	2.88	0.48
1:A:500:GLU:OE1	2:B:1143:ALA:C	2.57	0.48
2:B:414:ALA:O	2:B:415:GLN:C	2.57	0.48
2:B:756:ILE:O	2:B:759:PRO:HD3	2.14	0.48
5:E:13:TRP:O	5:E:16:PHE:HB3	2.14	0.48
5:E:55:ARG:C	5:E:57:MET:N	2.69	0.48
5:E:94:LYS:HE2	5:E:98:ILE:CD1	2.38	0.48
9:I:34:TYR:CD2	9:I:34:TYR:C	2.90	0.48
11:K:24:ASP:OD1	11:K:26:LYS:HB2	2.13	0.48
1:A:41:MET:HB3	1:A:48:ALA:O	2.13	0.48
1:A:71:GLN:C	1:A:73:GLY:N	2.69	0.48
1:A:332:LYS:O	1:A:334:GLY:N	2.46	0.48
1:A:340:LEU:HD21	2:B:1200:ALA:CA	2.43	0.48
1:A:341:MET:CE	2:B:1135:ARG:NH1	2.77	0.48
1:A:573:SER:O	1:A:576:GLN:HB2	2.12	0.48
1:A:1420:ASP:O	1:A:1421:CYS:HB2	2.13	0.48
2:B:210:LYS:HG3	2:B:461:LEU:O	2.13	0.48
2:B:552:MET:HA	2:B:555:ILE:HB	1.96	0.48
2:B:593:PRO:HG2	2:B:617:ARG:CZ	2.43	0.48
2:B:661:LEU:C	2:B:663:ALA:N	2.71	0.48
2:B:995:ARG:NH1	3:C:165:LYS:HG2	2.27	0.48
2:B:1099:VAL:C	2:B:1101:ASP:N	2.71	0.48
2:B:1159:ARG:HD3	2:B:1193:GLN:CG	2.37	0.48
3:C:46:ILE:HG23	3:C:157:CYS:HB3	1.96	0.48
5:E:153:HIS:HB3	5:E:196:VAL:CG1	2.44	0.48
1:A:427:GLN:O	1:A:428:TYR:C	2.56	0.48
1:A:1441:PHE:HZ	6:F:89:GLU:HA	1.78	0.48
2:B:234:ILE:HD12	2:B:234:ILE:H	1.79	0.48
2:B:1177:HIS:C	2:B:1179:GLN:H	2.22	0.48
2:B:1187:ASN:HD21	2:B:1190:ASP:HB3	1.79	0.48
3:C:147:LEU:HD23	3:C:147:LEU:N	2.28	0.48
4:D:38:ILE:HG22	4:D:39:ASN:O	2.14	0.48
7:G:80:LYS:HD3	7:G:80:LYS:H	1.77	0.48
1:A:942:PHE:C	1:A:942:PHE:CD2	2.91	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1101:LEU:O	1:A:1101:LEU:HD12	2.13	0.48
1:A:1333:ILE:HG22	1:A:1334:ASP:N	2.29	0.48
2:B:999:MET:HE3	2:B:999:MET:CA	2.35	0.48
3:C:194:GLU:O	3:C:195:GLN:HG3	2.14	0.48
10:J:53:HIS:CD2	10:J:54:VAL:C	2.92	0.48
11:K:93:SER:O	11:K:97:LYS:HG3	2.14	0.48
1:A:21:LEU:HD11	1:A:1414:ALA:HA	1.95	0.47
1:A:35:ILE:CG2	1:A:84:ILE:HD12	2.44	0.47
1:A:71:GLN:O	1:A:73:GLY:N	2.38	0.47
1:A:309:ALA:C	1:A:311:GLN:H	2.21	0.47
1:A:553:VAL:HG22	1:A:652:VAL:CG2	2.44	0.47
1:A:807:GLY:O	1:A:808:LEU:O	2.32	0.47
1:A:1369:ALA:O	1:A:1372:VAL:HG12	2.14	0.47
1:A:1450:LEU:HD11	6:F:108:PHE:CZ	2.49	0.47
2:B:192:LEU:O	2:B:193:LYS:CB	2.62	0.47
2:B:558:LEU:O	2:B:560:GLU:N	2.47	0.47
3:C:86:CYS:SG	3:C:92:CYS:SG	3.12	0.47
3:C:90:ASP:O	3:C:90:ASP:CG	2.56	0.47
3:C:183:TRP:O	3:C:185:LYS:N	2.48	0.47
7:G:115:MET:HB3	7:G:116:PRO:CD	2.41	0.47
11:K:47:ARG:HD2	11:K:47:ARG:C	2.38	0.47
1:A:450:LEU:HD12	1:A:450:LEU:H	1.78	0.47
1:A:567:LYS:HD2	1:A:568:PRO:CD	2.45	0.47
1:A:577:ILE:O	1:A:578:LEU:C	2.56	0.47
1:A:598:LEU:CA	8:H:122:LEU:HD13	2.39	0.47
2:B:102:VAL:CG2	2:B:112:LEU:HB2	2.41	0.47
2:B:542:MET:HG2	2:B:747:MET:HB3	1.96	0.47
2:B:803:LEU:HD12	2:B:1032:SER:HB3	1.95	0.47
2:B:918:ILE:HD12	2:B:935:ARG:HD3	1.97	0.47
4:D:20:GLU:O	4:D:21:GLU:O	2.32	0.47
5:E:18:THR:O	5:E:19:VAL:C	2.55	0.47
5:E:169:ARG:HH12	6:F:74:ILE:HD11	1.77	0.47
7:G:143:ILE:HG22	7:G:144:ARG:H	1.77	0.47
1:A:116:ASP:O	1:A:117:GLU:C	2.57	0.47
1:A:444:PHE:HB2	1:A:458:HIS:HD2	1.79	0.47
1:A:622:VAL:O	1:A:622:VAL:HG22	2.13	0.47
1:A:699:ALA:HB3	1:A:701:LEU:HG	1.96	0.47
1:A:1057:VAL:HG12	1:A:1058:VAL:N	2.29	0.47
1:A:1141:THR:OG1	1:A:1205:LYS:HD3	2.14	0.47
1:A:1222:ASN:O	1:A:1223:ASP:HB3	2.14	0.47
1:A:1451:VAL:O	1:A:1454:MET:HG2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:603:LEU:HD13	2:B:608:ASP:CB	2.43	0.47
2:B:653:VAL:HG22	2:B:689:LEU:HB3	1.95	0.47
2:B:806:THR:HG22	2:B:808:ALA:CB	2.44	0.47
2:B:806:THR:HG22	2:B:808:ALA:HB3	1.94	0.47
2:B:844:SER:O	2:B:847:ASP:HB2	2.14	0.47
2:B:847:ASP:O	2:B:849:GLY:N	2.47	0.47
2:B:882:THR:HG21	2:B:935:ARG:HA	1.95	0.47
2:B:954:VAL:O	12:L:55:ILE:O	2.31	0.47
3:C:167:HIS:CD2	3:C:168:ALA:H	2.31	0.47
3:C:208:GLU:C	3:C:210:GLU:H	2.22	0.47
4:D:35:LEU:HD12	4:D:35:LEU:N	2.29	0.47
5:E:124:VAL:HA	5:E:132:ILE:HD12	1.95	0.47
10:J:16:ASP:O	10:J:18:TRP:N	2.47	0.47
1:A:166:GLY:O	1:A:167:CYS:CB	2.62	0.47
1:A:167:CYS:SG	1:A:167:CYS:O	2.72	0.47
1:A:500:GLU:OE2	1:A:1438:THR:HG21	2.14	0.47
1:A:901:LEU:N	1:A:926:GLN:NE2	2.50	0.47
1:A:1015:VAL:O	1:A:1016:THR:C	2.57	0.47
1:A:1220:PHE:CD1	1:A:1224:LEU:HD23	2.49	0.47
2:B:185:THR:H	2:B:188:ASP:HB2	1.80	0.47
3:C:35:ARG:NH1	11:K:41:THR:H	2.12	0.47
3:C:209:TYR:HD1	3:C:209:TYR:H	1.60	0.47
4:D:51:ASN:O	4:D:52:LEU:C	2.57	0.47
6:F:132:LEU:HD23	6:F:132:LEU:N	2.29	0.47
10:J:56:LEU:O	10:J:57:ILE:C	2.58	0.47
1:A:279:LEU:O	1:A:284:ALA:HB2	2.14	0.47
1:A:381:THR:CG2	1:A:383:TYR:H	2.27	0.47
1:A:608:ILE:C	1:A:610:GLY:N	2.72	0.47
2:B:437:GLU:HB2	2:B:439:ALA:HA	1.96	0.47
2:B:461:LEU:N	2:B:461:LEU:HD12	2.29	0.47
2:B:520:GLY:HA2	2:B:748:ILE:HG22	1.95	0.47
2:B:950:ASP:O	2:B:951:GLN:HB2	2.13	0.47
7:G:66:GLY:O	7:G:67:SER:C	2.56	0.47
10:J:2:ILE:HG12	10:J:57:ILE:HD12	1.95	0.47
10:J:31:ASP:O	10:J:32:GLU:C	2.58	0.47
11:K:52:ASN:O	11:K:54:ARG:N	2.48	0.47
1:A:105:CYS:O	1:A:114:LEU:HG	2.15	0.47
1:A:496:GLU:O	1:A:499:ALA:HB3	2.15	0.47
1:A:500:GLU:OE2	2:B:1145:SER:CB	2.63	0.47
1:A:553:VAL:HG13	1:A:648:ASN:HB3	1.97	0.47
1:A:673:GLY:N	1:A:674:PRO:HD2	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:823:GLY:C	1:A:825:ILE:N	2.72	0.47
1:A:929:LEU:HD23	1:A:983:ILE:HG21	1.96	0.47
1:A:963:ILE:HD11	1:A:1048:ASN:CB	2.33	0.47
1:A:1127:ASP:HB3	1:A:1130:GLN:HB2	1.96	0.47
1:A:1162:VAL:O	1:A:1162:VAL:HG12	2.14	0.47
2:B:123:THR:O	2:B:125:SER:N	2.47	0.47
2:B:893:LEU:HD11	2:B:910:VAL:CG1	2.44	0.47
2:B:999:MET:HG2	2:B:1007:VAL:HG22	1.97	0.47
2:B:1214:PRO:O	2:B:1214:PRO:HG2	2.15	0.47
3:C:91:HIS:O	3:C:91:HIS:CD2	2.67	0.47
3:C:133:ILE:HD12	3:C:237:SER:HA	1.96	0.47
3:C:255:VAL:O	3:C:255:VAL:HG12	2.14	0.47
5:E:129:PRO:O	5:E:130:ALA:C	2.57	0.47
5:E:205:SER:O	5:E:206:GLY:C	2.58	0.47
8:H:58:THR:HB	8:H:143:LEU:HD13	1.96	0.47
8:H:110:ASP:O	8:H:128:ASN:ND2	2.48	0.47
1:A:65:LEU:O	1:A:66:LYS:C	2.57	0.47
1:A:120:GLU:C	1:A:122:MET:N	2.70	0.47
1:A:456:MET:HE1	1:A:474:VAL:CG2	2.44	0.47
1:A:774:ARG:H	1:A:774:ARG:HG2	1.50	0.47
1:A:775:ILE:HD12	1:A:818:MET:SD	2.54	0.47
1:A:977:LYS:HB3	1:A:978:PRO:HD2	1.95	0.47
1:A:1237:ILE:HG22	1:A:1238:ILE:N	2.29	0.47
2:B:225:VAL:HA	2:B:237:VAL:O	2.14	0.47
2:B:235:SER:C	2:B:236:HIS:CD2	2.93	0.47
2:B:373:ARG:CG	2:B:566:LEU:HD23	2.44	0.47
2:B:390:LEU:O	2:B:391:ASP:C	2.58	0.47
2:B:591:ARG:O	2:B:592:ASN:C	2.56	0.47
2:B:613:VAL:HG22	2:B:628:THR:HA	1.96	0.47
2:B:708:GLU:O	2:B:709:ASP:C	2.58	0.47
3:C:70:ILE:HD11	3:C:144:ILE:HG12	1.97	0.47
3:C:86:CYS:SG	3:C:88:CYS:SG	3.10	0.47
3:C:112:ASN:HB2	3:C:114:TYR:CE1	2.50	0.47
4:D:40:HIS:CE1	4:D:41:GLN:HG3	2.49	0.47
4:D:146:GLN:O	4:D:147:TYR:C	2.57	0.47
4:D:191:ALA:C	4:D:193:THR:N	2.73	0.47
4:D:206:GLU:C	4:D:208:GLU:H	2.23	0.47
5:E:35:VAL:O	5:E:37:LEU:N	2.48	0.47
8:H:15:VAL:HG22	8:H:26:ILE:HD11	1.96	0.47
8:H:58:THR:HG22	8:H:59:ILE:H	1.79	0.47
10:J:56:LEU:O	10:J:59:LYS:N	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:46:VAL:O	12:L:46:VAL:HG12	2.14	0.47
1:A:510:GLN:OE1	1:A:510:GLN:HA	2.14	0.47
1:A:1410:PHE:C	1:A:1412:ALA:H	2.23	0.47
2:B:118:ARG:HG2	2:B:204:ILE:HD13	1.97	0.47
2:B:284:ILE:HG23	2:B:324:ILE:CD1	2.45	0.47
2:B:879:ARG:O	2:B:880:THR:HB	2.15	0.47
3:C:238:ILE:HD11	3:C:246:ARG:NH1	2.30	0.47
3:C:253:LYS:O	3:C:256:ALA:HB3	2.15	0.47
5:E:35:VAL:C	5:E:37:LEU:N	2.72	0.47
6:F:123:LYS:O	6:F:124:GLU:C	2.58	0.47
7:G:13:LEU:O	7:G:67:SER:HA	2.15	0.47
1:A:218:ASP:O	1:A:219:PHE:C	2.56	0.47
1:A:236:LEU:N	1:A:236:LEU:HD23	2.30	0.47
1:A:298:PHE:O	1:A:301:ALA:HB3	2.15	0.47
1:A:344:ARG:HG2	1:A:344:ARG:HH11	1.80	0.47
1:A:475:THR:HG23	1:A:476:SER:H	1.76	0.47
1:A:552:TRP:O	1:A:554:PRO:HD3	2.13	0.47
1:A:570:PRO:C	1:A:571:LEU:HD12	2.40	0.47
1:A:1098:VAL:N	1:A:1099:PRO:HD2	2.30	0.47
2:B:230:ALA:N	2:B:231:PRO:CD	2.78	0.47
2:B:594:ALA:HA	2:B:617:ARG:HH12	1.76	0.47
3:C:170:TRP:O	3:C:171:GLY:C	2.57	0.47
3:C:179:GLU:O	3:C:180:TYR:HB3	2.14	0.47
3:C:214:ASN:HB3	3:C:217:ASP:OD2	2.14	0.47
5:E:157:SER:O	5:E:159:ASP:N	2.48	0.47
7:G:44:TYR:O	7:G:78:VAL:HA	2.14	0.47
7:G:50:ASP:O	7:G:51:TYR:C	2.58	0.47
7:G:81:PRO:C	7:G:82:PHE:CD1	2.93	0.47
1:A:2:VAL:HG21	2:B:1158:PHE:HA	1.97	0.47
1:A:2:VAL:CG2	2:B:1158:PHE:HA	2.45	0.47
1:A:551:TYR:CE2	11:K:62:LYS:HE2	2.49	0.47
1:A:786:HIS:HE1	2:B:705:MET:HE1	1.80	0.47
1:A:966:ASN:O	1:A:967:ALA:C	2.57	0.47
1:A:1019:CYS:O	1:A:1023:ARG:N	2.45	0.47
2:B:114:PRO:O	2:B:117:ALA:N	2.48	0.47
2:B:855:PHE:CD1	2:B:855:PHE:C	2.90	0.47
2:B:1034:VAL:C	2:B:1036:ALA:N	2.72	0.47
6:F:81:THR:HB	6:F:136:ARG:NH1	2.30	0.47
8:H:59:ILE:CG2	8:H:60:ALA:N	2.73	0.47
10:J:23:ASN:O	10:J:25:LEU:N	2.48	0.47
1:A:296:LEU:O	1:A:297:GLN:C	2.59	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:863:VAL:HG11	1:A:866:PHE:CE2	2.49	0.46
1:A:886:ILE:CD1	1:A:943:LEU:HB3	2.41	0.46
1:A:1261:LYS:HA	1:A:1264:GLU:HB3	1.96	0.46
1:A:1441:PHE:HB2	6:F:135:ARG:O	2.15	0.46
2:B:27:ALA:O	2:B:29:ASP:N	2.48	0.46
2:B:168:GLY:HA2	2:B:454:THR:OG1	2.15	0.46
2:B:653:VAL:HG22	2:B:689:LEU:HD13	1.97	0.46
2:B:681:TRP:O	2:B:683:SER:N	2.49	0.46
2:B:864:LYS:N	2:B:872:GLU:OE1	2.45	0.46
2:B:1160:VAL:HG11	2:B:1169:MET:SD	2.55	0.46
2:B:1198:TYR:C	2:B:1198:TYR:CD2	2.93	0.46
6:F:103:MET:HE1	7:G:65:ASP:HB2	1.97	0.46
8:H:82:PRO:O	8:H:84:ALA:N	2.35	0.46
8:H:89:LEU:C	8:H:91:ASP:N	2.68	0.46
9:I:61:ASP:O	9:I:63:GLY:N	2.48	0.46
1:A:134:ARG:HD3	1:A:221:SER:O	2.15	0.46
1:A:319:GLY:CA	2:B:472:ALA:HB3	2.44	0.46
1:A:332:LYS:HG3	1:A:333:GLU:N	2.30	0.46
1:A:335:ARG:CA	1:A:339:ASN:HB2	2.40	0.46
1:A:935:GLN:O	1:A:936:LEU:C	2.59	0.46
1:A:1343:ALA:HB2	5:E:150:VAL:CG2	2.45	0.46
2:B:104:GLU:OE1	12:L:54:ARG:NH2	2.49	0.46
2:B:205:ILE:HG22	2:B:206:ASN:N	2.30	0.46
2:B:710:LEU:C	2:B:711:GLU:HG2	2.40	0.46
2:B:711:GLU:H	2:B:712:PRO:HD2	1.80	0.46
2:B:1034:VAL:HG23	2:B:1059:LEU:HD13	1.97	0.46
3:C:259:LEU:CD1	11:K:91:CYS:HB2	2.45	0.46
4:D:47:LEU:CD1	4:D:48:ILE:N	2.77	0.46
4:D:154:PHE:HB2	4:D:160:VAL:HG22	1.97	0.46
5:E:145:THR:HG21	5:E:187:TYR:CE2	2.50	0.46
6:F:109:VAL:HG21	6:F:124:GLU:HA	1.97	0.46
7:G:14:HIS:HD2	7:G:16:SER:CB	2.28	0.46
7:G:77:VAL:O	7:G:77:VAL:HG12	2.14	0.46
8:H:91:ASP:C	8:H:93:TYR:N	2.72	0.46
1:A:289:ILE:C	1:A:291:GLU:N	2.73	0.46
1:A:402:ALA:HB1	1:A:433:GLU:O	2.15	0.46
1:A:1431:GLY:HA3	2:B:1152:MET:SD	2.55	0.46
2:B:199:MET:HE2	2:B:492:LEU:CD2	2.42	0.46
2:B:376:PHE:HB3	2:B:586:TRP:CZ3	2.49	0.46
3:C:146:LYS:HB2	10:J:61:LEU:HD11	1.97	0.46
3:C:257:SER:C	3:C:258:ILE:HD12	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:147:SER:OG	6:F:150:GLU:HG3	2.15	0.46
7:G:43:GLY:CA	7:G:80:LYS:HB3	2.42	0.46
10:J:34:THR:O	10:J:35:ALA:C	2.59	0.46
11:K:46:ILE:O	11:K:46:ILE:HG22	2.15	0.46
1:A:231:PRO:C	1:A:233:TRP:N	2.74	0.46
1:A:343:LYS:NZ	2:B:1151:LEU:O	2.47	0.46
1:A:871:ASP:HB3	5:E:204:THR:HG23	1.96	0.46
1:A:1291:VAL:HG13	1:A:1292:PRO:N	2.29	0.46
1:A:1344:GLY:O	1:A:1345:ARG:C	2.56	0.46
2:B:298:LEU:HD13	2:B:314:LEU:HD13	1.97	0.46
2:B:307:ASP:O	2:B:308:TRP:C	2.58	0.46
2:B:865:LYS:HE2	2:B:871:THR:OG1	2.15	0.46
2:B:1072:MET:HE1	2:B:1085:ILE:HB	1.92	0.46
2:B:1131:GLY:O	2:B:1132:GLU:C	2.58	0.46
5:E:129:PRO:O	5:E:130:ALA:O	2.34	0.46
7:G:14:HIS:CD2	7:G:16:SER:CB	2.98	0.46
7:G:108:VAL:HG13	7:G:159:ALA:O	2.16	0.46
10:J:7:CYS:CA	10:J:49:MET:HE3	2.45	0.46
1:A:399:HIS:O	1:A:400:PRO:C	2.58	0.46
1:A:1019:CYS:O	1:A:1022:LEU:N	2.48	0.46
1:A:1076:ALA:HA	1:A:1079:MET:CE	2.41	0.46
2:B:405:ARG:HA	2:B:631:GLY:O	2.16	0.46
2:B:563:MET:CE	2:B:580:VAL:HB	2.43	0.46
2:B:595:ARG:O	2:B:596:LEU:C	2.59	0.46
2:B:654:ARG:C	2:B:656:GLY:H	2.23	0.46
2:B:654:ARG:O	2:B:656:GLY:N	2.48	0.46
2:B:834:ASN:HA	2:B:838:SER:O	2.15	0.46
2:B:842:ASN:ND2	2:B:845:SER:OG	2.44	0.46
6:F:132:LEU:O	6:F:148:VAL:HG22	2.15	0.46
7:G:99:PHE:CD1	7:G:99:PHE:C	2.93	0.46
7:G:121:PHE:HB2	7:G:130:TYR:CE2	2.50	0.46
8:H:93:TYR:N	8:H:93:TYR:CD1	2.84	0.46
12:L:38:LEU:O	12:L:39:SER:CB	2.63	0.46
1:A:17:VAL:HA	2:B:1215:ARG:O	2.15	0.46
1:A:608:ILE:HG13	1:A:613:ILE:HD12	1.97	0.46
1:A:655:PHE:O	1:A:658:LEU:HB3	2.16	0.46
1:A:1015:VAL:O	1:A:1018:PHE:N	2.49	0.46
1:A:1193:LEU:HD12	1:A:1193:LEU:C	2.41	0.46
1:A:1265:ASN:C	1:A:1267:MET:H	2.23	0.46
2:B:108:VAL:CG1	2:B:109:THR:H	2.28	0.46
2:B:168:GLY:N	2:B:450:ALA:HB1	2.19	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:769:TYR:C	2:B:771:SER:N	2.73	0.46
2:B:854:LEU:HB3	2:B:856:PHE:HE1	1.81	0.46
2:B:1152:MET:O	2:B:1154:ALA:N	2.49	0.46
3:C:67:LEU:HD11	3:C:155:LEU:HD12	1.97	0.46
3:C:133:ILE:CD1	3:C:237:SER:HA	2.45	0.46
3:C:181:ASP:OD1	3:C:186:LEU:HD13	2.16	0.46
5:E:161:LYS:O	5:E:163:GLU:N	2.49	0.46
11:K:59:ALA:HA	11:K:74:ARG:O	2.15	0.46
1:A:7:SER:CB	2:B:1175:LEU:HD22	2.45	0.46
1:A:626:ASN:O	1:A:628:GLY:N	2.44	0.46
1:A:817:ALA:HA	2:B:764:SER:OG	2.16	0.46
1:A:901:LEU:O	1:A:921:GLY:N	2.48	0.46
1:A:1227:ILE:CG2	1:A:1228:TRP:N	2.78	0.46
2:B:582:VAL:HG12	2:B:587:HIS:NE2	2.30	0.46
2:B:979:LYS:HG3	2:B:989:THR:HG22	1.98	0.46
2:B:1001:PHE:CD2	3:C:34:ARG:NH2	2.84	0.46
3:C:142:VAL:N	10:J:16:ASP:HB3	2.14	0.46
3:C:236:GLY:C	3:C:238:ILE:N	2.73	0.46
4:D:66:ARG:CD	4:D:133:THR:HB	2.43	0.46
6:F:143:PHE:C	6:F:143:PHE:HD1	2.23	0.46
9:I:110:PHE:H	9:I:110:PHE:HD2	1.64	0.46
12:L:27:LEU:HD23	12:L:27:LEU:N	2.30	0.46
1:A:563:PRO:HG3	1:A:572:TRP:CE2	2.49	0.46
1:A:1195:LEU:HD11	1:A:1267:MET:CE	2.46	0.46
1:A:1334:ASP:C	1:A:1336:MET:N	2.73	0.46
1:A:1435:PRO:O	1:A:1436:ILE:HG13	2.15	0.46
2:B:579:ARG:CB	2:B:586:TRP:HE1	2.24	0.46
2:B:948:ILE:C	2:B:949:VAL:O	2.56	0.46
2:B:999:MET:HE2	2:B:1000:PRO:HD2	1.98	0.46
2:B:1084:GLN:HG2	3:C:201:TRP:CZ2	2.51	0.46
2:B:1147:LEU:CD2	2:B:1151:LEU:HD22	2.46	0.46
2:B:1169:MET:HE1	2:B:1201:LYS:CA	2.45	0.46
5:E:17:ARG:O	5:E:20:LYS:HB2	2.16	0.46
7:G:127:PRO:HG2	7:G:138:THR:HG21	1.98	0.46
1:A:43:GLU:O	1:A:44:THR:CB	2.64	0.46
1:A:92:HIS:HB2	1:A:236:LEU:HD21	1.96	0.46
1:A:877:HIS:C	1:A:878:ILE:CG1	2.88	0.46
1:A:1265:ASN:O	1:A:1268:LEU:N	2.41	0.46
2:B:305:VAL:O	2:B:305:VAL:HG12	2.15	0.46
2:B:820:GLY:C	2:B:1091:TYR:CE1	2.94	0.46
2:B:873:THR:O	2:B:914:LYS:HA	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1007:VAL:HG22	2:B:1008:PRO:CD	2.38	0.46
3:C:29:MET:HE2	11:K:98:LEU:HD21	1.97	0.46
3:C:66:ARG:CZ	10:J:2:ILE:HG21	2.46	0.46
3:C:76:ASP:OD2	3:C:128:ASN:N	2.49	0.46
4:D:19:GLU:O	4:D:21:GLU:N	2.49	0.46
9:I:56:ALA:O	9:I:57:GLY:O	2.34	0.46
10:J:8:PHE:H	10:J:49:MET:CE	2.28	0.46
1:A:84:ILE:O	1:A:84:ILE:CG2	2.63	0.46
1:A:373:THR:HG21	2:B:1105:ALA:HB3	1.98	0.46
1:A:603:ASN:HB3	1:A:604:GLY:H	1.57	0.46
1:A:761:MET:HA	1:A:804:TYR:HB2	1.97	0.46
1:A:800:VAL:HG13	1:A:808:LEU:HG	1.98	0.46
1:A:809:THR:O	1:A:810:PRO:C	2.59	0.46
1:A:1161:THR:CG2	1:A:1163:ILE:HG13	2.46	0.46
1:A:1313:LEU:C	1:A:1315:GLU:H	2.24	0.46
1:A:1389:PHE:CD1	1:A:1389:PHE:C	2.94	0.46
2:B:589:VAL:CG1	2:B:590:HIS:H	2.11	0.46
2:B:642:ASP:CB	2:B:649:LYS:HG3	2.42	0.46
2:B:726:ALA:HB1	2:B:1051:THR:HG21	1.97	0.46
2:B:882:THR:CG2	2:B:884:ARG:HB2	2.46	0.46
3:C:90:ASP:O	3:C:90:ASP:OD1	2.33	0.46
4:D:54:GLU:OE1	4:D:164:ILE:HD11	2.16	0.46
4:D:196:PRO:C	4:D:198:LEU:H	2.23	0.46
6:F:99:LEU:HD21	7:G:64:THR:O	2.16	0.46
9:I:4:PHE:HE1	9:I:6:PHE:CE2	2.34	0.46
9:I:75:CYS:SG	9:I:80:SER:N	2.85	0.46
11:K:58:PHE:HB3	11:K:76:GLN:HE21	1.81	0.46
12:L:62:LYS:O	12:L:63:ARG:C	2.59	0.46
1:A:82:GLY:O	1:A:241:VAL:N	2.42	0.45
1:A:332:LYS:C	1:A:334:GLY:H	2.25	0.45
1:A:474:VAL:C	1:A:477:PRO:HD2	2.41	0.45
1:A:807:GLY:C	1:A:808:LEU:O	2.59	0.45
1:A:964:ILE:O	1:A:965:GLN:C	2.59	0.45
1:A:1132:LYS:O	1:A:1134:ILE:N	2.49	0.45
1:A:1150:SER:O	1:A:1151:GLU:HG3	2.15	0.45
1:A:1334:ASP:C	1:A:1336:MET:H	2.23	0.45
1:A:1342:GLU:HG3	5:E:198:ILE:HD13	1.98	0.45
1:A:1364:ASN:HD22	1:A:1364:ASN:C	2.24	0.45
2:B:39:ARG:HH21	2:B:665:GLU:CG	2.26	0.45
2:B:180:TYR:CD1	2:B:180:TYR:N	2.82	0.45
2:B:333:PHE:O	2:B:334:ILE:CG1	2.61	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:365:THR:HG23	2:B:367:LEU:N	2.27	0.45
2:B:546:SER:OG	2:B:631:GLY:N	2.39	0.45
2:B:638:PHE:HB2	2:B:741:CYS:O	2.16	0.45
2:B:729:ILE:O	2:B:729:ILE:HG22	2.15	0.45
2:B:969:ARG:NH1	3:C:61:GLU:OE1	2.49	0.45
2:B:981:ALA:HB3	2:B:1095:LEU:HD21	1.97	0.45
2:B:1068:GLY:O	2:B:1069:PHE:C	2.59	0.45
2:B:1189:ILE:HG22	2:B:1190:ASP:N	2.31	0.45
3:C:6:PRO:HB3	3:C:25:VAL:CG1	2.45	0.45
3:C:70:ILE:HG12	3:C:142:VAL:HG11	1.98	0.45
3:C:104:PHE:HD2	3:C:105:GLY:N	2.14	0.45
4:D:180:LEU:HD23	4:D:180:LEU:HA	1.75	0.45
1:A:70:CYS:O	1:A:71:GLN:C	2.59	0.45
1:A:853:ASP:O	1:A:854:ASN:CB	2.64	0.45
1:A:1027:ALA:O	1:A:1028:THR:C	2.59	0.45
1:A:1100:ARG:NH2	1:A:1351:GLU:HG2	2.31	0.45
2:B:766:ARG:HD3	2:B:766:ARG:HA	1.70	0.45
2:B:839:MET:HG3	2:B:1010:LEU:CD1	2.44	0.45
2:B:990:ILE:HG22	2:B:991:GLY:N	2.31	0.45
6:F:128:LYS:HD3	6:F:149:GLU:O	2.15	0.45
8:H:7:ASP:O	8:H:8:ASP:HB2	2.15	0.45
11:K:24:ASP:OD2	11:K:74:ARG:NH1	2.49	0.45
1:A:250:ILE:O	1:A:258:GLY:HA3	2.16	0.45
1:A:474:VAL:HG22	1:A:474:VAL:O	2.16	0.45
1:A:871:ASP:OD1	1:A:1366:ARG:NH2	2.49	0.45
1:A:874:ASP:O	1:A:875:ALA:C	2.59	0.45
1:A:1011:GLN:O	1:A:1012:ARG:C	2.60	0.45
2:B:293:PRO:HG2	2:B:296:GLU:HB3	1.98	0.45
2:B:789:MET:HE2	2:B:953:LEU:HD22	1.98	0.45
2:B:1050:ILE:CG2	2:B:1051:THR:N	2.78	0.45
3:C:105:GLY:HA3	3:C:149:LYS:O	2.17	0.45
7:G:106:MET:HG2	7:G:107:LYS:N	2.31	0.45
7:G:115:MET:CB	7:G:116:PRO:HD2	2.41	0.45
9:I:8:ARG:NE	9:I:9:ASP:OD1	2.41	0.45
9:I:15:TYR:N	9:I:15:TYR:CD1	2.84	0.45
11:K:31:VAL:HG12	11:K:32:VAL:H	1.79	0.45
1:A:108:MET:HB3	1:A:210:ILE:CD1	2.47	0.45
1:A:369:SER:HB3	11:K:2:ASN:HD21	1.80	0.45
1:A:524:VAL:CG1	1:A:525:GLN:H	2.18	0.45
1:A:567:LYS:CB	8:H:95:TYR:HA	2.46	0.45
1:A:765:VAL:HG21	1:A:808:LEU:HD11	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:779:PHE:O	1:A:780:VAL:C	2.59	0.45
1:A:829:VAL:C	1:A:831:THR:N	2.74	0.45
1:A:874:ASP:O	1:A:876:ALA:N	2.50	0.45
1:A:947:PHE:CD2	1:A:954:TRP:CZ2	3.04	0.45
2:B:113:TYR:CD2	2:B:192:LEU:HD22	2.51	0.45
2:B:324:ILE:CG2	2:B:325:GLN:N	2.80	0.45
2:B:1060:ARG:HA	2:B:1060:ARG:HD2	1.53	0.45
2:B:1207:LEU:HB3	2:B:1212:ILE:HG22	1.99	0.45
3:C:100:THR:HG22	3:C:101:LEU:N	2.31	0.45
3:C:123:ASN:ND2	3:C:125:MET:SD	2.90	0.45
3:C:259:LEU:HD11	11:K:91:CYS:HB2	1.99	0.45
5:E:192:ARG:HH11	5:E:192:ARG:CG	2.26	0.45
6:F:106:PRO:HG2	7:G:19:GLY:HA2	1.97	0.45
6:F:111:LEU:O	6:F:113:GLY:N	2.48	0.45
8:H:111:LEU:HD23	8:H:127:GLY:O	2.16	0.45
12:L:30:ILE:HG22	12:L:31:CYS:N	2.32	0.45
1:A:7:SER:C	1:A:9:ALA:H	2.23	0.45
1:A:34:LYS:HD3	1:A:34:LYS:N	2.31	0.45
1:A:353:ILE:HB	1:A:470:LEU:CD2	2.47	0.45
1:A:626:ASN:O	1:A:631:HIS:CD2	2.69	0.45
2:B:48:LEU:O	2:B:49:ASP:C	2.59	0.45
2:B:115:GLN:HG2	2:B:193:LYS:HB2	1.98	0.45
2:B:115:GLN:HG2	2:B:193:LYS:CB	2.46	0.45
2:B:329:THR:O	2:B:332:ASP:HB3	2.16	0.45
2:B:435:THR:C	2:B:437:GLU:H	2.23	0.45
2:B:784:ASN:O	2:B:788:ARG:HG3	2.17	0.45
2:B:1002:THR:O	2:B:1003:ALA:C	2.59	0.45
3:C:73:GLN:HE21	3:C:74:SER:H	1.65	0.45
3:C:91:HIS:CD2	3:C:91:HIS:C	2.94	0.45
3:C:99:LEU:HD23	3:C:99:LEU:N	2.26	0.45
8:H:11:GLN:O	8:H:28:ALA:HB1	2.17	0.45
1:A:95:PHE:CD1	1:A:234:MET:HG2	2.51	0.45
1:A:116:ASP:C	1:A:118:HIS:N	2.71	0.45
1:A:324:SER:O	1:A:325:ILE:C	2.56	0.45
1:A:407:ARG:HG2	1:A:430:TRP:CZ3	2.52	0.45
1:A:492:PRO:HB2	1:A:497:THR:HG22	1.98	0.45
1:A:618:GLU:O	1:A:619:LYS:C	2.60	0.45
1:A:929:LEU:CD2	1:A:983:ILE:HG21	2.47	0.45
1:A:1019:CYS:O	1:A:1020:CYS:C	2.60	0.45
1:A:1057:VAL:HG12	1:A:1058:VAL:H	1.82	0.45
1:A:1156:PRO:HA	1:A:1190:PRO:CB	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1283:VAL:HG12	1:A:1284:MET:H	1.81	0.45
1:A:1343:ALA:O	1:A:1346:ALA:HB3	2.16	0.45
2:B:560:GLU:O	2:B:561:TRP:CD1	2.69	0.45
2:B:906:SER:O	2:B:907:GLY:O	2.34	0.45
2:B:1152:MET:HE1	2:B:1157:ALA:HA	1.99	0.45
3:C:181:ASP:CG	3:C:186:LEU:HD13	2.42	0.45
7:G:18:PHE:HA	7:G:22:MET:HE3	1.95	0.45
7:G:31:LEU:HD22	7:G:48:VAL:HG21	1.99	0.45
10:J:7:CYS:HA	10:J:49:MET:HE3	1.98	0.45
1:A:418:SER:C	1:A:420:ARG:H	2.25	0.45
1:A:596:THR:C	1:A:598:LEU:N	2.73	0.45
1:A:1011:GLN:NE2	1:A:1015:VAL:HG21	2.31	0.45
1:A:1053:PHE:O	1:A:1055:ARG:N	2.50	0.45
1:A:1173:HIS:C	1:A:1174:PHE:CD1	2.94	0.45
2:B:130:VAL:HG23	2:B:167:ILE:HD12	1.98	0.45
2:B:515:HIS:HD2	2:B:517:THR:N	2.05	0.45
3:C:144:ILE:O	3:C:145:CYS:HB3	2.17	0.45
5:E:16:PHE:O	5:E:17:ARG:C	2.59	0.45
5:E:98:ILE:O	5:E:99:HIS:C	2.59	0.45
5:E:135:PHE:CD2	5:E:140:LEU:HD21	2.37	0.45
9:I:111:THR:CG2	9:I:112:SER:N	2.77	0.45
10:J:47:ARG:NH1	10:J:47:ARG:HG2	2.30	0.45
11:K:40:HIS:O	11:K:41:THR:C	2.59	0.45
1:A:499:ALA:O	1:A:503:GLN:HB2	2.17	0.45
1:A:603:ASN:O	1:A:604:GLY:C	2.60	0.45
1:A:896:ARG:NH2	1:A:1030:ARG:HH21	2.14	0.45
1:A:1205:LYS:O	1:A:1206:ASP:C	2.60	0.45
2:B:45:SER:O	2:B:46:GLN:C	2.60	0.45
2:B:284:ILE:HD13	2:B:333:PHE:HD2	1.81	0.45
2:B:785:TYR:C	2:B:787:VAL:N	2.71	0.45
2:B:1065:GLN:HE21	2:B:1066:SER:CA	2.30	0.45
3:C:36:VAL:HG21	3:C:251:LEU:HB2	1.98	0.45
3:C:92:CYS:C	3:C:94:LYS:N	2.72	0.45
4:D:51:ASN:C	4:D:52:LEU:O	2.59	0.45
8:H:58:THR:HG22	8:H:59:ILE:N	2.31	0.45
8:H:123:MET:HG2	8:H:124:ARG:N	2.31	0.45
10:J:21:TYR:HB2	10:J:39:LEU:CD1	2.46	0.45
1:A:524:VAL:HG12	1:A:525:GLN:HE21	1.81	0.45
1:A:668:ASP:HA	1:A:741:ASN:OD1	2.17	0.45
1:A:767:GLN:HB2	1:A:799:PHE:HD1	1.82	0.45
1:A:791:ASP:C	1:A:791:ASP:OD1	2.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:971:PHE:HE2	1:A:1040:GLN:HG2	1.80	0.45
1:A:1153:TYR:CD2	1:A:1163:ILE:HD11	2.52	0.45
1:A:1349:TYR:O	1:A:1350:LYS:C	2.60	0.45
1:A:1409:LEU:O	1:A:1412:ALA:HB3	2.17	0.45
1:A:1445:ILE:H	1:A:1445:ILE:CD1	2.19	0.45
2:B:345:LYS:O	2:B:347:LYS:HG2	2.17	0.45
2:B:581:PHE:HA	2:B:585:VAL:O	2.17	0.45
2:B:640:VAL:O	2:B:640:VAL:HG12	2.17	0.45
2:B:826:ALA:HB2	2:B:1008:PRO:HB3	1.99	0.45
2:B:1008:PRO:HB2	2:B:1010:LEU:O	2.17	0.45
3:C:38:ILE:HA	3:C:173:ALA:HB2	1.98	0.45
4:D:51:ASN:ND2	4:D:54:GLU:OE2	2.50	0.45
5:E:136:ASN:OD1	5:E:137:GLU:N	2.50	0.45
7:G:48:VAL:HG13	7:G:74:TYR:HD1	1.82	0.45
9:I:111:THR:HG21	9:I:113:ASP:HB2	1.99	0.45
12:L:58:LYS:O	12:L:59:ALA:O	2.35	0.45
1:A:1135:ARG:C	1:A:1137:ALA:H	2.24	0.45
1:A:1438:THR:O	1:A:1438:THR:HG22	2.17	0.45
2:B:308:TRP:CZ3	9:I:45:ARG:HG2	2.51	0.45
2:B:435:THR:C	2:B:437:GLU:N	2.74	0.45
2:B:492:LEU:O	2:B:493:SER:C	2.59	0.45
2:B:882:THR:O	2:B:883:LEU:CB	2.65	0.45
2:B:899:ILE:O	2:B:952:VAL:HG21	2.16	0.45
2:B:1087:PHE:CD2	2:B:1088:GLY:N	2.80	0.45
2:B:1137:CYS:O	2:B:1140:ALA:HB3	2.17	0.45
3:C:246:ARG:HA	3:C:249:ASP:HB3	1.99	0.45
4:D:115:HIS:O	4:D:116:SER:CB	2.64	0.45
5:E:124:VAL:CG1	5:E:132:ILE:HB	2.43	0.45
8:H:4:THR:O	8:H:5:LEU:HD23	2.17	0.45
1:A:164:ARG:CG	1:A:165:GLY:H	2.19	0.44
1:A:382:PRO:CB	1:A:428:TYR:HE2	2.30	0.44
1:A:556:TRP:CZ2	1:A:558:GLY:HA2	2.52	0.44
1:A:1213:GLY:O	1:A:1214:GLU:C	2.59	0.44
1:A:1422:ARG:NH2	2:B:1224:PHE:C	2.69	0.44
2:B:237:VAL:HG12	2:B:238:ALA:N	2.31	0.44
2:B:308:TRP:HA	2:B:311:LEU:HD12	1.99	0.44
2:B:769:TYR:O	2:B:772:ALA:N	2.50	0.44
2:B:838:SER:CB	2:B:989:THR:O	2.65	0.44
3:C:163:ILE:C	3:C:165:LYS:H	2.25	0.44
4:D:153:ARG:HB3	4:D:154:PHE:CE1	2.52	0.44
4:D:192:LYS:NZ	4:D:199:ASN:HA	2.30	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:114:ASN:O	5:E:115:ASN:CB	2.65	0.44
7:G:14:HIS:CE1	7:G:15:PRO:HD2	2.52	0.44
8:H:116:TYR:HE2	8:H:140:ALA:CB	2.30	0.44
11:K:42:LEU:O	11:K:46:ILE:HG13	2.17	0.44
11:K:53:ASP:C	11:K:55:LYS:H	2.26	0.44
11:K:95:ILE:O	11:K:98:LEU:HB2	2.17	0.44
1:A:53:LEU:CD2	1:A:54:ASN:N	2.61	0.44
1:A:270:LEU:O	1:A:271:LYS:C	2.60	0.44
1:A:701:LEU:HD21	9:I:114:GLN:HB2	1.98	0.44
1:A:1018:PHE:O	1:A:1021:LEU:HB3	2.17	0.44
1:A:1265:ASN:O	1:A:1267:MET:N	2.50	0.44
2:B:410:GLY:O	2:B:412:LEU:N	2.50	0.44
2:B:753:ALA:HA	2:B:756:ILE:HD12	2.00	0.44
2:B:1197:PRO:O	2:B:1200:ALA:N	2.48	0.44
5:E:134:THR:C	5:E:135:PHE:HD1	2.25	0.44
5:E:147:HIS:O	5:E:148:GLU:C	2.61	0.44
8:H:25:ARG:HA	8:H:41:ASP:HA	1.98	0.44
10:J:51:LEU:O	10:J:51:LEU:HD12	2.17	0.44
1:A:278:THR:O	1:A:278:THR:HG22	2.17	0.44
1:A:528:LEU:O	1:A:529:CYS:C	2.60	0.44
1:A:567:LYS:HZ1	8:H:46:LEU:HB2	1.82	0.44
1:A:595:THR:O	1:A:596:THR:HG23	2.18	0.44
1:A:665:GLY:C	1:A:666:ILE:HD12	2.42	0.44
1:A:709:THR:HB	1:A:712:GLU:HG3	1.99	0.44
1:A:841:LEU:O	1:A:845:LEU:HG	2.16	0.44
1:A:963:ILE:HD13	1:A:1049:ILE:CG1	2.47	0.44
1:A:1006:ILE:HD12	5:E:163:GLU:CG	2.47	0.44
1:A:1348:LEU:O	1:A:1352:VAL:HG23	2.16	0.44
1:A:1349:TYR:CA	1:A:1372:VAL:HG21	2.47	0.44
1:A:1409:LEU:CD1	2:B:1207:LEU:HD21	2.42	0.44
2:B:258:LEU:O	2:B:259:TYR:O	2.35	0.44
3:C:44:LEU:HD23	3:C:45:ALA:N	2.33	0.44
3:C:89:GLU:O	3:C:90:ASP:HB3	2.15	0.44
3:C:226:ASP:O	3:C:227:THR:CB	2.66	0.44
7:G:22:MET:O	7:G:23:LYS:C	2.60	0.44
11:K:53:ASP:O	11:K:55:LYS:N	2.50	0.44
1:A:18:GLN:H	2:B:1215:ARG:HB2	1.82	0.44
1:A:33:ALA:O	1:A:83:HIS:HD2	1.99	0.44
1:A:58:LEU:HD13	1:A:243:PRO:HA	2.00	0.44
1:A:63:ARG:HA	1:A:74:MET:HE2	1.99	0.44
1:A:103:CYS:O	1:A:106:VAL:O	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:VAL:HG12	1:A:153:PRO:CD	2.47	0.44
1:A:418:SER:C	1:A:420:ARG:N	2.75	0.44
1:A:590:ARG:HH21	1:A:620:LYS:CB	2.28	0.44
1:A:853:ASP:OD1	1:A:853:ASP:C	2.60	0.44
1:A:1001:ARG:HG2	1:A:1001:ARG:HH11	1.82	0.44
1:A:1044:TRP:O	1:A:1045:VAL:C	2.59	0.44
1:A:1339:LEU:HD13	5:E:147:HIS:CD2	2.53	0.44
1:A:1370:LEU:O	1:A:1374:VAL:HG23	2.17	0.44
1:A:1373:ASP:HA	1:A:1376:THR:CG2	2.47	0.44
2:B:26:THR:O	2:B:29:ASP:HB2	2.18	0.44
2:B:307:ASP:O	2:B:309:GLN:N	2.50	0.44
2:B:570:VAL:HG23	2:B:573:GLN:HB3	1.99	0.44
2:B:825:VAL:HG12	2:B:826:ALA:N	2.32	0.44
2:B:1084:GLN:N	2:B:1084:GLN:NE2	2.66	0.44
2:B:1110:PRO:HG3	2:B:1124:ARG:O	2.18	0.44
3:C:27:LEU:O	3:C:30:ALA:N	2.50	0.44
4:D:53:SER:HB3	4:D:152:SER:HA	1.98	0.44
5:E:31:THR:OG1	5:E:34:GLU:N	2.50	0.44
7:G:73:LYS:HE3	7:G:74:TYR:O	2.17	0.44
10:J:16:ASP:C	10:J:18:TRP:H	2.26	0.44
1:A:48:ALA:C	1:A:49:LYS:HG3	2.43	0.44
1:A:350:ARG:HH11	1:A:350:ARG:HG3	1.83	0.44
1:A:709:THR:HG22	1:A:710:LEU:N	2.32	0.44
1:A:982:THR:O	1:A:985:ASP:HB2	2.16	0.44
1:A:1388:GLY:C	1:A:1390:ASN:H	2.25	0.44
2:B:181:LEU:CD2	2:B:189:LEU:HD22	2.47	0.44
2:B:432:MET:C	2:B:434:ARG:H	2.26	0.44
2:B:604:ARG:C	2:B:606:LYS:H	2.26	0.44
2:B:705:MET:HE2	2:B:745:PRO:HB3	2.00	0.44
2:B:758:PHE:N	2:B:759:PRO:CD	2.80	0.44
6:F:103:MET:CE	7:G:66:GLY:H	2.29	0.44
7:G:45:ILE:HD13	7:G:45:ILE:HA	1.90	0.44
7:G:119:LEU:HD13	7:G:132:SER:HB2	2.00	0.44
8:H:10:PHE:N	8:H:10:PHE:CD1	2.85	0.44
9:I:106:CYS:O	9:I:107:SER:HB2	2.16	0.44
10:J:2:ILE:C	10:J:53:HIS:CE1	2.95	0.44
1:A:206:GLU:O	1:A:207:ILE:C	2.60	0.44
1:A:224:PHE:CZ	1:A:231:PRO:HG3	2.52	0.44
1:A:244:PRO:HG2	1:A:245:PRO:HD2	1.99	0.44
1:A:282:ASN:O	1:A:284:ALA:N	2.51	0.44
1:A:336:ILE:HG22	1:A:337:ARG:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:427:GLN:HB2	1:A:430:TRP:NE1	2.32	0.44
1:A:559:VAL:O	1:A:559:VAL:HG12	2.17	0.44
1:A:935:GLN:C	1:A:937:VAL:N	2.72	0.44
1:A:1115:SER:C	1:A:1308:THR:CG2	2.90	0.44
2:B:108:VAL:HG12	2:B:109:THR:N	2.33	0.44
2:B:113:TYR:HB3	2:B:114:PRO:HD2	2.00	0.44
2:B:562:GLY:HA3	2:B:590:HIS:CE1	2.53	0.44
2:B:579:ARG:HA	2:B:589:VAL:HG13	1.99	0.44
2:B:624:LEU:HD12	2:B:624:LEU:HA	1.84	0.44
2:B:680:THR:O	2:B:684:LEU:HD12	2.18	0.44
2:B:859:TYR:CE1	2:B:941:LEU:HD12	2.53	0.44
2:B:1017:ILE:CB	2:B:1018:PRO:HD3	2.44	0.44
2:B:1177:HIS:O	2:B:1179:GLN:N	2.50	0.44
3:C:91:HIS:ND1	3:C:158:VAL:HG11	2.33	0.44
3:C:248:ILE:HG23	11:K:98:LEU:HD22	1.99	0.44
4:D:170:THR:HB	4:D:172:LEU:H	1.83	0.44
7:G:115:MET:CB	7:G:116:PRO:CD	2.96	0.44
11:K:35:PHE:CD1	11:K:71:PHE:CE1	3.05	0.44
11:K:58:PHE:CB	11:K:76:GLN:HE21	2.31	0.44
1:A:44:THR:O	1:A:45:GLN:HB2	2.17	0.44
1:A:247:ARG:O	1:A:247:ARG:HG3	2.18	0.44
1:A:252:PHE:HB2	1:A:256:GLN:CD	2.42	0.44
1:A:334:GLY:O	1:A:335:ARG:C	2.60	0.44
1:A:352:VAL:HG12	1:A:353:ILE:N	2.32	0.44
1:A:356:ASP:C	1:A:358:ASN:H	2.24	0.44
1:A:508:PRO:O	1:A:511:ILE:HG13	2.18	0.44
1:A:800:VAL:HG11	1:A:808:LEU:HG	2.00	0.44
1:A:1101:LEU:HB2	1:A:1355:VAL:HG11	1.99	0.44
1:A:1335:ILE:O	1:A:1335:ILE:CG2	2.65	0.44
1:A:1441:PHE:CE2	6:F:89:GLU:HG2	2.52	0.44
2:B:558:LEU:C	2:B:560:GLU:N	2.74	0.44
2:B:840:ILE:CG2	2:B:994:TYR:HD1	2.30	0.44
2:B:846:ILE:HG23	2:B:974:PRO:HG2	1.99	0.44
3:C:44:LEU:HD23	3:C:44:LEU:C	2.42	0.44
3:C:189:THR:CG2	3:C:190:ASP:H	2.29	0.44
6:F:85:MET:HE2	6:F:93:ILE:HD12	1.99	0.44
9:I:8:ARG:CG	9:I:34:TYR:CE1	2.94	0.44
12:L:40:LEU:HB3	12:L:41:SER:H	1.57	0.44
1:A:47:ARG:HH22	1:A:254:GLU:HA	1.83	0.44
1:A:49:LYS:HZ1	1:A:61:ILE:HG13	1.82	0.44
1:A:51:GLY:HA2	1:A:56:PRO:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:432:VAL:O	1:A:433:GLU:C	2.60	0.44
1:A:547:LEU:HD22	11:K:58:PHE:HD1	1.78	0.44
1:A:932:GLU:O	1:A:936:LEU:HG	2.18	0.44
1:A:1036:ARG:HG2	1:A:1036:ARG:HH11	1.83	0.44
1:A:1129:GLU:O	1:A:1130:GLN:C	2.61	0.44
2:B:62:ILE:HG23	2:B:418:LYS:HG2	1.99	0.44
2:B:400:HIS:CG	2:B:517:THR:HG21	2.53	0.44
2:B:424:LEU:O	2:B:428:ILE:HG13	2.18	0.44
2:B:765:PRO:O	2:B:767:ASN:N	2.51	0.44
3:C:83:SER:O	3:C:85:ASP:N	2.51	0.44
7:G:139:ILE:HG22	7:G:140:LYS:N	2.31	0.44
1:A:73:GLY:O	1:A:74:MET:C	2.61	0.44
1:A:224:PHE:CZ	1:A:234:MET:HE2	2.53	0.44
1:A:494:SER:H	1:A:497:THR:HB	1.82	0.44
1:A:526:ASP:OD1	2:B:1013:ASN:ND2	2.49	0.44
1:A:883:LEU:CD2	1:A:1021:LEU:HB2	2.48	0.44
1:A:1132:LYS:O	1:A:1135:ARG:N	2.51	0.44
2:B:60:GLN:O	2:B:63:ILE:HG22	2.18	0.44
2:B:129:PHE:CD2	2:B:166:PHE:HA	2.53	0.44
2:B:172:ILE:CG2	2:B:173:MET:N	2.81	0.44
2:B:203:PHE:N	2:B:203:PHE:CD1	2.86	0.44
2:B:730:ARG:O	2:B:731:VAL:O	2.36	0.44
2:B:1072:MET:HE3	2:B:1085:ILE:HD13	2.00	0.44
7:G:18:PHE:HZ	7:G:68:ALA:HB2	1.83	0.44
10:J:28:ASP:O	10:J:29:GLU:C	2.61	0.44
12:L:61:THR:CG2	12:L:63:ARG:HG2	2.48	0.44
1:A:86:LEU:HD13	1:A:90:VAL:HG23	2.00	0.43
1:A:93:VAL:CG2	1:A:301:ALA:HA	2.48	0.43
1:A:244:PRO:O	1:A:245:PRO:C	2.61	0.43
1:A:456:MET:HB2	1:A:478:TYR:OH	2.18	0.43
1:A:578:LEU:HD23	1:A:612:ILE:HD11	2.00	0.43
2:B:744:HIS:CD2	2:B:745:PRO:HD2	2.52	0.43
2:B:862:GLN:O	2:B:914:LYS:HE3	2.18	0.43
3:C:161:LYS:O	3:C:170:TRP:NE1	2.51	0.43
5:E:212:ARG:HG3	5:E:212:ARG:HH11	1.82	0.43
7:G:3:PHE:CD1	7:G:80:LYS:HE2	2.53	0.43
8:H:40:LEU:HD21	8:H:142:LEU:HD21	2.00	0.43
10:J:13:VAL:O	10:J:14:VAL:CG2	2.66	0.43
11:K:87:LEU:O	11:K:88:LYS:C	2.60	0.43
1:A:215:SER:O	1:A:218:ASP:HB2	2.17	0.43
1:A:277:GLU:C	1:A:279:LEU:N	2.73	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:660:ASN:O	1:A:661:GLY:O	2.36	0.43
1:A:682:THR:HG23	1:A:728:LYS:HE3	2.00	0.43
1:A:909:ASP:C	1:A:911:SER:H	2.25	0.43
2:B:58:THR:O	2:B:62:ILE:HG13	2.18	0.43
2:B:134:LYS:HD2	2:B:442:PHE:HA	1.08	0.43
2:B:386:LEU:O	2:B:387:LEU:C	2.61	0.43
2:B:410:GLY:O	2:B:411:PRO:C	2.60	0.43
2:B:549:THR:CG2	2:B:550:ASP:N	2.74	0.43
2:B:824:ILE:CD1	10:J:48:ARG:NH1	2.81	0.43
2:B:1181:GLU:O	2:B:1182:CYS:HB2	2.18	0.43
4:D:153:ARG:C	4:D:154:PHE:CG	2.95	0.43
5:E:22:MET:O	5:E:26:ARG:HG3	2.18	0.43
11:K:100:ALA:O	11:K:103:THR:HB	2.18	0.43
1:A:347:PHE:H	2:B:1107:ALA:HA	1.82	0.43
1:A:737:LEU:HA	1:A:737:LEU:HD23	1.70	0.43
1:A:1209:MET:O	1:A:1210:GLY:C	2.61	0.43
1:A:1236:LEU:C	1:A:1237:ILE:HG13	2.43	0.43
2:B:237:VAL:HG22	2:B:257:LYS:HA	1.99	0.43
2:B:281:PRO:C	2:B:283:VAL:N	2.76	0.43
2:B:282:ILE:CD1	2:B:382:ILE:HD13	2.37	0.43
2:B:460:ALA:C	2:B:462:ALA:H	2.26	0.43
4:D:49:ALA:HB2	4:D:174:PRO:HB3	1.99	0.43
5:E:124:VAL:HB	5:E:125:PRO:HD3	1.99	0.43
7:G:9:LEU:CD1	7:G:10:ASN:H	2.30	0.43
7:G:17:PHE:C	7:G:19:GLY:N	2.77	0.43
8:H:82:PRO:C	8:H:84:ALA:N	2.75	0.43
9:I:103:CYS:HB3	9:I:107:SER:H	1.83	0.43
12:L:61:THR:HG22	12:L:63:ARG:HG2	2.01	0.43
1:A:89:PRO:HB2	1:A:204:THR:CG2	2.48	0.43
1:A:344:ARG:C	1:A:345:VAL:CG1	2.91	0.43
1:A:839:ARG:O	1:A:840:ARG:C	2.59	0.43
1:A:1142:THR:O	1:A:1143:LEU:C	2.61	0.43
1:A:1450:LEU:CD1	6:F:108:PHE:CZ	3.02	0.43
2:B:641:GLU:C	2:B:643:ASP:H	2.25	0.43
3:C:80:LEU:HD11	3:C:95:CYS:CA	2.48	0.43
3:C:90:ASP:O	3:C:91:HIS:HB3	2.16	0.43
6:F:138:LEU:CB	6:F:139:PRO:HD2	2.45	0.43
12:L:47:ARG:HG3	12:L:47:ARG:NH1	2.33	0.43
1:A:241:VAL:O	1:A:242:PRO:C	2.61	0.43
1:A:289:ILE:O	1:A:291:GLU:N	2.50	0.43
1:A:401:GLY:O	1:A:435:HIS:CD2	2.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:441:PRO:HD2	1:A:498:ARG:CZ	2.49	0.43
1:A:1124:HIS:HB3	1:A:1130:GLN:HG2	2.01	0.43
1:A:1209:MET:SD	1:A:1236:LEU:HD22	2.59	0.43
2:B:51:PHE:HB2	2:B:173:MET:CE	2.48	0.43
2:B:293:PRO:HG2	2:B:296:GLU:CB	2.47	0.43
2:B:294:ASP:O	2:B:296:GLU:N	2.48	0.43
2:B:294:ASP:OD2	2:B:294:ASP:N	2.50	0.43
2:B:418:LYS:O	2:B:420:LEU:N	2.51	0.43
2:B:694:ASP:O	2:B:698:GLU:HB2	2.18	0.43
2:B:702:LEU:HD12	2:B:703:ILE:H	1.84	0.43
2:B:763:GLN:HG2	2:B:765:PRO:CG	2.48	0.43
3:C:256:ALA:C	3:C:258:ILE:N	2.77	0.43
4:D:138:ASN:O	4:D:140:ASP:N	2.52	0.43
8:H:11:GLN:HA	8:H:53:ASP:O	2.18	0.43
8:H:103:LYS:HG2	8:H:104:PHE:N	2.34	0.43
9:I:75:CYS:SG	9:I:79:HIS:CA	3.07	0.43
1:A:106:VAL:HG13	1:A:112:LYS:C	2.43	0.43
1:A:473:SER:C	1:A:475:THR:H	2.27	0.43
1:A:608:ILE:HD12	1:A:613:ILE:CD1	2.47	0.43
1:A:645:LEU:O	1:A:646:PHE:C	2.59	0.43
1:A:659:HIS:C	1:A:661:GLY:H	2.26	0.43
1:A:873:MET:C	1:A:1058:VAL:HG23	2.43	0.43
1:A:1193:LEU:HD21	1:A:1267:MET:HE2	2.00	0.43
1:A:1215:ARG:HA	1:A:1215:ARG:HD2	1.72	0.43
1:A:1401:SER:O	1:A:1402:PHE:HB2	2.18	0.43
2:B:593:PRO:O	2:B:596:LEU:N	2.52	0.43
2:B:603:LEU:HB3	2:B:609:ILE:HD11	1.99	0.43
2:B:806:THR:C	2:B:808:ALA:N	2.75	0.43
4:D:141:LEU:O	4:D:142:LYS:C	2.61	0.43
5:E:43:LYS:O	5:E:45:LYS:N	2.48	0.43
10:J:53:HIS:NE2	10:J:55:ASP:HA	2.33	0.43
10:J:64:ASN:CB	10:J:65:PRO:CD	2.88	0.43
11:K:17:SER:O	11:K:18:LYS:C	2.62	0.43
1:A:18:GLN:O	2:B:1215:ARG:CG	2.66	0.43
1:A:29:ALA:HB1	2:B:1184:GLY:HA2	2.00	0.43
1:A:33:ALA:HB1	1:A:35:ILE:HG13	2.00	0.43
1:A:93:VAL:HG23	1:A:304:MET:HE3	2.00	0.43
1:A:98:LYS:C	1:A:100:LYS:N	2.77	0.43
1:A:552:TRP:HE3	1:A:651:LYS:HB3	1.83	0.43
1:A:666:ILE:CD1	1:A:667:GLY:N	2.80	0.43
1:A:854:ASN:CB	1:A:1000:LEU:HD21	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1067:LEU:O	1:A:1068:ALA:C	2.62	0.43
1:A:1148:ILE:HB	1:A:1196:GLU:O	2.18	0.43
1:A:1340:GLY:O	1:A:1343:ALA:N	2.43	0.43
1:A:1435:PRO:HA	1:A:1439:GLY:O	2.18	0.43
2:B:32:ALA:O	2:B:35:SER:HB2	2.19	0.43
2:B:63:ILE:HA	2:B:421:PHE:CE2	2.54	0.43
2:B:286:PHE:CD1	2:B:297:ILE:HG23	2.53	0.43
2:B:575:PRO:C	2:B:577:ALA:H	2.27	0.43
3:C:58:LEU:CD2	3:C:58:LEU:N	2.81	0.43
3:C:238:ILE:HD11	3:C:246:ARG:HH11	1.83	0.43
3:C:262:LEU:HD23	3:C:262:LEU:HA	1.75	0.43
5:E:175:LEU:HA	5:E:176:PRO:HD3	1.91	0.43
6:F:89:GLU:HB3	6:F:134:ILE:CD1	2.48	0.43
6:F:98:ALA:O	6:F:99:LEU:C	2.62	0.43
9:I:4:PHE:CD1	9:I:4:PHE:C	2.97	0.43
9:I:8:ARG:HG3	9:I:34:TYR:CD1	2.54	0.43
10:J:1:MET:HE2	10:J:60:PHE:HE2	1.78	0.43
1:A:42:ASP:C	1:A:44:THR:N	2.77	0.43
1:A:100:LYS:O	1:A:102:VAL:N	2.52	0.43
1:A:148:CYS:O	1:A:168:GLY:HA2	2.19	0.43
1:A:498:ARG:O	1:A:501:LEU:N	2.47	0.43
1:A:853:ASP:OD1	1:A:855:THR:HG22	2.18	0.43
1:A:1029:ARG:HG3	1:A:1029:ARG:NH1	2.34	0.43
1:A:1164:PRO:C	1:A:1166:ASP:N	2.76	0.43
2:B:263:GLY:O	2:B:264:SER:C	2.62	0.43
2:B:418:LYS:C	2:B:420:LEU:N	2.75	0.43
2:B:521:LEU:HB3	2:B:633:VAL:CG1	2.46	0.43
2:B:753:ALA:HA	2:B:756:ILE:CD1	2.48	0.43
2:B:936:ASP:OD1	2:B:938:SER:N	2.43	0.43
2:B:1029:CYS:HA	2:B:1089:PRO:O	2.19	0.43
2:B:1031:LEU:CD2	2:B:1044:ALA:HB2	2.48	0.43
4:D:52:LEU:CD2	4:D:147:TYR:HE2	2.32	0.43
9:I:34:TYR:C	9:I:35:VAL:HG23	2.44	0.43
1:A:209:ASN:O	1:A:210:ILE:C	2.62	0.43
1:A:224:PHE:CD2	1:A:231:PRO:HG3	2.54	0.43
1:A:535:THR:O	1:A:575:LYS:HG3	2.19	0.43
1:A:575:LYS:NZ	1:A:615:GLY:H	2.16	0.43
1:A:940:ARG:O	1:A:941:LYS:C	2.62	0.43
1:A:1385:THR:HG22	1:A:1386:ARG:H	1.84	0.43
1:A:1437:GLY:C	1:A:1439:GLY:N	2.77	0.43
2:B:291:ILE:HD13	2:B:300:HIS:CD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:371:GLU:CD	2:B:371:GLU:N	2.77	0.43
2:B:377:PHE:C	2:B:379:GLY:H	2.27	0.43
2:B:593:PRO:O	2:B:594:ALA:C	2.60	0.43
2:B:1001:PHE:HD2	3:C:34:ARG:HH21	1.66	0.43
2:B:1106:ARG:HD3	2:B:1127:GLY:CA	2.49	0.43
3:C:70:ILE:HD11	3:C:144:ILE:CG1	2.49	0.43
4:D:51:ASN:OD1	4:D:52:LEU:O	2.36	0.43
5:E:177:ARG:C	5:E:212:ARG:HD3	2.44	0.43
7:G:9:LEU:CG	7:G:10:ASN:N	2.81	0.43
8:H:15:VAL:HG22	8:H:26:ILE:CG1	2.49	0.43
9:I:110:PHE:CD2	9:I:110:PHE:N	2.85	0.43
1:A:12:ARG:O	2:B:1194:ILE:HG22	2.18	0.43
1:A:42:ASP:HB3	1:A:45:GLN:HA	2.00	0.43
1:A:62:ASP:O	1:A:63:ARG:C	2.61	0.43
1:A:210:ILE:O	1:A:214:ILE:HG13	2.19	0.43
1:A:679:ILE:O	1:A:682:THR:N	2.51	0.43
1:A:693:VAL:HA	1:A:696:GLU:HB3	2.01	0.43
1:A:760:GLN:OE1	2:B:1021:MET:HE1	2.19	0.43
1:A:940:ARG:HG2	1:A:940:ARG:NH1	2.34	0.43
1:A:1131:ALA:O	1:A:1132:LYS:C	2.62	0.43
1:A:1226:VAL:HG22	1:A:1240:CYS:HB3	2.00	0.43
1:A:1342:GLU:OE2	5:E:212:ARG:NH1	2.51	0.43
2:B:164:LYS:NZ	2:B:443:ASN:CA	2.81	0.43
2:B:582:VAL:HA	2:B:626:ILE:O	2.19	0.43
2:B:603:LEU:HD22	2:B:603:LEU:HA	1.86	0.43
2:B:794:ASN:O	2:B:795:ILE:HD12	2.18	0.43
3:C:189:THR:CG2	3:C:190:ASP:N	2.80	0.43
4:D:53:SER:CB	4:D:153:ARG:H	2.32	0.43
4:D:66:ARG:O	4:D:67:ARG:C	2.61	0.43
5:E:20:LYS:O	5:E:21:GLU:C	2.62	0.43
5:E:117:THR:C	5:E:119:SER:H	2.27	0.43
9:I:111:THR:CG2	9:I:113:ASP:HB2	2.49	0.43
10:J:1:MET:H2	10:J:55:ASP:C	2.26	0.43
10:J:41:LEU:CD1	10:J:50:ILE:HG13	2.49	0.43
10:J:41:LEU:HD11	10:J:50:ILE:HG13	2.00	0.43
1:A:42:ASP:O	1:A:44:THR:N	2.45	0.42
1:A:472:LEU:HD11	2:B:835:GLN:CD	2.44	0.42
1:A:1039:LYS:HE3	1:A:1043:ASP:OD2	2.19	0.42
1:A:1208:THR:O	1:A:1209:MET:C	2.62	0.42
1:A:1444:MET:O	6:F:133:VAL:N	2.48	0.42
1:A:1450:LEU:HD11	6:F:108:PHE:HZ	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:458:LYS:O	2:B:459:TYR:C	2.61	0.42
2:B:460:ALA:C	2:B:462:ALA:N	2.76	0.42
2:B:1162:ILE:CG2	2:B:1163:CYS:H	2.25	0.42
3:C:62:PHE:O	3:C:63:ILE:C	2.62	0.42
3:C:92:CYS:O	3:C:94:LYS:N	2.52	0.42
3:C:101:LEU:HD12	3:C:101:LEU:HA	1.80	0.42
3:C:241:ASP:CG	3:C:242:GLN:N	2.77	0.42
5:E:191:LYS:O	5:E:192:ARG:C	2.62	0.42
8:H:38:LEU:HD13	8:H:125:LEU:CD1	2.49	0.42
8:H:80:ARG:HA	8:H:81:PRO:HD3	1.77	0.42
9:I:83:ASN:HA	9:I:102:VAL:O	2.19	0.42
9:I:84:VAL:HG13	9:I:84:VAL:O	2.19	0.42
10:J:2:ILE:HG22	10:J:3:VAL:O	2.18	0.42
11:K:96:ASN:O	11:K:97:LYS:C	2.62	0.42
1:A:268:ASP:O	1:A:269:ILE:C	2.62	0.42
1:A:779:PHE:CE1	1:A:785:PRO:CD	2.93	0.42
1:A:901:LEU:H	1:A:926:GLN:HE21	1.56	0.42
1:A:1409:LEU:O	1:A:1410:PHE:C	2.62	0.42
2:B:128:LEU:HD12	2:B:128:LEU:HA	1.87	0.42
2:B:189:LEU:O	2:B:190:TYR:C	2.61	0.42
2:B:257:LYS:N	2:B:270:LYS:O	2.53	0.42
2:B:312:GLU:O	2:B:313:MET:C	2.63	0.42
2:B:615:MET:HE3	2:B:615:MET:HB2	1.97	0.42
2:B:844:SER:O	2:B:845:SER:C	2.62	0.42
2:B:957:ASN:O	2:B:958:GLN:C	2.63	0.42
7:G:145:VAL:CG1	7:G:146:LYS:N	2.81	0.42
9:I:86:PHE:CD1	9:I:86:PHE:C	2.97	0.42
10:J:8:PHE:O	10:J:9:SER:C	2.60	0.42
11:K:53:ASP:C	11:K:55:LYS:N	2.76	0.42
11:K:101:LEU:O	11:K:101:LEU:HD23	2.19	0.42
1:A:41:MET:O	1:A:50:ILE:HG13	2.20	0.42
1:A:120:GLU:C	1:A:122:MET:H	2.26	0.42
1:A:203:SER:O	1:A:204:THR:C	2.62	0.42
1:A:275:SER:O	1:A:279:LEU:HG	2.19	0.42
1:A:367:PRO:HB3	1:A:465:TYR:O	2.19	0.42
1:A:415:LEU:HD23	1:A:415:LEU:HA	1.75	0.42
1:A:443:LEU:HD11	1:A:455:MET:SD	2.59	0.42
1:A:457:ALA:HB3	1:A:506:ALA:HA	2.01	0.42
1:A:573:SER:O	1:A:574:GLY:C	2.61	0.42
1:A:682:THR:HA	1:A:685:GLU:HG2	2.00	0.42
1:A:853:ASP:OD1	1:A:855:THR:CG2	2.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1289:ARG:NH1	1:A:1326:ARG:NH1	2.67	0.42
1:A:1446:ASP:HB2	6:F:133:VAL:CG2	2.49	0.42
1:A:1453:TYR:O	1:A:1454:MET:HB3	2.18	0.42
2:B:167:ILE:HG22	2:B:453:ILE:HD12	2.01	0.42
2:B:578:THR:O	2:B:579:ARG:C	2.62	0.42
2:B:769:TYR:C	2:B:771:SER:H	2.26	0.42
2:B:1106:ARG:HG3	2:B:1107:ALA:N	2.34	0.42
2:B:1117:GLN:HE21	2:B:1199:ALA:HB2	1.84	0.42
2:B:1182:CYS:O	2:B:1183:LYS:O	2.37	0.42
3:C:22:LEU:HD23	3:C:25:VAL:HG21	2.00	0.42
7:G:21:ARG:HD3	7:G:21:ARG:HA	1.85	0.42
1:A:87:ALA:HB1	1:A:276:LEU:HD23	2.00	0.42
1:A:339:ASN:O	1:A:343:LYS:HG2	2.20	0.42
1:A:477:PRO:HG2	1:A:521:MET:HG2	2.00	0.42
1:A:522:GLY:O	1:A:646:PHE:HE2	2.01	0.42
1:A:525:GLN:O	1:A:526:ASP:C	2.63	0.42
1:A:1111:MET:CE	1:A:1330:ASN:OD1	2.68	0.42
1:A:1116:LEU:CD1	1:A:1118:VAL:HG13	2.48	0.42
1:A:1168:GLU:O	1:A:1172:LEU:HG	2.19	0.42
2:B:20:ASP:O	2:B:22:SER:N	2.45	0.42
2:B:33:VAL:O	2:B:34:ILE:C	2.63	0.42
2:B:436:VAL:O	2:B:436:VAL:HG12	2.18	0.42
2:B:596:LEU:O	2:B:600:LEU:HG	2.19	0.42
4:D:33:PHE:CE2	7:G:80:LYS:NZ	2.72	0.42
5:E:101:GLN:NE2	5:E:127:ILE:HG21	2.34	0.42
7:G:10:ASN:OD1	7:G:71:ASN:HA	2.19	0.42
10:J:32:GLU:O	10:J:33:GLY:C	2.62	0.42
1:A:242:PRO:O	1:A:247:ARG:NE	2.52	0.42
1:A:277:GLU:O	1:A:279:LEU:N	2.52	0.42
1:A:298:PHE:HD2	1:A:299:HIS:CD2	2.37	0.42
1:A:306:ASN:ND2	1:A:322:VAL:CG1	2.83	0.42
1:A:383:TYR:CD2	1:A:383:TYR:N	2.86	0.42
1:A:807:GLY:O	1:A:808:LEU:C	2.61	0.42
1:A:1335:ILE:HG23	1:A:1339:LEU:HD12	2.01	0.42
1:A:1381:LEU:HD23	1:A:1381:LEU:HA	1.77	0.42
2:B:288:ALA:HA	2:B:331:LEU:HD12	2.02	0.42
2:B:408:LEU:HD12	2:B:408:LEU:HA	1.86	0.42
2:B:1115:THR:CG2	2:B:1117:GLN:CG	2.97	0.42
3:C:31:ASN:O	3:C:35:ARG:HG3	2.18	0.42
3:C:75:MET:O	3:C:246:ARG:NH2	2.49	0.42
3:C:179:GLU:CG	3:C:180:TYR:N	2.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:206:GLU:O	4:D:208:GLU:N	2.53	0.42
7:G:149:GLY:O	7:G:159:ALA:HB1	2.20	0.42
9:I:61:ASP:C	9:I:63:GLY:N	2.73	0.42
1:A:23:SER:CB	1:A:233:TRP:NE1	2.82	0.42
1:A:514:PRO:C	1:A:516:SER:N	2.75	0.42
1:A:590:ARG:HD3	1:A:604:GLY:C	2.44	0.42
1:A:685:GLU:HG3	1:A:686:ALA:N	2.33	0.42
1:A:807:GLY:HA2	2:B:760:ASP:O	2.19	0.42
1:A:901:LEU:HA	1:A:907:THR:OG1	2.20	0.42
1:A:1161:THR:HG22	1:A:1163:ILE:HG13	2.02	0.42
1:A:1365:TYR:O	1:A:1366:ARG:C	2.63	0.42
2:B:233:PRO:HG2	2:B:234:ILE:CD1	2.40	0.42
2:B:654:ARG:C	2:B:656:GLY:N	2.77	0.42
2:B:814:PHE:C	2:B:816:GLU:H	2.27	0.42
2:B:986:GLN:O	2:B:987:LYS:C	2.62	0.42
4:D:29:LEU:O	4:D:30:GLY:C	2.62	0.42
7:G:88:ASP:OD2	7:G:88:ASP:N	2.49	0.42
9:I:101:PHE:HD1	9:I:110:PHE:O	2.02	0.42
1:A:76:GLU:O	1:A:76:GLU:CG	2.57	0.42
1:A:356:ASP:OD2	11:K:65:HIS:CE1	2.71	0.42
1:A:481:ASP:OD1	1:A:483:ASP:OD2	2.38	0.42
1:A:497:THR:HG22	1:A:498:ARG:N	2.34	0.42
1:A:606:LEU:HB3	1:A:614:PHE:CE2	2.54	0.42
1:A:817:ALA:O	1:A:820:GLY:N	2.52	0.42
2:B:693:ILE:HD13	2:B:701:ILE:HD13	2.00	0.42
2:B:860:MET:HE2	2:B:965:LYS:HE2	2.02	0.42
2:B:900:ALA:O	2:B:903:VAL:HG23	2.19	0.42
3:C:92:CYS:C	3:C:94:LYS:H	2.27	0.42
4:D:167:LEU:C	4:D:169:SER:H	2.27	0.42
5:E:90:VAL:CA	5:E:120:ALA:HB2	2.49	0.42
11:K:12:LEU:H	11:K:12:LEU:CD1	2.32	0.42
11:K:45:LEU:HG	11:K:94:ILE:CD1	2.43	0.42
1:A:31:SER:OG	1:A:82:GLY:HA2	2.19	0.42
1:A:73:GLY:O	1:A:75:ASN:N	2.52	0.42
1:A:427:GLN:HB2	1:A:430:TRP:CE2	2.55	0.42
1:A:825:ILE:HG22	1:A:826:ASP:N	2.33	0.42
1:A:1313:LEU:C	1:A:1315:GLU:N	2.78	0.42
2:B:25:ILE:HD11	2:B:653:VAL:C	2.42	0.42
2:B:193:LYS:HD3	2:B:787:VAL:HG11	2.01	0.42
2:B:278:GLN:HG2	2:B:279:ASP:H	1.85	0.42
2:B:758:PHE:HB3	2:B:761:HIS:CD2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1032:SER:O	2:B:1036:ALA:HB2	2.19	0.42
2:B:1147:LEU:O	2:B:1148:LYS:C	2.62	0.42
4:D:113:PHE:CA	4:D:156:ASP:OD1	2.60	0.42
5:E:201:LYS:HA	5:E:206:GLY:O	2.20	0.42
9:I:58:VAL:O	9:I:58:VAL:HG12	2.19	0.42
9:I:111:THR:CG2	9:I:112:SER:H	2.31	0.42
1:A:57:ARG:C	1:A:58:LEU:O	2.62	0.42
1:A:466:SER:HB2	2:B:1099:VAL:HG11	2.02	0.42
1:A:567:LYS:HG3	1:A:568:PRO:CD	2.39	0.42
1:A:825:ILE:O	1:A:826:ASP:C	2.62	0.42
1:A:1111:MET:H	1:A:1111:MET:HG2	1.56	0.42
1:A:1147:THR:HA	1:A:1197:LEU:HD23	2.00	0.42
1:A:1157:ASP:C	1:A:1159:ARG:N	2.77	0.42
1:A:1164:PRO:C	1:A:1166:ASP:H	2.28	0.42
1:A:1362:TYR:CD1	1:A:1362:TYR:C	2.97	0.42
2:B:604:ARG:HG3	2:B:611:PRO:HA	2.02	0.42
2:B:651:LEU:HD11	2:B:707:PRO:CB	2.49	0.42
2:B:762:ASN:OD1	2:B:1022:THR:HA	2.19	0.42
2:B:770:GLN:OE1	2:B:983:ARG:CA	2.66	0.42
2:B:911:ILE:HG22	2:B:912:ILE:HG13	2.00	0.42
2:B:1084:GLN:NE2	2:B:1084:GLN:H	2.17	0.42
2:B:1197:PRO:O	2:B:1200:ALA:HB3	2.20	0.42
2:B:1223:ASP:HB3	2:B:1224:PHE:H	1.72	0.42
4:D:7:THR:CB	7:G:42:PHE:CZ	3.03	0.42
5:E:112:TYR:CZ	5:E:136:ASN:HB2	2.54	0.42
5:E:124:VAL:HG13	5:E:132:ILE:CB	2.45	0.42
6:F:97:ARG:NH1	6:F:100:GLN:OE1	2.53	0.42
11:K:31:VAL:CG1	11:K:32:VAL:H	2.31	0.42
11:K:68:PHE:N	11:K:68:PHE:CD2	2.86	0.42
1:A:231:PRO:O	1:A:233:TRP:N	2.52	0.42
1:A:306:ASN:HB2	1:A:324:SER:HB3	2.02	0.42
1:A:414:ASP:OD1	1:A:416:ARG:CG	2.68	0.42
1:A:537:ARG:NH1	8:H:120:GLY:O	2.44	0.42
1:A:1150:SER:C	1:A:1151:GLU:HG3	2.45	0.42
2:B:31:TRP:O	2:B:32:ALA:C	2.62	0.42
2:B:54:PHE:CE2	2:B:59:LEU:HD13	2.55	0.42
2:B:644:GLU:C	2:B:646:LEU:N	2.77	0.42
2:B:737:THR:O	2:B:738:PHE:C	2.62	0.42
2:B:986:GLN:OE1	2:B:986:GLN:HA	2.20	0.42
2:B:1006:ILE:HG22	10:J:45:CYS:HB3	2.02	0.42
2:B:1106:ARG:NH2	2:B:1109:GLY:H	2.17	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:183:TRP:CE2	3:C:207:CYS:HB3	2.54	0.42
5:E:177:ARG:O	5:E:212:ARG:CD	2.68	0.42
6:F:93:ILE:HD13	6:F:148:VAL:HG13	2.02	0.42
8:H:83:GLN:C	8:H:85:GLY:N	2.73	0.42
10:J:27:GLU:C	10:J:29:GLU:N	2.78	0.42
11:K:49:GLU:HG3	11:K:94:ILE:HG13	2.00	0.42
11:K:113:THR:O	11:K:114:LEU:CB	2.63	0.42
1:A:481:ASP:OD1	1:A:483:ASP:CG	2.62	0.41
1:A:574:GLY:O	1:A:575:LYS:C	2.62	0.41
1:A:667:GLY:HA3	3:C:192:TRP:CH2	2.55	0.41
1:A:765:VAL:HG23	1:A:802:ASN:O	2.20	0.41
1:A:896:ARG:HD3	1:A:897:TYR:HE1	1.84	0.41
1:A:1010:ALA:O	1:A:1013:ASP:HB2	2.20	0.41
2:B:351:TYR:CD1	2:B:355:ILE:HD11	2.53	0.41
2:B:954:VAL:HA	2:B:964:VAL:HG22	2.01	0.41
2:B:1187:ASN:OD1	2:B:1189:ILE:N	2.52	0.41
2:B:1216:LEU:N	2:B:1216:LEU:HD23	2.35	0.41
3:C:9:LYS:O	3:C:10:ILE:C	2.62	0.41
4:D:153:ARG:O	4:D:154:PHE:CG	2.73	0.41
1:A:55:ASP:N	1:A:56:PRO:CD	2.83	0.41
1:A:106:VAL:HA	1:A:114:LEU:HD21	2.03	0.41
1:A:269:ILE:HD11	1:A:300:VAL:HA	2.01	0.41
1:A:332:LYS:C	1:A:334:GLY:N	2.78	0.41
1:A:365:GLY:HA3	1:A:463:ILE:CD1	2.51	0.41
1:A:416:ARG:O	1:A:417:TYR:HD2	2.03	0.41
1:A:526:ASP:O	1:A:527:THR:C	2.63	0.41
1:A:794:PRO:C	1:A:796:SER:N	2.78	0.41
1:A:1001:ARG:O	1:A:1002:GLY:C	2.64	0.41
1:A:1376:THR:O	1:A:1377:THR:C	2.62	0.41
2:B:293:PRO:C	2:B:294:ASP:O	2.59	0.41
2:B:437:GLU:OE1	2:B:439:ALA:O	2.38	0.41
2:B:610:ASN:C	2:B:612:GLU:H	2.28	0.41
2:B:796:LEU:HD12	2:B:852:ARG:O	2.19	0.41
2:B:834:ASN:ND2	2:B:1013:ASN:HB2	2.34	0.41
2:B:992:ILE:HD11	11:K:66:PRO:HB2	2.01	0.41
2:B:1219:ASP:OD1	2:B:1219:ASP:O	2.38	0.41
3:C:80:LEU:HD22	3:C:129:ILE:HD13	2.01	0.41
4:D:40:HIS:C	4:D:42:GLY:N	2.78	0.41
4:D:217:LEU:O	4:D:219:THR:N	2.53	0.41
5:E:82:PHE:CD1	5:E:82:PHE:N	2.88	0.41
6:F:74:ILE:HG23	6:F:75:PRO:HD2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:127:GLY:HA3	8:H:130:ARG:NH2	2.35	0.41
10:J:3:VAL:HG21	10:J:18:TRP:CG	2.55	0.41
11:K:58:PHE:HE2	11:K:74:ARG:HE	1.57	0.41
1:A:53:LEU:HD22	1:A:54:ASN:HD22	1.85	0.41
1:A:90:VAL:HG13	1:A:297:GLN:OE1	2.20	0.41
1:A:137:ALA:O	1:A:138:ILE:C	2.64	0.41
1:A:152:VAL:HG13	1:A:153:PRO:HD2	1.97	0.41
1:A:331:GLY:O	1:A:332:LYS:HB3	2.20	0.41
1:A:586:ILE:CG2	1:A:587:HIS:N	2.83	0.41
1:A:630:ILE:O	1:A:631:HIS:C	2.63	0.41
1:A:1115:SER:OG	1:A:1116:LEU:N	2.53	0.41
1:A:1206:ASP:O	1:A:1274:ARG:NH1	2.51	0.41
1:A:1279:ILE:HG23	1:A:1308:THR:OG1	2.19	0.41
1:A:1299:VAL:CG1	1:A:1300:LYS:N	2.83	0.41
1:A:1340:GLY:O	1:A:1341:ILE:C	2.62	0.41
1:A:1425:SER:O	1:A:1426:GLU:C	2.61	0.41
2:B:20:ASP:C	2:B:22:SER:H	2.27	0.41
2:B:309:GLN:HG3	9:I:52:ILE:HD11	2.02	0.41
2:B:619:ILE:O	2:B:622:LYS:N	2.51	0.41
2:B:635:ARG:HB2	2:B:636:PRO:HD2	2.02	0.41
2:B:644:GLU:C	2:B:646:LEU:H	2.28	0.41
2:B:681:TRP:C	2:B:683:SER:N	2.78	0.41
2:B:801:LYS:O	10:J:52:THR:CG2	2.63	0.41
2:B:827:ILE:O	2:B:827:ILE:HG22	2.19	0.41
3:C:229:TYR:CD1	3:C:229:TYR:N	2.88	0.41
3:C:232:VAL:HG21	3:C:244:VAL:CG2	2.42	0.41
3:C:245:VAL:C	3:C:247:GLY:N	2.74	0.41
4:D:179:GLN:O	4:D:183:LEU:HB2	2.20	0.41
5:E:61:GLN:HG2	5:E:62:ALA:N	2.35	0.41
5:E:116:ILE:CG2	5:E:117:THR:N	2.83	0.41
5:E:133:GLU:HB3	5:E:135:PHE:HE1	1.84	0.41
8:H:106:GLU:O	8:H:108:SER:N	2.48	0.41
1:A:19:PHE:HB3	1:A:1413:GLY:HA2	2.02	0.41
1:A:93:VAL:CG2	1:A:304:MET:HE3	2.50	0.41
1:A:241:VAL:HA	1:A:242:PRO:HD2	1.87	0.41
1:A:274:ILE:O	1:A:275:SER:C	2.62	0.41
1:A:450:LEU:N	1:A:450:LEU:CD1	2.80	0.41
1:A:1041:ALA:O	1:A:1044:TRP:HB3	2.20	0.41
1:A:1070:GLN:O	1:A:1071:SER:C	2.62	0.41
1:A:1118:VAL:O	1:A:1118:VAL:HG23	2.21	0.41
2:B:205:ILE:CG2	2:B:206:ASN:N	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:214:ALA:HB3	2:B:498:THR:HA	2.01	0.41
2:B:314:LEU:O	2:B:315:LYS:C	2.63	0.41
2:B:579:ARG:CA	2:B:589:VAL:HG13	2.51	0.41
2:B:610:ASN:O	2:B:612:GLU:N	2.53	0.41
2:B:638:PHE:HD2	2:B:690:VAL:HG22	1.86	0.41
2:B:731:VAL:CG1	2:B:732:SER:H	2.27	0.41
4:D:138:ASN:O	4:D:141:LEU:N	2.54	0.41
5:E:23:VAL:O	5:E:28:TYR:HD1	2.03	0.41
5:E:58:MET:O	5:E:59:SER:C	2.63	0.41
6:F:72:LYS:O	6:F:73:ALA:HB3	2.19	0.41
1:A:774:ARG:CZ	1:A:797:LYS:CB	2.98	0.41
1:A:909:ASP:C	1:A:911:SER:N	2.79	0.41
1:A:1072:ILE:O	1:A:1075:PRO:HD2	2.20	0.41
2:B:34:ILE:O	2:B:35:SER:C	2.63	0.41
2:B:37:PHE:CE1	2:B:41:LYS:CG	2.96	0.41
2:B:170:LEU:HA	2:B:171:PRO:HD2	1.94	0.41
2:B:211:VAL:HG23	2:B:483:LEU:HB2	2.03	0.41
2:B:291:ILE:HD13	2:B:300:HIS:NE2	2.35	0.41
2:B:298:LEU:N	2:B:298:LEU:CD2	2.83	0.41
2:B:366:GLN:O	2:B:367:LEU:O	2.38	0.41
2:B:479:VAL:O	2:B:480:SER:HB3	2.20	0.41
2:B:552:MET:O	2:B:554:ILE:N	2.53	0.41
2:B:637:LEU:HD23	2:B:742:GLU:HA	2.02	0.41
2:B:790:ASP:OD2	2:B:790:ASP:N	2.51	0.41
2:B:918:ILE:HG21	2:B:935:ARG:NH1	2.36	0.41
2:B:1030:LEU:HD12	2:B:1030:LEU:HA	1.92	0.41
2:B:1164:GLY:HA3	2:B:1190:ASP:OD2	2.21	0.41
3:C:116:LYS:HD3	3:C:140:ASN:HA	2.03	0.41
4:D:128:VAL:O	4:D:129:LEU:C	2.64	0.41
4:D:170:THR:HG22	4:D:172:LEU:HG	1.99	0.41
4:D:209:ARG:O	4:D:212:LYS:HB2	2.20	0.41
5:E:124:VAL:N	5:E:125:PRO:HD2	2.36	0.41
5:E:127:ILE:O	5:E:130:ALA:HB3	2.19	0.41
6:F:75:PRO:C	6:F:77:ASP:N	2.78	0.41
9:I:56:ALA:O	9:I:57:GLY:C	2.63	0.41
1:A:808:LEU:CD2	1:A:813:PHE:HA	2.46	0.41
1:A:1332:PHE:HA	1:A:1335:ILE:HB	2.03	0.41
2:B:130:VAL:CG2	2:B:167:ILE:HD12	2.50	0.41
2:B:1200:ALA:O	2:B:1201:LYS:C	2.63	0.41
3:C:240:VAL:O	3:C:244:VAL:HG23	2.21	0.41
5:E:78:LEU:C	5:E:78:LEU:CD2	2.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:7:PHE:CD1	11:K:7:PHE:C	2.98	0.41
11:K:52:ASN:O	11:K:53:ASP:C	2.64	0.41
1:A:264:PHE:O	1:A:267:ALA:HB3	2.20	0.41
1:A:409:SER:O	1:A:410:GLY:C	2.64	0.41
1:A:444:PHE:CB	1:A:458:HIS:CD2	3.03	0.41
1:A:446:ARG:NH1	1:A:479:ASN:O	2.53	0.41
1:A:566:ILE:O	1:A:567:LYS:O	2.39	0.41
1:A:567:LYS:CE	8:H:46:LEU:HB2	2.51	0.41
1:A:599:SER:HB2	1:A:603:ASN:H	1.85	0.41
1:A:823:GLY:O	1:A:824:LEU:C	2.64	0.41
1:A:836:TYR:O	1:A:837:ILE:C	2.63	0.41
1:A:1125:ALA:C	1:A:1127:ASP:H	2.28	0.41
1:A:1127:ASP:O	1:A:1130:GLN:HB3	2.20	0.41
1:A:1333:ILE:O	1:A:1337:GLU:HG3	2.21	0.41
2:B:69:LEU:HD22	2:B:429:PHE:CE1	2.56	0.41
2:B:204:ILE:O	2:B:204:ILE:HG22	2.21	0.41
2:B:542:MET:CG	2:B:747:MET:HB3	2.50	0.41
2:B:593:PRO:O	2:B:595:ARG:N	2.53	0.41
2:B:687:GLU:O	2:B:689:LEU:HG	2.20	0.41
2:B:765:PRO:C	2:B:767:ASN:N	2.77	0.41
2:B:792:MET:HA	2:B:856:PHE:O	2.19	0.41
2:B:1029:CYS:HB3	2:B:1086:PHE:CZ	2.55	0.41
3:C:15:LYS:O	3:C:240:VAL:HG22	2.20	0.41
3:C:99:LEU:HD22	3:C:120:ILE:HG12	2.01	0.41
3:C:123:ASN:HD21	3:C:125:MET:HA	1.85	0.41
5:E:39:LEU:O	5:E:40:GLU:C	2.64	0.41
5:E:60:PHE:CE2	5:E:80:VAL:HB	2.56	0.41
11:K:65:HIS:CG	11:K:66:PRO:HD2	2.56	0.41
1:A:95:PHE:O	1:A:98:LYS:N	2.49	0.41
1:A:408:ASP:O	1:A:410:GLY:N	2.53	0.41
1:A:444:PHE:CB	1:A:458:HIS:HD2	2.33	0.41
1:A:636:GLU:OE2	1:A:962:ARG:NH1	2.51	0.41
1:A:659:HIS:C	1:A:661:GLY:N	2.79	0.41
1:A:697:ALA:C	1:A:699:ALA:H	2.29	0.41
1:A:852:TYR:CD2	1:A:1060:PRO:CB	3.03	0.41
1:A:1291:VAL:HA	1:A:1292:PRO:HD3	1.87	0.41
1:A:1410:PHE:HA	1:A:1410:PHE:HD2	1.77	0.41
2:B:810:GLU:CB	2:B:815:ARG:HH22	2.33	0.41
2:B:1085:ILE:N	2:B:1085:ILE:CD1	2.81	0.41
3:C:94:LYS:HE3	3:C:94:LYS:HB2	1.86	0.41
4:D:128:VAL:C	4:D:130:LEU:N	2.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:42:PHE:CE1	5:E:58:MET:HE3	2.55	0.41
5:E:98:ILE:C	5:E:100:ILE:N	2.78	0.41
5:E:127:ILE:O	5:E:127:ILE:HG13	2.21	0.41
5:E:145:THR:HG21	5:E:187:TYR:CD2	2.56	0.41
5:E:195:VAL:HG12	5:E:196:VAL:N	2.36	0.41
7:G:31:LEU:CD2	7:G:48:VAL:HG21	2.51	0.41
7:G:49:LEU:N	7:G:49:LEU:HD23	2.35	0.41
10:J:48:ARG:HD2	10:J:48:ARG:C	2.45	0.41
1:A:249:SER:HB2	1:A:250:ILE:H	1.66	0.41
1:A:276:LEU:O	1:A:279:LEU:N	2.47	0.41
1:A:472:LEU:O	1:A:475:THR:CB	2.68	0.41
1:A:482:PHE:O	1:A:484:GLY:N	2.53	0.41
1:A:527:THR:O	1:A:531:ILE:HB	2.21	0.41
1:A:621:THR:O	1:A:629:LEU:HB2	2.21	0.41
1:A:744:LYS:O	1:A:747:VAL:N	2.54	0.41
1:A:822:GLU:O	1:A:825:ILE:HB	2.21	0.41
1:A:875:ALA:HA	1:A:878:ILE:CD1	2.48	0.41
1:A:1059:HIS:CE1	6:F:87:LYS:H	2.39	0.41
1:A:1074:GLU:C	1:A:1076:ALA:N	2.78	0.41
1:A:1157:ASP:O	1:A:1159:ARG:N	2.54	0.41
1:A:1226:VAL:HG12	1:A:1227:ILE:N	2.35	0.41
1:A:1242:VAL:O	1:A:1243:VAL:CB	2.68	0.41
1:A:1388:GLY:C	1:A:1390:ASN:N	2.79	0.41
2:B:121:ASN:ND2	2:B:207:GLY:HA3	2.36	0.41
2:B:388:CYS:C	2:B:390:LEU:N	2.79	0.41
2:B:487:THR:CG2	2:B:488:TYR:N	2.84	0.41
2:B:519:TRP:HE1	2:B:635:ARG:NH2	2.19	0.41
2:B:603:LEU:HB3	2:B:609:ILE:CG1	2.50	0.41
2:B:662:MET:HA	2:B:665:GLU:HB2	2.03	0.41
2:B:700:SER:C	2:B:701:ILE:CG2	2.93	0.41
2:B:758:PHE:O	2:B:760:ASP:N	2.54	0.41
2:B:759:PRO:C	2:B:761:HIS:H	2.29	0.41
2:B:901:PRO:O	2:B:949:VAL:HB	2.21	0.41
2:B:918:ILE:HD12	2:B:935:ARG:CD	2.51	0.41
2:B:1027:ILE:O	2:B:1028:GLU:C	2.64	0.41
2:B:1208:MET:HA	2:B:1212:ILE:O	2.20	0.41
4:D:52:LEU:C	4:D:54:GLU:H	2.29	0.41
4:D:113:PHE:N	4:D:156:ASP:OD1	2.52	0.41
4:D:193:THR:O	4:D:196:PRO:HD3	2.21	0.41
5:E:98:ILE:O	5:E:100:ILE:N	2.54	0.41
6:F:111:LEU:N	6:F:111:LEU:CD1	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:138:THR:O	7:G:139:ILE:C	2.64	0.41
8:H:40:LEU:CD2	8:H:142:LEU:HD21	2.50	0.41
8:H:48:PRO:O	8:H:49:VAL:HG23	2.20	0.41
8:H:96:VAL:HA	8:H:142:LEU:O	2.21	0.41
9:I:98:VAL:C	9:I:99:LEU:HD23	2.45	0.41
9:I:99:LEU:C	9:I:100:PHE:CD1	2.96	0.41
11:K:10:PHE:CD1	11:K:11:LEU:CD2	3.04	0.41
1:A:172:PRO:HD3	1:A:185:TRP:HE1	1.86	0.41
1:A:326:ARG:NH2	1:A:1407:GLU:HG3	2.36	0.41
1:A:1059:HIS:CE1	6:F:86:THR:HA	2.55	0.41
2:B:100:PRO:HD2	2:B:180:TYR:CE1	2.55	0.41
2:B:388:CYS:C	2:B:390:LEU:H	2.28	0.41
2:B:496:ARG:HB3	2:B:496:ARG:NH1	2.35	0.41
2:B:619:ILE:C	2:B:621:GLU:N	2.79	0.41
2:B:758:PHE:HZ	2:B:1031:LEU:HD22	1.86	0.41
2:B:821:GLN:NE2	2:B:851:PHE:HA	2.35	0.41
2:B:822:ASN:ND2	10:J:52:THR:HG21	2.36	0.41
2:B:842:ASN:HD21	2:B:845:SER:H	1.60	0.41
2:B:856:PHE:CD1	2:B:856:PHE:N	2.89	0.41
2:B:910:VAL:HG12	2:B:911:ILE:N	2.35	0.41
2:B:952:VAL:O	2:B:953:LEU:HB3	2.21	0.41
5:E:134:THR:C	5:E:135:PHE:CD1	2.99	0.41
5:E:167:ARG:HD3	5:E:167:ARG:HA	1.78	0.41
7:G:111:THR:O	7:G:112:LYS:C	2.64	0.41
1:A:7:SER:HB2	2:B:1175:LEU:HD22	2.03	0.40
1:A:69:THR:O	1:A:71:GLN:HG2	2.20	0.40
1:A:78:PRO:HA	2:B:1201:LYS:HZ1	1.84	0.40
1:A:244:PRO:HB2	1:A:245:PRO:CD	2.41	0.40
1:A:255:SER:O	1:A:256:GLN:HG3	2.20	0.40
1:A:269:ILE:CD1	1:A:300:VAL:HA	2.51	0.40
1:A:343:LYS:HE2	2:B:1156:ASP:OD2	2.21	0.40
1:A:453:MET:C	1:A:455:MET:N	2.76	0.40
1:A:695:LYS:C	1:A:697:ALA:N	2.79	0.40
1:A:789:LYS:HE3	9:I:67:THR:HB	2.03	0.40
1:A:1031:VAL:O	1:A:1031:VAL:HG12	2.20	0.40
1:A:1132:LYS:C	1:A:1134:ILE:N	2.79	0.40
1:A:1136:SER:O	1:A:1274:ARG:HG2	2.21	0.40
2:B:166:PHE:C	2:B:167:ILE:HG13	2.45	0.40
2:B:281:PRO:HG2	2:B:284:ILE:HG13	2.03	0.40
2:B:515:HIS:O	2:B:518:HIS:HB2	2.20	0.40
2:B:579:ARG:HG2	2:B:579:ARG:NH1	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:622:LYS:HE3	9:I:59:VAL:HG22	2.03	0.40
2:B:814:PHE:C	2:B:816:GLU:N	2.77	0.40
2:B:836:GLU:O	2:B:837:ASP:HB2	2.21	0.40
2:B:1068:GLY:C	2:B:1069:PHE:O	2.63	0.40
2:B:1080:LYS:HD2	3:C:188:HIS:HB2	2.03	0.40
2:B:1200:ALA:O	2:B:1203:LEU:HB3	2.21	0.40
3:C:8:VAL:HG12	3:C:9:LYS:H	1.84	0.40
3:C:62:PHE:O	3:C:66:ARG:HG3	2.21	0.40
3:C:239:PRO:O	3:C:240:VAL:C	2.65	0.40
4:D:138:ASN:HD21	7:G:35:GLU:HB3	1.86	0.40
4:D:196:PRO:C	4:D:198:LEU:N	2.79	0.40
6:F:135:ARG:NH1	6:F:143:PHE:CE2	2.90	0.40
7:G:123:ALA:C	7:G:125:SER:H	2.28	0.40
9:I:34:TYR:HD2	9:I:34:TYR:C	2.24	0.40
9:I:75:CYS:SG	9:I:78:CYS:C	3.04	0.40
12:L:29:TYR:N	12:L:29:TYR:CD2	2.88	0.40
1:A:23:SER:O	1:A:25:GLU:N	2.55	0.40
1:A:514:PRO:C	1:A:516:SER:H	2.29	0.40
1:A:560:ILE:HA	1:A:561:PRO:HD2	1.95	0.40
1:A:626:ASN:HB3	1:A:627:GLY:H	1.70	0.40
1:A:826:ASP:O	1:A:827:THR:C	2.65	0.40
2:B:295:GLY:N	2:B:298:LEU:HD23	2.34	0.40
2:B:511:PRO:O	2:B:513:GLN:N	2.54	0.40
2:B:575:PRO:HG2	2:B:576:ASP:H	1.86	0.40
2:B:838:SER:CA	2:B:989:THR:O	2.70	0.40
2:B:854:LEU:HD23	2:B:854:LEU:HA	1.83	0.40
2:B:983:ARG:HD2	2:B:1091:TYR:HB3	2.02	0.40
2:B:1106:ARG:HD3	2:B:1126:GLY:C	2.46	0.40
2:B:1124:ARG:O	2:B:1125:ASP:CB	2.68	0.40
3:C:18:VAL:O	3:C:19:ASP:C	2.64	0.40
3:C:163:ILE:C	3:C:165:LYS:N	2.79	0.40
3:C:206:ASN:OD1	3:C:229:TYR:CD2	2.74	0.40
3:C:247:GLY:C	3:C:249:ASP:N	2.77	0.40
4:D:62:ALA:C	4:D:64:VAL:N	2.78	0.40
4:D:156:ASP:O	4:D:158:GLU:N	2.54	0.40
6:F:95:GLY:O	6:F:96:THR:C	2.64	0.40
6:F:109:VAL:HG23	6:F:124:GLU:HG2	2.03	0.40
8:H:62:SER:OG	8:H:63:LEU:N	2.53	0.40
9:I:95:THR:HG22	9:I:96:SER:N	2.36	0.40
10:J:2:ILE:CG2	10:J:3:VAL:N	2.83	0.40
10:J:52:THR:O	10:J:53:HIS:C	2.63	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:SER:HB3	1:A:233:TRP:NE1	2.35	0.40
1:A:649:ILE:O	1:A:653:VAL:HG23	2.22	0.40
1:A:1163:ILE:HG22	1:A:1164:PRO:HD2	2.03	0.40
1:A:1434:ALA:CB	1:A:1436:ILE:HD12	2.52	0.40
2:B:487:THR:O	2:B:490:SER:HB3	2.21	0.40
2:B:702:LEU:C	2:B:703:ILE:HG13	2.46	0.40
2:B:800:GLN:CA	10:J:52:THR:HG22	2.51	0.40
2:B:802:PRO:HB3	2:B:1091:TYR:CD2	2.57	0.40
2:B:822:ASN:HD22	10:J:52:THR:HG21	1.86	0.40
2:B:827:ILE:HD12	2:B:1086:PHE:HD2	1.86	0.40
2:B:980:PHE:HE2	2:B:1094:ARG:HB2	1.85	0.40
3:C:73:GLN:HE21	3:C:74:SER:N	2.19	0.40
5:E:14:ARG:NH2	5:E:141:VAL:HG12	2.37	0.40
6:F:99:LEU:O	6:F:103:MET:CG	2.69	0.40
7:G:44:TYR:O	7:G:78:VAL:HG12	2.22	0.40
7:G:101:VAL:HG12	7:G:102:GLN:N	2.35	0.40
9:I:88:SER:C	9:I:90:GLN:H	2.29	0.40
12:L:55:ILE:HG12	12:L:55:ILE:H	1.53	0.40
1:A:24:PRO:O	1:A:28:ARG:HG3	2.21	0.40
1:A:79:GLY:C	1:A:243:PRO:HG3	2.47	0.40
1:A:220:THR:O	1:A:221:SER:C	2.64	0.40
1:A:335:ARG:HB3	1:A:336:ILE:H	1.65	0.40
1:A:403:LYS:O	1:A:404:TYR:CG	2.74	0.40
1:A:532:ARG:O	1:A:533:LYS:C	2.64	0.40
1:A:535:THR:HG22	1:A:536:LEU:N	2.36	0.40
1:A:867:ILE:O	1:A:868:TYR:C	2.63	0.40
1:A:920:LEU:C	1:A:920:LEU:HD23	2.47	0.40
1:A:958:VAL:HG22	1:A:1052:GLN:HB3	2.03	0.40
1:A:1066:VAL:O	1:A:1067:LEU:C	2.65	0.40
1:A:1125:ALA:C	1:A:1127:ASP:N	2.80	0.40
1:A:1215:ARG:O	1:A:1216:ILE:C	2.64	0.40
1:A:1293:SER:HB2	1:A:1299:VAL:HG23	2.03	0.40
1:A:1369:ALA:C	1:A:1373:ASP:OD2	2.64	0.40
1:A:1392:SER:C	1:A:1394:THR:H	2.29	0.40
2:B:410:GLY:C	2:B:412:LEU:N	2.79	0.40
2:B:488:TYR:O	2:B:489:SER:C	2.65	0.40
2:B:778:MET:CE	2:B:1094:ARG:CD	2.96	0.40
2:B:801:LYS:N	10:J:52:THR:HG22	2.36	0.40
2:B:1060:ARG:C	2:B:1062:HIS:N	2.78	0.40
2:B:1183:LYS:HE3	2:B:1183:LYS:O	2.20	0.40
2:B:1197:PRO:O	2:B:1198:TYR:C	2.64	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:11:ARG:NH2	3:C:206:ASN:OD1	2.54	0.40
3:C:59:ALA:O	3:C:60:ASP:C	2.64	0.40
4:D:31:GLN:O	4:D:34:GLN:HG3	2.21	0.40
5:E:8:ASN:OD1	5:E:8:ASN:O	2.40	0.40
5:E:117:THR:O	5:E:120:ALA:N	2.45	0.40
6:F:75:PRO:HG2	6:F:78:GLN:HB2	2.04	0.40
9:I:34:TYR:O	9:I:35:VAL:CG2	2.69	0.40
1:A:23:SER:C	1:A:25:GLU:N	2.78	0.40
1:A:70:CYS:O	1:A:70:CYS:SG	2.78	0.40
1:A:785:PRO:HG2	1:A:786:HIS:CD2	2.56	0.40
1:A:1149:ALA:HB2	9:I:47:GLU:HA	2.03	0.40
1:A:1372:VAL:CG1	1:A:1373:ASP:N	2.82	0.40
1:A:1385:THR:CG2	1:A:1386:ARG:N	2.84	0.40
2:B:126:SER:O	2:B:169:ARG:HA	2.22	0.40
2:B:235:SER:O	2:B:236:HIS:HD2	2.04	0.40
2:B:258:LEU:O	2:B:258:LEU:CG	2.66	0.40
2:B:386:LEU:O	2:B:388:CYS:N	2.55	0.40
2:B:700:SER:O	2:B:701:ILE:HG22	2.22	0.40
2:B:841:MET:O	2:B:993:THR:HA	2.21	0.40
2:B:1119:VAL:HG22	2:B:1126:GLY:HA2	2.03	0.40
2:B:1135:ARG:O	2:B:1138:MET:N	2.54	0.40
3:C:238:ILE:CG2	3:C:243:VAL:HG23	2.50	0.40
4:D:204:ASP:O	4:D:208:GLU:HB2	2.22	0.40
7:G:104:GLY:HA3	7:G:105:PRO:HD2	1.96	0.40
10:J:16:ASP:OD1	10:J:16:ASP:N	2.54	0.40
11:K:43:GLY:HA3	11:K:61:TYR:CE1	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1406/1733 (81%)	949 (68%)	293 (21%)	164 (12%)	0	4
2	B	1096/1224 (90%)	744 (68%)	226 (21%)	126 (12%)	0	5
3	C	264/318 (83%)	159 (60%)	66 (25%)	39 (15%)	0	2
4	D	178/221 (80%)	124 (70%)	35 (20%)	19 (11%)	0	6
5	E	212/215 (99%)	147 (69%)	50 (24%)	15 (7%)	1	11
6	F	82/155 (53%)	64 (78%)	14 (17%)	4 (5%)	1	16
7	G	169/215 (79%)	131 (78%)	26 (15%)	12 (7%)	1	11
8	H	129/146 (88%)	84 (65%)	29 (22%)	16 (12%)	0	4
9	I	117/122 (96%)	79 (68%)	31 (26%)	7 (6%)	1	14
10	J	63/70 (90%)	37 (59%)	10 (16%)	16 (25%)	0	1
11	K	113/120 (94%)	89 (79%)	18 (16%)	6 (5%)	1	16
12	L	44/70 (63%)	19 (43%)	14 (32%)	11 (25%)	0	1
All	All	3873/4609 (84%)	2626 (68%)	812 (21%)	435 (11%)	0	6

All (435) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	48	ALA
1	A	54	ASN
1	A	55	ASP
1	A	57	ARG
1	A	62	ASP
1	A	65	LEU
1	A	74	MET
1	A	76	GLU
1	A	78	PRO
1	A	93	VAL
1	A	130	ASP
1	A	154	SER
1	A	167	CYS
1	A	250	ILE
1	A	255	SER
1	A	286	HIS
1	A	311	GLN
1	A	322	VAL
1	A	333	GLU
1	A	335	ARG
1	A	385	ILE

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Mol	Chain	Res	Type
1	A	418	SER
1	A	423	ASP
1	A	424	ILE
1	A	536	LEU
1	A	567	LYS
1	A	619	LYS
1	A	626	ASN
1	A	666	ILE
1	A	808	LEU
1	A	968	GLN
1	A	1002	GLY
1	A	1036	ARG
1	A	1115	SER
1	A	1122	PRO
1	A	1223	ASP
1	A	1281	ARG
1	A	1314	SER
1	A	1341	ILE
1	A	1365	TYR
1	A	1366	ARG
1	A	1378	GLN
1	A	1397	LEU
1	A	1403	GLU
1	A	1405	THR
1	A	1438	THR
2	B	108	VAL
2	B	115	GLN
2	B	186	GLU
2	B	206	ASN
2	B	258	LEU
2	B	259	TYR
2	B	334	ILE
2	B	367	LEU
2	B	443	ASN
2	B	472	ALA
2	B	629	ASP
2	B	643	ASP
2	B	709	ASP
2	B	727	LYS
2	B	731	VAL
2	B	746	SER
2	B	751	VAL

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Mol	Chain	Res	Type
2	B	881	ASN
2	B	891	ASP
2	B	907	GLY
2	B	958	GLN
2	B	1006	ILE
2	B	1046	PRO
2	B	1069	PHE
2	B	1100	ASP
2	B	1108	ARG
2	B	1156	ASP
2	B	1171	VAL
2	B	1175	LEU
2	B	1181	GLU
2	B	1182	CYS
2	B	1183	LYS
2	B	1186	ASP
2	B	1188	LYS
3	C	56	THR
3	C	78	GLU
3	C	91	HIS
3	C	141	GLY
3	C	149	LYS
3	C	156	THR
3	C	161	LYS
3	C	184	ASN
3	C	202	PRO
3	C	209	TYR
3	C	213	PRO
3	C	214	ASN
3	C	215	GLU
3	C	231	ASN
3	C	240	VAL
4	D	6	SER
4	D	8	PHE
4	D	12	ARG
4	D	19	GLU
4	D	20	GLU
4	D	21	GLU
4	D	52	LEU
4	D	114	MET
4	D	116	SER
4	D	120	GLU

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Mol	Chain	Res	Type
4	D	131	GLU
4	D	177	VAL
4	D	192	LYS
4	D	199	ASN
5	E	106	GLN
5	E	130	ALA
7	G	62	LEU
7	G	63	PRO
7	G	139	ILE
8	H	81	PRO
8	H	128	ASN
8	H	140	ALA
9	I	9	ASP
9	I	106	CYS
10	J	2	ILE
10	J	6	ARG
10	J	8	PHE
10	J	9	SER
10	J	17	LYS
10	J	28	ASP
10	J	32	GLU
10	J	64	ASN
11	K	114	LEU
12	L	50	ASP
12	L	53	HIS
12	L	59	ALA
1	A	4	GLN
1	A	42	ASP
1	A	44	THR
1	A	59	GLY
1	A	61	ILE
1	A	66	LYS
1	A	70	CYS
1	A	101	LYS
1	A	111	GLY
1	A	113	LEU
1	A	244	PRO
1	A	263	THR
1	A	290	GLU
1	A	312	PRO
1	A	318	SER
1	A	336	ILE

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Mol	Chain	Res	Type
1	A	364	VAL
1	A	409	SER
1	A	421	ALA
1	A	483	ASP
1	A	661	GLY
1	A	753	GLY
1	A	765	VAL
1	A	775	ILE
1	A	780	VAL
1	A	789	LYS
1	A	818	MET
1	A	824	LEU
1	A	846	GLU
1	A	847	ASP
1	A	875	ALA
1	A	986	ILE
1	A	1008	GLN
1	A	1016	THR
1	A	1116	LEU
1	A	1120	LEU
1	A	1133	LEU
1	A	1165	GLU
1	A	1212	VAL
1	A	1221	LYS
1	A	1233	ASP
1	A	1335	ILE
1	A	1377	THR
1	A	1386	ARG
1	A	1389	PHE
1	A	1393	ASN
2	B	21	GLU
2	B	28	GLU
2	B	45	SER
2	B	46	GLN
2	B	114	PRO
2	B	229	ALA
2	B	260	GLY
2	B	266	ALA
2	B	282	ILE
2	B	308	TRP
2	B	446	LEU
2	B	447	ALA

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Mol	Chain	Res	Type
2	B	475	SER
2	B	513	GLN
2	B	559	SER
2	B	641	GLU
2	B	655	LYS
2	B	869	SER
2	B	888	GLY
2	B	1003	ALA
2	B	1035	ALA
2	B	1041	GLU
2	B	1126	GLY
2	B	1153	GLU
2	B	1155	SER
2	B	1157	ALA
2	B	1167	GLY
2	B	1176	ASN
2	B	1178	ASN
3	C	84	ARG
3	C	87	PHE
3	C	110	THR
3	C	142	VAL
3	C	164	ALA
3	C	169	LYS
3	C	175	ALA
3	C	216	GLY
3	C	255	VAL
3	C	264	GLN
4	D	15	LEU
4	D	218	GLU
5	E	36	GLU
5	E	44	ALA
5	E	59	SER
5	E	73	PRO
5	E	74	ASP
5	E	192	ARG
5	E	206	GLY
6	F	81	THR
7	G	118	ASP
7	G	154	VAL
8	H	32	THR
8	H	59	ILE
8	H	82	PRO

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Mol	Chain	Res	Type
8	H	84	ALA
8	H	92	ASP
8	H	107	VAL
9	I	3	THR
9	I	57	GLY
9	I	62	ILE
10	J	14	VAL
10	J	29	GLU
10	J	33	GLY
11	K	53	ASP
12	L	35	SER
1	A	58	LEU
1	A	71	GLN
1	A	117	GLU
1	A	131	SER
1	A	170	THR
1	A	219	PHE
1	A	223	GLY
1	A	232	GLU
1	A	253	ASN
1	A	278	THR
1	A	317	LYS
1	A	357	PRO
1	A	399	HIS
1	A	419	LYS
1	A	439	ASN
1	A	465	TYR
1	A	517	ASN
1	A	543	LEU
1	A	592	ASP
1	A	605	MET
1	A	731	ARG
1	A	817	ALA
1	A	940	ARG
1	A	1164	PRO
1	A	1309	ASP
1	A	1411	GLU
2	B	58	THR
2	B	383	ASN
2	B	450	ALA
2	B	512	ARG
2	B	571	PRO

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Mol	Chain	Res	Type
2	B	590	HIS
2	B	591	ARG
2	B	605	ARG
2	B	648	HIS
2	B	682	SER
2	B	711	GLU
2	B	738	PHE
2	B	792	MET
2	B	797	TYR
2	B	848	ARG
2	B	878	GLN
2	B	884	ARG
2	B	943	SER
2	B	1017	ILE
2	B	1082	MET
3	C	60	ASP
3	C	89	GLU
3	C	93	ASP
3	C	167	HIS
5	E	115	ASN
7	G	53	ASN
8	H	17	PRO
8	H	77	ARG
8	H	108	SER
8	H	135	LEU
9	I	78	CYS
10	J	24	LEU
10	J	51	LEU
10	J	55	ASP
11	K	54	ARG
11	K	88	LYS
12	L	40	LEU
12	L	54	ARG
1	A	69	THR
1	A	276	LEU
1	A	283	GLY
1	A	400	PRO
1	A	756	ILE
1	A	795	GLU
1	A	910	PRO
1	A	958	VAL
1	A	1011	GLN

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Mol	Chain	Res	Type
1	A	1028	THR
1	A	1114	PRO
1	A	1240	CYS
1	A	1242	VAL
1	A	1395	GLY
2	B	67	SER
2	B	68	THR
2	B	100	PRO
2	B	124	TYR
2	B	257	LYS
2	B	369	GLY
2	B	419	THR
2	B	459	TYR
2	B	594	ALA
2	B	620	ARG
2	B	735	ALA
2	B	883	LEU
2	B	951	GLN
2	B	1011	ILE
2	B	1097	HIS
2	B	1144	ALA
3	C	77	ILE
3	C	198	ALA
4	D	30	GLY
4	D	168	LYS
7	G	19	GLY
7	G	26	LEU
8	H	44	VAL
8	H	52	GLN
9	I	47	GLU
10	J	27	GLU
11	K	29	ASN
12	L	43	THR
12	L	56	LEU
12	L	60	ARG
1	A	68	GLN
1	A	128	ILE
1	A	226	GLU
1	A	598	LEU
1	A	599	SER
1	A	633	VAL
1	A	648	ASN

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Mol	Chain	Res	Type
1	A	649	ILE
1	A	739	ASP
1	A	755	PHE
1	A	841	LEU
1	A	871	ASP
1	A	969	GLN
1	A	1054	LEU
1	A	1266	THR
1	A	1297	GLU
1	A	1396	ALA
2	B	27	ALA
2	B	48	LEU
2	B	65	GLU
2	B	197	PHE
2	B	309	GLN
2	B	414	ALA
2	B	418	LYS
2	B	530	GLY
2	B	636	PRO
2	B	758	PHE
2	B	766	ARG
2	B	867	GLY
2	B	1016	ALA
3	C	108	GLU
5	E	40	GLU
5	E	45	LYS
6	F	112	GLU
6	F	150	GLU
7	G	34	VAL
1	A	84	ILE
1	A	245	PRO
1	A	492	PRO
1	A	525	GLN
1	A	1158	PRO
2	B	313	MET
2	B	364	ILE
2	B	480	SER
2	B	836	GLU
2	B	1214	PRO
3	C	18	VAL
3	C	176	ILE
3	C	230	MET

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Mol	Chain	Res	Type
4	D	69	ALA
5	E	158	SER
7	G	115	MET
8	H	21	ASN
10	J	63	TYR
11	K	90	ALA
12	L	28	LYS
12	L	46	VAL
1	A	196	GLU
1	A	300	VAL
1	A	627	GLY
2	B	501	PRO
2	B	611	PRO
2	B	712	PRO
3	C	172	PRO
3	C	212	PRO
1	A	652	VAL
1	A	653	VAL
2	B	551	PRO
5	E	37	LEU
1	A	546	VAL
1	A	825	ILE
1	A	1379	GLY
1	A	1454	MET
2	B	411	PRO
2	B	818	PRO
2	B	1018	PRO
3	C	171	GLY
2	B	524	PRO
3	C	126	GLY
6	F	131	PRO
7	G	20	PRO
7	G	116	PRO
2	B	592	ASN
5	E	129	PRO

5.3.2 Protein sidechains ⓘ

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1
2	B	1
9	I	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	807:GLY	C	808:LEU	N	1.20
1	B	442:PHE	C	443:ASN	N	1.14
1	I	39:GLY	C	40:SER	N	0.84

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1416/1733 (81%)	1.28	279 (19%) 3 6	96, 165, 229, 265	0
2	B	1114/1224 (91%)	1.26	209 (18%) 3 7	20, 162, 239, 270	0
3	C	266/318 (83%)	1.08	35 (13%) 7 11	114, 157, 215, 237	0
4	D	182/221 (82%)	1.50	45 (24%) 2 5	20, 170, 207, 228	0
5	E	214/215 (99%)	1.19	39 (18%) 3 7	111, 196, 241, 247	0
6	F	84/155 (54%)	1.02	9 (10%) 11 14	109, 143, 189, 209	0
7	G	171/215 (79%)	0.98	19 (11%) 10 14	119, 147, 177, 201	0
8	H	133/146 (91%)	1.64	43 (32%) 1 3	173, 210, 246, 255	0
9	I	119/122 (97%)	1.80	45 (37%) 1 3	104, 200, 236, 277	0
10	J	65/70 (92%)	0.92	8 (12%) 8 12	119, 156, 197, 204	0
11	K	115/120 (95%)	1.07	16 (13%) 6 10	119, 160, 191, 199	0
12	L	46/70 (65%)	2.08	22 (47%) 0 2	153, 214, 245, 253	0
All	All	3925/4609 (85%)	1.27	769 (19%) 3 6	20, 164, 234, 277	0

All (769) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	472	ALA	9.5
1	A	1081	LEU	7.9
2	B	471	LYS	7.3
4	D	116	SER	7.2
2	B	882	THR	6.8
2	B	665	GLU	6.6
8	H	63	LEU	6.4
2	B	473	MET	6.4
4	D	155	ARG	6.2
2	B	441	ASP	6.1
2	B	444	MET	6.1

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Mol	Chain	Res	Type	RSRZ
2	B	70	ILE	6.1
2	B	919	SER	5.9
4	D	115	HIS	5.8
4	D	4	SER	5.7
9	I	76	PRO	5.7
2	B	134	LYS	5.7
2	B	476	ARG	5.6
2	B	443	ASN	5.6
2	B	478	GLY	5.5
2	B	933	SER	5.5
1	A	1254	ALA	5.5
1	A	830	LYS	5.5
4	D	117	GLU	5.4
2	B	474	SER	5.4
2	B	467	GLY	5.4
2	B	437	GLU	5.3
2	B	335	GLY	5.3
2	B	475	SER	5.2
9	I	105	SER	5.2
8	H	139	ASN	5.2
2	B	164	LYS	5.2
2	B	477	ALA	5.2
1	A	158	PRO	5.1
8	H	132	LEU	5.0
2	B	438	GLU	5.0
2	B	442	PHE	5.0
1	A	132	LYS	4.9
2	B	918	ILE	4.9
4	D	114	MET	4.9
3	C	106	GLU	4.9
2	B	1224	PHE	4.9
1	A	153	PRO	4.8
1	A	171	GLN	4.8
2	B	646	LEU	4.8
1	A	112	LYS	4.8
8	H	136	LYS	4.8
1	A	69	THR	4.8
2	B	734	HIS	4.7
1	A	258	GLY	4.7
1	A	1320	PRO	4.7
2	B	723	VAL	4.6
1	A	257	ARG	4.6

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Mol	Chain	Res	Type	RSRZ
1	A	558	GLY	4.6
4	D	6	SER	4.6
1	A	1126	ALA	4.5
2	B	439	ALA	4.5
2	B	469	GLN	4.5
2	B	662	MET	4.5
8	H	50	ALA	4.5
2	B	470	LYS	4.5
1	A	250	ILE	4.4
12	L	25	ALA	4.4
1	A	1093	LYS	4.4
2	B	446	LEU	4.3
2	B	440	HIS	4.3
4	D	10	THR	4.3
4	D	113	PHE	4.3
1	A	734	GLU	4.3
1	A	251	SER	4.3
1	A	56	PRO	4.3
8	H	37	LYS	4.3
1	A	47	ARG	4.2
6	F	72	LYS	4.2
4	D	11	ARG	4.2
2	B	883	LEU	4.2
2	B	509	ALA	4.2
11	K	115	ALA	4.2
4	D	118	THR	4.2
2	B	359	GLU	4.1
1	A	1173	HIS	4.1
2	B	468	GLU	4.1
12	L	33	GLU	4.0
4	D	221	TYR	4.0
1	A	1290	LYS	4.0
1	A	65	LEU	4.0
2	B	709	ASP	4.0
1	A	1080	THR	4.0
1	A	880	LYS	3.9
1	A	486	GLU	3.9
5	E	131	THR	3.9
12	L	32	ALA	3.9
9	I	42	LEU	3.9
1	A	1455	PRO	3.9
2	B	465	ASN	3.9

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Mol	Chain	Res	Type	RSRZ
3	C	152	GLU	3.9
9	I	40	SER	3.9
1	A	1128	GLN	3.9
2	B	502	ILE	3.9
2	B	230	ALA	3.8
2	B	727	LYS	3.8
1	A	68	GLN	3.8
1	A	1187	GLN	3.8
8	H	51	ALA	3.8
1	A	1288	ASP	3.8
8	H	112	ILE	3.8
2	B	774	GLY	3.7
2	B	641	GLU	3.7
12	L	35	SER	3.7
8	H	138	GLU	3.7
2	B	351	TYR	3.7
8	H	90	ALA	3.7
5	E	121	MET	3.7
11	K	113	THR	3.7
1	A	888	GLY	3.7
1	A	290	GLU	3.7
1	A	538	ASP	3.7
9	I	116	ASN	3.7
1	A	1176	LEU	3.7
7	G	21	ARG	3.6
1	A	1136	SER	3.6
2	B	419	THR	3.6
1	A	165	GLY	3.6
1	A	249	SER	3.6
2	B	248	SER	3.6
5	E	91	LYS	3.6
4	D	20	GLU	3.6
12	L	45	ALA	3.6
1	A	2	VAL	3.6
1	A	601	LYS	3.6
2	B	562	GLY	3.6
2	B	1220	ARG	3.6
1	A	790	ASP	3.6
2	B	731	VAL	3.6
1	A	1454	MET	3.6
1	A	149	GLU	3.6
9	I	108	HIS	3.5

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Mol	Chain	Res	Type	RSRZ
2	B	431	TYR	3.5
12	L	49	LYS	3.5
12	L	47	ARG	3.5
2	B	436	VAL	3.5
4	D	121	LYS	3.5
2	B	870	ILE	3.5
1	A	44	THR	3.5
4	D	120	GLU	3.5
2	B	108	VAL	3.5
2	B	249	ARG	3.5
3	C	203	GLN	3.5
1	A	975	HIS	3.4
1	A	1236	LEU	3.4
1	A	1317	MET	3.4
12	L	53	HIS	3.4
1	A	1003	LYS	3.4
8	H	109	LYS	3.4
12	L	62	LYS	3.4
9	I	114	GLN	3.4
3	C	150	GLY	3.4
9	I	49	ILE	3.4
3	C	190	ASP	3.3
2	B	881	ASN	3.3
2	B	725	PRO	3.3
2	B	245	GLU	3.3
2	B	625	LYS	3.3
2	B	730	ARG	3.3
1	A	1269	GLU	3.3
1	A	1307	GLU	3.3
2	B	64	CYS	3.3
2	B	791	THR	3.3
8	H	140	ALA	3.3
2	B	1134	GLU	3.3
3	C	79	GLN	3.3
2	B	358	LYS	3.3
9	I	77	LYS	3.3
1	A	318	SER	3.3
9	I	107	SER	3.3
1	A	749	ALA	3.3
12	L	50	ASP	3.3
1	A	40	THR	3.3
12	L	26	THR	3.3

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Mol	Chain	Res	Type	RSRZ
9	I	120	GLN	3.3
2	B	601	ARG	3.3
3	C	47	ASP	3.3
2	B	568	ASP	3.2
1	A	1415	SER	3.2
1	A	768	GLN	3.2
9	I	43	VAL	3.2
1	A	253	ASN	3.2
4	D	9	GLN	3.2
4	D	157	GLN	3.2
9	I	118	ARG	3.2
1	A	1257	ASP	3.2
2	B	724	ASP	3.2
5	E	95	THR	3.2
1	A	455	MET	3.2
1	A	1109	LYS	3.2
4	D	153	ARG	3.2
1	A	154	SER	3.2
1	A	1403	GLU	3.2
5	E	43	LYS	3.2
1	A	57	ARG	3.2
1	A	286	HIS	3.2
1	A	145	LYS	3.1
1	A	949	ASP	3.2
1	A	159	THR	3.1
1	A	1404	GLU	3.1
2	B	650	GLU	3.1
8	H	135	LEU	3.1
8	H	119	GLY	3.1
1	A	1400	CYS	3.1
1	A	176	LYS	3.1
4	D	65	GLU	3.1
1	A	1096	SER	3.1
3	C	210	GLU	3.1
4	D	31	GLN	3.1
8	H	4	THR	3.1
2	B	773	MET	3.1
1	A	146	MET	3.1
1	A	66	LYS	3.1
2	B	864	LYS	3.1
1	A	1359	ASP	3.1
2	B	1062	HIS	3.1

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Mol	Chain	Res	Type	RSRZ
2	B	728	ARG	3.1
1	A	254	GLU	3.1
2	B	251	ILE	3.1
2	B	415	GLN	3.0
9	I	60	GLN	3.0
11	K	114	LEU	3.0
1	A	48	ALA	3.0
1	A	175	ARG	3.0
2	B	445	LYS	3.0
1	A	932	GLU	3.0
11	K	25	THR	3.0
1	A	186	LYS	3.0
2	B	655	LYS	3.0
2	B	987	LYS	3.0
2	B	935	ARG	3.0
4	D	23	ASN	3.0
1	A	701	LEU	3.0
1	A	147	VAL	3.0
1	A	948	VAL	3.0
2	B	253	THR	3.0
2	B	868	MET	3.0
2	B	786	ASN	3.0
4	D	76	LYS	3.0
2	B	729	ILE	3.0
1	A	85	ASP	3.0
1	A	131	SER	3.0
1	A	64	ASN	3.0
5	E	6	GLU	3.0
2	B	888	GLY	2.9
1	A	118	HIS	2.9
7	G	85	GLU	2.9
2	B	642	ASP	2.9
9	I	13	MET	2.9
1	A	1078	GLN	2.9
1	A	827	THR	2.9
8	H	48	PRO	2.9
8	H	129	TYR	2.9
1	A	708	MET	2.9
2	B	262	GLU	2.9
11	K	26	LYS	2.9
1	A	806	ARG	2.9
2	B	20	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
8	H	2	SER	2.9
2	B	708	GLU	2.9
3	C	179	GLU	2.9
1	A	49	LYS	2.9
1	A	179	LEU	2.9
1	A	173	THR	2.9
1	A	1008	GLN	2.9
1	A	74	MET	2.9
2	B	887	HIS	2.9
3	C	9	LYS	2.9
5	E	71	LYS	2.9
11	K	55	LYS	2.9
1	A	589	GLN	2.9
1	A	996	ASN	2.9
2	B	766	ARG	2.8
1	A	1284	MET	2.8
1	A	60	SER	2.8
8	H	88	SER	2.8
1	A	161	LEU	2.8
2	B	867	GLY	2.8
8	H	85	GLY	2.8
2	B	241	ARG	2.8
2	B	663	ALA	2.8
1	A	591	PHE	2.8
1	A	739	ASP	2.8
2	B	643	ASP	2.8
2	B	668	ASP	2.8
1	A	256	GLN	2.8
2	B	175	ARG	2.8
5	E	51	GLY	2.8
5	E	199	ILE	2.8
2	B	712	PRO	2.8
2	B	715	ALA	2.8
1	A	226	GLU	2.8
2	B	529	GLU	2.8
2	B	860	MET	2.8
3	C	102	GLN	2.8
10	J	40	GLY	2.8
2	B	24	PRO	2.8
2	B	347	LYS	2.8
3	C	178	PHE	2.8
3	C	108	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
8	H	108	SER	2.8
2	B	1223	ASP	2.8
5	E	32	GLN	2.8
1	A	924	LYS	2.8
5	E	44	ALA	2.8
1	A	1172	LEU	2.8
2	B	988	GLY	2.8
2	B	133	LYS	2.8
8	H	76	THR	2.8
9	I	82	GLU	2.8
1	A	529	CYS	2.8
2	B	103	ASN	2.8
12	L	48	CYS	2.8
1	A	1023	ARG	2.8
1	A	319	GLY	2.8
1	A	904	THR	2.8
1	A	918	GLU	2.8
2	B	880	THR	2.8
7	G	152	SER	2.8
8	H	29	ALA	2.8
5	E	114	ASN	2.7
1	A	280	GLU	2.7
2	B	713	ALA	2.7
1	A	425	GLN	2.7
2	B	736	THR	2.7
1	A	899	VAL	2.7
1	A	1132	LYS	2.7
1	A	51	GLY	2.7
1	A	238	CYS	2.7
1	A	597	LEU	2.7
5	E	194	GLU	2.7
8	H	106	GLU	2.7
2	B	869	SER	2.7
2	B	871	THR	2.7
1	A	346	ASP	2.7
1	A	1206	ASP	2.7
2	B	94	LYS	2.7
1	A	117	GLU	2.7
6	F	143	PHE	2.7
8	H	137	GLN	2.7
12	L	68	GLU	2.7
2	B	264	SER	2.7

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Mol	Chain	Res	Type	RSRZ
3	C	137	LYS	2.7
1	A	55	ASP	2.7
2	B	879	ARG	2.7
2	B	252	SER	2.7
2	B	266	ALA	2.7
7	G	57	GLN	2.7
1	A	67	CYS	2.7
9	I	111	THR	2.7
2	B	895	ASP	2.7
1	A	34	LYS	2.7
1	A	216	VAL	2.7
2	B	510	LYS	2.7
5	E	57	MET	2.7
1	A	3	GLY	2.7
1	A	355	GLY	2.7
4	D	136	GLY	2.7
2	B	250	PHE	2.7
2	B	1049	ASP	2.6
5	E	139	ALA	2.6
2	B	345	LYS	2.6
4	D	14	ARG	2.6
1	A	39	GLU	2.6
2	B	1041	GLU	2.6
2	B	1163	CYS	2.6
12	L	51	CYS	2.6
8	H	84	ALA	2.6
1	A	1112	LYS	2.6
7	G	55	ASP	2.6
5	E	50	MET	2.6
1	A	168	GLY	2.6
1	A	50	ILE	2.6
1	A	1201	ALA	2.6
8	H	146	ARG	2.6
1	A	515	GLN	2.6
11	K	110	ASN	2.6
1	A	815	PHE	2.6
1	A	1174	PHE	2.6
1	A	136	ALA	2.6
2	B	726	ALA	2.6
2	B	265	SER	2.6
3	C	229	TYR	2.6
5	E	77	SER	2.6

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Mol	Chain	Res	Type	RSRZ
9	I	45	ARG	2.6
5	E	129	PRO	2.6
1	A	1204	ASP	2.6
4	D	21	GLU	2.6
1	A	778	GLY	2.6
2	B	937	ALA	2.6
9	I	91	ARG	2.6
9	I	64	SER	2.6
1	A	1378	GLN	2.6
5	E	101	GLN	2.6
5	E	7	ARG	2.6
1	A	1158	PRO	2.6
2	B	963	PHE	2.6
3	C	16	ASP	2.6
3	C	166	GLU	2.6
7	G	111	THR	2.6
1	A	167	CYS	2.5
1	A	1135	ARG	2.5
2	B	553	PRO	2.5
1	A	180	LYS	2.5
6	F	76	LYS	2.5
2	B	710	LEU	2.5
2	B	61	ASP	2.5
2	B	111	ALA	2.5
3	C	3	GLU	2.5
1	A	148	CYS	2.5
1	A	383	TYR	2.5
1	A	973	ILE	2.5
9	I	119	THR	2.5
1	A	178	GLY	2.5
1	A	754	SER	2.5
2	B	447	ALA	2.5
5	E	215	MET	2.5
2	B	678	GLU	2.5
1	A	1381	LEU	2.5
1	A	152	VAL	2.5
2	B	1173	ALA	2.5
2	B	623	GLU	2.5
2	B	945	GLU	2.5
2	B	1053	GLU	2.5
7	G	150	CYS	2.5
1	A	635	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	1131	ALA	2.5
1	A	1175	SER	2.5
2	B	22	SER	2.5
2	B	831	SER	2.5
4	D	45	GLU	2.5
1	A	151	ASP	2.5
1	A	791	ASP	2.5
2	B	866	TYR	2.5
4	D	204	ASP	2.5
5	E	125	PRO	2.5
4	D	13	ARG	2.5
11	K	107	THR	2.5
1	A	5	GLN	2.5
7	G	171	ILE	2.5
10	J	65	PRO	2.5
4	D	12	ARG	2.5
8	H	127	GLY	2.5
1	A	1387	HIS	2.5
1	A	121	LEU	2.4
2	B	1175	LEU	2.4
1	A	124	GLN	2.4
2	B	666	TYR	2.4
2	B	369	GLY	2.4
3	C	206	ASN	2.4
4	D	35	LEU	2.4
1	A	1234	GLU	2.4
2	B	513	GLN	2.4
4	D	73	SER	2.4
1	A	412	ARG	2.4
11	K	28	PRO	2.4
2	B	315	LYS	2.4
1	A	1137	ALA	2.4
6	F	155	LEU	2.4
5	E	8	ASN	2.4
1	A	61	ILE	2.4
2	B	602	THR	2.4
1	A	914	GLU	2.4
4	D	119	ARG	2.4
8	H	82	PRO	2.4
1	A	895	LYS	2.4
10	J	59	LYS	2.4
3	C	87	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
9	I	67	THR	2.4
12	L	70	ARG	2.4
1	A	398	GLU	2.4
5	E	172	GLU	2.4
1	A	129	LYS	2.4
1	A	705	LYS	2.4
5	E	2	ASP	2.4
1	A	109	HIS	2.4
1	A	169	ASN	2.4
2	B	113	TYR	2.4
2	B	836	GLU	2.4
3	C	212	PRO	2.4
5	E	56	LYS	2.4
5	E	133	GLU	2.4
8	H	35	GLN	2.4
9	I	41	PRO	2.4
1	A	1224	LEU	2.4
2	B	1190	ASP	2.4
1	A	344	ARG	2.4
2	B	617	ARG	2.4
1	A	619	LYS	2.4
2	B	277	LYS	2.4
3	C	149	LYS	2.4
1	A	120	GLU	2.4
1	A	333	GLU	2.4
1	A	760	GLN	2.4
2	B	875	GLU	2.4
3	C	81	GLU	2.4
1	A	111	GLY	2.4
1	A	354	SER	2.4
12	L	36	SER	2.4
2	B	323	VAL	2.4
1	A	752	LYS	2.4
3	C	151	GLN	2.3
5	E	106	GLN	2.3
1	A	150	THR	2.3
2	B	956	THR	2.3
2	B	559	SER	2.3
1	A	1421	CYS	2.3
9	I	104	LEU	2.3
2	B	733	HIS	2.3
7	G	148	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	170	THR	2.3
1	A	237	THR	2.3
1	A	788	SER	2.3
1	A	28	ARG	2.3
1	A	1205	LYS	2.3
3	C	91	HIS	2.3
2	B	832	GLY	2.3
8	H	120	GLY	2.3
1	A	696	GLU	2.3
1	A	133	LYS	2.3
8	H	116	TYR	2.3
1	A	281	HIS	2.3
1	A	1099	PRO	2.3
6	F	116	ASP	2.3
1	A	310	GLY	2.3
1	A	623	GLY	2.3
1	A	1275	GLY	2.3
2	B	644	GLU	2.3
1	A	1235	LYS	2.3
1	A	1452	LYS	2.3
2	B	979	LYS	2.3
9	I	117	LYS	2.3
4	D	219	THR	2.3
8	H	46	LEU	2.3
2	B	569	TYR	2.3
3	C	204	SER	2.3
2	B	648	HIS	2.3
7	G	128	PRO	2.3
2	B	804	GLY	2.3
4	D	205	ASP	2.3
9	I	46	HIS	2.3
1	A	1041	ALA	2.3
1	A	107	CYS	2.3
2	B	533	CYS	2.3
3	C	12	GLU	2.3
5	E	26	ARG	2.3
9	I	70	ARG	2.3
9	I	4	PHE	2.3
1	A	59	GLY	2.3
1	A	798	GLY	2.3
1	A	972	HIS	2.3
11	K	22	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	4	GLN	2.3
1	A	521	MET	2.3
1	A	1001	ARG	2.3
2	B	1222	ARG	2.3
6	F	85	MET	2.3
9	I	47	GLU	2.3
1	A	1229	SER	2.3
9	I	96	SER	2.3
1	A	637	LYS	2.3
1	A	115	LEU	2.3
1	A	213	HIS	2.3
2	B	535	LEU	2.3
7	G	58	ARG	2.3
1	A	160	GLN	2.3
11	K	79	GLU	2.2
1	A	1304	TRP	2.2
1	A	1393	ASN	2.2
2	B	737	THR	2.2
7	G	12	THR	2.2
1	A	203	SER	2.2
1	A	255	SER	2.2
8	H	62	SER	2.2
1	A	1289	ARG	2.2
12	L	42	ARG	2.2
4	D	19	GLU	2.2
7	G	69	GLU	2.2
1	A	569	LYS	2.2
2	B	934	LYS	2.2
8	H	36	CYS	2.2
8	H	89	LEU	2.2
9	I	106	CYS	2.2
1	A	1098	VAL	2.2
1	A	816	HIS	2.2
4	D	156	ASP	2.2
8	H	126	GLU	2.2
10	J	26	GLN	2.2
11	K	106	GLU	2.2
5	E	122	LYS	2.2
1	A	46	THR	2.2
1	A	144	THR	2.2
2	B	463	THR	2.2
2	B	792	MET	2.2

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Mol	Chain	Res	Type	RSRZ
11	K	59	ALA	2.2
11	K	77	THR	2.2
1	A	45	GLN	2.2
1	A	1211	GLN	2.2
2	B	1125	ASP	2.2
3	C	52	GLU	2.2
3	C	264	GLN	2.2
1	A	356	ASP	2.2
1	A	164	ARG	2.2
1	A	854	ASN	2.2
2	B	563	MET	2.2
8	H	130	ARG	2.2
11	K	89	ASN	2.2
2	B	109	THR	2.2
12	L	61	THR	2.2
3	C	197	SER	2.2
9	I	78	CYS	2.2
1	A	607	ILE	2.2
9	I	6	PHE	2.2
1	A	611	GLN	2.2
2	B	28	GLU	2.2
2	B	908	GLU	2.2
12	L	27	LEU	2.2
10	J	28	ASP	2.2
1	A	1379	GLY	2.2
2	B	636	PRO	2.2
7	G	112	LYS	2.2
1	A	311	GLN	2.2
1	A	1165	GLU	2.2
8	H	45	GLU	2.2
1	A	157	ASP	2.2
1	A	556	TRP	2.2
5	E	90	VAL	2.2
7	G	87	VAL	2.2
2	B	333	PHE	2.2
1	A	633	VAL	2.2
1	A	994	GLN	2.2
1	A	1103	GLU	2.2
2	B	567	GLU	2.2
9	I	17	ARG	2.2
1	A	1223	ASP	2.1
1	A	1380	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
8	H	94	ASP	2.1
9	I	72	ASP	2.1
1	A	358	ASN	2.1
1	A	936	LEU	2.1
2	B	658	ILE	2.1
8	H	21	ASN	2.1
10	J	17	LYS	2.1
2	B	435	THR	2.1
2	B	971	THR	2.1
2	B	572	HIS	2.1
1	A	599	SER	2.1
1	A	678	GLU	2.1
2	B	698	GLU	2.1
7	G	134	GLU	2.1
10	J	58	GLU	2.1
1	A	309	ALA	2.1
4	D	69	ALA	2.1
1	A	116	ASP	2.1
1	A	197	PRO	2.1
3	C	226	ASP	2.1
1	A	252	PHE	2.1
4	D	212	LYS	2.1
9	I	27	PHE	2.1
1	A	471	ASN	2.1
1	A	584	ASN	2.1
10	J	64	ASN	2.1
3	C	224	GLN	2.1
9	I	39	GLY	2.1
5	E	53	PRO	2.1
1	A	672	ASP	2.1
1	A	522	GLY	2.1
2	B	490	SER	2.1
2	B	423	LYS	2.1
6	F	112	GLU	2.1
9	I	54	GLU	2.1
5	E	38	PRO	2.1
1	A	557	ASP	2.1
1	A	1231	ASP	2.1
1	A	1309	ASP	2.1
2	B	394	ASP	2.1
4	D	189	ASP	2.1
7	G	52	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
11	K	24	ASP	2.1
8	H	107	VAL	2.1
12	L	60	ARG	2.1
1	A	885	THR	2.1
5	E	107	THR	2.1
2	B	652	LYS	2.1
5	E	201	LYS	2.1
12	L	28	LYS	2.1
1	A	413	ILE	2.1
1	A	942	PHE	2.1
4	D	158	GLU	2.1
5	E	40	GLU	2.1
9	I	28	GLU	2.1
2	B	261	ARG	2.1
2	B	320	ASP	2.1
2	B	1009	ASP	2.1
3	C	90	ASP	2.1
3	C	191	TYR	2.1
4	D	40	HIS	2.1
1	A	166	GLY	2.1
1	A	323	LYS	2.1
1	A	887	GLY	2.1
2	B	876	LYS	2.1
7	G	169	GLY	2.1
4	D	28	GLN	2.1
9	I	87	GLN	2.1
2	B	216	GLU	2.1
2	B	1221	SER	2.1
6	F	102	SER	2.1
9	I	66	PRO	2.1
1	A	36	ARG	2.1
6	F	137	TYR	2.1
1	A	223	GLY	2.1
1	A	776	ALA	2.1
2	B	92	PHE	2.1
2	B	466	TRP	2.1
1	A	898	ARG	2.0
1	A	199	LEU	2.0
3	C	222	LYS	2.0
1	A	707	GLY	2.0
2	B	95	ILE	2.0
2	B	295	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
2	B	793	ALA	2.0
4	D	70	PHE	2.0
9	I	56	ALA	2.0
1	A	77	CYS	2.0
1	A	1122	PRO	2.0
1	A	1141	THR	2.0
4	D	26	THR	2.0
12	L	43	THR	2.0
2	B	732	SER	2.0
1	A	940	ARG	2.0
1	A	1336	MET	2.0
2	B	267	ARG	2.0
2	B	432	MET	2.0
2	B	884	ARG	2.0
2	B	1072	MET	2.0
2	B	246	LYS	2.0
1	A	893	PHE	2.0
2	B	459	TYR	2.0
1	A	423	ASP	2.0
1	A	1097	GLY	2.0
5	E	25	ASP	2.0
1	A	654	ASN	2.0
1	A	1171	GLN	2.0
2	B	46	GLN	2.0
1	A	676	MET	2.0
1	A	1129	GLU	2.0
1	A	1159	ARG	2.0
2	B	21	GLU	2.0
2	B	346	GLU	2.0
8	H	31	THR	2.0
4	D	209	ARG	2.0
9	I	97	MET	2.0
5	E	49	SER	2.0
1	A	6	TYR	2.0
9	I	44	TYR	2.0
1	A	704	ALA	2.0
1	A	307	ASP	2.0
1	A	387	ARG	2.0
1	A	688	LYS	2.0
2	B	566	LEU	2.0
2	B	889	THR	2.0
7	G	142	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
5	E	186	LEU	2.0
9	I	93	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
13	ZN	B	1225	1/1	0.95	0.21	20,20,20,20	0
13	ZN	A	1735	1/1	0.97	0.20	20,20,20,20	0
13	ZN	A	1734	1/1	0.98	0.27	20,20,20,20	0
13	ZN	C	319	1/1	0.98	0.17	20,20,20,20	0
13	ZN	I	124	1/1	0.99	0.26	20,20,20,20	0
13	ZN	L	71	1/1	0.99	0.24	20,20,20,20	0
13	ZN	J	71	1/1	1.00	0.18	20,20,20,20	0
13	ZN	I	123	1/1	1.00	0.20	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.