



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 06:53 PM UTC

PDB ID : 5IY6 / pdb_00005iy6
EMDB ID : EMD-3307
Title : Human holo-PIC in the closed state
Authors : He, Y.; Yan, C.; Fang, J.; Inouye, C.; Tjian, R.; Ivanov, I.; Nogales, E.
Deposited on : 2016-03-24
Resolution : 7.20 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>

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:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

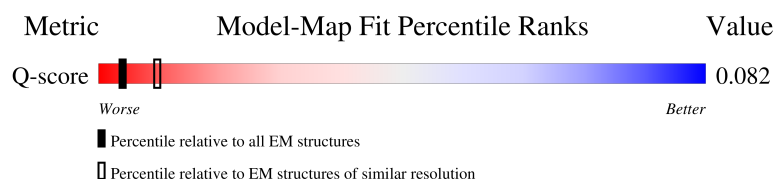
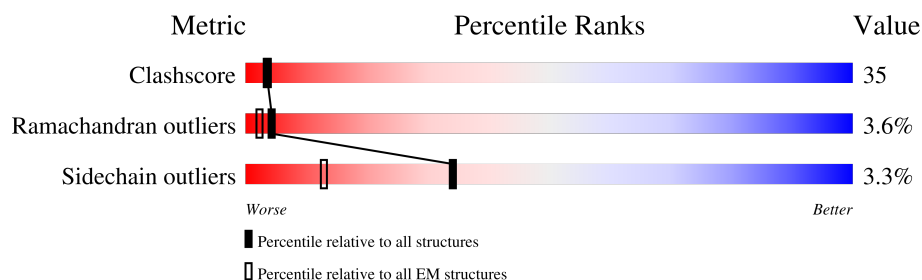
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.20 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)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	444 (6.70 - 7.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1970	
2	B	1174	
3	C	275	
4	D	142	

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Mol	Chain	Length	Quality of chain
5	E	210	
6	F	127	
7	G	172	
8	H	150	
9	I	125	
10	J	67	
11	K	117	
12	L	58	
13	M	316	
14	N	376	
15	O	109	
16	P	339	
17	Q	439	
18	R	291	
19	S	517	
20	T	249	
21	U	301	
22	V	782	
23	W	760	
24	0	395	
25	1	71	
26	2	462	
27	3	308	
28	X	65	
29	Y	65	

2 Entry composition

There are 31 unique types of molecules in this entry. The entry contains 61839 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 subunit RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1454	Total	C	N	O	S	0	0
			11515	7234	2058	2150	73		

- Molecule 2 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1165	Total	C	N	O	S	0	0
			9317	5878	1637	1738	64		

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	275	Total	C	N	O	S	0	0
			2213	1386	380	440	7		

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	129	Total	C	N	O	S	0	0
			1062	665	179	214	4		

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit RPB5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	210	Total	C	N	O	S	0	0
			1723	1088	301	325	9		

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit RPB6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	86	Total	C	N	O	S	0	0
			689	437	120	127	5		

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	171	Total	C	N	O	S	0	0
			1351	875	219	249	8		

- Molecule 8 is a protein called DNA-directed RNA polymerase II subunit RPB8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	150	Total	C	N	O	S	0	0
			1205	764	196	239	6		

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	125	Total	C	N	O	S	0	0
			1013	626	177	198	12		

- Molecule 10 is a protein called DNA-directed RNA polymerase II subunit RPB10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	67	Total	C	N	O	S	0	0
			533	345	90	92	6		

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB11-a.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	117	Total	C	N	O	S	0	0
			937	604	154	177	2		

- Molecule 12 is a protein called DNA-directed RNA polymerase II subunit RPB12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	46	Total	C	N	O	S	0	0
			388	241	75	66	6		

- Molecule 13 is a protein called Transcription initiation factor IIB.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	260	Total	C	N	O	S	0	0
			2018	1265	360	376	17		

- Molecule 14 is a protein called Transcription initiation factor IIA subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	113	Total	C	N	O	S	0	0
			930	585	152	189	4		

- Molecule 15 is a protein called Transcription initiation factor IIA subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	99	Total	C	N	O	S	0	0
			806	510	142	151	3		

- Molecule 16 is a protein called TATA-box-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	185	Total	C	N	O	S	0	0
			1462	946	257	252	7		

- Molecule 17 is a protein called General transcription factor IIE subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	180	Total	C	N	O	S	0	0
			1484	938	262	273	11		

- Molecule 18 is a protein called Transcription initiation factor IIE subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	165	Total	C	N	O	S	0	0
			1357	865	235	253	4		

- Molecule 19 is a protein called General transcription factor IIF subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	138	Total	C	N	O	S	0	0
			1138	719	208	208	3		

- Molecule 20 is a protein called General transcription factor IIF subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	222	Total	C	N	O	S	0	0
			1788	1127	320	338	3		

- Molecule 21 is a protein called Transcription elongation factor A protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	170	Total	C	N	O	S	0	0
			1343	818	247	263	15		

- Molecule 22 is a protein called TFIIH basal transcription factor complex helicase XPB subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	475	Total	C	N	O	S	0	0
			3855	2454	663	712	26		

- Molecule 23 is a protein called TFIIH basal transcription factor complex helicase XPD subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	665	Total	C	N	O	S	0	0
			5348	3415	932	975	26		

- Molecule 24 is a protein called General transcription factor IIH subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	0	188	Total	C	N	O	S	0	0
			1479	935	258	276	10		

- Molecule 25 is a protein called General transcription factor IIH subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	1	62	Total	C	N	O	S	0	0
			491	317	77	93	4		

- Molecule 26 is a protein called General transcription factor IIH subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	2	274	Total	C	N	O	S	0	0
			2196	1417	377	392	10		

- Molecule 27 is a protein called General transcription factor IIH subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	3	193	Total	C	N	O	S	0	0
			1526	978	252	284	12		

- Molecule 28 is a DNA chain called SCP-X.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	65	Total	C	N	O	P	0	0
			1343	633	261	385	64		

- Molecule 29 is a DNA chain called SCP-Y.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	65	Total	C	N	O	P	0	0
			1316	625	236	391	64		

- Molecule 30 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
30	A	1	Total	Mg	0
			1	1	
30	B	1	Total	Mg	0
			1	1	

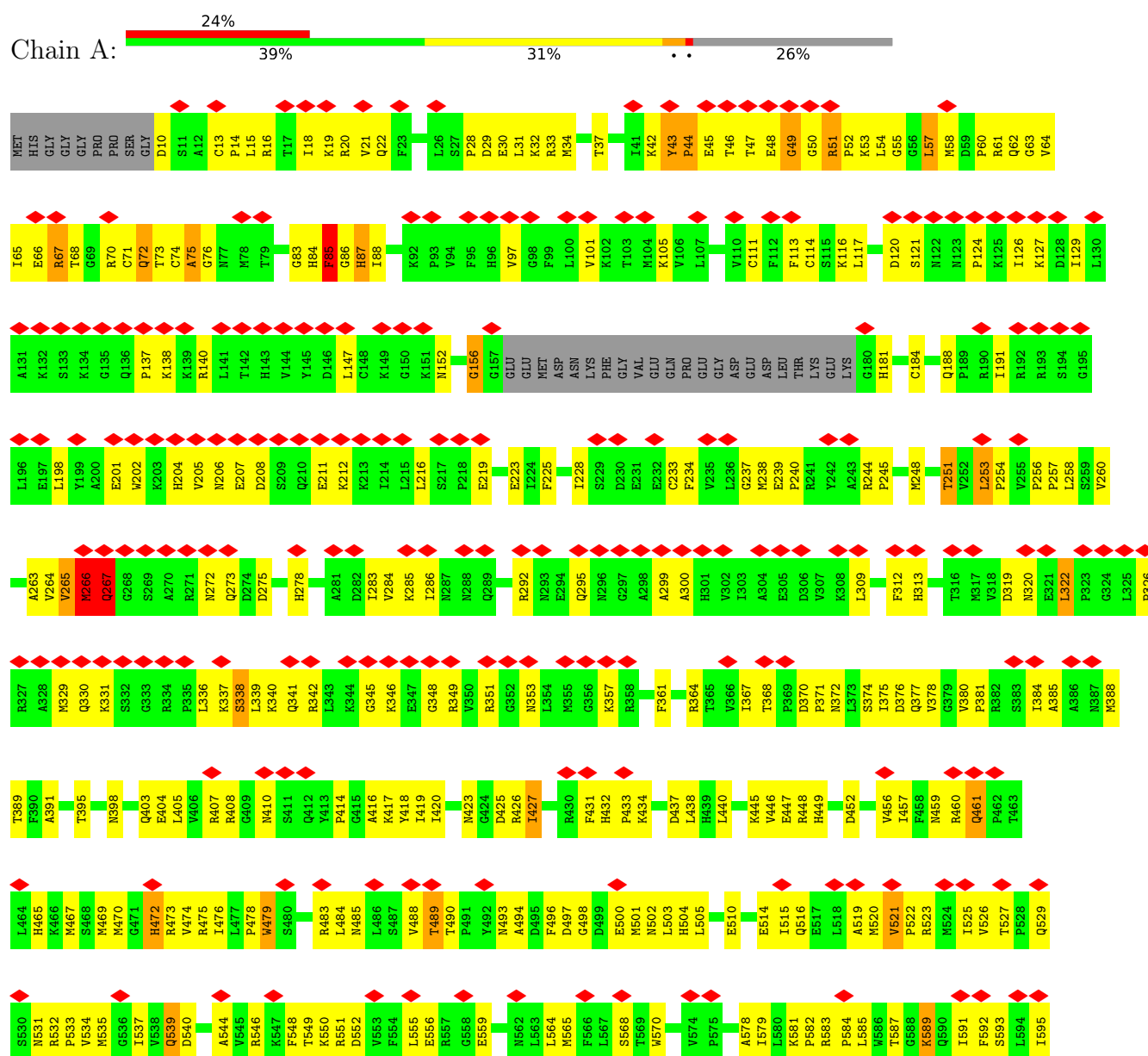
- Molecule 31 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
31	A	2	Total	Zn	0
			2	2	
31	B	1	Total	Zn	0
			1	1	
31	C	1	Total	Zn	0
			1	1	
31	I	2	Total	Zn	0
			2	2	
31	J	1	Total	Zn	0
			1	1	
31	L	1	Total	Zn	0
			1	1	
31	M	1	Total	Zn	0
			1	1	
31	Q	1	Total	Zn	0
			1	1	
31	U	1	Total	Zn	0
			1	1	

3 Residue-property plots

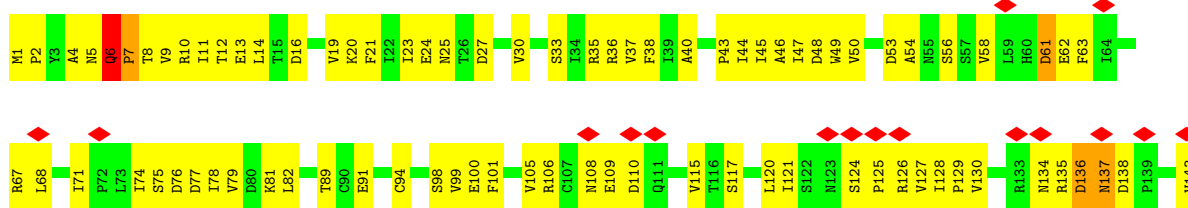
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

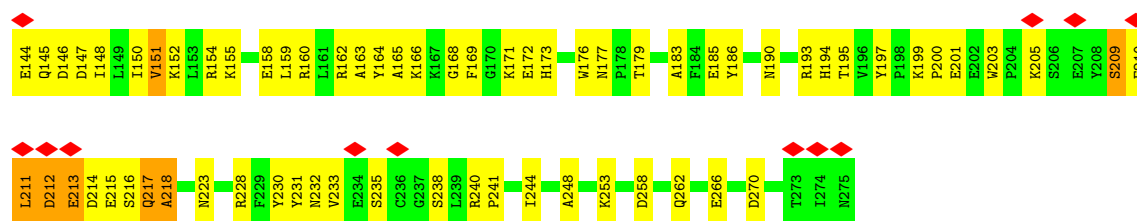
• Molecule 1: DNA-directed RNA polymerase II subunit RPB1



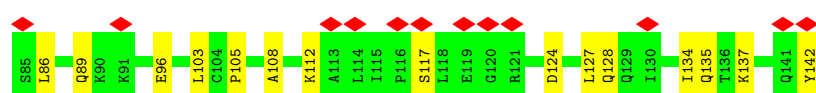
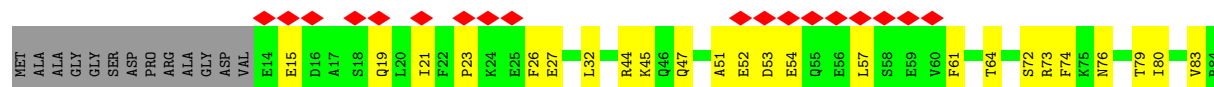
P1450	M451	G1452	G1453	V1454	S1455	E1456	N1457	I1458	M1459	L1460	G1461	Q1462	L1463	A1464	P1465	A1466	G1467	T1468	G1469	C1470	L1473	L1474	L1475	D1476	A1477	E1478	K1479	E1485	PRO	THR	THR	ASN	ILE	PRO	PRO	GLY	GLY	ALA	ALA	GLY	PRO	THR	GLY	GLY	MET	PHE	PHE	GLY	SER	SER	ALA	PRO	SER	PRO	MET	GLY	GLY	ILE	SER																																																																																																																																																																																																																																																																																																																																		
V1365	T1366	S1367	F1368	D1369	G1370	G1371	G1372	S1373	S1374	S1375	S1376	S1377	S1378	S1379	S1380	S1381	S1382	S1383	S1384	S1385	S1386	S1387	S1388	S1389	S1390	S1391	S1392	S1393	S1394	S1395	S1396	S1397	S1398	S1399	S1400	S1401	S1402	S1403	S1404	S1405	S1406	S1407	S1408	S1409	S1410	S1411	S1412	S1413	S1414	S1415	S1416	S1417	S1418	S1419	S1420	S1421	S1422	S1423	S1424	S1425	S1426	S1427	S1428	S1429	S1430	S1431	S1432	S1433	S1434	S1435	S1436	S1437	S1438	S1439	S1440	S1441	S1442	S1443	S1444	D1449																																																																																																																																																																																																																																																																																																													
D1250	M1251	A1252	E1253	L1254	L1255	R1256	I1257	R1258	I1259	R1260	I1261	M1262	N1263	S1264	E1265	E1266	N1267	K1268	M1269	Q1270	E1271	E1272	E1273	E1274	V1275	V1276	D1277	K1278	M1279	D1280	D1281	D1282	V1283	R1286	C1287	I1288	E1289	N1291	M1292	L1293	T1294	D1295	M1296	T1297	L1298	Q1299	D1300	I1301	E1302	Q1303	S1304	S1305	F1306	M1307	M1308	M1309	H1310	L1311																																																																																																																																																																																																																																																																																																																																			
P1312	Q1313	T1314	D1315	N1316	K1317	K1318	K1319	T1320	T1321	T1322	T1323	T1324	T1325	F1326	L1327	L1328	L1329	L1330	L1331	L1332	L1333	L1334	L1335	L1336	L1337	L1338	L1339	L1340	L1341	L1342	L1343	L1344	L1345	L1346	L1347	L1348	L1349	L1350	L1351	L1352	L1353	L1354	L1355	L1356	L1357	L1358	L1359	L1360	L1361	L1362	L1363	L1364	L1365	L1366	L1367	L1368	L1369	L1370	L1371	L1372	L1373	L1374	L1375	L1376	L1377	L1378	L1379	L1380	L1381	L1382	L1383	L1384	L1385	L1386	L1387	L1388	L1389	L1390	L1391	L1392	L1393	L1394	L1395	L1396	L1397	L1398	L1399	L1400	L1401	L1402	L1403	L1404	L1405	L1406	L1407	L1408	L1409	L1410	L1411	L1412	L1413	L1414	L1415	L1416	L1417	L1418	L1419	L1420	L1421	L1422	L1423	L1424	L1425	L1426	L1427	L1428	L1429	L1430	L1431	L1432	L1433	L1434	L1435	L1436	L1437	L1438	L1439	L1440	L1441	L1442	L1443	L1444	D1449																																																																																																																																																																																																																																																								
D1178	T1179	V1180	V1181	V1182	V1183	V1184	V1185	V1186	V1187	V1188	V1189	V1190	V1191	V1192	V1193	V1194	V1195	V1196	V1197	V1198	V1199	V1200	V1201	V1202	V1203	V1204	V1205	V1206	V1207	V1208	V1209	V1210	V1211	V1212	V1213	V1214	V1215	V1216	V1217	V1218	V1219	V1220	V1221	V1222	V1223	V1224	V1225	V1226	V1227	V1228	V1229	V1230	V1231	V1232	V1233	V1234	V1235	V1236	V1237	V1238	V1239	V1240	V1241	V1242	V1243	V1244	V1245	V1246	V1247	V1248	V1249	V1250	V1251	V1252	V1253	V1254	V1255	V1256	V1257	V1258	V1259	V1260	V1261	V1262	V1263	V1264	V1265	V1266	V1267	V1268	V1269	V1270	V1271	V1272	V1273	V1274	V1275	V1276	V1277	V1278	V1279	V1280	V1281	V1282	V1283	V1284	V1285	V1286	V1287	V1288	V1289	V1290	V1291	V1292	V1293	V1294	V1295	V1296	V1297	V1298	V1299	V1300	V1301	V1302	V1303	V1304	V1305	V1306	V1307	V1308	V1309	V1310	V1311	V1312	V1313	V1314	V1315	V1316	V1317	V1318	V1319	V1320	V1321	V1322	V1323	V1324	V1325	V1326	V1327	V1328	V1329	V1330	V1331	V1332	V1333	V1334	V1335	V1336	V1337	V1338	V1339	V1340	V1341	V1342	V1343	V1344	V1345	V1346	V1347	V1348	V1349	V1350	V1351	V1352	V1353	V1354	V1355	V1356	V1357	V1358	V1359	V1360	V1361	V1362	V1363	V1364	V1365	V1366	V1367	V1368	V1369	V1370	V1371	V1372	V1373	V1374	V1375	V1376	V1377	V1378	V1379	V1380	V1381	V1382	V1383	V1384	V1385	V1386	V1387	V1388	V1389	V1390	V1391	V1392	V1393	V1394	V1395	V1396	V1397	V1398	V1399	V1400	V1401	V1402	V1403	V1404	V1405	V1406	V1407	V1408	V1409	V1410	V1411	V1412	V1413	V1414	V1415	V1416	V1417	V1418	V1419	V1420	V1421	V1422	V1423	V1424	V1425	V1426	V1427	V1428	V1429	V1430	V1431	V1432	V1433	V1434	V1435	V1436	V1437	V1438	V1439	V1440	V1441	V1442	V1443	V1444	D1449																																																																																																																		
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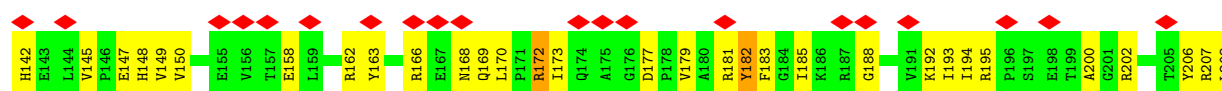
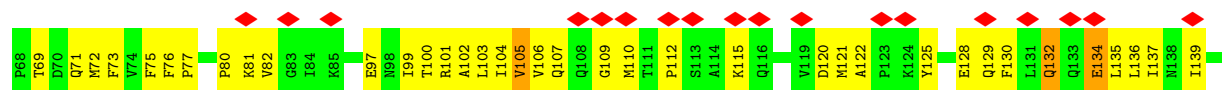
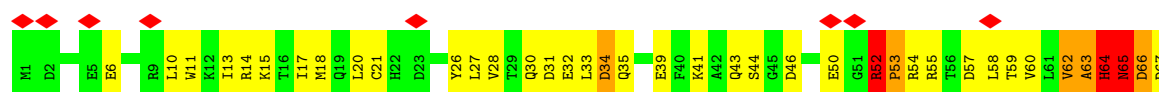




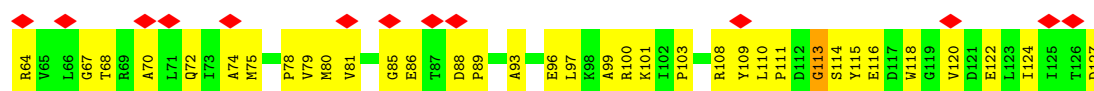
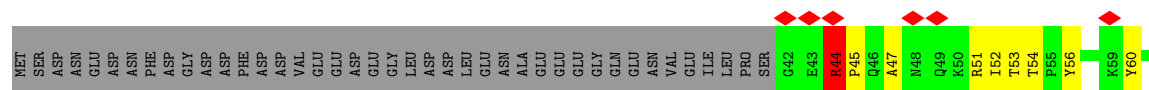
• Molecule 4: DNA-directed RNA polymerase II subunit RPB4



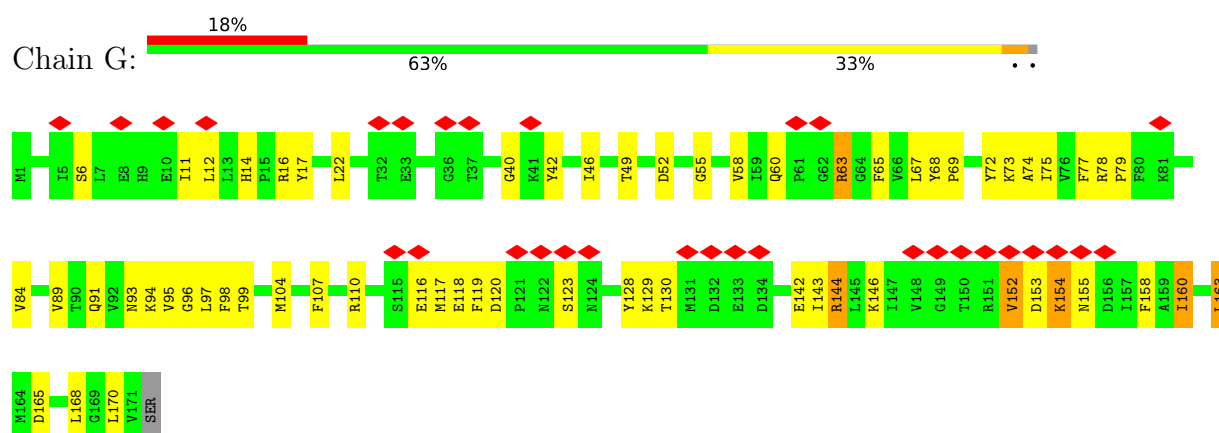
• Molecule 5: DNA-directed RNA polymerase II subunit RPB5



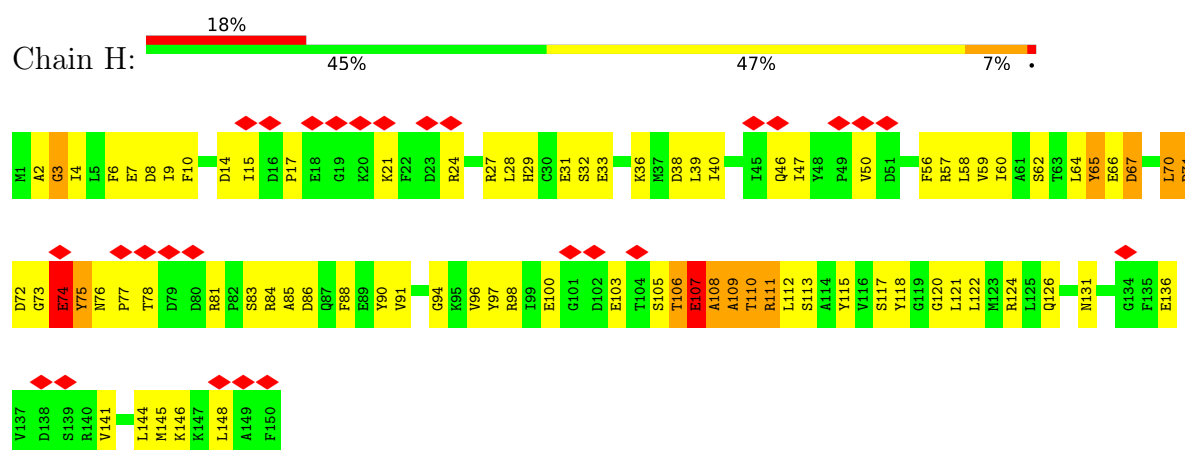
• Molecule 6: DNA-directed RNA polymerase II subunit RPB6



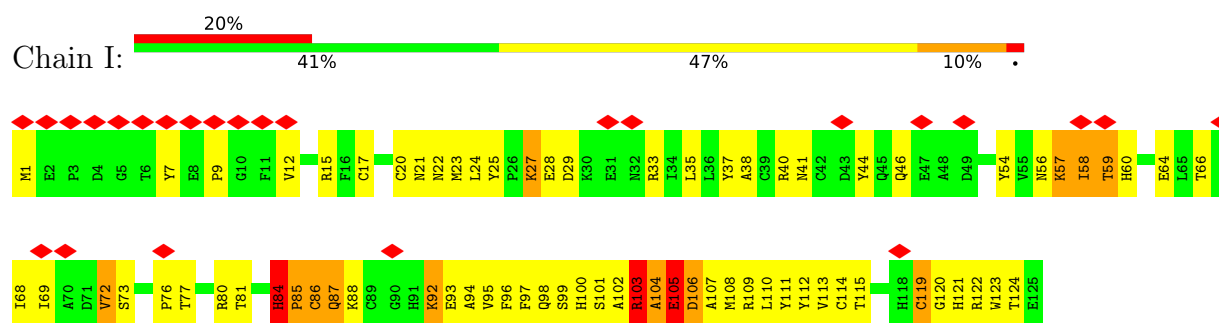
• Molecule 7: DNA-directed RNA polymerase II subunit RPB7



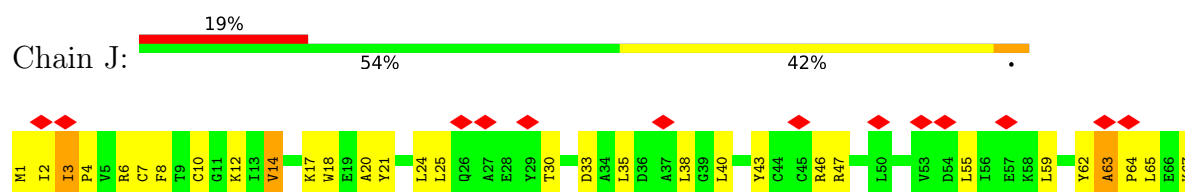
• Molecule 8: DNA-directed RNA polymerase II subunit RPB8



• Molecule 9: DNA-directed RNA polymerase II subunit RPB9

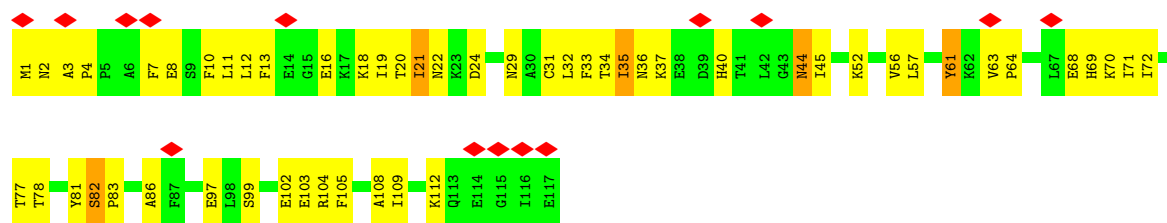


• Molecule 10: DNA-directed RNA polymerase II subunit RPB10

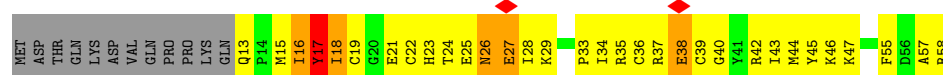
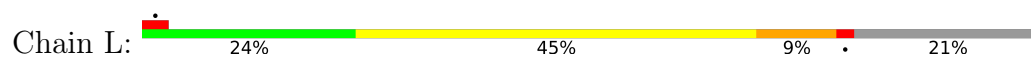


• Molecule 11: DNA-directed RNA polymerase II subunit RPB11-a

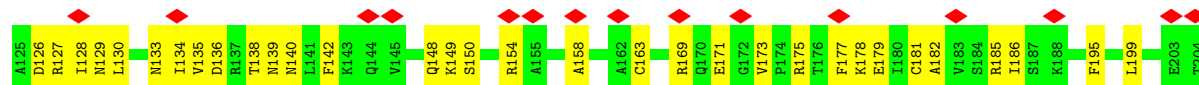
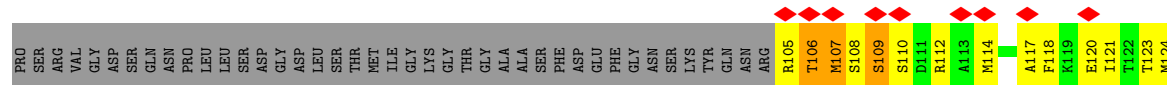
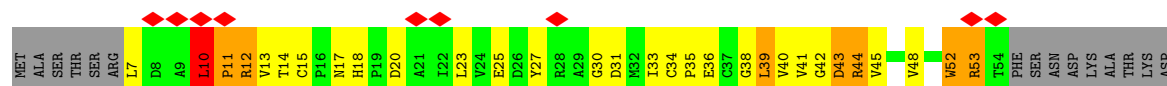




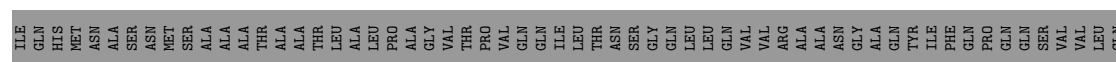
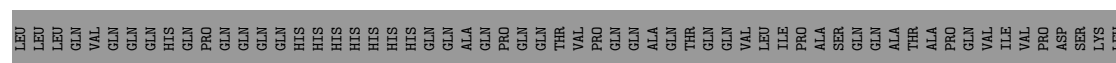
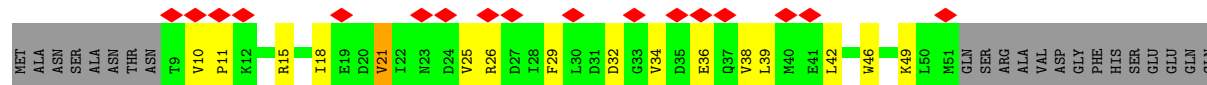
• Molecule 12: DNA-directed RNA polymerase II subunit RPB12

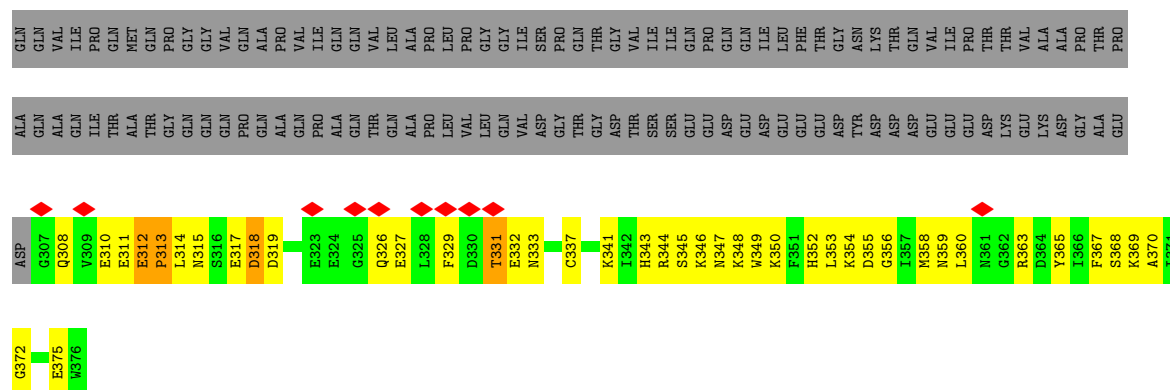


• Molecule 13: Transcription initiation factor IIB

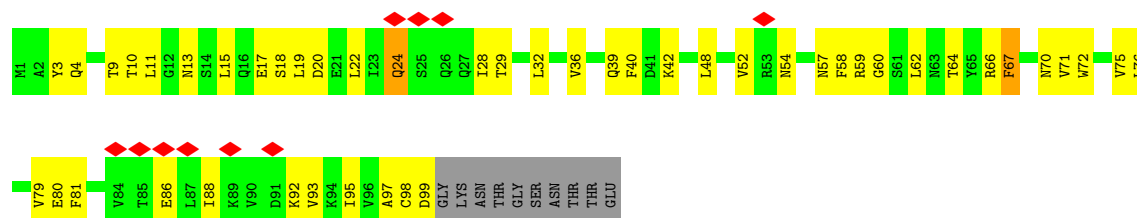


• Molecule 14: Transcription initiation factor IIA subunit 1

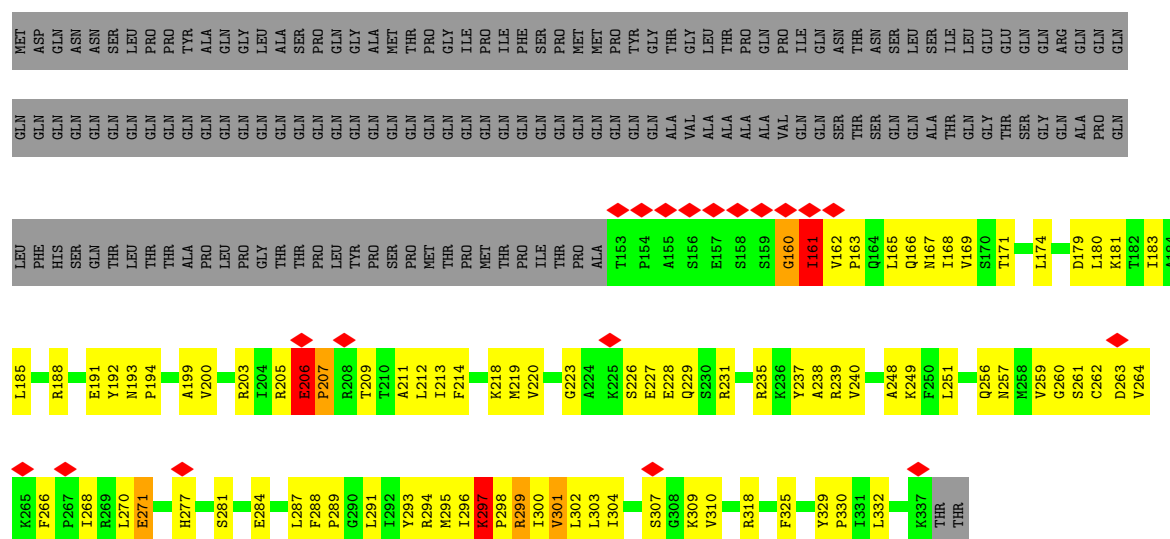
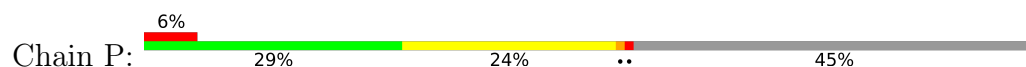




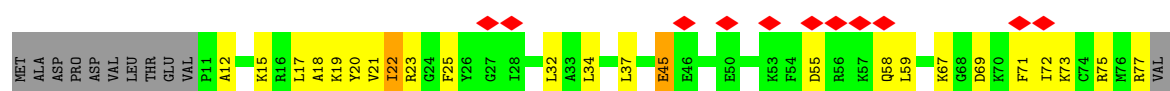
- Molecule 15: Transcription initiation factor IIA subunit 2

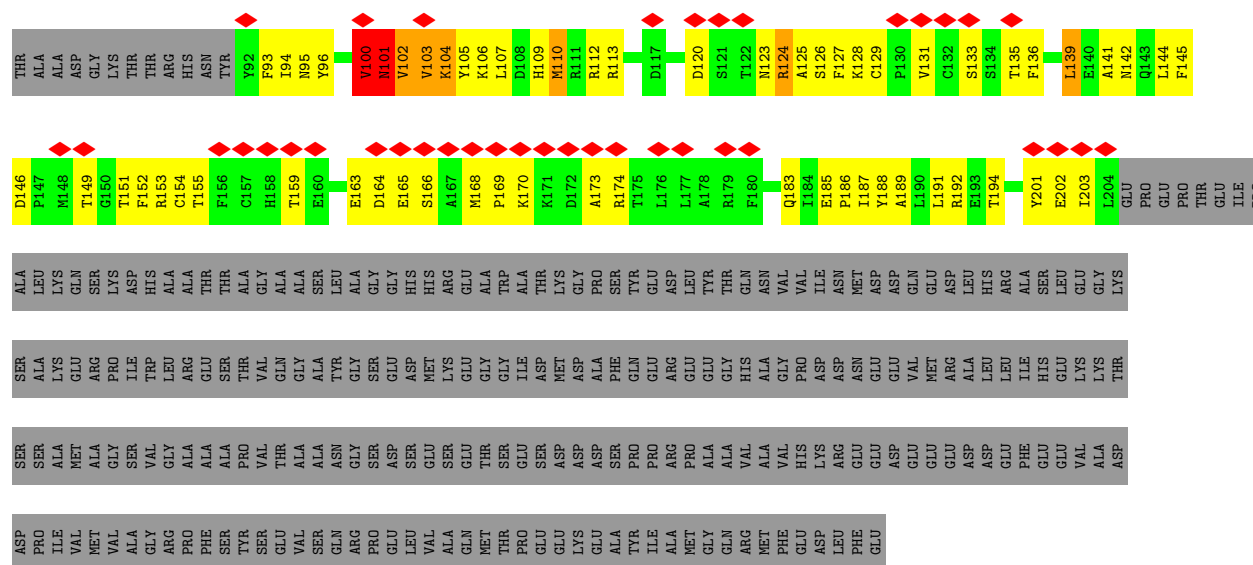


- Molecule 16: TATA-box-binding protein

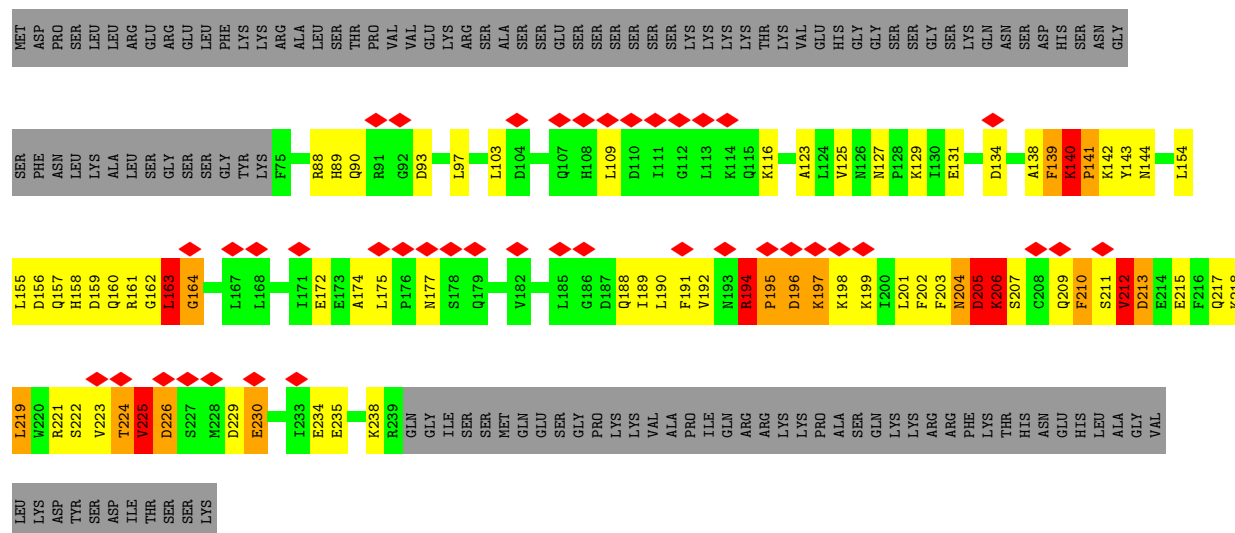
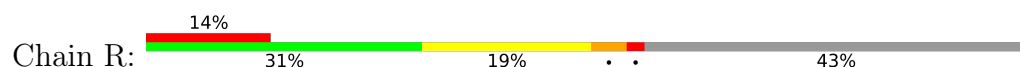


- Molecule 17: General transcription factor IIE subunit 1

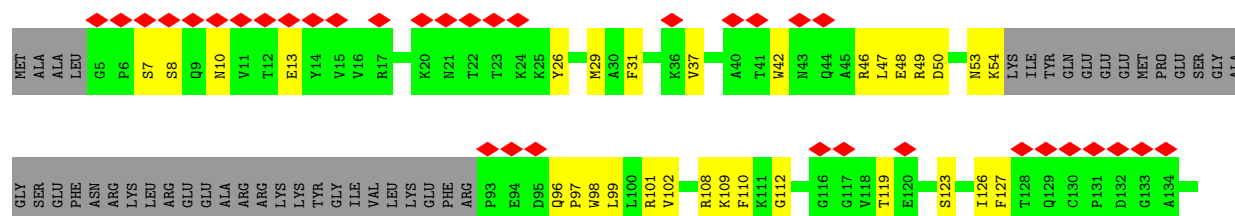


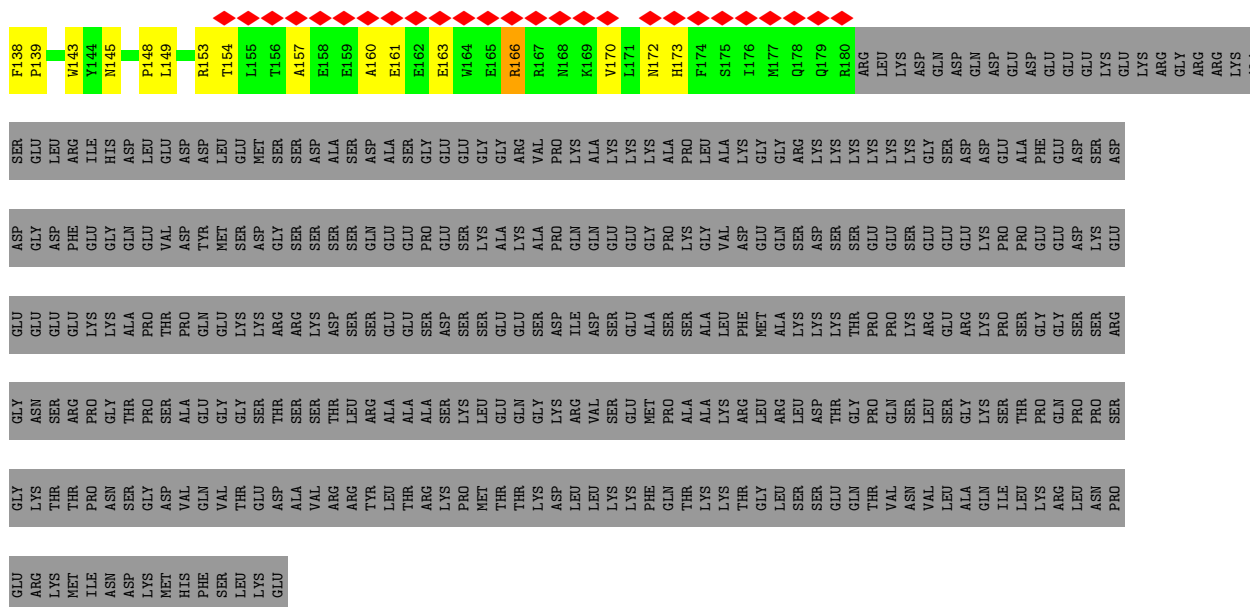


• Molecule 18: Transcription initiation factor IIE subunit beta

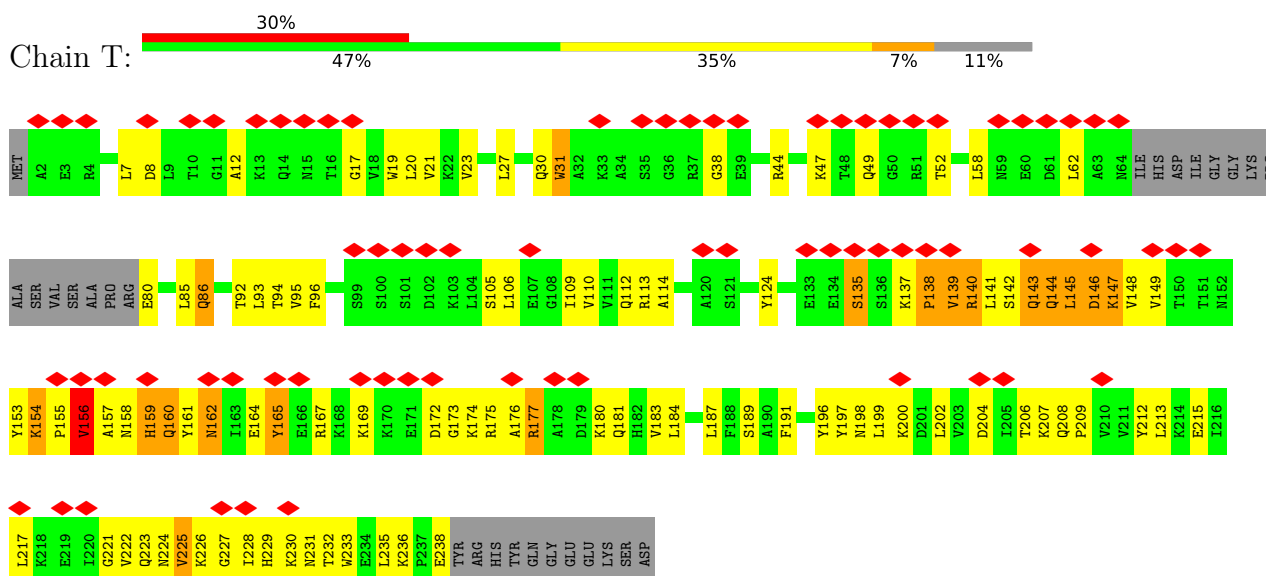


• Molecule 19: General transcription factor IIF subunit 1

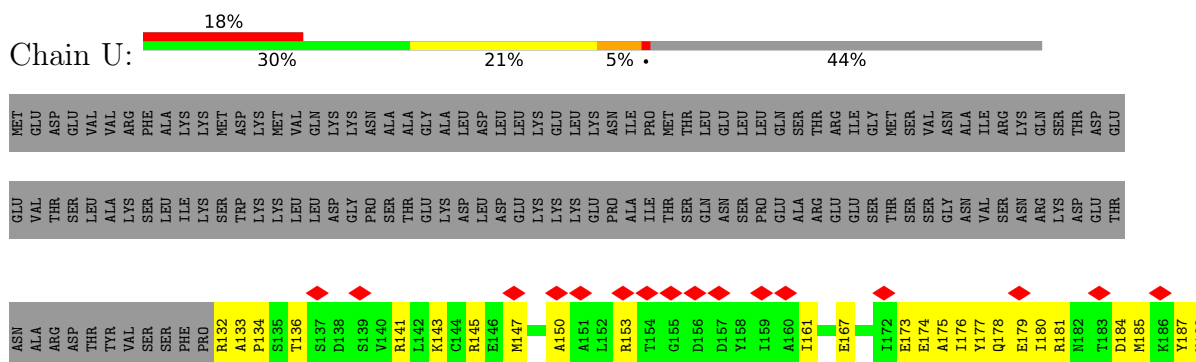


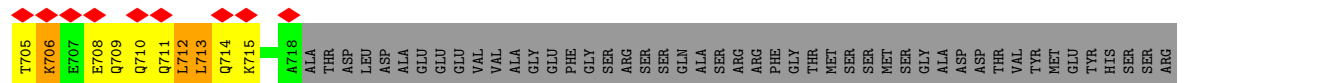


- Molecule 20: General transcription factor IIF subunit 2



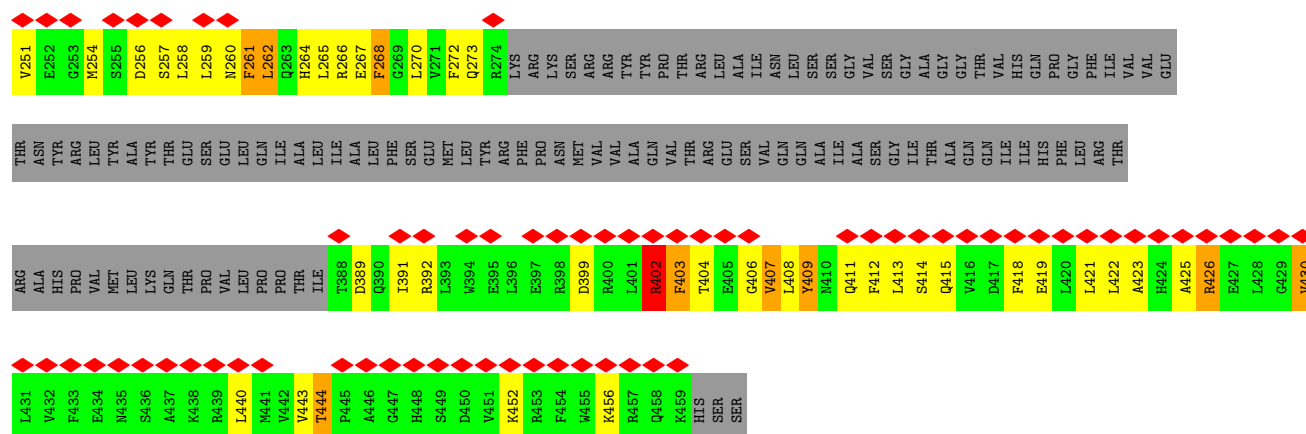
- Molecule 21: Transcription elongation factor A protein 1



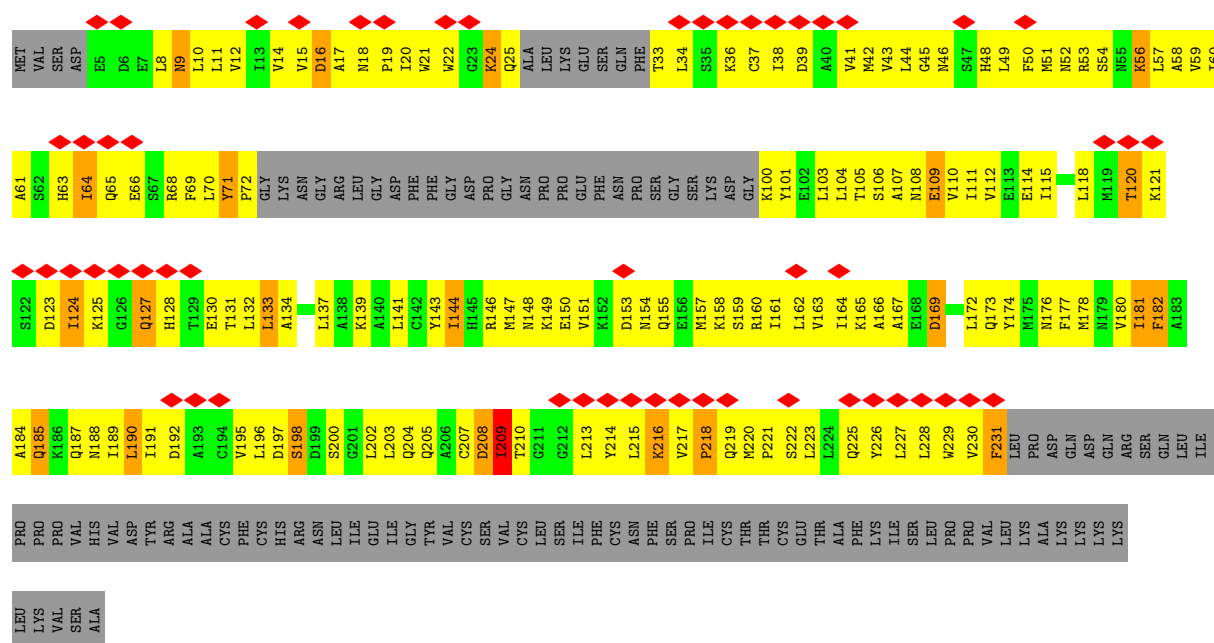


- Molecule 24: General transcription factor IIH subunit 2

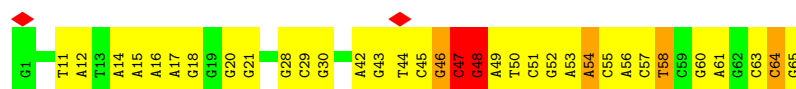




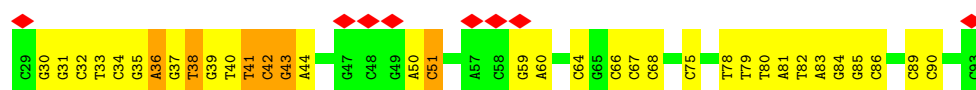
• Molecule 27: General transcription factor IIH subunit 3



• Molecule 28: SCP-X



• Molecule 29: SCP-Y



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	34728	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	27500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.218	Depositor
Minimum map value	-0.111	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.045	Depositor
Map size (Å)	506.88, 506.88, 506.88	wwPDB
Map dimensions	192, 192, 192	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.64, 2.64, 2.64	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	0.48	13/11727 (0.1%)	1.08	85/15833 (0.5%)
2	B	0.38	0/9503	0.97	36/12831 (0.3%)
3	C	0.38	0/2259	0.95	4/3073 (0.1%)
4	D	0.34	0/1077	0.86	0/1446
5	E	0.36	0/1753	1.02	10/2368 (0.4%)
6	F	0.33	0/700	0.96	5/946 (0.5%)
7	G	0.36	0/1382	0.90	3/1874 (0.2%)
8	H	0.34	0/1227	1.00	8/1654 (0.5%)
9	I	0.32	0/1038	1.07	8/1407 (0.6%)
10	J	0.37	0/542	0.95	2/730 (0.3%)
11	K	0.37	0/956	0.92	5/1294 (0.4%)
12	L	0.39	0/394	1.08	5/524 (1.0%)
13	M	0.35	0/2049	1.01	9/2769 (0.3%)
14	N	0.39	0/945	1.02	5/1274 (0.4%)
15	O	0.34	0/816	0.82	1/1105 (0.1%)
16	P	0.33	0/1489	0.94	4/2005 (0.2%)
17	Q	0.38	0/1507	1.02	7/2023 (0.3%)
18	R	0.54	0/1380	1.20	10/1854 (0.5%)
19	S	0.33	0/1167	0.77	0/1576
20	T	0.37	0/1817	0.97	9/2445 (0.4%)
21	U	0.44	0/1358	1.01	5/1820 (0.3%)
22	V	1.85	72/3931 (1.8%)	2.27	229/5298 (4.3%)
23	W	2.01	129/5460 (2.4%)	2.38	339/7390 (4.6%)
24	0	2.07	33/1506 (2.2%)	2.31	71/2038 (3.5%)
25	1	1.29	1/496 (0.2%)	1.79	13/669 (1.9%)
26	2	1.23	0/2243	1.70	41/3024 (1.4%)
27	3	1.27	0/1548	1.67	19/2090 (0.9%)
28	X	0.73	3/1510 (0.2%)	1.24	24/2332 (1.0%)
29	Y	0.70	2/1472 (0.1%)	1.12	20/2267 (0.9%)
All	All	0.95	253/63252 (0.4%)	1.39	977/85959 (1.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
17	Q	0	1
18	R	0	8
20	T	0	1
22	V	0	8
23	W	0	11
24	0	0	1
25	1	0	1
26	2	0	8
28	X	0	8
29	Y	0	6
All	All	0	54

All (253) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1116	ASN	CA-C	-14.44	1.35	1.52
1	A	1117	VAL	N-CA	-12.01	1.31	1.46
29	Y	51	DC	O3'-P	-11.94	1.43	1.61
1	A	1115	LYS	CA-C	-10.42	1.38	1.52
24	0	142	GLU	N-CA	-10.17	1.37	1.45
24	0	158	HIS	CA-C	10.00	1.65	1.52
24	0	99	ASN	CA-CB	9.65	1.63	1.53
23	W	465	ASP	CA-C	9.19	1.64	1.52
1	A	620	HIS	N-CA	-9.09	1.33	1.46
22	V	590	MET	CA-C	8.93	1.64	1.52
24	0	122	GLY	N-CA	8.49	1.55	1.45
22	V	255	MET	N-CA	8.44	1.54	1.47
22	V	376	ALA	CA-C	8.42	1.63	1.52
24	0	142	GLU	CA-C	8.35	1.60	1.52
23	W	237	HIS	CE1-NE2	8.31	1.40	1.32
1	A	1115	LYS	N-CA	8.30	1.57	1.46
1	A	622	SER	N-CA	-7.91	1.37	1.46
24	0	235	HIS	CE1-NE2	7.91	1.40	1.32
1	A	1116	ASN	N-CA	-7.89	1.36	1.46
24	0	186	ILE	N-CA	7.81	1.55	1.46
23	W	670	GLY	CA-C	7.67	1.59	1.52
23	W	302	ASP	CA-C	7.65	1.62	1.53
22	V	289	TYR	N-CA	7.59	1.54	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	W	606	GLU	CA-CB	7.56	1.65	1.53
22	V	554	ARG	NE-CZ	7.45	1.41	1.33
24	O	112	LYS	N-CA	7.32	1.56	1.46
23	W	566	LEU	CA-C	7.28	1.61	1.52
22	V	391	ARG	CZ-NH2	-7.27	1.24	1.33
23	W	168	VAL	CA-CB	7.26	1.58	1.54
24	O	135	VAL	N-CA	7.24	1.55	1.46
23	W	521	GLY	N-CA	7.21	1.55	1.45
24	O	203	ALA	CA-C	7.17	1.61	1.52
23	W	556	GLY	N-CA	7.13	1.52	1.45
23	W	272	ARG	CA-CB	7.07	1.64	1.53
23	W	706	LEU	CA-C	7.06	1.62	1.52
23	W	546	GLU	C-N	7.04	1.43	1.33
24	O	169	ILE	CA-CB	7.02	1.63	1.54
23	W	531	VAL	C-N	7.01	1.39	1.33
23	W	327	GLU	CA-C	7.00	1.61	1.52
22	V	626	ILE	N-CA	6.98	1.55	1.46
1	A	1116	ASN	CA-CB	6.93	1.64	1.53
23	W	272	ARG	N-CA	6.88	1.54	1.45
23	W	615	GLY	N-CA	6.74	1.52	1.44
24	O	188	THR	N-CA	6.72	1.54	1.46
23	W	474	HIS	CD2-NE2	-6.70	1.30	1.37
23	W	429	ALA	CA-C	6.68	1.61	1.52
23	W	698	GLN	N-CA	6.66	1.54	1.46
22	V	706	LYS	N-CA	-6.60	1.38	1.46
22	V	353	ALA	C-N	6.57	1.42	1.33
23	W	683	ARG	CZ-NH2	-6.56	1.25	1.33
23	W	115	LEU	N-CA	6.53	1.54	1.46
22	V	425	ARG	C-O	-6.53	1.16	1.24
23	W	321	GLY	N-CA	6.52	1.54	1.45
23	W	674	TYR	N-CA	6.52	1.54	1.45
24	O	202	SER	CA-C	6.50	1.62	1.53
24	O	96	PHE	CA-C	6.45	1.61	1.52
23	W	522	ASN	CA-C	6.44	1.60	1.52
22	V	382	SER	N-CA	6.41	1.54	1.46
24	O	171	PHE	CA-C	6.41	1.60	1.52
23	W	291	GLY	CA-C	6.40	1.59	1.52
22	V	453	ARG	CZ-NH2	-6.39	1.25	1.33
23	W	245	ASP	N-CA	6.37	1.53	1.46
22	V	414	GLY	CA-C	6.36	1.58	1.51
22	V	479	ASP	N-CA	-6.34	1.38	1.46
22	V	348	LEU	C-O	-6.32	1.16	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	V	712	LEU	CA-C	6.31	1.60	1.52
23	W	301	THR	N-CA	6.30	1.54	1.45
23	W	494	ILE	C-O	-6.29	1.17	1.24
23	W	685	ALA	N-CA	6.26	1.54	1.46
1	A	619	LYS	CA-C	-6.25	1.45	1.52
23	W	47	GLY	N-CA	6.24	1.54	1.45
1	A	924	TYR	N-CA	-6.23	1.39	1.46
23	W	265	THR	N-CA	6.21	1.54	1.46
23	W	608	ILE	CA-CB	6.21	1.63	1.54
23	W	523	LEU	N-CA	6.20	1.53	1.46
23	W	693	LEU	CA-CB	6.17	1.61	1.54
23	W	67	VAL	N-CA	6.15	1.54	1.46
24	O	128	ILE	CA-C	6.13	1.60	1.52
22	V	618	PRO	C-O	6.12	1.31	1.23
22	V	332	ARG	CA-C	6.11	1.60	1.52
23	W	432	ILE	CA-CB	6.11	1.62	1.54
28	X	51	DC	O3'-P	-6.11	1.51	1.61
23	W	491	CYS	N-CA	6.11	1.53	1.46
23	W	490	LEU	CA-C	6.09	1.59	1.52
23	W	158	TYR	N-CA	6.08	1.54	1.46
23	W	492	PRO	CA-C	6.08	1.59	1.52
23	W	69	LYS	CA-C	6.05	1.59	1.52
23	W	511	ARG	NE-CZ	-6.05	1.26	1.33
22	V	383	THR	CB-OG1	-6.04	1.34	1.43
24	O	142	GLU	CA-CB	-6.04	1.46	1.54
22	V	609	LYS	N-CA	6.00	1.54	1.46
23	W	18	TYR	CA-CB	6.00	1.62	1.53
22	V	647	LYS	CA-C	5.99	1.60	1.52
24	O	171	PHE	N-CA	-5.99	1.39	1.46
23	W	698	GLN	CA-C	5.98	1.60	1.52
22	V	306	ILE	N-CA	-5.97	1.38	1.46
22	V	633	ARG	CZ-NH1	-5.97	1.24	1.32
23	W	701	LEU	N-CA	5.96	1.54	1.46
29	Y	36	DA	C1'-N9	5.95	1.58	1.46
23	W	559	GLU	C-O	-5.93	1.16	1.23
23	W	83	VAL	CA-C	5.93	1.60	1.52
24	O	199	ILE	C-N	5.93	1.41	1.33
22	V	620	ALA	N-CA	5.92	1.54	1.46
22	V	638	GLN	N-CA	5.91	1.53	1.46
22	V	252	TYR	CA-CB	5.91	1.62	1.53
22	V	325	ARG	CZ-NH1	-5.91	1.24	1.32
23	W	244	ILE	CA-CB	5.90	1.61	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	V	551	HIS	CA-C	5.88	1.60	1.52
23	W	448	PHE	CA-C	5.82	1.60	1.52
23	W	632	ILE	N-CA	5.82	1.53	1.46
22	V	468	ALA	N-CA	5.81	1.53	1.46
22	V	690	ILE	CA-CB	5.81	1.61	1.54
23	W	237	HIS	CA-C	5.79	1.60	1.52
24	O	162	HIS	CA-C	5.79	1.60	1.52
22	V	269	SER	N-CA	5.79	1.53	1.46
23	W	648	GLU	C-N	5.78	1.41	1.33
23	W	106	GLY	CA-C	5.77	1.56	1.51
23	W	705	ASN	C-O	-5.76	1.16	1.24
23	W	242	VAL	N-CA	5.74	1.53	1.46
23	W	42	MET	CA-C	5.74	1.60	1.52
28	X	54	DA	C1'-N9	5.73	1.57	1.46
22	V	452	ARG	CZ-NH2	-5.73	1.26	1.33
22	V	332	ARG	CZ-NH2	-5.72	1.26	1.33
24	O	147	ASN	CA-C	5.71	1.60	1.52
23	W	666	ARG	NE-CZ	-5.70	1.26	1.33
23	W	334	ARG	CZ-NH2	-5.68	1.26	1.33
24	O	207	VAL	CA-CB	5.68	1.61	1.54
23	W	508	PHE	CA-CB	5.67	1.57	1.53
22	V	437	LEU	C-N	5.65	1.41	1.33
22	V	392	PHE	C-N	5.65	1.38	1.33
22	V	657	ALA	CA-C	5.65	1.59	1.52
23	W	152	LEU	N-CA	5.64	1.54	1.46
23	W	343	ARG	CA-C	5.63	1.60	1.52
23	W	286	ARG	CZ-NH2	-5.62	1.26	1.33
23	W	283	ASP	CA-CB	5.62	1.62	1.53
24	O	131	LEU	CA-C	5.61	1.60	1.52
23	W	645	GLN	N-CA	5.60	1.53	1.46
22	V	252	TYR	C-N	5.60	1.41	1.33
22	V	474	ASP	N-CA	5.59	1.53	1.46
23	W	160	GLU	CA-C	5.59	1.60	1.52
22	V	639	ARG	N-CA	5.59	1.53	1.46
23	W	703	ASP	CA-C	5.59	1.60	1.53
22	V	565	VAL	N-CA	5.58	1.53	1.46
23	W	155	CYS	C-N	5.58	1.43	1.34
23	W	600	ALA	N-CA	5.58	1.53	1.46
24	O	190	LYS	N-CA	5.56	1.53	1.46
23	W	256	LEU	C-N	-5.56	1.26	1.33
22	V	629	HIS	CE1-NE2	5.56	1.38	1.32
1	A	589	LYS	N-CA	5.54	1.53	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	1	47	ALA	CA-C	-5.54	1.48	1.53
24	0	195	ARG	CA-CB	5.53	1.61	1.53
23	W	663	CYS	N-CA	-5.53	1.39	1.46
23	W	291	GLY	C-N	5.52	1.41	1.34
22	V	560	VAL	N-CA	-5.51	1.39	1.46
22	V	640	LEU	CA-C	5.51	1.59	1.52
22	V	415	HIS	CD2-NE2	5.49	1.43	1.37
23	W	77	VAL	CA-C	5.49	1.57	1.52
23	W	331	GLY	N-CA	-5.46	1.39	1.45
22	V	310	LEU	CA-C	5.46	1.60	1.52
23	W	693	LEU	N-CA	5.44	1.51	1.45
23	W	110	SER	CA-CB	5.44	1.63	1.53
23	W	518	ARG	CZ-NH2	-5.44	1.26	1.33
23	W	405	THR	N-CA	5.42	1.52	1.46
23	W	552	TRP	C-O	-5.42	1.17	1.24
22	V	323	SER	CA-C	5.42	1.59	1.52
23	W	298	ALA	CA-C	5.41	1.60	1.52
23	W	630	SER	CA-C	5.39	1.59	1.52
22	V	699	GLU	CA-C	5.38	1.59	1.52
23	W	185	ARG	CA-CB	5.37	1.61	1.53
22	V	296	ASP	CA-C	5.37	1.59	1.52
22	V	626	ILE	CB-CG1	5.36	1.64	1.53
23	W	85	GLU	CA-C	5.35	1.59	1.52
22	V	692	LYS	CA-C	5.33	1.59	1.52
23	W	263	LEU	N-CA	5.33	1.52	1.46
22	V	561	PHE	C-N	5.33	1.40	1.33
22	V	705	THR	CB-OG1	-5.32	1.35	1.43
23	W	95	GLU	CA-C	5.31	1.59	1.52
23	W	510	THR	CA-C	-5.31	1.45	1.52
23	W	548	THR	N-CA	5.30	1.52	1.46
23	W	48	LYS	N-CA	5.30	1.52	1.46
22	V	618	PRO	CA-CB	5.30	1.62	1.53
23	W	66	GLU	N-CA	5.29	1.53	1.46
23	W	229	ALA	N-CA	5.29	1.52	1.46
24	0	97	ASP	N-CA	5.29	1.52	1.46
24	0	136	ASP	N-CA	5.29	1.52	1.46
28	X	53	DA	P-O5'	-5.29	1.49	1.60
23	W	96	LYS	N-CA	5.28	1.53	1.46
23	W	713	GLY	CA-C	5.27	1.57	1.52
1	A	521	VAL	CA-CB	5.26	1.57	1.53
22	V	386	ASP	N-CA	5.26	1.51	1.46
23	W	154	HIS	CA-CB	5.26	1.62	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	W	412	LYS	N-CA	5.26	1.53	1.46
23	W	592	ARG	CD-NE	5.25	1.53	1.46
22	V	636	GLU	N-CA	5.25	1.52	1.46
23	W	426	PRO	CA-CB	-5.24	1.47	1.53
23	W	675	GLY	N-CA	5.24	1.52	1.45
1	A	610	PRO	CA-C	-5.23	1.46	1.52
22	V	332	ARG	NE-CZ	-5.23	1.27	1.33
22	V	420	SER	N-CA	5.21	1.52	1.46
24	O	217	GLY	N-CA	5.20	1.52	1.45
23	W	257	ASP	CA-C	5.20	1.59	1.52
23	W	341	LYS	CA-CB	5.20	1.61	1.53
23	W	482	THR	N-CA	5.19	1.52	1.46
23	W	310	LEU	CA-CB	5.18	1.60	1.53
24	O	80	ARG	CA-CB	5.18	1.61	1.53
23	W	452	GLN	CA-CB	5.18	1.61	1.53
24	O	197	SER	N-CA	-5.18	1.39	1.46
23	W	30	ARG	N-CA	5.18	1.52	1.46
23	W	567	LEU	N-CA	-5.17	1.40	1.45
23	W	658	ARG	CZ-NH2	-5.17	1.26	1.33
23	W	75	ARG	CZ-NH2	-5.17	1.26	1.33
22	V	316	LEU	CA-CB	5.16	1.61	1.53
22	V	408	SER	CA-C	-5.16	1.46	1.52
24	O	195	ARG	CZ-NH1	-5.16	1.25	1.32
23	W	651	PHE	N-CA	-5.16	1.40	1.46
22	V	367	SER	N-CA	-5.16	1.39	1.46
23	W	398	THR	CB-OG1	-5.15	1.35	1.43
23	W	501	GLN	CA-C	5.15	1.59	1.52
22	V	303	ASN	C-N	5.15	1.37	1.33
23	W	210	HIS	CE1-NE2	5.13	1.37	1.32
22	V	532	LEU	CA-CB	5.13	1.61	1.53
22	V	607	ILE	C-O	-5.13	1.18	1.24
22	V	410	TYR	N-CA	5.12	1.52	1.46
23	W	491	CYS	CA-C	5.12	1.58	1.53
22	V	398	ASP	N-CA	5.12	1.52	1.45
22	V	693	LEU	CA-C	5.11	1.59	1.53
23	W	672	THR	N-CA	5.11	1.52	1.46
22	V	521	GLU	CA-CB	5.11	1.61	1.53
23	W	122	THR	CA-C	5.10	1.58	1.52
23	W	20	GLU	C-N	-5.10	1.26	1.33
23	W	626	VAL	N-CA	5.09	1.52	1.46
23	W	699	GLU	N-CA	5.09	1.52	1.46
23	W	303	ALA	CA-C	5.09	1.59	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	W	531	VAL	C-O	-5.09	1.18	1.24
23	W	679	PHE	CA-CB	5.09	1.62	1.53
23	W	286	ARG	CZ-NH1	-5.09	1.25	1.32
22	V	617	LEU	N-CA	5.08	1.51	1.45
22	V	420	SER	CA-C	-5.07	1.46	1.52
22	V	623	LEU	C-O	-5.07	1.18	1.24
23	W	61	ARG	CA-C	5.07	1.59	1.52
23	W	168	VAL	N-CA	5.07	1.52	1.46
24	O	140	HIS	ND1-CE1	5.06	1.37	1.32
23	W	418	ILE	N-CA	5.06	1.52	1.46
22	V	338	ILE	CA-C	5.05	1.58	1.52
23	W	322	SER	N-CA	5.05	1.52	1.46
23	W	185	ARG	NE-CZ	-5.04	1.27	1.33
23	W	79	GLU	N-CA	5.03	1.52	1.46
24	O	61	LEU	N-CA	5.01	1.52	1.46
23	W	417	ILE	CA-C	-5.01	1.46	1.52
23	W	328	HIS	ND1-CE1	5.01	1.37	1.32
23	W	629	GLN	N-CA	-5.01	1.39	1.46
22	V	333	ALA	CA-C	-5.00	1.45	1.52
23	W	275	GLU	C-N	5.00	1.40	1.33

All (977) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	3	209	ILE	N-CA-CB	19.76	143.84	111.23
1	A	622	SER	N-CA-C	-16.44	75.33	108.21
27	3	208	ASP	N-CA-C	-16.06	82.98	109.96
1	A	1116	ASN	N-CA-C	15.36	133.44	108.41
28	X	42	DA	O3'-P-O5'	-14.36	82.46	104.00
23	W	421	PHE	N-CA-C	14.31	141.29	110.80
9	I	84	HIS	C-N-CD	-14.31	66.32	125.00
1	A	603	ILE	N-CA-C	14.11	127.92	108.17
1	A	619	LYS	O-C-N	12.88	139.18	122.43
24	O	77	LYS	C-N-CD	-12.78	72.60	125.00
22	V	520	ARG	O-C-N	12.56	136.55	122.11
3	C	6	GLN	C-N-CD	-12.42	74.06	125.00
28	X	46	DG	O3'-P-O5'	-12.31	85.53	104.00
13	M	10	LEU	C-N-CD	-12.29	74.63	125.00
27	3	71	TYR	C-N-CD	-12.16	75.13	125.00
1	A	924	TYR	N-CA-C	-12.09	93.88	110.68
22	V	520	ARG	CA-C-N	-11.99	100.08	120.58
22	V	520	ARG	C-N-CA	-11.99	100.08	120.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	W	175	TYR	N-CA-C	11.94	127.79	110.24
1	A	923	ASP	N-CA-C	11.91	127.98	109.52
2	B	497	LYS	C-N-CD	-11.76	76.80	125.00
23	W	26	ARG	NE-CZ-NH2	11.71	129.74	119.20
8	H	74	GLU	N-CA-C	-11.50	86.31	110.80
1	A	1117	VAL	N-CA-CB	11.46	130.13	111.23
26	2	236	PHE	CA-CB-CG	-11.10	102.70	113.80
22	V	358	ARG	NE-CZ-NH2	11.06	129.16	119.20
1	A	610	PRO	CA-C-O	11.01	133.89	121.34
23	W	335	ARG	NE-CZ-NH1	-10.97	110.53	121.50
16	P	161	ILE	N-CA-C	-10.81	86.85	109.34
28	X	46	DG	C2'-C3'-O3'	10.77	127.66	111.50
22	V	270	PHE	CA-CB-CG	10.66	124.46	113.80
23	W	167	GLU	CA-C-N	10.44	128.68	120.33
23	W	167	GLU	C-N-CA	10.44	128.68	120.33
27	3	208	ASP	CB-CA-C	-10.14	92.80	109.53
1	A	1116	ASN	O-C-N	9.89	134.74	123.27
2	B	133	ILE	N-CA-C	-9.89	98.76	112.50
23	W	287	ARG	NE-CZ-NH2	9.88	128.09	119.20
23	W	26	ARG	NH1-CZ-NH2	-9.87	106.46	119.30
1	A	619	LYS	CA-C-O	9.80	132.55	121.58
23	W	117	ILE	N-CA-C	9.77	119.72	110.53
18	R	194	ARG	C-N-CD	-9.73	85.11	125.00
25	1	44	PHE	CA-CB-CG	-9.60	104.20	113.80
22	V	638	GLN	OE1-CD-NE2	-9.56	113.04	122.60
22	V	634	ARG	NE-CZ-NH2	9.52	127.77	119.20
1	A	619	LYS	CA-C-N	9.51	137.99	123.05
1	A	619	LYS	C-N-CA	9.51	137.99	123.05
22	V	388	GLN	OE1-CD-NE2	-9.50	113.10	122.60
23	W	645	GLN	OE1-CD-NE2	-9.47	113.13	122.60
22	V	621	ASN	CA-CB-CG	9.41	122.01	112.60
22	V	377	GLN	OE1-CD-NE2	-9.30	113.30	122.60
1	A	49	GLY	N-CA-C	-9.24	91.29	113.18
23	W	419	GLU	C-N-CD	-9.07	87.79	125.00
27	3	231	PHE	CA-CB-CG	-9.07	104.72	113.80
23	W	335	ARG	NE-CZ-NH2	9.06	127.36	119.20
12	L	27	GLU	N-CA-C	9.00	123.99	111.92
23	W	530	VAL	N-CA-CB	9.00	120.82	110.65
22	V	668	GLN	OE1-CD-NE2	-8.98	113.62	122.60
26	2	61	PHE	CB-CA-C	-8.97	97.04	110.95
18	R	224	THR	N-CA-C	-8.95	101.21	110.97
22	V	334	ARG	CD-NE-CZ	8.91	136.87	124.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	W	270	VAL	CA-C-O	8.86	131.86	120.78
23	W	112	ARG	CA-C-N	8.77	132.04	120.28
23	W	112	ARG	C-N-CA	8.77	132.04	120.28
22	V	665	GLN	OE1-CD-NE2	-8.76	113.84	122.60
29	Y	51	DC	O3'-P-O5'	8.76	117.13	104.00
25	1	34	ILE	CA-C-N	-8.73	111.77	123.12
25	1	34	ILE	C-N-CA	-8.73	111.77	123.12
1	A	266	MET	N-CA-C	-8.72	92.22	110.80
26	2	268	PHE	CA-CB-CG	-8.71	105.09	113.80
23	W	76	THR	CA-CB-OG1	8.71	122.66	109.60
23	W	332	PHE	CA-CB-CG	8.70	122.50	113.80
29	Y	32	DC	O4'-C1'-N1	8.67	121.41	108.40
8	H	109	ALA	N-CA-C	-8.55	99.44	111.24
1	A	610	PRO	N-CA-C	8.53	124.44	111.14
25	1	47	ALA	CB-CA-C	-8.50	106.76	116.54
22	V	484	ILE	N-CA-C	8.50	119.12	111.81
17	Q	73	LYS	N-CA-C	-8.44	96.44	109.52
23	W	263	LEU	N-CA-CB	-8.43	97.72	110.12
23	W	343	ARG	NE-CZ-NH2	8.41	126.77	119.20
23	W	469	LYS	CA-C-N	8.41	131.33	120.56
23	W	469	LYS	C-N-CA	8.41	131.33	120.56
23	W	193	PHE	CA-CB-CG	8.39	122.19	113.80
1	A	48	GLU	N-CA-C	-8.32	100.50	111.74
28	X	48	DG	C2'-C3'-O3'	8.23	123.85	111.50
22	V	392	PHE	CA-CB-CG	8.23	122.03	113.80
12	L	26	ASN	N-CA-C	-8.23	100.19	112.04
21	U	232	GLU	N-CA-C	8.21	128.28	110.80
23	W	157	PHE	CA-CB-CG	8.21	122.01	113.80
1	A	1117	VAL	N-CA-C	-8.18	92.32	109.34
23	W	420	PRO	CA-C-N	8.16	137.13	121.54
23	W	420	PRO	C-N-CA	8.16	137.13	121.54
23	W	77	VAL	N-CA-CB	-8.14	105.37	110.50
23	W	521	GLY	CA-C-N	8.13	131.01	120.44
23	W	521	GLY	C-N-CA	8.13	131.01	120.44
1	A	621	ILE	CA-C-O	8.11	130.91	120.78
26	2	47	GLU	N-CA-C	8.10	120.02	111.03
22	V	433	GLN	N-CA-C	8.05	121.67	112.57
28	X	45	DC	O3'-P-O5'	-8.04	91.95	104.00
28	X	65	DG	O4'-C1'-N9	8.02	120.43	108.40
13	M	43	ASP	N-CA-C	8.02	127.88	110.80
18	R	205	ASP	CA-C-N	8.01	136.12	121.70
18	R	205	ASP	C-N-CA	8.01	136.12	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	W	106	GLY	CA-C-O	-8.00	114.61	121.57
23	W	667	ALA	N-CA-C	7.99	119.62	111.07
5	E	52	ARG	C-N-CD	-7.96	92.37	125.00
1	A	621	ILE	CA-C-N	7.92	134.15	123.46
1	A	621	ILE	C-N-CA	7.92	134.15	123.46
23	W	395	SER	CA-C-O	-7.91	110.67	118.34
5	E	63	ALA	N-CA-C	7.91	124.35	107.67
17	Q	102	VAL	CA-C-N	-7.90	107.75	121.97
17	Q	102	VAL	C-N-CA	-7.90	107.75	121.97
22	V	333	ALA	N-CA-C	7.89	121.85	111.75
22	V	394	SER	N-CA-C	7.89	122.01	112.38
14	N	318	ASP	N-CA-C	7.83	120.42	110.24
23	W	16	TYR	N-CA-C	7.81	118.29	108.45
23	W	345	ARG	N-CA-C	7.80	122.14	112.47
23	W	696	TRP	N-CA-C	7.80	120.82	110.53
1	A	925	THR	N-CA-C	-7.79	100.89	113.19
22	V	415	HIS	CG-CD2-NE2	-7.79	99.41	107.20
23	W	499	ASN	OD1-CG-ND2	-7.78	114.83	122.60
29	Y	42	DC	O3'-P-O5'	-7.77	92.34	104.00
26	2	160	LEU	N-CA-C	-7.77	102.81	111.28
26	2	162	PHE	CA-CB-CG	-7.76	106.03	113.80
2	B	880	LEU	N-CA-C	7.75	125.51	113.72
17	Q	104	LYS	N-CA-C	7.72	119.33	111.07
23	W	724	MET	CA-C-N	7.71	130.61	120.28
23	W	724	MET	C-N-CA	7.71	130.61	120.28
23	W	304	HIS	CB-CG-CD2	-7.67	121.23	131.20
22	V	710	GLN	CA-C-N	7.65	130.39	120.44
22	V	710	GLN	C-N-CA	7.65	130.39	120.44
14	N	319	ASP	N-CA-C	7.62	127.03	110.80
24	0	237	SER	CA-C-N	7.62	128.22	120.38
24	0	237	SER	C-N-CA	7.62	128.22	120.38
22	V	422	GLU	CA-C-O	7.61	128.84	119.11
27	3	182	PHE	CA-CB-CG	-7.60	106.20	113.80
22	V	640	LEU	O-C-N	7.57	130.18	122.08
23	W	295	ALA	N-CA-C	7.57	119.31	111.14
23	W	250	ASN	OD1-CG-ND2	-7.55	115.05	122.60
8	H	110	THR	N-CA-C	7.54	119.82	109.11
22	V	355	CYS	CA-C-N	7.52	130.67	120.44
22	V	355	CYS	C-N-CA	7.52	130.67	120.44
27	3	127	GLN	N-CA-C	-7.51	103.17	111.36
23	W	41	GLU	O-C-N	7.51	131.76	123.27
23	W	165	GLY	CA-C-N	7.51	130.95	120.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	W	165	GLY	C-N-CA	7.51	130.95	120.29
23	W	509	GLU	N-CA-C	7.50	122.08	112.34
26	2	35	TYR	CA-CB-CG	-7.48	100.43	113.90
23	W	329	PHE	CA-CB-CG	7.47	121.27	113.80
24	0	123	ASN	CA-C-N	7.47	127.49	119.28
24	0	123	ASN	C-N-CA	7.47	127.49	119.28
24	0	206	ARG	NH1-CZ-NH2	-7.47	109.59	119.30
3	C	136	ASP	N-CA-C	7.45	122.86	112.72
22	V	669	GLU	CA-C-N	7.42	131.59	120.31
22	V	669	GLU	C-N-CA	7.42	131.59	120.31
2	B	579	ASP	CA-C-N	7.41	127.05	119.19
2	B	579	ASP	C-N-CA	7.41	127.05	119.19
20	T	85	LEU	CA-C-N	-7.39	110.99	122.59
20	T	85	LEU	C-N-CA	-7.39	110.99	122.59
23	W	302	ASP	CA-C-O	7.38	126.83	119.08
26	2	245	LEU	N-CA-C	-7.38	101.33	110.41
24	0	92	VAL	O-C-N	7.38	129.14	121.91
24	0	98	GLN	OE1-CD-NE2	-7.37	115.23	122.60
2	B	78	VAL	CB-CA-C	-7.37	102.54	111.97
20	T	225	VAL	N-CA-C	-7.35	105.42	113.43
23	W	487	ARG	N-CA-C	7.34	120.15	111.71
24	0	195	ARG	NE-CZ-NH1	7.32	128.81	121.50
27	3	16	ASP	CA-C-N	7.29	132.90	120.72
27	3	16	ASP	C-N-CA	7.29	132.90	120.72
12	L	17	TYR	N-CA-C	7.29	126.33	110.80
23	W	654	PHE	CA-C-N	7.29	130.05	120.28
23	W	654	PHE	C-N-CA	7.29	130.05	120.28
22	V	580	ILE	CA-C-O	7.28	128.08	120.36
23	W	683	ARG	NE-CZ-NH2	7.24	125.72	119.20
23	W	288	LEU	O-C-N	-7.24	114.50	122.03
22	V	486	PRO	CA-C-N	7.20	132.72	121.99
22	V	486	PRO	C-N-CA	7.20	132.72	121.99
11	K	82	SER	CA-C-N	7.20	127.19	119.28
11	K	82	SER	C-N-CA	7.20	127.19	119.28
23	W	690	ARG	NE-CZ-NH2	7.16	125.65	119.20
23	W	323	ILE	CA-C-N	7.15	129.86	120.28
23	W	323	ILE	C-N-CA	7.15	129.86	120.28
26	2	89	LEU	N-CA-C	-7.13	103.59	111.36
13	M	52	TRP	N-CA-C	7.12	121.22	112.54
28	X	63	DC	C6-N1-C1'	7.09	130.34	119.70
1	A	265	VAL	N-CA-C	7.08	118.84	109.21
22	V	393	THR	O-C-N	-7.04	113.88	122.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	U	232	GLU	CA-C-N	-7.04	108.10	121.54
21	U	232	GLU	C-N-CA	-7.04	108.10	121.54
22	V	267	THR	CA-C-O	-7.04	112.02	120.32
26	2	193	PRO	N-CA-C	7.02	119.26	110.70
23	W	232	VAL	CA-CB-CG1	7.02	122.33	110.40
24	0	147	ASN	OD1-CG-ND2	-7.01	115.59	122.60
23	W	340	VAL	CA-C-N	7.01	129.67	120.28
23	W	340	VAL	C-N-CA	7.01	129.67	120.28
23	W	653	THR	CA-C-N	7.00	129.66	120.28
23	W	653	THR	C-N-CA	7.00	129.66	120.28
23	W	186	ARG	NE-CZ-NH1	6.97	128.47	121.50
28	X	64	DC	C4'-C3'-O3'	-6.95	99.58	110.00
23	W	715	GLN	OE1-CD-NE2	-6.95	115.66	122.60
26	2	225	SER	N-CA-C	-6.94	103.65	111.14
1	A	1271	GLU	N-CA-C	6.93	118.49	111.07
2	B	78	VAL	N-CA-C	-6.93	103.77	110.42
22	V	558	ILE	N-CA-CB	-6.92	101.42	111.52
23	W	98	GLU	CA-C-N	6.90	130.22	122.15
23	W	98	GLU	C-N-CA	6.90	130.22	122.15
22	V	715	LYS	N-CA-C	6.89	118.79	111.28
26	2	193	PRO	CA-N-CD	-6.88	102.37	112.00
22	V	274	GLN	O-C-N	-6.88	116.65	123.46
28	X	63	DC	C2-N1-C1'	-6.87	109.39	119.70
25	1	45	VAL	CA-C-N	-6.86	113.52	122.51
25	1	45	VAL	C-N-CA	-6.86	113.52	122.51
23	W	97	GLN	OE1-CD-NE2	-6.86	115.74	122.60
28	X	60	DG	N9-C1'-C2'	6.84	123.77	113.50
24	0	145	LEU	N-CA-C	6.83	118.72	111.28
23	W	328	HIS	CB-CG-CD2	-6.82	122.33	131.20
23	W	562	GLN	OE1-CD-NE2	-6.82	115.78	122.60
2	B	665	ILE	N-CA-C	6.82	117.86	107.77
23	W	34	ALA	CA-C-N	6.80	132.48	122.82
23	W	34	ALA	C-N-CA	6.80	132.48	122.82
23	W	343	ARG	NE-CZ-NH1	-6.80	114.70	121.50
23	W	66	GLU	CA-C-N	6.79	134.18	121.97
23	W	66	GLU	C-N-CA	6.79	134.18	121.97
23	W	703	ASP	N-CA-C	6.78	120.89	111.74
22	V	348	LEU	CA-C-O	-6.78	113.36	120.55
23	W	595	ILE	CB-CA-C	6.78	122.41	111.29
23	W	462	SER	CA-C-N	6.78	126.46	119.82
23	W	462	SER	C-N-CA	6.78	126.46	119.82
23	W	473	PHE	CA-CB-CG	-6.76	107.04	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	620	HIS	N-CA-C	6.76	121.11	112.86
22	V	317	ARG	CA-C-O	-6.76	113.05	120.69
23	W	659	HIS	CA-CB-CG	6.76	120.56	113.80
23	W	270	VAL	CA-C-N	6.74	130.54	120.17
23	W	270	VAL	C-N-CA	6.74	130.54	120.17
24	O	236	VAL	CA-CB-CG1	6.74	121.85	110.40
1	A	1121	VAL	CB-CA-C	-6.73	107.31	113.70
23	W	131	ASP	CA-C-N	6.73	127.45	119.98
23	W	131	ASP	C-N-CA	6.73	127.45	119.98
1	A	646	GLY	N-CA-C	6.73	120.25	110.63
22	V	711	GLN	OE1-CD-NE2	-6.73	115.87	122.60
23	W	467	TYR	CA-C-N	6.73	126.68	119.28
23	W	467	TYR	C-N-CA	6.73	126.68	119.28
22	V	641	GLY	N-CA-C	6.72	120.79	112.73
22	V	331	GLY	CA-C-N	6.71	129.27	120.28
22	V	331	GLY	C-N-CA	6.71	129.27	120.28
23	W	263	LEU	O-C-N	-6.70	115.01	122.12
24	O	64	VAL	O-C-N	-6.70	116.03	123.26
22	V	629	HIS	CB-CG-CD2	-6.69	122.50	131.20
22	V	608	SER	O-C-N	-6.69	113.91	122.20
23	W	591	GLY	CA-C-O	-6.69	113.78	121.47
23	W	723	GLN	OE1-CD-NE2	-6.68	115.92	122.60
22	V	553	ARG	NE-CZ-NH2	6.68	125.21	119.20
28	X	48	DG	C5'-C4'-O4'	6.67	119.41	109.40
24	O	92	VAL	CA-C-O	-6.66	114.11	121.17
23	W	629	GLN	CA-C-O	-6.64	113.72	120.96
23	W	80	ILE	N-CA-CB	6.61	119.52	110.54
16	P	160	GLY	N-CA-C	6.59	128.81	113.18
22	V	358	ARG	NH1-CZ-NH2	-6.59	110.73	119.30
28	X	51	DC	O3'-P-O5'	6.59	113.88	104.00
22	V	701	LEU	O-C-N	-6.58	115.53	123.10
26	2	242	PHE	CA-CB-CG	-6.58	107.22	113.80
20	T	183	VAL	N-CA-C	6.57	117.36	110.72
23	W	540	THR	O-C-N	-6.57	114.19	122.27
24	O	59	ARG	NE-CZ-NH2	6.57	125.11	119.20
26	2	272	PHE	CA-CB-CG	-6.57	107.23	113.80
22	V	714	GLN	OE1-CD-NE2	-6.56	116.04	122.60
22	V	624	ILE	N-CA-CB	-6.55	103.12	111.64
23	W	152	LEU	O-C-N	-6.55	113.79	121.32
22	V	388	GLN	CG-CD-NE2	6.54	126.20	116.40
22	V	366	ASN	CA-CB-CG	6.53	119.13	112.60
5	E	65	ASN	N-CA-C	-6.53	96.89	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	W	314	VAL	N-CA-CB	6.52	118.18	110.55
23	W	120	GLU	CA-C-N	6.52	128.91	120.56
23	W	120	GLU	C-N-CA	6.52	128.91	120.56
23	W	187	GLN	OE1-CD-NE2	-6.52	116.08	122.60
1	A	619	LYS	CB-CA-C	6.51	122.62	111.68
5	E	34	ASP	N-CA-C	6.51	120.48	112.54
16	P	160	GLY	CA-C-N	6.51	133.68	121.97
16	P	160	GLY	C-N-CA	6.51	133.68	121.97
22	V	409	THR	CA-C-N	6.49	131.09	120.63
22	V	409	THR	C-N-CA	6.49	131.09	120.63
24	O	58	MET	O-C-N	6.48	131.17	123.27
23	W	33	ASP	N-CA-C	6.46	119.14	111.71
23	W	491	CYS	CA-C-N	6.46	126.84	119.92
23	W	491	CYS	C-N-CA	6.46	126.84	119.92
23	W	406	LEU	CA-C-O	-6.46	114.22	121.00
22	V	328	PHE	CA-C-N	6.46	134.07	121.41
22	V	328	PHE	C-N-CA	6.46	134.07	121.41
23	W	410	TYR	N-CA-C	-6.46	105.32	113.72
22	V	709	GLN	CA-C-N	6.45	128.93	120.28
22	V	709	GLN	C-N-CA	6.45	128.93	120.28
11	K	61	TYR	N-CA-C	6.45	118.98	109.24
22	V	434	GLU	N-CA-C	6.44	118.38	111.36
23	W	138	THR	CA-C-O	-6.44	113.73	120.55
22	V	467	THR	N-CA-C	6.43	118.63	108.79
22	V	454	VAL	CA-C-N	6.43	129.42	120.29
22	V	454	VAL	C-N-CA	6.43	129.42	120.29
23	W	166	ARG	CD-NE-CZ	6.42	133.39	124.40
9	I	105	GLU	N-CA-C	6.42	124.48	110.80
26	2	238	PHE	CA-CB-CG	-6.42	107.38	113.80
23	W	88	ARG	CA-C-N	6.42	129.40	120.29
23	W	88	ARG	C-N-CA	6.42	129.40	120.29
29	Y	41	DT	N1-C1'-C2'	6.41	123.12	113.50
23	W	416	ILE	CA-C-N	6.41	131.91	123.06
23	W	416	ILE	C-N-CA	6.41	131.91	123.06
2	B	77	GLU	N-CA-C	-6.41	100.01	109.11
22	V	281	GLN	O-C-N	6.40	128.75	122.09
23	W	210	HIS	ND1-CG-CD2	6.40	112.50	106.10
22	V	373	GLN	OE1-CD-NE2	-6.40	116.20	122.60
1	A	603	ILE	CA-C-O	6.40	127.26	120.48
6	F	44	ARG	CA-C-N	-6.39	113.39	119.85
6	F	44	ARG	C-N-CA	-6.39	113.39	119.85
22	V	643	VAL	CA-CB-CG1	6.39	121.26	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	W	258	ARG	CA-C-O	-6.39	113.65	120.42
22	V	251	PHE	N-CA-C	6.39	117.86	108.86
23	W	161	PHE	CA-CB-CG	6.39	120.19	113.80
23	W	698	GLN	OE1-CD-NE2	-6.39	116.21	122.60
23	W	196	ARG	CA-C-N	6.38	128.83	120.28
23	W	196	ARG	C-N-CA	6.38	128.83	120.28
23	W	662	GLN	OE1-CD-NE2	-6.38	116.22	122.60
23	W	299	ARG	NE-CZ-NH1	6.38	127.88	121.50
18	R	205	ASP	O-C-N	-6.37	115.36	123.26
22	V	391	ARG	NE-CZ-NH1	-6.37	115.13	121.50
23	W	511	ARG	NE-CZ-NH2	6.37	124.93	119.20
24	0	105	GLY	CA-C-O	-6.36	116.03	121.57
24	0	224	ASP	N-CA-CB	-6.36	101.51	111.56
2	B	63	PRO	N-CA-C	6.36	118.46	110.70
27	3	218	PRO	N-CA-C	-6.34	99.19	111.69
23	W	416	ILE	O-C-N	-6.34	115.72	122.95
23	W	83	VAL	CA-C-N	6.34	128.55	120.56
23	W	83	VAL	C-N-CA	6.34	128.55	120.56
22	V	396	ALA	CA-C-N	6.33	132.91	121.89
22	V	396	ALA	C-N-CA	6.33	132.91	121.89
23	W	552	TRP	N-CA-C	-6.33	104.30	111.14
23	W	257	ASP	CA-CB-CG	-6.32	106.28	112.60
13	M	34	CYS	CA-C-N	6.32	126.06	119.05
13	M	34	CYS	C-N-CA	6.32	126.06	119.05
23	W	70	LEU	CA-C-O	-6.31	113.61	120.36
23	W	238	ASN	OD1-CG-ND2	-6.31	116.29	122.60
22	V	480	LEU	CA-C-N	6.30	128.73	120.28
22	V	480	LEU	C-N-CA	6.30	128.73	120.28
22	V	689	VAL	O-C-N	-6.30	116.57	123.18
29	Y	39	DG	C4-N9-C1'	-6.30	117.55	127.00
24	0	111	SER	CA-C-N	6.29	132.92	123.05
24	0	111	SER	C-N-CA	6.29	132.92	123.05
1	A	1310	HIS	N-CA-C	6.28	120.05	109.76
27	3	181	ILE	CB-CA-C	-6.27	103.95	111.97
22	V	341	PRO	CB-CA-C	-6.27	103.37	111.39
23	W	299	ARG	N-CA-C	-6.26	104.85	113.18
15	O	67	PHE	N-CA-C	6.26	118.65	108.26
3	C	137	ASN	N-CA-C	-6.26	97.47	110.80
22	V	449	LYS	N-CA-C	6.26	118.10	111.28
7	G	152	VAL	N-CA-C	6.25	117.74	107.24
23	W	286	ARG	NE-CZ-NH2	6.25	124.82	119.20
2	B	1114	TYR	N-CA-C	6.25	118.80	108.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	932	ARG	CA-C-N	-6.24	110.22	121.14
1	A	932	ARG	C-N-CA	-6.24	110.22	121.14
22	V	545	GLN	N-CA-C	6.24	118.08	111.28
23	W	242	VAL	CA-C-O	-6.23	114.24	120.85
23	W	113	LYS	CA-C-O	-6.23	113.95	120.55
23	W	592	ARG	NH1-CZ-NH2	-6.22	111.21	119.30
6	F	88	ASP	CA-C-N	6.22	126.13	119.28
6	F	88	ASP	C-N-CA	6.22	126.13	119.28
23	W	63	TYR	CA-C-N	6.22	126.12	119.28
23	W	63	TYR	C-N-CA	6.22	126.12	119.28
13	M	217	ARG	N-CA-C	6.22	118.06	111.28
23	W	447	VAL	O-C-N	6.21	127.90	121.87
23	W	662	GLN	CG-CD-NE2	6.21	125.72	116.40
23	W	50	VAL	CA-CB-CG1	6.21	120.95	110.40
1	A	331	LYS	N-CA-C	6.20	121.42	113.18
29	Y	33	DT	O4'-C1'-N1	6.20	117.69	108.40
24	0	123	ASN	OD1-CG-ND2	-6.19	116.41	122.60
27	3	209	ILE	N-CA-C	-6.19	96.46	109.34
22	V	524	ALA	N-CA-C	6.19	118.02	111.28
2	B	882	SER	N-CA-C	-6.18	97.63	110.80
9	I	59	THR	N-CA-C	6.18	120.20	111.92
22	V	341	PRO	N-CA-CB	6.18	108.51	103.32
26	2	229	ASP	CA-CB-CG	-6.18	106.42	112.60
23	W	461	LEU	CA-C-N	6.18	128.74	120.58
23	W	461	LEU	C-N-CA	6.18	128.74	120.58
22	V	337	VAL	CA-C-N	6.17	131.57	122.99
22	V	337	VAL	C-N-CA	6.17	131.57	122.99
23	W	125	ARG	CD-NE-CZ	6.17	133.03	124.40
23	W	272	ARG	NH1-CZ-NH2	-6.17	111.28	119.30
18	R	226	ASP	CA-CB-CG	6.16	118.76	112.60
23	W	345	ARG	CD-NE-CZ	6.16	133.02	124.40
23	W	585	GLN	O-C-N	6.15	130.23	122.23
22	V	474	ASP	CA-C-N	6.15	133.28	121.54
22	V	474	ASP	C-N-CA	6.15	133.28	121.54
23	W	312	ASP	N-CA-C	6.14	117.77	111.14
24	0	62	TYR	CA-C-O	6.14	126.92	120.54
22	V	330	ASN	CA-C-O	-6.14	113.43	120.24
29	Y	37	DG	P-O5'-C5'	6.14	129.21	120.00
24	0	140	HIS	CB-CG-CD2	-6.13	123.22	131.20
24	0	206	ARG	NE-CZ-NH1	6.13	127.63	121.50
28	X	48	DG	O3'-P-O5'	-6.13	94.81	104.00
22	V	367	SER	CA-C-N	6.11	128.97	120.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	V	367	SER	C-N-CA	6.11	128.97	120.29
23	W	301	THR	CA-C-N	6.11	130.43	120.23
23	W	301	THR	C-N-CA	6.11	130.43	120.23
18	R	225	VAL	CA-C-N	-6.10	110.90	121.52
18	R	225	VAL	C-N-CA	-6.10	110.90	121.52
22	V	337	VAL	CA-C-O	-6.09	115.61	121.63
24	O	184	ASP	CA-CB-CG	6.08	118.68	112.60
23	W	332	PHE	O-C-N	-6.08	115.67	122.12
23	W	30	ARG	CD-NE-CZ	6.08	132.91	124.40
18	R	225	VAL	N-CA-C	6.08	121.98	109.34
23	W	463	PRO	N-CA-CB	6.07	109.29	103.52
22	V	709	GLN	OE1-CD-NE2	-6.06	116.54	122.60
22	V	529	LYS	O-C-N	-6.05	115.30	122.20
23	W	210	HIS	CB-CG-CD2	-6.05	123.33	131.20
1	A	1160	ARG	N-CA-C	6.05	117.95	111.36
22	V	713	LEU	CA-C-O	-6.05	114.43	120.90
22	V	278	GLU	CA-C-O	-6.04	112.63	120.25
29	Y	42	DC	C2-N1-C1'	-6.04	110.64	119.70
22	V	404	SER	CB-CA-C	6.04	122.43	110.42
29	Y	32	DC	C6-N1-C1'	6.04	128.75	119.70
1	A	490	THR	CA-C-N	-6.03	112.80	119.19
1	A	490	THR	C-N-CA	-6.03	112.80	119.19
29	Y	39	DG	C8-N9-C1'	6.03	136.04	127.00
22	V	651	VAL	CA-C-O	-6.02	113.25	120.78
23	W	621	PHE	CA-CB-CG	-6.02	107.78	113.80
22	V	379	LYS	N-CA-C	6.01	119.45	111.75
23	W	183	LEU	CA-C-N	6.01	126.61	120.00
23	W	183	LEU	C-N-CA	6.01	126.61	120.00
23	W	314	VAL	N-CA-C	6.01	116.19	110.42
1	A	859	TYR	N-CA-C	6.01	117.63	111.14
26	2	79	PHE	CA-CB-CG	-6.01	107.79	113.80
23	W	122	THR	CA-C-N	6.01	127.35	119.84
23	W	122	THR	C-N-CA	6.01	127.35	119.84
26	2	203	PHE	CA-CB-CG	-6.01	107.79	113.80
26	2	171	VAL	CB-CA-C	-6.00	104.29	111.97
14	N	372	GLY	N-CA-C	6.00	119.86	111.10
22	V	603	ASN	CA-CB-CG	6.00	118.60	112.60
23	W	164	HIS	CB-CG-CD2	-5.99	123.42	131.20
23	W	569	ILE	N-CA-CB	-5.99	105.25	112.07
22	V	561	PHE	O-C-N	-5.98	116.52	123.27
1	A	1314	THR	N-CA-C	-5.97	105.70	112.87
22	V	607	ILE	CA-CB-CG1	5.96	120.53	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	0	235	HIS	CB-CG-CD2	-5.96	123.45	131.20
23	W	590	ASN	N-CA-C	5.95	119.78	110.32
22	V	410	TYR	CA-C-N	5.95	129.57	120.82
22	V	410	TYR	C-N-CA	5.95	129.57	120.82
23	W	161	PHE	O-C-N	-5.95	115.90	122.09
23	W	470	ILE	CB-CG1-CD1	-5.95	101.31	113.80
23	W	592	ARG	NE-CZ-NH1	5.95	127.45	121.50
24	0	130	SER	N-CA-C	5.94	117.84	111.36
22	V	459	GLN	CA-C-N	5.94	132.88	121.54
22	V	459	GLN	C-N-CA	5.94	132.88	121.54
22	V	307	ASN	CA-CB-CG	5.94	118.54	112.60
1	A	1115	LYS	CA-C-N	-5.92	114.65	123.00
1	A	1115	LYS	C-N-CA	-5.92	114.65	123.00
23	W	289	VAL	N-CA-C	5.92	116.66	110.62
2	B	72	GLN	O-C-N	5.92	130.34	122.41
23	W	416	ILE	CA-C-O	5.92	127.40	120.71
29	Y	32	DC	C2-N1-C1'	-5.91	110.83	119.70
22	V	633	ARG	NE-CZ-NH2	-5.91	113.88	119.20
22	V	403	CYS	N-CA-CB	-5.91	102.07	110.46
23	W	20	GLU	CA-C-O	-5.91	114.29	120.55
23	W	92	ASN	OD1-CG-ND2	-5.91	116.69	122.60
23	W	280	ARG	CA-C-O	-5.91	114.16	120.42
29	Y	37	DG	O5'-C5'-C4'	5.91	119.66	110.80
23	W	442	LEU	CA-C-N	5.90	128.67	120.29
23	W	442	LEU	C-N-CA	5.90	128.67	120.29
1	A	256	PRO	CA-C-N	5.90	125.88	120.21
1	A	256	PRO	C-N-CA	5.90	125.88	120.21
9	I	84	HIS	CA-C-N	5.90	127.22	119.84
9	I	84	HIS	C-N-CA	5.90	127.22	119.84
23	W	623	VAL	N-CA-C	-5.90	103.56	108.63
24	0	158	HIS	CB-CG-CD2	-5.89	123.54	131.20
22	V	485	GLY	CA-C-N	5.89	126.22	119.92
22	V	485	GLY	C-N-CA	5.89	126.22	119.92
24	0	74	GLN	OE1-CD-NE2	-5.89	116.71	122.60
22	V	527	THR	CA-C-O	-5.88	115.29	121.99
28	X	47	DC	O4'-C1'-N1	5.88	117.22	108.40
1	A	604	ARG	N-CA-C	5.88	123.32	110.80
22	V	369	VAL	CA-CB-CG1	5.88	120.39	110.40
23	W	722	ARG	CD-NE-CZ	5.88	132.62	124.40
23	W	152	LEU	CA-C-N	5.87	125.81	119.76
23	W	152	LEU	C-N-CA	5.87	125.81	119.76
23	W	650	ASP	CA-C-O	-5.87	114.65	120.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	W	480	THR	CA-CB-OG1	5.87	118.41	109.60
27	3	64	ILE	CB-CA-C	-5.87	104.45	111.97
23	W	207	TYR	CA-C-O	-5.87	115.14	121.36
24	0	203	ALA	N-CA-C	5.87	119.04	108.48
23	W	37	HIS	N-CA-C	5.86	117.75	108.79
26	2	175	LEU	N-CA-CB	5.86	119.24	110.22
25	1	34	ILE	N-CA-C	5.86	116.04	110.42
2	B	1128	ALA	N-CA-C	-5.85	105.81	113.12
23	W	239	ILE	N-CA-C	5.84	116.57	110.62
23	W	685	ALA	N-CA-C	5.83	118.39	111.33
23	W	606	GLU	O-C-N	-5.83	115.40	122.22
24	0	190	LYS	N-CA-C	-5.82	105.01	111.36
27	3	153	ASP	N-CA-C	-5.82	104.94	111.28
23	W	716	VAL	N-CA-CB	5.82	119.31	110.58
23	W	206	VAL	CA-CB-CG1	5.82	120.29	110.40
22	V	276	MET	CA-C-O	-5.81	114.75	121.26
22	V	594	GLN	O-C-N	-5.80	115.82	122.09
22	V	674	THR	CA-C-N	5.80	127.98	120.44
22	V	674	THR	C-N-CA	5.80	127.98	120.44
23	W	312	ASP	N-CA-CB	-5.80	101.65	110.07
24	0	56	GLY	CA-C-N	5.80	131.73	122.10
24	0	56	GLY	C-N-CA	5.80	131.73	122.10
22	V	335	SER	N-CA-C	5.79	117.87	109.07
23	W	683	ARG	CD-NE-CZ	5.79	132.50	124.40
23	W	92	ASN	CB-CG-ND2	5.79	125.08	116.40
23	W	154	HIS	CB-CG-ND1	5.79	131.38	122.70
1	A	1286	ARG	N-CA-C	5.78	117.66	111.36
5	E	209	VAL	N-CA-C	5.78	116.52	108.89
11	K	44	ASN	N-CA-C	5.78	117.58	111.28
22	V	281	GLN	N-CA-C	5.78	118.05	111.11
22	V	332	ARG	NE-CZ-NH1	5.78	127.28	121.50
23	W	586	GLU	N-CA-C	5.78	117.25	111.07
9	I	86	CYS	N-CA-C	-5.78	101.36	109.96
23	W	213	LEU	N-CA-C	5.78	118.35	111.71
23	W	218	ALA	N-CA-C	5.77	117.57	111.28
9	I	103	ARG	N-CA-C	-5.77	98.52	110.80
23	W	672	THR	N-CA-C	5.76	119.94	113.02
22	V	412	MET	O-C-N	-5.76	115.07	122.21
1	A	924	TYR	CB-CA-C	5.75	120.00	111.88
23	W	112	ARG	NE-CZ-NH1	5.75	127.25	121.50
23	W	702	THR	N-CA-C	5.75	119.91	113.01
2	B	235	ILE	N-CA-C	5.75	116.22	108.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	1	48	GLU	N-CA-C	-5.75	98.56	110.80
24	0	160	PRO	CA-C-N	5.74	132.67	121.41
24	0	160	PRO	C-N-CA	5.74	132.67	121.41
22	V	479	ASP	N-CA-C	5.74	118.48	111.82
1	A	1113	SER	N-CA-C	5.73	116.65	108.74
1	A	1315	ASP	N-CA-C	5.73	117.99	111.11
23	W	415	THR	CA-C-O	5.73	127.59	120.54
22	V	656	ASN	CA-CB-CG	5.73	118.33	112.60
26	2	403	PHE	CA-C-N	5.72	132.74	122.09
26	2	403	PHE	C-N-CA	5.72	132.74	122.09
23	W	548	THR	CA-C-O	-5.72	114.81	120.82
22	V	488	LEU	N-CA-C	5.72	117.59	111.36
22	V	665	GLN	CG-CD-NE2	5.72	124.98	116.40
22	V	702	ALA	N-CA-CB	-5.72	102.47	110.25
23	W	593	GLY	CA-C-N	5.72	132.83	122.02
23	W	593	GLY	C-N-CA	5.72	132.83	122.02
22	V	520	ARG	NE-CZ-NH2	5.71	124.34	119.20
24	0	92	VAL	CB-CA-C	-5.71	104.66	111.97
22	V	527	THR	N-CA-C	5.70	117.42	110.41
22	V	497	GLN	OE1-CD-NE2	-5.70	116.90	122.60
23	W	447	VAL	CA-C-O	-5.70	115.02	120.95
22	V	526	LYS	CA-C-N	5.70	131.77	121.06
22	V	526	LYS	C-N-CA	5.70	131.77	121.06
22	V	393	THR	N-CA-C	5.70	115.54	108.19
22	V	532	LEU	N-CA-C	5.70	118.43	111.82
23	W	109	LEU	CA-C-N	5.70	133.47	121.91
23	W	109	LEU	C-N-CA	5.70	133.47	121.91
27	3	120	THR	CA-C-N	5.70	127.91	120.28
27	3	120	THR	C-N-CA	5.70	127.91	120.28
22	V	338	ILE	CA-C-O	-5.69	114.33	120.36
23	W	669	ARG	NE-CZ-NH1	5.69	127.19	121.50
1	A	1178	ASP	CA-C-N	5.69	125.80	119.32
1	A	1178	ASP	C-N-CA	5.69	125.80	119.32
22	V	354	ALA	N-CA-C	5.69	117.48	111.28
29	Y	42	DC	O4'-C1'-N1	5.69	116.93	108.40
5	E	182	TYR	N-CA-C	5.68	117.15	111.07
22	V	567	ALA	CA-C-N	5.68	128.21	120.54
22	V	567	ALA	C-N-CA	5.68	128.21	120.54
29	Y	33	DT	O3'-P-O5'	5.68	112.52	104.00
22	V	295	TYR	N-CA-C	5.68	118.02	110.53
22	V	307	ASN	N-CA-CB	-5.68	102.18	111.66
23	W	272	ARG	NE-CZ-NH1	5.68	127.18	121.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	V	636	GLU	N-CA-C	-5.67	105.00	111.07
2	B	719	SER	CA-C-N	-5.67	113.18	119.19
2	B	719	SER	C-N-CA	-5.67	113.18	119.19
23	W	339	TYR	CA-C-N	5.67	128.48	120.42
23	W	339	TYR	C-N-CA	5.67	128.48	120.42
23	W	651	PHE	CA-CB-CG	5.67	119.47	113.80
23	W	154	HIS	CA-CB-CG	-5.67	108.13	113.80
24	0	178	ASP	O-C-N	-5.67	116.25	121.30
1	A	251	THR	CB-CA-C	-5.67	108.26	116.54
26	2	444	THR	CA-CB-OG1	5.67	118.10	109.60
23	W	414	PHE	CA-CB-CG	5.66	119.46	113.80
22	V	579	TYR	N-CA-C	5.66	118.44	109.50
23	W	270	VAL	O-C-N	-5.65	115.51	122.57
23	W	44	SER	CA-C-O	5.65	126.32	119.49
23	W	193	PHE	N-CA-C	5.65	117.44	111.28
1	A	1120	GLY	N-CA-C	5.64	120.54	110.95
23	W	177	LEU	N-CA-C	5.64	117.11	111.07
23	W	216	LYS	CA-C-O	-5.64	114.57	120.55
1	A	620	HIS	CA-C-O	-5.64	113.67	120.32
23	W	305	LEU	CA-C-N	5.63	127.82	120.28
23	W	305	LEU	C-N-CA	5.63	127.82	120.28
8	H	73	GLY	CA-C-N	5.63	132.29	121.54
8	H	73	GLY	C-N-CA	5.63	132.29	121.54
23	W	697	ILE	N-CA-C	5.63	121.04	109.34
1	A	239	GLU	CA-C-N	5.62	126.00	119.47
1	A	239	GLU	C-N-CA	5.62	126.00	119.47
22	V	477	ILE	CA-CB-CG1	5.62	119.96	110.40
22	V	506	GLN	OE1-CD-NE2	-5.62	116.98	122.60
23	W	207	TYR	CA-CB-CG	5.62	124.02	113.90
23	W	215	PRO	CA-C-N	5.62	127.81	120.28
23	W	215	PRO	C-N-CA	5.62	127.81	120.28
1	A	644	SER	N-CA-C	-5.61	104.56	111.40
14	N	331	THR	N-CA-C	-5.61	105.31	111.82
23	W	103	PRO	CB-CA-C	5.60	120.81	111.56
22	V	444	HIS	CA-C-N	5.60	128.56	120.38
22	V	444	HIS	C-N-CA	5.60	128.56	120.38
1	A	267	GLN	CA-C-N	-5.60	113.32	121.44
1	A	267	GLN	C-N-CA	-5.60	113.32	121.44
22	V	405	VAL	CB-CA-C	5.60	120.47	111.29
22	V	551	HIS	CA-CB-CG	-5.60	108.20	113.80
22	V	355	CYS	O-C-N	-5.59	116.19	122.12
23	W	220	LEU	O-C-N	-5.59	115.77	122.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	M	43	ASP	CA-C-N	-5.59	110.86	121.54
13	M	43	ASP	C-N-CA	-5.59	110.86	121.54
26	2	61	PHE	N-CA-CB	5.59	118.09	109.98
23	W	16	TYR	CA-C-N	5.59	129.83	122.51
23	W	16	TYR	C-N-CA	5.59	129.83	122.51
24	0	194	ILE	CA-C-O	5.58	127.22	120.74
23	W	703	ASP	CA-C-N	5.58	132.20	121.54
23	W	703	ASP	C-N-CA	5.58	132.20	121.54
2	B	81	PRO	CA-C-N	5.58	125.58	119.89
2	B	81	PRO	C-N-CA	5.58	125.58	119.89
26	2	262	LEU	CB-CA-C	-5.57	102.14	110.88
22	V	439	ILE	CB-CG1-CD1	5.57	125.49	113.80
24	0	113	ARG	N-CA-C	5.57	117.87	109.41
23	W	306	ALA	CA-C-O	-5.56	114.66	120.55
22	V	375	LYS	CA-C-N	5.56	127.73	120.28
22	V	375	LYS	C-N-CA	5.56	127.73	120.28
23	W	590	ASN	CA-C-N	5.56	129.06	121.83
23	W	590	ASN	C-N-CA	5.56	129.06	121.83
22	V	677	GLN	N-CA-C	5.55	117.01	111.07
5	E	69	THR	N-CA-C	-5.55	105.23	112.23
22	V	429	TRP	CA-C-N	5.55	133.19	122.53
22	V	429	TRP	C-N-CA	5.55	133.19	122.53
23	W	197	TYR	CA-C-O	5.55	126.43	120.55
24	0	99	ASN	N-CA-C	5.55	119.89	110.02
23	W	601	ARG	NE-CZ-NH2	-5.54	114.21	119.20
1	A	952	LEU	N-CA-C	5.54	117.40	111.36
23	W	439	ASP	CA-C-O	5.53	127.24	120.60
29	Y	51	DC	OP1-P-O3'	-5.53	91.41	108.00
24	0	79	ASN	CA-C-N	-5.53	112.87	120.28
24	0	79	ASN	C-N-CA	-5.53	112.87	120.28
24	0	227	HIS	CA-CB-CG	5.53	119.33	113.80
23	W	53	LEU	CA-C-O	-5.52	114.70	120.55
23	W	726	GLN	OE1-CD-NE2	-5.52	117.08	122.60
2	B	546	GLU	CA-CB-CG	5.52	125.13	114.10
23	W	685	ALA	CA-C-O	5.52	126.59	120.63
26	2	45	PHE	CA-CB-CG	-5.52	108.28	113.80
22	V	268	VAL	CA-C-N	5.51	129.07	120.75
22	V	268	VAL	C-N-CA	5.51	129.07	120.75
1	A	253	LEU	CA-C-N	5.51	125.78	119.83
1	A	253	LEU	C-N-CA	5.51	125.78	119.83
22	V	572	ALA	N-CA-C	5.51	117.29	111.28
22	V	457	ILE	N-CA-CB	-5.50	102.15	111.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	W	251	LEU	CB-CA-C	5.50	119.43	109.37
23	W	468	PRO	CA-N-CD	-5.50	104.30	112.00
24	0	123	ASN	O-C-N	-5.50	114.85	121.12
23	W	334	ARG	N-CA-CB	-5.50	102.04	110.01
24	0	75	ASP	N-CA-C	5.50	117.27	111.28
1	A	87	HIS	N-CA-C	5.49	117.42	109.07
22	V	675	LYS	N-CA-C	5.49	116.94	111.07
23	W	68	THR	CA-C-O	-5.49	115.83	121.87
29	Y	38	DT	N1-C1'-C2'	5.49	121.73	113.50
23	W	57	MET	CA-C-N	5.49	129.38	120.60
23	W	57	MET	C-N-CA	5.49	129.38	120.60
1	A	603	ILE	CA-C-N	5.48	132.00	121.54
1	A	603	ILE	C-N-CA	5.48	132.00	121.54
24	0	98	GLN	CA-C-O	5.47	126.22	120.42
23	W	606	GLU	CA-C-O	5.47	126.28	120.10
23	W	454	VAL	CA-C-N	5.47	131.08	122.33
23	W	454	VAL	C-N-CA	5.47	131.08	122.33
1	A	322	LEU	CA-C-N	5.46	125.22	119.76
1	A	322	LEU	C-N-CA	5.46	125.22	119.76
2	B	1044	GLY	CA-C-N	5.46	125.37	119.85
2	B	1044	GLY	C-N-CA	5.46	125.37	119.85
18	R	139	PHE	N-CA-C	5.46	117.33	110.24
22	V	637	ALA	N-CA-C	5.46	118.15	111.82
24	0	226	SER	N-CA-CB	-5.46	102.10	110.12
26	2	267	GLU	CA-C-N	-5.46	115.75	122.84
26	2	267	GLU	C-N-CA	-5.46	115.75	122.84
24	0	236	VAL	CB-CA-C	-5.46	104.78	112.14
22	V	567	ALA	O-C-N	5.45	128.37	122.15
23	W	435	PHE	CA-C-N	5.45	129.30	121.50
23	W	435	PHE	C-N-CA	5.45	129.30	121.50
24	0	186	ILE	N-CA-C	5.45	116.18	110.62
22	V	514	MET	CB-CA-C	5.45	118.86	110.14
13	M	307	ASP	N-CA-C	-5.45	107.00	113.97
25	1	51	ASN	CA-CB-CG	-5.44	107.16	112.60
1	A	871	VAL	N-CA-C	5.43	116.55	108.46
23	W	463	PRO	CA-C-N	5.43	131.91	121.54
23	W	463	PRO	C-N-CA	5.43	131.91	121.54
23	W	76	THR	N-CA-C	5.43	117.32	109.07
22	V	662	LEU	N-CA-CB	-5.42	101.59	110.43
28	X	61	DA	C2'-C3'-O3'	5.42	119.63	111.50
26	2	98	THR	CA-C-N	5.42	128.09	120.28
26	2	98	THR	C-N-CA	5.42	128.09	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	2	182	ALA	N-CA-C	-5.42	102.86	110.50
23	W	197	TYR	O-C-N	-5.42	116.38	122.12
10	J	59	LEU	N-CA-C	-5.41	105.29	111.14
23	W	487	ARG	NH1-CZ-NH2	-5.41	112.26	119.30
23	W	75	ARG	NE-CZ-NH1	5.41	126.91	121.50
23	W	489	CYS	CA-C-N	5.41	130.39	122.39
23	W	489	CYS	C-N-CA	5.41	130.39	122.39
2	B	364	PHE	N-CA-C	5.41	117.25	111.36
2	B	575	GLY	N-CA-C	5.40	118.14	110.74
26	2	35	TYR	CB-CA-C	5.40	121.03	110.67
22	V	253	GLU	CA-C-N	5.39	131.84	121.54
22	V	253	GLU	C-N-CA	5.39	131.84	121.54
22	V	433	GLN	OE1-CD-NE2	-5.39	117.21	122.60
1	A	31	LEU	N-CA-C	-5.39	105.41	111.28
22	V	252	TYR	O-C-N	-5.39	116.93	123.29
22	V	360	ARG	CD-NE-CZ	5.39	131.95	124.40
24	0	142	GLU	O-C-N	5.39	125.75	121.55
2	B	446	TYR	N-CA-C	5.39	116.83	111.07
23	W	455	ILE	N-CA-C	5.38	115.65	108.27
6	F	113	GLY	N-CA-C	-5.38	107.82	113.58
8	H	85	ALA	N-CA-C	-5.38	105.81	112.38
28	X	63	DC	C2'-C3'-O3'	5.38	119.57	111.50
23	W	645	GLN	CA-C-N	5.38	131.65	121.97
23	W	645	GLN	C-N-CA	5.38	131.65	121.97
25	1	33	PHE	CA-CB-CG	-5.37	108.43	113.80
22	V	576	ASN	N-CA-CB	-5.37	103.84	111.84
2	B	1105	GLU	N-CA-C	-5.37	105.33	111.07
23	W	600	ALA	CA-C-N	5.36	128.00	120.28
23	W	600	ALA	C-N-CA	5.36	128.00	120.28
21	U	281	ALA	CA-C-O	5.36	121.05	117.94
24	0	178	ASP	CA-C-N	5.36	124.87	119.19
24	0	178	ASP	C-N-CA	5.36	124.87	119.19
29	Y	40	DT	C2'-C3'-O3'	5.36	119.54	111.50
17	Q	110	MET	N-CA-C	5.36	116.80	111.07
22	V	265	THR	CA-C-O	-5.35	115.29	121.07
22	V	339	VAL	CA-C-O	5.35	126.01	120.39
22	V	252	TYR	N-CA-C	5.35	117.69	109.07
23	W	156	ARG	CD-NE-CZ	5.35	131.89	124.40
23	W	686	ARG	CA-C-N	5.35	127.01	120.22
23	W	686	ARG	C-N-CA	5.35	127.01	120.22
28	X	46	DG	P-O3'-C3'	5.35	128.22	120.20
22	V	542	ARG	NE-CZ-NH2	5.35	124.01	119.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	W	562	GLN	CB-CG-CD	5.35	121.69	112.60
22	V	564	ASN	CA-C-N	5.34	127.78	120.46
22	V	564	ASN	C-N-CA	5.34	127.78	120.46
23	W	313	GLU	N-CA-C	5.34	116.78	111.07
24	O	134	ALA	CA-C-O	5.34	126.08	120.42
28	X	61	DA	C1'-O4'-C4'	-5.34	101.69	109.70
22	V	361	CYS	N-CA-CB	-5.33	101.55	110.83
20	T	31	TRP	N-CA-C	5.33	117.84	111.71
23	W	141	TYR	N-CA-C	5.33	117.09	111.28
28	X	48	DG	P-O5'-C5'	5.33	127.99	120.00
2	B	257	VAL	N-CA-C	5.33	120.42	109.34
22	V	677	GLN	OE1-CD-NE2	-5.32	117.28	122.60
28	X	46	DG	C5'-C4'-C3'	-5.32	106.92	114.90
22	V	332	ARG	CA-CB-CG	5.32	124.73	114.10
22	V	575	LEU	CA-C-N	5.32	129.67	122.07
22	V	575	LEU	C-N-CA	5.32	129.67	122.07
23	W	118	HIS	CB-CG-CD2	-5.32	124.29	131.20
9	I	58	ILE	N-CA-C	5.31	120.39	109.34
22	V	555	ASN	N-CA-C	5.31	118.77	111.54
23	W	37	HIS	CA-C-N	5.31	127.82	120.92
23	W	37	HIS	C-N-CA	5.31	127.82	120.92
24	O	73	ASP	CA-CB-CG	5.31	117.91	112.60
1	A	785	ILE	N-CA-C	5.30	116.38	111.45
23	W	202	ALA	N-CA-C	5.30	118.19	109.76
23	W	450	ARG	N-CA-C	5.30	122.09	110.80
1	A	83	GLY	N-CA-C	-5.30	105.08	112.18
23	W	282	ARG	CA-C-N	5.30	127.38	120.28
23	W	282	ARG	C-N-CA	5.30	127.38	120.28
23	W	560	ASN	CA-CB-CG	-5.30	107.30	112.60
23	W	253	ARG	N-CA-C	5.29	117.05	111.28
27	3	50	PHE	CA-CB-CG	-5.29	108.51	113.80
22	V	469	THR	CA-C-N	5.29	131.64	121.54
22	V	469	THR	C-N-CA	5.29	131.64	121.54
23	W	534	GLY	O-C-N	-5.29	118.87	122.62
24	O	99	ASN	OD1-CG-ND2	-5.29	117.31	122.60
23	W	669	ARG	NH1-CZ-NH2	-5.28	112.43	119.30
1	A	85	PHE	CA-C-N	-5.28	118.09	122.16
1	A	85	PHE	C-N-CA	-5.28	118.09	122.16
22	V	381	TRP	CZ3-CH2-CZ2	-5.28	114.64	121.50
24	O	131	LEU	O-C-N	-5.28	115.77	122.27
22	V	272	VAL	O-C-N	5.28	126.99	121.87
24	O	170	ILE	CA-CB-CG1	5.28	119.37	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	V	525	ILE	CA-C-O	-5.27	114.48	120.65
22	V	576	ASN	CA-C-O	5.27	127.66	121.54
1	A	1336	LEU	CA-C-N	-5.27	115.76	122.77
1	A	1336	LEU	C-N-CA	-5.27	115.76	122.77
1	A	702	ILE	N-CA-C	5.27	115.47	110.42
23	W	455	ILE	CA-C-O	-5.26	115.01	120.64
24	O	90	TYR	CA-C-N	5.26	127.33	120.28
24	O	90	TYR	C-N-CA	5.26	127.33	120.28
29	Y	42	DC	C6-N1-C1'	5.26	127.59	119.70
23	W	516	VAL	N-CA-C	5.26	115.98	110.62
1	A	427	ILE	N-CA-C	5.26	115.69	108.12
22	V	297	PHE	N-CA-C	5.26	117.06	109.07
22	V	332	ARG	NH1-CZ-NH2	-5.26	112.47	119.30
12	L	27	GLU	CA-C-N	-5.25	115.23	122.69
12	L	27	GLU	C-N-CA	-5.25	115.23	122.69
23	W	454	VAL	N-CA-CB	-5.25	105.82	112.60
28	X	47	DC	P-O5'-C5'	5.25	127.88	120.00
22	V	317	ARG	O-C-N	5.25	127.31	121.43
22	V	634	ARG	NE-CZ-NH1	-5.25	116.25	121.50
24	O	59	ARG	NH1-CZ-NH2	-5.25	112.47	119.30
22	V	341	PRO	N-CA-C	5.25	119.46	111.11
23	W	457	THR	N-CA-CB	-5.25	103.43	111.56
29	Y	39	DG	C1'-O4'-C4'	-5.25	101.83	109.70
22	V	282	LYS	CG-CD-CE	5.25	123.37	111.30
22	V	574	ARG	O-C-N	-5.25	116.17	122.15
24	O	237	SER	N-CA-C	5.24	116.02	109.57
23	W	102	LEU	CA-C-N	5.24	126.39	119.84
23	W	102	LEU	C-N-CA	5.24	126.39	119.84
1	A	299	ALA	CB-CA-C	-5.24	110.52	116.54
23	W	50	VAL	O-C-N	5.24	127.22	121.83
23	W	711	ASP	CA-CB-CG	-5.24	107.36	112.60
23	W	87	LEU	CB-CA-C	5.24	119.75	110.85
1	A	43	TYR	CA-C-N	5.23	126.38	119.84
1	A	43	TYR	C-N-CA	5.23	126.38	119.84
1	A	1035	GLU	N-CA-C	5.23	116.67	111.07
23	W	169	PRO	N-CA-CB	5.23	109.04	103.39
3	C	209	SER	N-CA-C	-5.23	105.70	111.71
22	V	366	ASN	N-CA-C	5.23	119.37	112.89
22	V	699	GLU	N-CA-C	5.23	116.75	108.96
23	W	284	GLU	N-CA-CB	5.23	117.59	110.01
1	A	621	ILE	O-C-N	5.22	129.10	122.57
22	V	341	PRO	CA-C-N	5.22	129.92	122.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	V	341	PRO	C-N-CA	5.22	129.92	122.08
22	V	704	SER	N-CA-C	5.22	119.52	113.20
26	2	60	LEU	CB-CA-C	-5.22	102.68	110.88
22	V	708	GLU	O-C-N	5.22	127.65	122.12
23	W	46	THR	CA-CB-OG1	5.22	117.43	109.60
23	W	205	VAL	CA-C-N	5.22	130.31	123.11
23	W	205	VAL	C-N-CA	5.22	130.31	123.11
26	2	402	ARG	N-CA-C	5.22	117.60	110.24
22	V	562	ALA	CA-C-N	5.22	131.50	121.54
22	V	562	ALA	C-N-CA	5.22	131.50	121.54
23	W	494	ILE	O-C-N	-5.21	117.26	123.05
22	V	552	GLU	N-CA-C	5.21	117.70	111.71
26	2	261	PHE	CB-CA-C	-5.21	102.70	110.88
28	X	61	DA	P-O3'-C3'	5.21	128.01	120.20
22	V	399	LYS	CA-C-N	5.20	124.81	119.56
22	V	399	LYS	C-N-CA	5.20	124.81	119.56
23	W	707	ASN	OD1-CG-ND2	-5.20	117.40	122.60
24	O	179	PRO	CA-C-O	-5.20	111.69	119.34
17	Q	101	ASN	N-CA-C	-5.20	106.02	112.93
22	V	315	VAL	CA-C-O	-5.20	114.93	120.39
23	W	319	VAL	CA-C-N	5.20	126.34	119.84
23	W	319	VAL	C-N-CA	5.20	126.34	119.84
23	W	128	LYS	CA-C-N	5.19	128.09	120.71
23	W	128	LYS	C-N-CA	5.19	128.09	120.71
7	G	160	ILE	N-CA-C	5.19	115.95	108.48
2	B	132	VAL	N-CA-C	5.19	120.13	109.34
2	B	150	GLY	N-CA-C	5.19	118.15	110.42
23	W	399	LEU	CA-C-O	-5.19	115.36	120.70
22	V	285	ILE	CA-CB-CG2	5.18	119.31	110.50
23	W	153	PRO	CB-CA-C	5.18	118.14	111.46
5	E	163	TYR	N-CA-C	5.18	119.31	112.89
23	W	199	ILE	O-C-N	-5.18	116.85	121.87
21	U	256	THR	N-CA-C	5.17	121.81	110.80
22	V	305	ASP	CA-C-N	5.17	131.27	121.97
22	V	305	ASP	C-N-CA	5.17	131.27	121.97
23	W	96	LYS	N-CA-C	5.16	121.80	110.80
23	W	152	LEU	N-CA-C	5.16	121.22	109.81
23	W	564	ASN	OD1-CG-ND2	-5.16	117.44	122.60
24	O	65	VAL	CA-CB-CG1	5.16	119.17	110.40
1	A	1078	GLN	N-CA-C	5.16	116.90	111.28
23	W	71	ILE	N-CA-C	5.16	115.91	108.48
22	V	678	ARG	CA-C-O	-5.15	115.09	120.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	T	165	TYR	N-CA-C	5.15	116.58	111.07
24	0	212	ALA	CA-C-N	5.15	127.44	120.44
24	0	212	ALA	C-N-CA	5.15	127.44	120.44
2	B	871	VAL	N-CA-C	5.15	115.46	107.28
22	V	344	ALA	N-CA-CB	-5.15	101.36	111.60
23	W	660	ALA	CA-C-N	5.14	127.69	120.28
23	W	660	ALA	C-N-CA	5.14	127.69	120.28
22	V	357	VAL	N-CA-CB	5.14	117.53	110.54
23	W	511	ARG	CA-C-N	5.14	131.37	122.32
23	W	511	ARG	C-N-CA	5.14	131.37	122.32
22	V	564	ASN	CB-CA-C	5.14	118.54	109.80
23	W	87	LEU	CA-C-N	5.14	127.17	120.28
23	W	87	LEU	C-N-CA	5.14	127.17	120.28
11	K	21	ILE	N-CA-C	5.14	115.25	107.80
22	V	419	ARG	CD-NE-CZ	5.14	131.59	124.40
22	V	283	ARG	NE-CZ-NH2	-5.13	114.58	119.20
23	W	693	LEU	CB-CA-C	5.13	116.93	109.08
20	T	189	SER	N-CA-C	5.13	116.56	111.07
27	3	169	ASP	CA-CB-CG	-5.13	107.47	112.60
22	V	545	GLN	CA-C-N	5.13	127.15	120.28
22	V	545	GLN	C-N-CA	5.13	127.15	120.28
23	W	98	GLU	O-C-N	-5.13	115.77	122.59
1	A	539	GLN	CB-CA-C	-5.12	110.26	117.23
23	W	154	HIS	CG-CD2-NE2	5.12	112.32	107.20
23	W	538	PHE	O-C-N	5.12	129.10	123.16
23	W	641	ARG	CD-NE-CZ	5.12	131.57	124.40
22	V	363	VAL	CA-C-N	-5.12	115.93	123.00
22	V	363	VAL	C-N-CA	-5.12	115.93	123.00
23	W	69	LYS	CG-CD-CE	5.12	123.08	111.30
22	V	397	LYS	CA-CB-CG	5.12	124.33	114.10
22	V	628	SER	CA-C-N	5.12	131.31	121.54
22	V	628	SER	C-N-CA	5.12	131.31	121.54
7	G	96	GLY	N-CA-C	5.11	117.74	110.74
23	W	158	TYR	CA-C-N	5.11	127.64	120.28
23	W	158	TYR	C-N-CA	5.11	127.64	120.28
24	0	80	ARG	CD-NE-CZ	5.11	131.56	124.40
24	0	233	THR	CA-CB-OG1	5.11	117.26	109.60
22	V	580	ILE	O-C-N	-5.11	117.68	123.20
24	0	124	PRO	CA-C-N	5.11	127.12	120.28
24	0	124	PRO	C-N-CA	5.11	127.12	120.28
25	1	62	ASP	CA-CB-CG	-5.10	107.50	112.60
2	B	75	SER	CA-C-N	5.10	131.41	121.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	75	SER	C-N-CA	5.10	131.41	121.41
23	W	483	MET	N-CA-CB	-5.10	102.67	110.42
2	B	449	ALA	N-CA-C	5.10	116.69	111.03
10	J	63	ALA	O-C-N	5.10	127.18	121.32
22	V	452	ARG	CA-CB-CG	5.10	124.30	114.10
23	W	64	PRO	CA-N-CD	-5.10	104.86	112.00
17	Q	22	ILE	N-CA-C	-5.09	105.53	110.42
23	W	31	THR	CA-CB-CG2	5.09	119.16	110.50
23	W	519	ASN	CA-CB-CG	5.09	117.69	112.60
28	X	46	DG	C4'-C3'-O3'	-5.09	102.36	110.00
5	E	132	GLN	N-CA-C	5.09	116.83	111.28
26	2	128	ALA	CA-C-N	-5.09	115.59	123.17
26	2	128	ALA	C-N-CA	-5.09	115.59	123.17
22	V	543	ALA	N-CA-C	5.08	116.82	111.28
23	W	24	TYR	N-CA-C	5.08	119.64	111.81
29	Y	39	DG	C4'-C3'-O3'	-5.08	102.37	110.00
2	B	48	ASP	N-CA-C	5.08	116.82	111.28
2	B	546	GLU	N-CA-C	-5.08	105.74	111.28
8	H	15	ILE	N-CA-C	-5.08	108.17	113.10
1	A	923	ASP	CA-C-N	-5.08	114.46	122.08
1	A	923	ASP	C-N-CA	-5.08	114.46	122.08
20	T	204	ASP	N-CA-C	5.08	116.82	111.28
5	E	105	VAL	N-CA-C	5.08	114.89	107.37
27	3	9	ASN	CA-CB-CG	-5.08	107.52	112.60
26	2	48	LEU	N-CA-C	5.08	121.03	109.81
23	W	570	GLU	CA-C-N	5.07	129.81	122.36
23	W	570	GLU	C-N-CA	5.07	129.81	122.36
22	V	465	GLY	CA-C-O	-5.07	115.97	120.94
23	W	23	SER	CB-CA-C	-5.07	102.92	110.88
23	W	621	PHE	O-C-N	5.07	129.40	122.41
1	A	621	ILE	CB-CA-C	5.07	119.60	111.29
2	B	926	VAL	N-CA-C	5.06	115.14	107.80
23	W	672	THR	CA-C-N	5.06	130.68	122.53
23	W	672	THR	C-N-CA	5.06	130.68	122.53
23	W	260	GLN	CA-C-N	5.06	125.60	119.98
23	W	260	GLN	C-N-CA	5.06	125.60	119.98
23	W	170	LEU	O-C-N	-5.06	115.98	120.48
23	W	205	VAL	CA-CB-CG1	5.06	119.00	110.40
20	T	86	GLN	CA-CB-CG	5.06	124.22	114.10
1	A	1409	GLY	N-CA-C	-5.05	108.27	115.30
22	V	577	LYS	CA-C-O	-5.05	115.49	120.19
22	V	466	LEU	N-CA-CB	-5.05	102.06	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	V	639	ARG	NE-CZ-NH2	5.05	123.75	119.20
23	W	414	PHE	CA-C-O	-5.05	115.72	121.68
26	2	244	THR	N-CA-C	-5.05	105.67	111.07
23	W	720	PHE	CA-CB-CG	5.04	118.84	113.80
23	W	459	GLY	O-C-N	5.04	129.25	122.70
26	2	249	TYR	CA-C-N	-5.04	114.59	122.05
26	2	249	TYR	C-N-CA	-5.04	114.59	122.05
22	V	316	LEU	CB-CA-C	-5.04	101.53	111.60
23	W	172	ALA	CA-C-N	5.04	131.28	121.41
23	W	172	ALA	C-N-CA	5.04	131.28	121.41
22	V	581	TYR	CA-C-O	-5.03	115.92	121.31
24	0	207	VAL	CA-C-N	5.03	127.43	120.29
24	0	207	VAL	C-N-CA	5.03	127.43	120.29
14	N	21	VAL	N-CA-C	5.03	115.26	110.53
22	V	311	LYS	CA-C-O	-5.03	113.27	120.16
22	V	366	ASN	OD1-CG-ND2	5.03	127.63	122.60
22	V	560	VAL	O-C-N	-5.03	117.22	123.10
23	W	699	GLU	CB-CA-C	5.03	118.35	109.80
25	1	3	ASN	CA-C-N	-5.03	115.14	122.58
25	1	3	ASN	C-N-CA	-5.03	115.14	122.58
8	H	36	LYS	N-CA-C	-5.02	107.83	114.31
22	V	634	ARG	N-CA-C	5.02	117.64	111.82
28	X	58	DT	C2'-C3'-O3'	-5.02	103.97	111.50
23	W	138	THR	N-CA-C	-5.02	105.81	111.28
23	W	444	ILE	N-CA-C	5.02	117.36	111.09
23	W	195	ALA	O-C-N	5.02	127.24	122.07
22	V	680	LEU	N-CA-C	5.01	116.75	111.28
23	W	557	ILE	CA-CB-CG1	5.01	118.92	110.40
22	V	487	LYS	CA-C-N	5.01	127.41	120.29
22	V	487	LYS	C-N-CA	5.01	127.41	120.29
23	W	629	GLN	OE1-CD-NE2	-5.01	117.59	122.60
23	W	299	ARG	O-C-N	-5.00	116.34	122.25
23	W	142	VAL	CA-C-O	-5.00	115.87	121.17
23	W	276	THR	CA-C-N	5.00	132.06	121.91
23	W	276	THR	C-N-CA	5.00	132.06	121.91

There are no chirality outliers.

All (54) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
24	0	143	PRO	Mainchain
25	1	17	LYS	Mainchain

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Mol	Chain	Res	Type	Group
26	2	389	ASP	Sidechain,Mainchain
26	2	399	ASP	Sidechain
26	2	403	PHE	Peptide,Mainchain
26	2	406	GLY	Peptide
26	2	409	TYR	Sidechain
26	2	425	ALA	Mainchain
1	A	85	PHE	Peptide
17	Q	100	VAL	Mainchain
18	R	204	ASN	Mainchain
18	R	205	ASP	Peptide,Mainchain
18	R	206	LYS	Mainchain
18	R	213	ASP	Sidechain
18	R	219	LEU	Mainchain
18	R	230	GLU	Mainchain
18	R	235	GLU	Sidechain
20	T	86	GLN	Sidechain
22	V	247	ASP	Mainchain
22	V	319	TYR	Sidechain
22	V	378	PHE	Sidechain
22	V	489	TYR	Sidechain
22	V	503	ALA	Peptide
22	V	519	TYR	Sidechain
22	V	530	ARG	Sidechain
22	V	674	THR	Mainchain
23	W	197	TYR	Sidechain
23	W	206	VAL	Mainchain
23	W	208	SER	Mainchain
23	W	211	TYR	Sidechain
23	W	282	ARG	Sidechain
23	W	286	ARG	Sidechain
23	W	616	ARG	Sidechain
23	W	641	ARG	Sidechain
23	W	669	ARG	Sidechain
23	W	674	TYR	Sidechain
23	W	719	TYR	Sidechain
28	X	43	DG	Sidechain
28	X	44	DT	Sidechain
28	X	46	DG	Sidechain
28	X	47	DC	Sidechain
28	X	48	DG	Sidechain
28	X	49	DA	Sidechain
28	X	50	DT	Sidechain

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Mol	Chain	Res	Type	Group
28	X	54	DA	Sidechain
29	Y	41	DT	Sidechain
29	Y	42	DC	Sidechain
29	Y	43	DG	Sidechain
29	Y	44	DA	Sidechain
29	Y	50	DA	Sidechain
29	Y	51	DC	Sidechain

5.2 Too-close contacts [i](#)

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	11515	0	11609	723	0
2	B	9317	0	9305	595	0
3	C	2213	0	2153	163	0
4	D	1062	0	1042	25	0
5	E	1723	0	1744	119	0
6	F	689	0	715	49	0
7	G	1351	0	1358	56	0
8	H	1205	0	1167	93	0
9	I	1013	0	932	97	0
10	J	533	0	553	52	0
11	K	937	0	959	49	0
12	L	388	0	393	72	0
13	M	2018	0	2059	138	0
14	N	930	0	888	68	0
15	O	806	0	818	50	0
16	P	1462	0	1549	111	0
17	Q	1484	0	1496	233	0
18	R	1357	0	1377	300	0
19	S	1138	0	1103	40	0
20	T	1788	0	1819	174	0
21	U	1343	0	1338	105	0
22	V	3855	0	3872	229	0
23	W	5348	0	5372	183	0
24	0	1479	0	1524	41	0
25	1	491	0	507	249	0
26	2	2196	0	2206	606	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	3	1526	0	1561	491	0
28	X	1343	0	725	35	0
29	Y	1316	0	730	36	0
30	A	1	0	0	0	0
30	B	1	0	0	0	0
31	A	2	0	0	0	0
31	B	1	0	0	0	0
31	C	1	0	0	0	0
31	I	2	0	0	0	0
31	J	1	0	0	0	0
31	L	1	0	0	0	0
31	M	1	0	0	0	0
31	Q	1	0	0	0	0
31	U	1	0	0	0	0
All	All	61839	0	60874	4257	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 35.

All (4257) 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)
23:W:421:PHE:CD1	23:W:431:PRO:HG3	1.15	1.65
5:E:27:LEU:HD12	5:E:64:HIS:CD2	1.29	1.64
27:3:59:VAL:HG12	27:3:71:TYR:CD1	1.24	1.64
5:E:27:LEU:HB2	5:E:64:HIS:CD2	1.33	1.63
22:V:315:VAL:HG13	23:W:500:ASP:CB	1.21	1.63
23:W:250:ASN:HB3	23:W:434:HIS:CD2	1.34	1.60
5:E:27:LEU:CB	5:E:64:HIS:CD2	1.85	1.59
1:A:621:ILE:CG2	1:A:623:PRO:HG3	1.13	1.57
22:V:531:ILE:HA	22:V:534:TYR:CE2	1.39	1.56
5:E:27:LEU:CB	5:E:64:HIS:HD2	0.95	1.56
17:Q:110:MET:HB2	18:R:218:LYS:CG	1.11	1.56
18:R:195:PRO:CG	18:R:199:LYS:HB2	1.32	1.56
22:V:516:PRO:CG	25:1:15:ALA:HB3	1.16	1.55
5:E:27:LEU:CD1	5:E:64:HIS:CD2	1.79	1.53
27:3:59:VAL:CG1	27:3:71:TYR:HD1	1.15	1.53
23:W:421:PHE:CD1	23:W:431:PRO:CG	1.87	1.53
24:0:54:ARG:HG3	27:3:182:PHE:CE1	1.42	1.53
1:A:621:ILE:C	1:A:623:PRO:HD3	1.10	1.53
17:Q:113:ARG:HD2	18:R:221:ARG:CD	1.37	1.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:27:LEU:CG	5:E:64:HIS:CD2	1.84	1.52
26:2:31:LEU:HD11	27:3:33:THR:CB	1.39	1.52
26:2:31:LEU:HD11	27:3:33:THR:CG2	1.42	1.49
22:V:516:PRO:HG3	25:1:15:ALA:CB	1.04	1.49
22:V:315:VAL:CG1	23:W:500:ASP:HB2	1.01	1.48
26:2:28:PRO:N	27:3:25:GLN:CA	1.70	1.48
18:R:195:PRO:CB	18:R:199:LYS:HB2	1.39	1.48
2:B:239:MET:SD	2:B:256:ILE:HG23	1.55	1.47
22:V:321:GLU:HB3	23:W:499:ASN:CG	1.38	1.45
26:2:117:ASN:HD21	27:3:108:ASN:CB	1.27	1.45
26:2:117:ASN:CG	27:3:108:ASN:HB2	1.39	1.45
2:B:93:LEU:N	20:T:145:LEU:HD23	1.29	1.45
26:2:117:ASN:ND2	27:3:108:ASN:CB	1.76	1.44
17:Q:109:HIS:O	18:R:221:ARG:CZ	1.64	1.43
16:P:206:GLU:HB3	16:P:207:PRO:CD	1.41	1.43
17:Q:105:TYR:CD1	18:R:234:GLU:HG2	1.52	1.43
1:A:621:ILE:HG23	1:A:623:PRO:CG	1.49	1.42
17:Q:110:MET:CE	18:R:213:ASP:HB3	1.47	1.42
1:A:1310:HIS:CB	21:U:252:LYS:HE3	1.50	1.42
22:V:321:GLU:HB3	23:W:499:ASN:ND2	1.25	1.42
18:R:155:LEU:CG	18:R:204:ASN:ND2	1.79	1.41
1:A:731:ASN:OD1	21:U:253:THR:CG2	1.69	1.41
12:L:16:ILE:HG13	12:L:28:ILE:N	1.33	1.40
17:Q:23:ARG:NH1	18:R:207:SER:HB3	1.32	1.40
17:Q:110:MET:CB	18:R:218:LYS:CG	2.00	1.40
1:A:621:ILE:CG2	1:A:623:PRO:CG	2.01	1.39
26:2:30:VAL:HG12	27:3:25:GLN:C	1.44	1.39
17:Q:187:ILE:HG23	18:R:212:VAL:CA	1.49	1.39
3:C:200:PRO:HG2	3:C:217:GLN:CG	1.51	1.38
13:M:178:LYS:O	20:T:154:LYS:CB	1.69	1.38
23:W:421:PHE:CE1	23:W:431:PRO:HG2	1.57	1.38
26:2:31:LEU:HD21	27:3:33:THR:N	1.34	1.37
17:Q:110:MET:HE1	18:R:213:ASP:CB	1.43	1.36
17:Q:113:ARG:CD	18:R:221:ARG:HD2	1.56	1.36
24:0:54:ARG:CG	27:3:182:PHE:HE1	1.35	1.36
1:A:621:ILE:C	1:A:623:PRO:CD	1.97	1.35
26:2:117:ASN:OD1	27:3:108:ASN:ND2	1.57	1.34
26:2:118:LEU:CD2	27:3:39:ASP:OD1	1.75	1.34
22:V:325:ARG:NH2	23:W:499:ASN:HB3	1.02	1.33
17:Q:110:MET:CB	18:R:218:LYS:HG3	1.55	1.33
22:V:523:VAL:HG11	25:1:20:LEU:CD2	1.56	1.33

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:731:ASN:CG	21:U:253:THR:HG22	1.53	1.32
17:Q:113:ARG:HB2	18:R:221:ARG:CD	1.58	1.31
20:T:177:ARG:HG2	20:T:208:GLN:CD	1.54	1.31
9:I:99:SER:OG	9:I:105:GLU:HB2	1.26	1.31
17:Q:109:HIS:O	18:R:221:ARG:NH1	1.62	1.31
2:B:242:ARG:O	2:B:252:ILE:CG2	1.77	1.31
5:E:65:ASN:O	5:E:67:ASP:N	1.59	1.31
22:V:516:PRO:CG	22:V:706:LYS:HZ3	1.43	1.30
26:2:118:LEU:HD22	27:3:39:ASP:OD1	1.16	1.30
9:I:105:GLU:O	9:I:107:ALA:N	1.62	1.30
17:Q:110:MET:CG	18:R:218:LYS:HB2	1.59	1.30
17:Q:113:ARG:CD	18:R:221:ARG:CD	2.08	1.30
17:Q:110:MET:HE1	18:R:213:ASP:CA	1.61	1.29
25:1:1:MET:O	26:2:413:LEU:HG	1.25	1.28
24:0:97:ASP:O	27:3:208:ASP:HB3	1.12	1.28
22:V:325:ARG:NH2	23:W:499:ASN:CB	1.97	1.28
17:Q:110:MET:HB2	18:R:218:LYS:CB	1.63	1.27
20:T:177:ARG:CG	20:T:208:GLN:OE1	1.80	1.27
22:V:321:GLU:CB	23:W:499:ASN:HD21	1.45	1.27
2:B:242:ARG:O	2:B:252:ILE:HG23	1.23	1.26
22:V:321:GLU:HB3	23:W:499:ASN:OD1	1.30	1.26
2:B:160:TYR:CZ	20:T:144:GLN:HG2	1.69	1.26
8:H:74:GLU:O	8:H:76:ASN:N	1.64	1.26
26:2:118:LEU:HD21	27:3:39:ASP:O	1.23	1.26
1:A:427:ILE:HG12	13:M:38:GLY:O	1.14	1.26
18:R:225:VAL:HG13	18:R:226:ASP:OD1	1.13	1.25
13:M:179:GLU:CA	20:T:154:LYS:HG2	1.65	1.25
22:V:516:PRO:CG	25:1:15:ALA:CB	1.84	1.25
22:V:674:THR:HG23	26:2:392:ARG:NH2	1.50	1.25
1:A:926:ASN:OD1	1:A:931:ARG:NE	1.70	1.25
17:Q:102:VAL:O	17:Q:103:VAL:C	1.78	1.25
22:V:321:GLU:OE2	23:W:500:ASP:CB	1.85	1.24
27:3:59:VAL:CG1	27:3:71:TYR:CD1	1.98	1.24
1:A:1310:HIS:HB3	21:U:252:LYS:CE	1.66	1.24
3:C:200:PRO:HB2	3:C:217:GLN:OE1	1.33	1.24
5:E:27:LEU:CD1	5:E:64:HIS:NE2	1.80	1.24
2:B:160:TYR:HE1	20:T:144:GLN:CD	1.44	1.24
18:R:155:LEU:HG	18:R:204:ASN:ND2	0.93	1.24
1:A:612:ASP:O	1:A:614:ASP:N	1.69	1.24
22:V:366:ASN:HD21	22:V:613:THR:CG2	1.49	1.24
23:W:59:TYR:CZ	23:W:62:ALA:CB	2.21	1.24

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:0:165:ARG:NH1	24:0:192:ALA:O	1.68	1.24
2:B:881:GLU:C	2:B:883:THR:H	1.41	1.23
12:L:16:ILE:HD12	12:L:28:ILE:O	1.32	1.23
23:W:209:TYR:OH	23:W:233:PHE:HA	1.37	1.23
23:W:410:TYR:O	23:W:412:LYS:N	1.71	1.23
26:2:30:VAL:HG12	27:3:25:GLN:O	1.36	1.23
18:R:212:VAL:CG2	18:R:213:ASP:H	1.46	1.22
22:V:321:GLU:CB	23:W:499:ASN:OD1	1.88	1.22
18:R:195:PRO:CG	18:R:199:LYS:CB	2.15	1.22
17:Q:105:TYR:CD1	18:R:234:GLU:CG	2.21	1.22
27:3:205:GLN:O	27:3:208:ASP:O	1.53	1.22
1:A:551:ARG:HD3	1:A:625:ASP:OD1	1.37	1.22
26:2:31:LEU:CD1	27:3:33:THR:HB	1.69	1.21
5:E:27:LEU:HD12	5:E:64:HIS:NE2	0.90	1.21
9:I:99:SER:OG	9:I:105:GLU:CB	1.88	1.21
22:V:531:ILE:CG2	22:V:534:TYR:OH	1.88	1.21
25:1:59:GLU:OE2	26:2:402:ARG:NH2	1.73	1.20
23:W:72:TYR:CE2	23:W:232:VAL:HG11	1.75	1.20
22:V:428:GLU:O	22:V:433:GLN:HA	1.42	1.19
3:C:212:ASP:O	3:C:213:GLU:O	1.59	1.19
23:W:59:TYR:CZ	23:W:62:ALA:HB1	1.77	1.19
17:Q:113:ARG:HD2	18:R:221:ARG:CG	1.70	1.19
22:V:611:GLY:HA2	22:V:615:PHE:CD2	1.76	1.19
23:W:250:ASN:CB	23:W:434:HIS:CD2	2.24	1.18
25:1:1:MET:CG	26:2:413:LEU:HB3	1.73	1.18
22:V:531:ILE:CA	22:V:534:TYR:CE2	2.25	1.18
26:2:30:VAL:CG1	27:3:24:LYS:O	1.91	1.18
27:3:58:ALA:N	27:3:71:TYR:OH	1.76	1.18
18:R:202:PHE:O	18:R:203:PHE:CD1	1.96	1.18
23:W:250:ASN:HB3	23:W:434:HIS:NE2	1.56	1.18
26:2:30:VAL:HG11	27:3:24:LYS:O	1.01	1.18
13:M:179:GLU:HA	20:T:154:LYS:CG	1.72	1.17
22:V:366:ASN:ND2	22:V:613:THR:CG2	2.05	1.17
17:Q:187:ILE:HG23	18:R:212:VAL:N	1.57	1.17
17:Q:25:PHE:CD2	18:R:215:GLU:CD	2.23	1.17
26:2:31:LEU:CD1	27:3:33:THR:CG2	2.21	1.17
26:2:117:ASN:ND2	27:3:108:ASN:HB2	0.85	1.17
1:A:610:PRO:O	1:A:611:ASP:HB2	1.41	1.17
27:3:66:GLU:HA	27:3:132:LEU:HD12	1.22	1.17
2:B:497:LYS:N	2:B:498:PRO:CD	2.07	1.16
22:V:531:ILE:HG23	22:V:534:TYR:CZ	1.79	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:516:PRO:HB3	25:1:15:ALA:HB1	1.24	1.16
22:V:321:GLU:CB	23:W:499:ASN:ND2	2.05	1.16
3:C:200:PRO:CB	3:C:217:GLN:OE1	1.94	1.16
17:Q:105:TYR:CG	18:R:234:GLU:HG2	1.79	1.16
17:Q:107:LEU:CA	18:R:218:LYS:HE3	1.76	1.16
26:2:171:VAL:HG22	26:2:213:TRP:HA	1.27	1.16
25:1:28:ALA:HB1	25:1:31:LYS:HD2	1.27	1.16
5:E:27:LEU:H	5:E:64:HIS:CB	1.57	1.15
26:2:160:LEU:HD23	26:2:206:LEU:HD21	1.25	1.15
2:B:873:LEU:CB	2:B:874:PRO:HD3	1.76	1.15
25:1:2:VAL:CG1	26:2:456:LYS:HG2	1.75	1.15
27:3:59:VAL:HG13	27:3:70:LEU:HB2	1.27	1.15
2:B:93:LEU:N	20:T:145:LEU:CD2	2.09	1.15
3:C:200:PRO:CG	3:C:217:GLN:HG3	1.75	1.15
5:E:27:LEU:H	5:E:64:HIS:HB2	1.09	1.15
12:L:25:GLU:HG3	12:L:27:GLU:OE2	1.47	1.15
26:2:28:PRO:N	27:3:25:GLN:HA	0.83	1.15
1:A:731:ASN:OD1	21:U:253:THR:HG22	0.99	1.14
5:E:27:LEU:CG	5:E:64:HIS:HD2	1.38	1.14
1:A:427:ILE:CG1	13:M:38:GLY:O	1.95	1.14
17:Q:113:ARG:CG	18:R:221:ARG:HD2	1.77	1.14
3:C:136:ASP:HB2	3:C:145:GLN:OE1	1.46	1.14
17:Q:23:ARG:HH11	18:R:207:SER:CB	1.61	1.14
26:2:30:VAL:CG1	27:3:25:GLN:O	1.96	1.13
27:3:59:VAL:N	27:3:71:TYR:CE1	2.16	1.13
2:B:497:LYS:N	2:B:498:PRO:HD3	1.47	1.13
22:V:325:ARG:HH22	23:W:499:ASN:CB	1.55	1.13
22:V:516:PRO:CB	25:1:15:ALA:HB1	1.77	1.13
18:R:127:ASN:HD21	18:R:140:LYS:HE2	1.14	1.13
1:A:621:ILE:CA	1:A:623:PRO:HD3	1.79	1.13
2:B:160:TYR:OH	20:T:144:GLN:HG2	1.47	1.13
23:W:250:ASN:CB	23:W:434:HIS:NE2	2.12	1.13
25:1:5:LEU:CD2	26:2:408:LEU:HD13	1.79	1.13
2:B:160:TYR:OH	20:T:144:GLN:CG	1.97	1.13
18:R:129:LYS:O	18:R:140:LYS:HB3	1.43	1.13
2:B:873:LEU:HB2	2:B:874:PRO:HD3	1.22	1.12
18:R:212:VAL:HG23	18:R:213:ASP:H	1.06	1.12
16:P:297:LYS:HB3	16:P:298:PRO:HD3	1.20	1.12
26:2:163:MET:HE2	26:2:206:LEU:HD12	1.30	1.12
5:E:27:LEU:HD12	5:E:64:HIS:CE1	1.84	1.12
1:A:927:GLU:O	1:A:931:ARG:HG3	1.50	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:187:ILE:HG13	18:R:212:VAL:H	1.01	1.12
23:W:59:TYR:CE2	23:W:62:ALA:CB	2.32	1.12
25:1:2:VAL:HG13	26:2:422:LEU:HD11	1.18	1.11
26:2:31:LEU:HD11	27:3:33:THR:HB	1.15	1.11
1:A:926:ASN:CG	1:A:931:ARG:HD2	1.75	1.11
18:R:140:LYS:H	18:R:141:PRO:HD2	1.06	1.11
22:V:611:GLY:HA2	22:V:615:PHE:HD2	0.95	1.11
27:3:57:LEU:O	27:3:71:TYR:HE2	1.29	1.11
3:C:136:ASP:C	3:C:138:ASP:H	1.51	1.11
22:V:516:PRO:HG2	22:V:706:LYS:HZ3	0.96	1.11
12:L:25:GLU:HG3	12:L:27:GLU:CD	1.76	1.11
22:V:531:ILE:HG23	22:V:534:TYR:OH	0.93	1.11
25:1:5:LEU:HD11	26:2:408:LEU:HB3	1.15	1.11
26:2:30:VAL:CG1	27:3:25:GLN:C	2.23	1.11
2:B:239:MET:HE1	2:B:256:ILE:HD13	1.13	1.10
22:V:516:PRO:HA	25:1:15:ALA:O	1.50	1.10
26:2:31:LEU:CD1	27:3:33:THR:CB	2.27	1.10
1:A:425:ASP:HB3	13:M:39:LEU:HD21	1.19	1.10
2:B:133:ILE:HA	2:B:139:GLN:HA	1.25	1.10
27:3:137:LEU:HB3	27:3:180:VAL:HG11	1.34	1.10
23:W:424:ARG:O	23:W:425:THR:HG23	1.52	1.10
24:0:54:ARG:CG	27:3:182:PHE:CE1	2.17	1.10
3:C:154:ARG:CD	10:J:65:LEU:HD12	1.82	1.10
27:3:57:LEU:C	27:3:71:TYR:OH	1.93	1.10
17:Q:107:LEU:HA	18:R:218:LYS:HE3	1.15	1.09
21:U:256:THR:O	21:U:257:GLN:O	1.69	1.09
18:R:195:PRO:CB	18:R:199:LYS:CB	2.29	1.09
23:W:421:PHE:CE1	23:W:431:PRO:CG	2.20	1.09
17:Q:23:ARG:NH1	18:R:207:SER:CB	2.14	1.09
22:V:315:VAL:CG1	23:W:500:ASP:CB	1.94	1.09
25:1:2:VAL:HG11	26:2:456:LYS:CG	1.81	1.09
25:1:9:LEU:HD13	25:1:48:GLU:HA	1.32	1.09
1:A:926:ASN:OD1	1:A:931:ARG:CD	2.01	1.09
18:R:129:LYS:HB3	18:R:140:LYS:HB2	1.26	1.09
22:V:674:THR:HG23	26:2:392:ARG:CZ	1.83	1.09
25:1:5:LEU:HD21	26:2:408:LEU:CD1	1.81	1.09
9:I:99:SER:OG	9:I:105:GLU:CG	2.00	1.09
26:2:30:VAL:H	27:3:25:GLN:CB	1.66	1.09
26:2:42:LEU:HD21	26:2:55:TRP:HB2	1.20	1.08
2:B:160:TYR:CE1	20:T:144:GLN:CD	2.30	1.08
3:C:154:ARG:CD	10:J:65:LEU:CD1	2.31	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:1:18:GLN:HB2	25:1:44:PHE:CE2	1.87	1.08
3:C:200:PRO:CG	3:C:217:GLN:CG	2.30	1.08
12:L:17:TYR:CA	12:L:46:LYS:HA	1.81	1.08
27:3:49:LEU:HB3	27:3:101:TYR:HB3	1.15	1.08
12:L:16:ILE:CD1	12:L:28:ILE:O	2.02	1.08
17:Q:110:MET:SD	18:R:218:LYS:HD2	1.93	1.08
22:V:519:TYR:CE2	25:1:20:LEU:HG	1.87	1.07
26:2:211:GLN:HG3	26:2:257:SER:HB3	1.29	1.07
2:B:876:ASN:O	2:B:879:GLU:CG	2.02	1.07
18:R:212:VAL:HG23	18:R:213:ASP:N	1.59	1.07
25:1:2:VAL:HG11	26:2:456:LYS:HG2	1.09	1.07
16:P:206:GLU:CB	16:P:207:PRO:CD	2.26	1.07
17:Q:187:ILE:HG13	18:R:212:VAL:N	1.54	1.07
18:R:194:ARG:N	18:R:195:PRO:HD3	1.64	1.07
18:R:195:PRO:HG3	18:R:199:LYS:CB	1.82	1.07
22:V:321:GLU:OE2	23:W:500:ASP:HB3	0.91	1.07
2:B:876:ASN:O	2:B:879:GLU:HG3	1.55	1.07
8:H:65:TYR:CE2	8:H:70:LEU:HB3	1.89	1.07
25:1:1:MET:CB	26:2:413:LEU:HB3	1.83	1.07
27:3:33:THR:HG23	27:3:36:LYS:H	1.13	1.07
1:A:425:ASP:CB	13:M:39:LEU:HD21	1.82	1.07
1:A:621:ILE:HG23	1:A:623:PRO:CB	1.84	1.06
1:A:926:ASN:ND2	1:A:931:ARG:HD2	1.67	1.06
3:C:200:PRO:HG2	3:C:217:GLN:CD	1.79	1.06
5:E:62:VAL:HG23	5:E:72:MET:HB3	1.36	1.06
20:T:146:ASP:O	20:T:147:LYS:HG2	1.54	1.06
21:U:252:LYS:HE2	21:U:252:LYS:HA	1.35	1.06
26:2:30:VAL:H	27:3:25:GLN:HB3	0.89	1.06
25:1:5:LEU:HD12	26:2:409:TYR:O	1.55	1.06
26:2:30:VAL:N	27:3:25:GLN:HB3	1.71	1.06
26:2:117:ASN:CG	27:3:108:ASN:CB	2.20	1.06
26:2:159:VAL:HG13	26:2:161:HIS:H	1.16	1.06
27:3:59:VAL:HB	27:3:71:TYR:CE1	1.88	1.06
1:A:932:ARG:HB3	1:A:939:VAL:HG11	1.10	1.06
18:R:140:LYS:H	18:R:141:PRO:CD	1.68	1.06
1:A:622:SER:N	1:A:623:PRO:HD3	1.59	1.05
18:R:129:LYS:CB	18:R:140:LYS:HB2	1.85	1.05
22:V:516:PRO:HG2	22:V:706:LYS:NZ	1.70	1.05
24:0:97:ASP:O	27:3:208:ASP:CB	2.02	1.05
26:2:192:GLU:HG3	26:2:193:PRO:HD2	1.33	1.05
2:B:79:GLU:O	2:B:80:GLU:HG2	1.52	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:110:MET:HG3	18:R:218:LYS:HB2	1.15	1.05
12:L:15:MET:O	12:L:16:ILE:CD1	2.05	1.05
23:W:421:PHE:HD1	23:W:431:PRO:CG	1.38	1.05
17:Q:187:ILE:CG2	18:R:212:VAL:N	2.18	1.05
25:1:34:ILE:HG12	25:1:50:VAL:HG11	1.39	1.05
26:2:31:LEU:HD11	27:3:33:THR:HG22	1.37	1.05
3:C:6:GLN:O	11:K:104:ARG:NH1	1.90	1.04
25:1:4:VAL:HG12	26:2:411:GLN:O	1.56	1.04
20:T:177:ARG:HG2	20:T:208:GLN:OE1	1.48	1.04
23:W:70:LEU:HD21	23:W:72:TYR:CE1	1.92	1.04
26:2:28:PRO:CA	27:3:25:GLN:C	2.30	1.04
17:Q:25:PHE:HD2	18:R:215:GLU:CD	1.61	1.04
2:B:880:LEU:O	2:B:881:GLU:CB	2.03	1.04
22:V:426:VAL:O	22:V:427:MET:O	1.76	1.04
26:2:234:LEU:HD21	26:2:237:LEU:HD12	1.36	1.04
12:L:17:TYR:HA	12:L:46:LYS:HA	1.08	1.04
17:Q:102:VAL:HB	17:Q:105:TYR:HB3	1.09	1.04
26:2:30:VAL:HG12	27:3:25:GLN:CA	1.86	1.04
1:A:1309:MET:SD	21:U:252:LYS:CD	2.46	1.03
13:M:43:ASP:O	13:M:44:ARG:C	1.96	1.03
22:V:516:PRO:CG	22:V:706:LYS:NZ	2.20	1.03
1:A:330:GLN:HB3	13:M:107:MET:SD	1.98	1.03
18:R:224:THR:HG21	18:R:230:GLU:HB2	1.40	1.03
3:C:5:ASN:C	3:C:7:PRO:HD3	1.81	1.03
9:I:105:GLU:C	9:I:107:ALA:H	1.65	1.03
17:Q:113:ARG:CB	18:R:221:ARG:HD2	1.89	1.03
24:0:54:ARG:NE	27:3:182:PHE:CE1	2.26	1.03
1:A:932:ARG:CB	1:A:939:VAL:HG11	1.88	1.03
13:M:178:LYS:O	20:T:154:LYS:HB3	0.85	1.03
16:P:297:LYS:CB	16:P:298:PRO:CD	2.37	1.03
22:V:516:PRO:CB	25:1:15:ALA:CB	2.34	1.03
26:2:81:LYS:HE3	26:2:93:LEU:HD21	1.40	1.03
2:B:239:MET:SD	2:B:256:ILE:CG2	2.46	1.02
17:Q:110:MET:CE	18:R:213:ASP:CB	2.13	1.02
20:T:177:ARG:CD	20:T:208:GLN:OE1	2.06	1.02
23:W:72:TYR:CD2	23:W:232:VAL:CG1	2.41	1.02
27:3:57:LEU:O	27:3:71:TYR:CE2	2.11	1.02
1:A:266:MET:O	1:A:267:GLN:CB	2.03	1.02
17:Q:113:ARG:HB2	18:R:221:ARG:NE	1.72	1.02
2:B:499:ARG:O	2:B:500:GLN:O	1.75	1.02
16:P:206:GLU:HB3	16:P:207:PRO:HD2	1.42	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:113:ARG:HD2	18:R:221:ARG:HD2	1.04	1.02
22:V:366:ASN:HD21	22:V:613:THR:HG22	1.19	1.02
24:0:54:ARG:HB2	27:3:209:ILE:HG23	1.36	1.02
24:0:77:LYS:O	24:0:79:ASN:N	1.93	1.02
17:Q:113:ARG:CB	18:R:221:ARG:CD	2.36	1.01
23:W:59:TYR:CE2	23:W:62:ALA:HB3	1.94	1.01
23:W:209:TYR:HH	23:W:233:PHE:HA	1.11	1.01
23:W:70:LEU:CD2	23:W:72:TYR:HE1	1.73	1.01
16:P:297:LYS:HB3	16:P:298:PRO:CD	1.90	1.01
17:Q:113:ARG:HB2	18:R:221:ARG:HD2	1.40	1.01
20:T:145:LEU:CD1	20:T:148:VAL:HG22	1.89	1.01
22:V:523:VAL:HG11	25:1:20:LEU:HD21	1.01	1.01
1:A:621:ILE:HG22	1:A:623:PRO:HG3	1.07	1.01
21:U:232:GLU:O	21:U:233:LEU:HB2	1.58	1.01
27:3:59:VAL:CB	27:3:71:TYR:CE1	2.44	1.01
24:0:54:ARG:CD	27:3:182:PHE:HE1	1.72	1.00
17:Q:110:MET:CB	18:R:218:LYS:CD	2.38	1.00
17:Q:187:ILE:HG23	18:R:212:VAL:C	1.86	1.00
18:R:224:THR:CG2	18:R:230:GLU:HB2	1.91	1.00
18:R:225:VAL:CG1	18:R:226:ASP:OD1	2.07	1.00
27:3:196:LEU:HD21	27:3:223:LEU:HD23	1.42	1.00
16:P:161:ILE:HG21	16:P:263:ASP:O	1.62	1.00
23:W:209:TYR:OH	23:W:233:PHE:CA	2.09	1.00
26:2:199:ALA:HB3	26:2:202:GLN:HE22	1.22	1.00
3:C:154:ARG:HD2	10:J:65:LEU:CD1	1.91	1.00
5:E:27:LEU:HG	5:E:64:HIS:CD2	1.96	1.00
8:H:74:GLU:C	8:H:76:ASN:H	1.70	1.00
18:R:162:GLY:C	18:R:164:GLY:H	1.66	1.00
21:U:175:ALA:HB1	21:U:222:ARG:NH2	1.76	1.00
1:A:266:MET:O	1:A:267:GLN:HB2	1.19	0.99
1:A:1309:MET:SD	21:U:252:LYS:HD3	2.00	0.99
17:Q:102:VAL:O	17:Q:104:LYS:N	1.95	0.99
22:V:516:PRO:CG	25:1:15:ALA:HB1	1.89	0.99
1:A:927:GLU:O	1:A:931:ARG:CG	2.10	0.99
3:C:200:PRO:HG2	3:C:217:GLN:HG3	1.02	0.99
2:B:92:TYR:HB3	20:T:145:LEU:HB3	1.44	0.99
17:Q:110:MET:HE1	18:R:213:ASP:HA	1.44	0.99
17:Q:187:ILE:CG1	18:R:212:VAL:H	1.71	0.99
2:B:239:MET:CE	2:B:256:ILE:HD13	1.92	0.99
9:I:86:CYS:O	9:I:88:LYS:N	1.95	0.99
12:L:17:TYR:HA	12:L:46:LYS:CA	1.93	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:160:TYR:CE1	20:T:144:GLN:HG2	1.96	0.99
1:A:1310:HIS:N	21:U:252:LYS:HD2	1.78	0.99
27:3:58:ALA:CA	27:3:71:TYR:CZ	2.45	0.99
5:E:27:LEU:HD12	5:E:64:HIS:HE2	1.28	0.98
16:P:289:PRO:HB3	29:Y:84:DG:H5'	1.44	0.98
23:W:293:ARG:O	23:W:421:PHE:HZ	1.46	0.98
16:P:307:SER:OG	29:Y:83:DA:OP1	1.80	0.98
16:P:206:GLU:HB3	16:P:207:PRO:HD3	1.01	0.98
17:Q:110:MET:CB	18:R:218:LYS:CB	2.35	0.98
26:2:118:LEU:CD2	27:3:39:ASP:O	2.12	0.98
27:3:173:GLN:HA	27:3:176:ASN:HD21	1.28	0.98
22:V:325:ARG:HH21	23:W:499:ASN:HB3	1.20	0.97
1:A:1310:HIS:H	21:U:252:LYS:CD	1.76	0.97
1:A:1310:HIS:H	21:U:252:LYS:HD2	1.23	0.97
9:I:99:SER:CB	9:I:105:GLU:HG3	1.94	0.97
22:V:515:SER:HB3	22:V:539:ASN:HD21	1.25	0.97
23:W:584:TYR:CD1	23:W:594:ALA:HB2	1.99	0.97
27:3:148:ASN:HB2	27:3:157:MET:HE2	1.42	0.97
3:C:217:GLN:O	3:C:218:ALA:CB	2.12	0.97
18:R:140:LYS:N	18:R:141:PRO:HD2	1.78	0.97
26:2:118:LEU:HD11	27:3:43:VAL:CG2	1.94	0.97
9:I:64:GLU:OE1	9:I:103:ARG:NH2	1.97	0.97
18:R:195:PRO:HG3	18:R:199:LYS:HB2	1.36	0.97
25:1:1:MET:HE1	26:2:440:LEU:HD13	1.41	0.97
27:3:165:LYS:HD2	27:3:195:VAL:HG22	1.44	0.97
13:M:178:LYS:C	20:T:154:LYS:CB	2.37	0.97
17:Q:25:PHE:CE2	18:R:215:GLU:HG3	2.00	0.97
22:V:523:VAL:CG1	25:1:20:LEU:CD2	2.43	0.97
22:V:315:VAL:HG11	23:W:500:ASP:HB2	1.42	0.97
25:1:1:MET:HB3	26:2:413:LEU:CG	1.94	0.97
3:C:6:GLN:CG	3:C:25:ASN:ND2	2.28	0.97
26:2:176:ALA:HB1	26:2:178:LEU:HD13	1.47	0.96
2:B:499:ARG:HB3	2:B:499:ARG:NH1	1.79	0.96
17:Q:187:ILE:HG23	18:R:212:VAL:HA	1.44	0.96
22:V:523:VAL:CG1	25:1:20:LEU:HD21	1.94	0.96
27:3:59:VAL:CB	27:3:71:TYR:CD1	2.48	0.96
8:H:100:GLU:HB2	8:H:113:SER:HB2	1.48	0.96
26:2:196:ILE:HD11	26:2:210:ALA:HB2	1.45	0.96
23:W:59:TYR:CE1	23:W:62:ALA:HB1	2.01	0.96
2:B:497:LYS:H	2:B:498:PRO:HD3	1.03	0.96
17:Q:107:LEU:HA	18:R:218:LYS:CE	1.96	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1112:VAL:O	21:U:252:LYS:HB3	1.66	0.96
3:C:212:ASP:O	3:C:213:GLU:C	2.07	0.96
2:B:78:VAL:O	2:B:79:GLU:HB2	1.64	0.95
26:2:30:VAL:HG12	27:3:25:GLN:CB	1.94	0.95
27:3:133:LEU:HD23	27:3:177:PHE:CD1	2.01	0.95
1:A:621:ILE:HD12	1:A:623:PRO:HB3	1.47	0.95
26:2:100:LEU:HD11	26:2:119:ARG:HG3	1.46	0.95
2:B:75:SER:OG	2:B:78:VAL:HG22	1.67	0.95
1:A:425:ASP:HB3	13:M:39:LEU:CD2	1.94	0.95
13:M:178:LYS:C	20:T:154:LYS:HB3	1.89	0.95
22:V:531:ILE:HA	22:V:534:TYR:CD2	2.02	0.95
17:Q:32:LEU:HD11	18:R:203:PHE:CD2	2.00	0.95
17:Q:110:MET:CB	18:R:218:LYS:HD2	1.94	0.95
17:Q:110:MET:CB	18:R:218:LYS:HB2	1.93	0.95
17:Q:187:ILE:CG2	18:R:212:VAL:CA	2.45	0.95
25:1:2:VAL:CG1	26:2:422:LEU:HD11	1.96	0.95
26:2:35:TYR:CE1	26:2:62:LEU:HG	2.02	0.95
26:2:211:GLN:HA	26:2:261:PHE:CZ	2.02	0.95
12:L:15:MET:O	12:L:16:ILE:CG1	2.15	0.95
2:B:92:TYR:CB	20:T:145:LEU:HD22	1.97	0.95
1:A:1314:THR:OG1	1:A:1332:GLN:NE2	2.00	0.95
9:I:105:GLU:C	9:I:107:ALA:N	2.14	0.95
23:W:72:TYR:CE2	23:W:232:VAL:CG1	2.50	0.95
18:R:212:VAL:CG2	18:R:213:ASP:N	2.15	0.95
2:B:880:LEU:O	2:B:881:GLU:HB2	1.14	0.94
26:2:30:VAL:HB	27:3:25:GLN:HB2	1.48	0.94
22:V:321:GLU:CA	23:W:499:ASN:HD21	1.78	0.94
22:V:515:SER:CB	22:V:539:ASN:HD21	1.80	0.94
1:A:932:ARG:HB3	1:A:939:VAL:CG1	1.96	0.94
12:L:15:MET:O	12:L:16:ILE:HG12	1.67	0.94
20:T:177:ARG:HD3	20:T:208:GLN:OE1	1.66	0.94
18:R:140:LYS:NZ	20:T:238:GLU:OE2	2.00	0.94
26:2:31:LEU:CD2	27:3:33:THR:N	2.29	0.94
1:A:612:ASP:HB3	1:A:617:PRO:HD3	1.46	0.94
1:A:1309:MET:SD	21:U:252:LYS:HD2	2.08	0.94
8:H:64:LEU:H	8:H:70:LEU:HD21	1.30	0.94
17:Q:110:MET:HE3	18:R:213:ASP:HB3	1.48	0.94
25:1:1:MET:HB3	26:2:413:LEU:HB3	1.50	0.94
1:A:621:ILE:HG23	1:A:623:PRO:HG3	0.95	0.94
18:R:195:PRO:HB3	18:R:199:LYS:HB2	1.49	0.93
18:R:202:PHE:O	18:R:203:PHE:CG	2.21	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:15:MET:O	12:L:16:ILE:HD13	1.68	0.93
2:B:712:PRO:HB3	2:B:999:ALA:HB1	1.51	0.93
26:2:118:LEU:HD23	27:3:42:MET:HB2	1.50	0.93
27:3:190:LEU:HA	27:3:210:THR:HG22	1.50	0.93
18:R:129:LYS:C	18:R:140:LYS:HB3	1.92	0.93
23:W:696:TRP:CD1	23:W:697:ILE:HG12	2.03	0.93
26:2:117:ASN:N	27:3:104:LEU:HD21	1.83	0.93
23:W:421:PHE:HE1	23:W:431:PRO:HG2	1.25	0.93
22:V:392:PHE:O	22:V:418:LYS:HD2	1.69	0.93
25:1:18:GLN:HB2	25:1:44:PHE:HE2	1.28	0.93
3:C:154:ARG:HD3	10:J:65:LEU:CD1	1.98	0.93
25:1:8:VAL:HG11	25:1:45:VAL:CG1	1.99	0.93
25:1:9:LEU:HD22	25:1:51:ASN:HD22	1.33	0.93
22:V:631:GLY:O	22:V:632:SER:CB	2.14	0.93
25:1:13:ASP:OD2	25:1:17:LYS:HB3	1.69	0.93
26:2:159:VAL:HG22	26:2:160:LEU:HD12	1.51	0.93
27:3:187:GLN:HG3	27:3:189:ILE:HG12	1.51	0.93
12:L:16:ILE:HG13	12:L:28:ILE:H	1.32	0.92
17:Q:102:VAL:CB	17:Q:105:TYR:HB3	1.98	0.92
27:3:165:LYS:HE3	27:3:200:SER:CB	2.00	0.92
2:B:160:TYR:CE1	20:T:144:GLN:CG	2.52	0.92
18:R:195:PRO:HG2	18:R:199:LYS:HB2	1.52	0.92
1:A:625:ASP:O	1:A:638:GLY:HA2	1.68	0.92
23:W:59:TYR:CE1	23:W:62:ALA:CB	2.52	0.92
26:2:28:PRO:HA	27:3:25:GLN:C	1.92	0.92
22:V:366:ASN:HD21	22:V:613:THR:HG23	1.33	0.92
24:0:54:ARG:HG3	27:3:182:PHE:CZ	2.05	0.92
17:Q:110:MET:CG	18:R:218:LYS:CB	2.47	0.92
18:R:155:LEU:CG	18:R:204:ASN:HD21	1.55	0.92
24:0:97:ASP:OD1	27:3:208:ASP:OD1	1.87	0.92
3:C:136:ASP:C	3:C:138:ASP:N	2.23	0.92
23:W:432:ILE:HG12	23:W:434:HIS:CE1	2.04	0.92
20:T:154:LYS:HD2	20:T:154:LYS:H	1.33	0.92
23:W:72:TYR:CD2	23:W:232:VAL:HG13	2.05	0.92
1:A:1308:TYR:HB3	1:A:1336:LEU:HD13	1.52	0.92
2:B:93:LEU:H	20:T:145:LEU:HD23	1.24	0.92
26:2:177:GLN:HA	26:2:220:LEU:CD2	1.99	0.92
1:A:551:ARG:HH22	8:H:121:LEU:HA	1.34	0.91
17:Q:112:ARG:HB3	18:R:221:ARG:HH22	1.33	0.91
26:2:81:LYS:CE	26:2:93:LEU:HD21	2.00	0.91
26:2:118:LEU:HD22	27:3:39:ASP:CG	1.93	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:160:TYR:CZ	20:T:144:GLN:CG	2.51	0.91
2:B:881:GLU:C	2:B:883:THR:N	2.15	0.91
13:M:179:GLU:HA	20:T:154:LYS:HG2	0.92	0.91
16:P:206:GLU:CB	16:P:207:PRO:HD3	1.96	0.91
27:3:165:LYS:HG3	27:3:203:LEU:HD12	1.52	0.91
12:L:25:GLU:HB2	12:L:27:GLU:HG3	1.50	0.91
17:Q:25:PHE:CD2	18:R:215:GLU:CG	2.53	0.91
12:L:16:ILE:CG1	12:L:28:ILE:N	2.30	0.91
27:3:133:LEU:HD13	27:3:133:LEU:H	1.33	0.91
27:3:137:LEU:CB	27:3:180:VAL:HG11	2.01	0.91
27:3:11:LEU:HD22	27:3:160:ARG:HG2	1.51	0.91
27:3:59:VAL:HB	27:3:71:TYR:HE1	1.24	0.91
16:P:297:LYS:CB	16:P:298:PRO:HD3	1.98	0.91
25:1:1:MET:O	26:2:413:LEU:CG	2.19	0.91
25:1:1:MET:HB3	26:2:413:LEU:CB	2.01	0.91
17:Q:110:MET:HB2	18:R:218:LYS:CD	2.00	0.91
1:A:926:ASN:CG	1:A:931:ARG:CD	2.41	0.90
25:1:2:VAL:HG13	26:2:422:LEU:CD1	2.01	0.90
17:Q:23:ARG:HH11	18:R:207:SER:HB3	0.75	0.90
1:A:1287:CYS:HA	2:B:250:SER:HB2	1.52	0.90
1:A:1308:TYR:O	1:A:1336:LEU:HD22	1.70	0.90
17:Q:107:LEU:N	18:R:218:LYS:HE3	1.87	0.90
1:A:426:ARG:HB3	13:M:40:VAL:CG2	2.01	0.90
1:A:1310:HIS:H	21:U:252:LYS:CE	1.83	0.90
23:W:430:ASN:HB3	23:W:431:PRO:HD2	1.54	0.90
26:2:28:PRO:N	27:3:25:GLN:C	2.28	0.90
22:V:531:ILE:HA	22:V:534:TYR:HE2	1.09	0.90
9:I:102:ALA:C	9:I:104:ALA:H	1.69	0.90
27:3:22:TRP:O	27:3:25:GLN:HG2	1.71	0.90
2:B:93:LEU:CA	20:T:145:LEU:HD23	2.01	0.90
2:B:133:ILE:O	2:B:134:LYS:HG2	1.70	0.90
13:M:10:LEU:O	13:M:12:ARG:N	2.05	0.90
1:A:1310:HIS:CA	21:U:252:LYS:HE3	2.01	0.90
18:R:155:LEU:HG	18:R:204:ASN:HD21	1.12	0.90
23:W:432:ILE:HG12	23:W:434:HIS:HE1	1.37	0.89
8:H:65:TYR:CE2	8:H:70:LEU:CB	2.55	0.89
17:Q:113:ARG:NE	18:R:217:GLN:O	2.06	0.89
5:E:6:GLU:OE2	5:E:54:ARG:NH2	2.05	0.89
14:N:343:HIS:HB3	14:N:350:LYS:HB2	1.51	0.89
17:Q:187:ILE:CG2	18:R:212:VAL:O	2.20	0.89
1:A:621:ILE:HG22	1:A:623:PRO:CG	1.82	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:2:81:LYS:HD2	26:2:89:LEU:HD21	1.52	0.89
3:C:45:ILE:HG12	3:C:79:VAL:HB	1.55	0.89
3:C:200:PRO:CG	3:C:217:GLN:OE1	2.20	0.89
23:W:70:LEU:HD21	23:W:72:TYR:HE1	1.30	0.89
26:2:218:GLN:HB3	26:2:264:HIS:HD2	1.38	0.89
2:B:92:TYR:HB3	20:T:145:LEU:HD22	1.54	0.89
17:Q:25:PHE:CD2	18:R:215:GLU:HG3	2.07	0.89
17:Q:113:ARG:HB2	18:R:221:ARG:CZ	1.74	0.89
25:1:4:VAL:HG11	26:2:412:PHE:HD2	1.36	0.89
1:A:551:ARG:HD3	1:A:637:MET:HE1	1.55	0.89
20:T:231:ASN:HB2	29:Y:68:DC:H5''	1.53	0.89
26:2:117:ASN:CB	27:3:42:MET:CE	2.51	0.89
27:3:71:TYR:CD2	27:3:72:PRO:HD2	2.08	0.89
27:3:59:VAL:CG1	27:3:70:LEU:HB2	2.03	0.89
1:A:1310:HIS:CB	21:U:252:LYS:CE	2.39	0.88
22:V:516:PRO:CD	22:V:706:LYS:HZ3	1.86	0.88
26:2:30:VAL:CB	27:3:25:GLN:HB2	2.01	0.88
13:M:11:PRO:O	13:M:12:ARG:HB3	1.71	0.88
16:P:166:GLN:HG3	29:Y:81:DA:H5''	1.55	0.88
17:Q:110:MET:HB3	18:R:218:LYS:HD2	1.55	0.88
27:3:58:ALA:C	27:3:71:TYR:CZ	2.51	0.88
22:V:315:VAL:HG13	23:W:500:ASP:CA	2.03	0.88
23:W:250:ASN:HB2	23:W:434:HIS:CE1	2.08	0.88
27:3:177:PHE:CD2	27:3:181:ILE:HD11	2.08	0.88
3:C:154:ARG:HD2	10:J:65:LEU:HD12	1.52	0.88
9:I:99:SER:HB3	9:I:105:GLU:HG3	1.55	0.88
1:A:551:ARG:CD	1:A:625:ASP:OD1	2.22	0.88
2:B:876:ASN:O	2:B:879:GLU:HG2	1.74	0.88
20:T:145:LEU:O	20:T:147:LYS:N	2.07	0.88
22:V:393:THR:HA	22:V:418:LYS:CE	2.03	0.88
25:1:47:ALA:CB	25:1:50:VAL:HB	2.03	0.88
27:3:165:LYS:HE3	27:3:200:SER:HB2	1.56	0.88
12:L:17:TYR:O	12:L:18:ILE:HB	1.70	0.88
26:2:160:LEU:CB	26:2:206:LEU:HD11	2.04	0.88
18:R:129:LYS:O	18:R:140:LYS:CB	2.22	0.88
2:B:873:LEU:HB2	2:B:874:PRO:CD	2.03	0.88
17:Q:23:ARG:NH2	18:R:206:LYS:HB3	1.89	0.88
22:V:611:GLY:CA	22:V:615:PHE:HD2	1.83	0.88
27:3:177:PHE:CE2	27:3:181:ILE:HD11	2.08	0.88
2:B:490:GLY:O	2:B:491:ARG:C	2.14	0.88
8:H:110:THR:O	8:H:111:ARG:HB2	1.71	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:15:MET:C	12:L:16:ILE:HG12	1.98	0.88
26:2:160:LEU:CD2	26:2:206:LEU:HD21	2.04	0.88
26:2:224:GLN:HB2	26:2:268:PHE:CZ	2.09	0.88
21:U:175:ALA:HB1	21:U:222:ARG:HH21	1.35	0.88
22:V:516:PRO:HA	25:1:15:ALA:C	1.98	0.88
25:1:8:VAL:HG11	25:1:45:VAL:HG13	1.55	0.88
26:2:243:SER:CB	26:2:258:LEU:HD22	2.04	0.88
23:W:696:TRP:CD1	23:W:697:ILE:CG1	2.57	0.87
26:2:218:GLN:HB3	26:2:264:HIS:CD2	2.09	0.87
17:Q:106:LYS:HG2	18:R:218:LYS:HE2	1.54	0.87
26:2:118:LEU:HD11	27:3:43:VAL:HG22	1.56	0.87
23:W:37:HIS:CE1	23:W:454:VAL:HG13	2.09	0.87
26:2:28:PRO:CD	27:3:25:GLN:HA	2.03	0.87
26:2:163:MET:SD	26:2:196:ILE:HG21	2.14	0.87
26:2:177:GLN:HA	26:2:220:LEU:HD21	1.56	0.87
27:3:59:VAL:HG12	27:3:71:TYR:CG	2.08	0.87
27:3:178:MET:HE2	27:3:202:LEU:HD12	1.57	0.87
1:A:614:ASP:O	1:A:616:GLY:N	2.06	0.87
21:U:134:PRO:O	21:U:145:ARG:NH1	2.07	0.87
17:Q:102:VAL:HB	17:Q:105:TYR:CB	2.03	0.87
17:Q:113:ARG:CD	18:R:221:ARG:HD3	2.03	0.87
26:2:160:LEU:CA	26:2:206:LEU:HD11	2.04	0.87
27:3:64:ILE:HG13	27:3:123:ASP:HB3	1.57	0.87
26:2:160:LEU:HB3	26:2:206:LEU:HD11	1.52	0.87
26:2:211:GLN:HG3	26:2:257:SER:CB	2.05	0.87
1:A:624:GLY:HA3	8:H:122:LEU:HD11	1.55	0.87
2:B:881:GLU:O	2:B:883:THR:N	2.07	0.87
12:L:16:ILE:CD1	12:L:28:ILE:C	2.48	0.87
22:V:413:LEU:HD12	28:X:56:DA:H5'	1.56	0.87
23:W:584:TYR:CE2	23:W:614:TYR:HB2	2.10	0.87
27:3:58:ALA:HA	27:3:71:TYR:CE2	2.09	0.87
3:C:217:GLN:O	3:C:218:ALA:HB3	1.72	0.87
26:2:48:LEU:HB3	26:2:49:PRO:HD3	1.57	0.87
20:T:146:ASP:O	20:T:147:LYS:CG	2.23	0.87
27:3:69:PHE:CZ	27:3:139:LYS:HB3	2.10	0.86
23:W:59:TYR:CG	23:W:62:ALA:HB2	2.10	0.86
1:A:625:ASP:HA	1:A:637:MET:HE3	1.57	0.86
2:B:499:ARG:O	2:B:500:GLN:C	2.16	0.86
25:1:28:ALA:CB	25:1:31:LYS:HD2	2.04	0.86
26:2:221:GLN:HG2	26:2:268:PHE:CZ	2.11	0.86
3:C:6:GLN:HG3	3:C:25:ASN:ND2	1.88	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:27:LEU:N	5:E:64:HIS:HB2	1.89	0.86
23:W:293:ARG:O	23:W:421:PHE:CZ	2.28	0.86
27:3:178:MET:HE2	27:3:202:LEU:CD1	2.05	0.86
26:2:117:ASN:OD1	27:3:108:ASN:CG	2.18	0.86
26:2:167:PRO:O	26:2:171:VAL:HG23	1.76	0.86
17:Q:113:ARG:HD2	18:R:221:ARG:HG3	1.55	0.86
26:2:159:VAL:HG22	26:2:160:LEU:H	1.41	0.86
27:3:70:LEU:HD13	27:3:115:ILE:HD11	1.55	0.86
18:R:162:GLY:O	18:R:164:GLY:N	2.08	0.86
20:T:177:ARG:CG	20:T:208:GLN:CD	2.34	0.86
22:V:516:PRO:CD	25:1:15:ALA:HB3	2.06	0.86
26:2:138:PRO:HG3	26:2:189:GLU:HG3	1.57	0.86
27:3:14:VAL:HG21	27:3:163:VAL:HG22	1.57	0.86
1:A:426:ARG:O	13:M:39:LEU:HA	1.74	0.85
25:1:2:VAL:CG1	26:2:422:LEU:CD1	2.54	0.85
26:2:29:GLY:N	27:3:25:GLN:OE1	2.09	0.85
26:2:45:PHE:HB2	26:2:51:LEU:HD13	1.56	0.85
26:2:81:LYS:CD	26:2:89:LEU:HD21	2.06	0.85
27:3:184:ALA:HA	27:3:187:GLN:HG2	1.58	0.85
27:3:124:ILE:HD13	27:3:125:LYS:N	1.91	0.85
2:B:92:TYR:C	20:T:145:LEU:CD2	2.49	0.85
27:3:190:LEU:HA	27:3:210:THR:CG2	2.05	0.85
14:N:327:GLU:HB2	16:P:188:ARG:HH12	1.40	0.85
26:2:171:VAL:HG22	26:2:213:TRP:CA	2.06	0.85
2:B:92:TYR:HB3	20:T:145:LEU:CB	2.06	0.85
27:3:100:LYS:HB3	27:3:103:LEU:HD13	1.58	0.85
9:I:102:ALA:C	9:I:104:ALA:N	2.31	0.85
18:R:224:THR:HG21	18:R:230:GLU:CB	2.05	0.85
19:S:102:VAL:HB	19:S:108:ARG:HB3	1.59	0.85
23:W:70:LEU:CD2	23:W:72:TYR:CE1	2.55	0.85
23:W:696:TRP:NE1	23:W:697:ILE:HG12	1.91	0.85
17:Q:187:ILE:C	18:R:212:VAL:HA	2.01	0.85
22:V:315:VAL:HG12	23:W:500:ASP:HB2	1.54	0.85
22:V:531:ILE:HG23	22:V:534:TYR:HH	1.37	0.85
2:B:646:ARG:HD3	2:B:651:TYR:H	1.40	0.85
3:C:200:PRO:HG3	3:C:217:GLN:HB3	1.58	0.85
5:E:62:VAL:CG2	5:E:72:MET:HB3	2.07	0.85
23:W:59:TYR:CD2	23:W:62:ALA:HB2	2.12	0.85
26:2:78:GLU:O	26:2:81:LYS:HG2	1.77	0.85
26:2:117:ASN:OD1	27:3:108:ASN:CB	2.23	0.85
21:U:252:LYS:CE	21:U:252:LYS:HA	2.01	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:631:GLY:O	22:V:632:SER:HB2	1.76	0.84
2:B:133:ILE:HA	2:B:139:GLN:CA	2.08	0.84
26:2:30:VAL:CG1	27:3:25:GLN:HB2	2.07	0.84
17:Q:191:LEU:HD21	18:R:212:VAL:HG11	1.59	0.84
26:2:118:LEU:HD12	26:2:119:ARG:N	1.92	0.84
2:B:133:ILE:O	2:B:134:LYS:CG	2.25	0.84
3:C:136:ASP:CB	3:C:145:GLN:OE1	2.26	0.84
26:2:118:LEU:CD2	27:3:39:ASP:HA	2.08	0.84
26:2:118:LEU:CD2	27:3:42:MET:HB2	2.06	0.84
27:3:160:ARG:HB3	27:3:190:LEU:HD21	1.57	0.84
5:E:65:ASN:C	5:E:67:ASP:N	2.30	0.84
1:A:731:ASN:ND2	21:U:253:THR:HG22	1.92	0.84
3:C:154:ARG:CD	10:J:65:LEU:HD13	2.05	0.84
27:3:216:LYS:H	27:3:216:LYS:HD2	1.43	0.84
1:A:643:LYS:NZ	21:U:301:CYS:O	2.11	0.84
22:V:674:THR:CG2	26:2:392:ARG:CZ	2.55	0.84
1:A:426:ARG:HB3	13:M:40:VAL:HG22	1.59	0.84
2:B:718:GLN:HG2	2:B:720:PRO:HD2	1.57	0.84
22:V:523:VAL:HG11	25:1:20:LEU:HD23	1.60	0.83
27:3:49:LEU:CB	27:3:101:TYR:HB3	2.05	0.83
22:V:674:THR:CG2	26:2:392:ARG:NH2	2.39	0.83
26:2:176:ALA:CB	26:2:178:LEU:HD13	2.07	0.83
10:J:63:ALA:HB3	10:J:64:PRO:HD3	1.59	0.83
2:B:24:GLU:OE1	2:B:762:ARG:NH1	2.11	0.83
17:Q:187:ILE:CG2	18:R:212:VAL:C	2.52	0.83
26:2:31:LEU:CD1	27:3:33:THR:HG22	1.96	0.83
26:2:86:SER:HB3	26:2:140:LYS:HE2	1.60	0.83
26:2:229:ASP:O	26:2:233:ILE:HG12	1.78	0.83
3:C:49:TRP:HB3	3:C:164:TYR:HB2	1.59	0.83
17:Q:110:MET:SD	18:R:218:LYS:CD	2.66	0.83
18:R:212:VAL:HG22	18:R:213:ASP:H	1.38	0.83
22:V:516:PRO:CA	25:1:15:ALA:O	2.27	0.83
26:2:81:LYS:CD	26:2:93:LEU:HD21	2.07	0.83
27:3:196:LEU:HD21	27:3:223:LEU:CD2	2.09	0.83
20:T:228:ILE:HA	28:X:30:DG:H5"	1.59	0.83
25:1:9:LEU:CD1	25:1:48:GLU:HA	2.09	0.83
12:L:19:CYS:HB3	12:L:22:CYS:SG	2.19	0.83
25:1:52:VAL:CG2	25:1:53:LEU:HD12	2.09	0.83
26:2:160:LEU:O	26:2:164:VAL:HG23	1.79	0.83
26:2:259:LEU:HD12	26:2:260:ASN:N	1.94	0.83
27:3:57:LEU:HD23	27:3:58:ALA:N	1.91	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:105:GLU:O	9:I:106:ASP:C	2.19	0.82
26:2:221:GLN:NE2	26:2:230:LEU:HB2	1.93	0.82
17:Q:105:TYR:CD1	18:R:234:GLU:HG3	2.14	0.82
26:2:37:HIS:HB3	26:2:38:PRO:HD3	1.61	0.82
5:E:147:GLU:HB3	5:E:194:ILE:HB	1.62	0.82
25:1:47:ALA:HB2	25:1:50:VAL:HB	1.61	0.82
23:W:293:ARG:HG2	23:W:421:PHE:CE1	2.14	0.82
26:2:174:ASP:O	26:2:220:LEU:HD23	1.79	0.82
12:L:16:ILE:HG13	12:L:27:GLU:C	2.03	0.82
22:V:316:LEU:HB2	22:V:321:GLU:HG3	1.59	0.82
22:V:415:HIS:CD2	22:V:416:THR:HG23	2.15	0.82
26:2:159:VAL:HG22	26:2:160:LEU:CD1	2.08	0.82
27:3:12:VAL:HG21	27:3:161:ILE:HG12	1.61	0.82
27:3:58:ALA:C	27:3:71:TYR:CE1	2.58	0.82
1:A:731:ASN:OD1	21:U:253:THR:HG21	1.80	0.82
26:2:160:LEU:HD23	26:2:206:LEU:CD2	2.07	0.82
5:E:15:LYS:NZ	5:E:35:GLN:OE1	2.12	0.82
22:V:366:ASN:ND2	22:V:613:THR:HG22	1.84	0.82
23:W:52:LEU:HD23	23:W:72:TYR:OH	1.80	0.82
26:2:57:MET:HA	26:2:60:LEU:CD1	2.09	0.82
25:1:9:LEU:HB2	25:1:51:ASN:HD21	1.43	0.82
27:3:49:LEU:HB3	27:3:101:TYR:CB	2.05	0.82
27:3:59:VAL:HG11	27:3:71:TYR:HD1	1.39	0.82
22:V:516:PRO:HG3	25:1:15:ALA:HB2	1.53	0.82
1:A:549:THR:O	1:A:589:LYS:NZ	2.13	0.82
1:A:1274:GLU:O	1:A:1276:VAL:HG23	1.80	0.82
2:B:133:ILE:CA	2:B:139:GLN:HA	2.05	0.82
5:E:21:CYS:SG	5:E:62:VAL:HG11	2.19	0.82
16:P:297:LYS:HA	16:P:297:LYS:CE	2.08	0.82
17:Q:110:MET:HB2	18:R:218:LYS:HG3	0.82	0.82
18:R:155:LEU:CD2	18:R:204:ASN:ND2	2.43	0.82
18:R:191:PHE:HB3	18:R:202:PHE:CE1	2.15	0.82
22:V:703:PHE:HZ	22:V:712:LEU:HD22	1.44	0.82
25:1:52:VAL:HG23	25:1:53:LEU:HD12	1.60	0.82
25:1:59:GLU:OE1	26:2:402:ARG:NH1	2.11	0.82
3:C:200:PRO:HG2	3:C:217:GLN:OE1	1.79	0.81
23:W:408:SER:O	23:W:409:THR:HB	1.77	0.81
25:1:1:MET:SD	26:2:415:GLN:O	2.38	0.81
26:2:174:ASP:OD1	26:2:179:LEU:HD12	1.80	0.81
1:A:723:ASN:HB2	9:I:109:ARG:HB2	1.61	0.81
18:R:127:ASN:HD21	18:R:140:LYS:CE	1.90	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:175:ARG:HD2	20:T:207:LYS:HB3	1.60	0.81
26:2:175:LEU:HB3	26:2:216:MET:SD	2.20	0.81
27:3:12:VAL:CG2	27:3:161:ILE:HG12	2.11	0.81
2:B:873:LEU:CB	2:B:874:PRO:CD	2.59	0.81
17:Q:102:VAL:C	17:Q:104:LYS:N	2.38	0.81
22:V:528:LYS:HE2	29:Y:36:DA:O3'	1.80	0.81
24:0:54:ARG:NE	27:3:182:PHE:HE1	1.73	0.81
22:V:321:GLU:HB2	23:W:499:ASN:OD1	1.77	0.81
1:A:1209:PRO:HB3	9:I:33:ARG:HH12	1.44	0.81
5:E:27:LEU:CD1	5:E:64:HIS:HE2	1.86	0.81
17:Q:106:LYS:NZ	18:R:219:LEU:HD13	1.94	0.81
26:2:221:GLN:OE1	26:2:224:GLN:HA	1.80	0.81
1:A:653:VAL:HG23	1:A:669:TYR:HE2	1.46	0.81
2:B:227:ASN:O	2:B:405:ARG:NH2	2.14	0.81
26:2:100:LEU:HG	26:2:119:ARG:HE	1.45	0.81
27:3:165:LYS:HE2	27:3:167:ALA:O	1.81	0.81
2:B:488:PRO:O	2:B:489:ILE:CG1	2.29	0.81
25:1:1:MET:HB3	26:2:413:LEU:HD23	1.63	0.81
2:B:289:ILE:HG13	2:B:291:ASP:H	1.43	0.81
22:V:427:MET:O	22:V:432:THR:O	1.98	0.81
23:W:59:TYR:CD1	23:W:62:ALA:HB2	2.16	0.81
25:1:1:MET:CB	26:2:413:LEU:CB	2.56	0.81
25:1:34:ILE:HG22	25:1:46:ILE:HD11	1.63	0.81
25:1:50:VAL:HG12	25:1:54:GLN:HG2	1.62	0.81
2:B:488:PRO:O	2:B:489:ILE:HG12	1.80	0.80
26:2:52:ALA:O	26:2:56:VAL:HG13	1.81	0.80
2:B:160:TYR:OH	20:T:144:GLN:HG3	1.79	0.80
10:J:67:LYS:HB2	12:L:23:HIS:HD2	1.47	0.80
17:Q:25:PHE:HD2	18:R:215:GLU:CG	1.90	0.80
8:H:40:ILE:HD12	8:H:124:ARG:HD3	1.61	0.80
22:V:523:VAL:HG21	25:1:20:LEU:HG	1.64	0.80
22:V:366:ASN:ND2	22:V:613:THR:HG23	1.88	0.80
26:2:42:LEU:HD12	26:2:59:MET:CE	2.11	0.80
10:J:67:LYS:HG3	12:L:23:HIS:HB3	1.63	0.80
23:W:250:ASN:CB	23:W:434:HIS:CE1	2.65	0.80
26:2:35:TYR:CD1	26:2:62:LEU:HG	2.16	0.80
26:2:205:LEU:O	26:2:209:PRO:HD2	1.81	0.80
17:Q:106:LYS:C	18:R:218:LYS:HE3	2.07	0.80
26:2:224:GLN:HB2	26:2:268:PHE:CE2	2.17	0.80
5:E:65:ASN:O	5:E:66:ASP:C	2.24	0.80
26:2:93:LEU:HA	26:2:96:TRP:CD1	2.17	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:195:PRO:HB2	18:R:199:LYS:HB2	1.61	0.80
27:3:214:TYR:O	27:3:215:LEU:HD23	1.82	0.80
8:H:106:THR:O	8:H:108:ALA:N	2.12	0.79
17:Q:110:MET:HB3	18:R:218:LYS:CD	2.09	0.79
18:R:196:ASP:O	18:R:197:LYS:HB2	1.81	0.79
26:2:190:PRO:O	26:2:194:PRO:HD2	1.83	0.79
27:3:64:ILE:HG23	27:3:128:HIS:CD2	2.17	0.79
27:3:144:ILE:CD1	27:3:147:MET:HE3	2.11	0.79
1:A:621:ILE:HG23	1:A:623:PRO:HB3	1.62	0.79
17:Q:106:LYS:C	18:R:218:LYS:CE	2.55	0.79
26:2:117:ASN:CG	27:3:42:MET:CE	2.55	0.79
1:A:637:MET:SD	8:H:120:GLY:O	2.40	0.79
1:A:1313:GLN:CB	1:A:1333:GLU:HG2	2.12	0.79
5:E:27:LEU:CG	5:E:64:HIS:CG	2.64	0.79
25:1:38:ILE:HA	25:1:44:PHE:HD1	1.48	0.79
26:2:77:LYS:HD3	26:2:78:GLU:N	1.97	0.79
26:2:234:LEU:O	26:2:234:LEU:HD23	1.83	0.79
27:3:11:LEU:CD2	27:3:160:ARG:HG2	2.12	0.79
1:A:425:ASP:CG	13:M:39:LEU:HD21	2.06	0.79
2:B:238:SER:O	2:B:256:ILE:O	1.99	0.79
26:2:177:GLN:CD	26:2:220:LEU:HD22	2.06	0.79
2:B:837:CYS:HB3	2:B:840:MET:HE3	1.63	0.79
18:R:163:LEU:O	18:R:164:GLY:O	2.00	0.79
25:1:1:MET:HB3	26:2:413:LEU:CD2	2.12	0.79
25:1:1:MET:HA	26:2:414:SER:H	1.47	0.79
26:2:256:ASP:O	26:2:259:LEU:HG	1.81	0.79
26:2:117:ASN:HB3	27:3:42:MET:HE3	1.62	0.79
2:B:79:GLU:O	2:B:80:GLU:CG	2.29	0.79
2:B:623:ARG:NH2	2:B:697:GLU:OE2	2.15	0.79
27:3:121:LYS:O	27:3:124:ILE:HB	1.81	0.79
5:E:27:LEU:HB2	5:E:64:HIS:CG	2.14	0.79
13:M:178:LYS:HG2	20:T:156:VAL:HG12	1.64	0.79
17:Q:71:PHE:HA	17:Q:100:VAL:HG22	1.65	0.79
22:V:523:VAL:CB	25:1:20:LEU:HD23	2.12	0.79
25:1:1:MET:CE	26:2:440:LEU:HD13	2.12	0.79
26:2:118:LEU:HD22	27:3:39:ASP:HA	1.65	0.79
27:3:185:GLN:HA	27:3:185:GLN:HE21	1.47	0.79
10:J:17:LYS:HB3	10:J:38:LEU:HD22	1.65	0.78
17:Q:104:LYS:HZ2	18:R:238:LYS:HD2	1.48	0.78
26:2:118:LEU:CD1	27:3:39:ASP:OD1	2.31	0.78
27:3:222:SER:O	27:3:225:GLN:HG2	1.83	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:206:GLU:CB	16:P:207:PRO:HD2	2.02	0.78
9:I:99:SER:CB	9:I:105:GLU:CG	2.58	0.78
25:1:1:MET:C	26:2:413:LEU:HG	2.09	0.78
25:1:38:ILE:HG22	25:1:44:PHE:CD1	2.19	0.78
26:2:203:PHE:CD2	26:2:205:LEU:HD23	2.18	0.78
13:M:43:ASP:O	13:M:45:VAL:N	2.15	0.78
25:1:34:ILE:CG2	25:1:46:ILE:HD11	2.13	0.78
26:2:30:VAL:HG22	26:2:34:LEU:HD23	1.65	0.78
26:2:208:THR:HG23	26:2:209:PRO:HD3	1.66	0.78
26:2:34:LEU:O	26:2:38:PRO:HD2	1.84	0.78
26:2:196:ILE:CD1	26:2:210:ALA:HB2	2.13	0.78
1:A:604:ARG:HA	1:A:628:VAL:O	1.83	0.78
24:0:54:ARG:HB2	27:3:209:ILE:CG2	2.14	0.78
1:A:30:GLU:HA	1:A:33:ARG:HB2	1.65	0.78
26:2:207:ASP:O	26:2:211:GLN:HG2	1.84	0.78
27:3:14:VAL:CG2	27:3:163:VAL:HG22	2.13	0.78
1:A:1112:VAL:O	21:U:252:LYS:HG3	1.83	0.78
18:R:195:PRO:HG3	18:R:199:LYS:C	2.09	0.78
25:1:25:GLU:CD	25:1:35:ILE:HG12	2.09	0.77
27:3:58:ALA:HA	27:3:71:TYR:CZ	2.19	0.77
27:3:147:MET:O	27:3:151:VAL:HG23	1.84	0.77
25:1:1:MET:HG3	26:2:415:GLN:O	1.84	0.77
26:2:42:LEU:HD21	26:2:55:TRP:CB	2.10	0.77
26:2:179:LEU:HB3	26:2:184:LEU:HD11	1.65	0.77
1:A:921:ARG:O	1:A:1052:ARG:NH1	2.17	0.77
18:R:155:LEU:CG	18:R:204:ASN:HD22	1.72	0.77
20:T:146:ASP:C	20:T:147:LYS:HG2	2.09	0.77
20:T:174:LYS:HB3	28:X:20:DG:H4'	1.65	0.77
27:3:57:LEU:C	27:3:71:TYR:CZ	2.62	0.77
18:R:155:LEU:CB	18:R:204:ASN:HD21	1.97	0.77
20:T:221:GLY:HA2	20:T:236:LYS:HG3	1.67	0.77
23:W:408:SER:O	23:W:409:THR:CB	2.31	0.77
27:3:57:LEU:C	27:3:71:TYR:CE2	2.63	0.77
27:3:58:ALA:N	27:3:71:TYR:CZ	2.53	0.77
22:V:703:PHE:CZ	22:V:712:LEU:HD22	2.18	0.77
26:2:181:GLN:OE1	26:2:229:ASP:HB2	1.84	0.77
27:3:185:GLN:NE2	27:3:210:THR:HA	2.00	0.77
17:Q:187:ILE:CG1	18:R:212:VAL:N	2.13	0.77
27:3:133:LEU:HD23	27:3:177:PHE:HD1	1.49	0.77
26:2:189:GLU:HB2	26:2:190:PRO:HD3	1.66	0.77
1:A:537:ILE:HB	1:A:645:LEU:HD21	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:611:ASP:OD2	1:A:617:PRO:HB3	1.84	0.77
1:A:731:ASN:HD21	21:U:253:THR:HA	1.47	0.77
3:C:154:ARG:HD2	10:J:65:LEU:HD13	1.64	0.77
26:2:29:GLY:N	27:3:25:GLN:HB3	1.99	0.77
26:2:53:LYS:O	26:2:56:VAL:HG22	1.84	0.77
26:2:118:LEU:CG	27:3:39:ASP:OD1	2.32	0.77
26:2:221:GLN:HE22	26:2:230:LEU:HB2	1.47	0.77
1:A:597:PRO:HB2	1:A:660:MET:HE3	1.67	0.77
18:R:195:PRO:HB3	18:R:199:LYS:CB	2.08	0.77
22:V:689:VAL:HB	26:2:391:ILE:HD11	1.67	0.77
27:3:151:VAL:HG12	27:3:155:GLN:O	1.84	0.77
1:A:1310:HIS:N	21:U:252:LYS:CD	2.40	0.77
17:Q:32:LEU:CD1	18:R:203:PHE:CD2	2.67	0.76
22:V:609:LYS:HZ2	29:Y:38:DT:P	2.08	0.76
23:W:424:ARG:O	23:W:425:THR:CG2	2.32	0.76
18:R:191:PHE:HB3	18:R:202:PHE:CD1	2.19	0.76
26:2:218:GLN:NE2	26:2:265:LEU:HA	2.00	0.76
2:B:1072:ARG:HH21	2:B:1113:PRO:HG2	1.50	0.76
5:E:27:LEU:N	5:E:64:HIS:CB	2.42	0.76
1:A:1169:VAL:HG21	1:A:1298:LEU:HD22	1.66	0.76
3:C:154:ARG:NH1	10:J:65:LEU:HB2	2.01	0.76
17:Q:191:LEU:CD2	18:R:212:VAL:HG11	2.15	0.76
20:T:174:LYS:HG2	28:X:20:DG:O3'	1.86	0.76
23:W:432:ILE:CG1	23:W:434:HIS:HE1	1.99	0.76
25:1:1:MET:SD	26:2:413:LEU:HB3	2.25	0.76
26:2:251:VAL:HG11	26:2:254:MET:CG	2.16	0.76
20:T:176:ALA:C	20:T:177:ARG:HG3	2.10	0.76
25:1:13:ASP:OD2	25:1:17:LYS:CB	2.33	0.76
3:C:130:VAL:O	3:C:134:ASN:ND2	2.19	0.76
25:1:24:ASP:OD2	25:1:57:VAL:HG11	1.85	0.76
1:A:137:PRO:HB3	1:A:237:GLY:HA3	1.68	0.76
22:V:444:HIS:O	22:V:447:PRO:HD2	1.85	0.76
23:W:410:TYR:C	23:W:412:LYS:H	1.94	0.76
1:A:884:ASN:ND2	6:F:111:PRO:O	2.18	0.76
2:B:92:TYR:HB3	20:T:145:LEU:CD2	2.15	0.76
9:I:73:SER:O	9:I:80:ARG:NH2	2.17	0.76
26:2:127:LYS:N	26:2:178:LEU:HD23	2.01	0.76
26:2:159:VAL:HG13	26:2:161:HIS:N	1.96	0.76
26:2:163:MET:HE2	26:2:206:LEU:CD1	2.15	0.76
1:A:1274:GLU:O	1:A:1276:VAL:N	2.19	0.76
19:S:50:ASP:HB3	19:S:97:PRO:HG2	1.66	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:3:172:LEU:HD13	27:3:172:LEU:O	1.86	0.76
12:L:18:ILE:O	12:L:45:TYR:N	2.18	0.76
21:U:250:MET:O	21:U:251:ALA:CB	2.33	0.76
27:3:147:MET:HE1	27:3:157:MET:SD	2.25	0.76
12:L:16:ILE:HG13	12:L:28:ILE:CA	2.17	0.75
17:Q:107:LEU:N	18:R:218:LYS:CE	2.50	0.75
21:U:173:GLU:OE2	21:U:187:TYR:OH	2.04	0.75
25:1:1:MET:HG2	26:2:413:LEU:C	2.11	0.75
27:3:190:LEU:HD23	27:3:190:LEU:H	1.51	0.75
12:L:40:GLY:O	12:L:42:ARG:NH1	2.19	0.75
20:T:177:ARG:NH1	28:X:20:DG:OP1	2.20	0.75
21:U:250:MET:O	21:U:251:ALA:HB2	1.83	0.75
26:2:86:SER:HB3	26:2:140:LYS:CE	2.16	0.75
1:A:611:ASP:CG	1:A:617:PRO:HG3	2.11	0.75
2:B:93:LEU:C	20:T:145:LEU:CD2	2.60	0.75
2:B:160:TYR:HE1	20:T:144:GLN:NE2	1.84	0.75
18:R:162:GLY:C	18:R:164:GLY:N	2.39	0.75
26:2:117:ASN:CG	27:3:42:MET:HE2	2.09	0.75
1:A:1206:ARG:HD3	1:A:1265:ASP:HA	1.69	0.75
26:2:35:TYR:CD2	26:2:62:LEU:HB3	2.22	0.75
26:2:44:VAL:HG13	26:2:45:PHE:CD1	2.20	0.75
26:2:251:VAL:HG12	26:2:254:MET:H	1.51	0.75
3:C:5:ASN:O	3:C:7:PRO:HD3	1.85	0.75
18:R:129:LYS:HB3	18:R:140:LYS:CB	2.12	0.75
27:3:14:VAL:CG2	27:3:163:VAL:HA	2.16	0.75
2:B:754:PRO:HB2	2:B:773:PRO:HG2	1.69	0.75
25:1:38:ILE:H	25:1:38:ILE:HD13	1.51	0.75
1:A:1208:SER:HB2	1:A:1261:ILE:HG12	1.69	0.75
25:1:10:ILE:CG2	26:2:407:VAL:HG21	2.16	0.75
26:2:51:LEU:HD23	26:2:51:LEU:O	1.87	0.75
27:3:148:ASN:CB	27:3:157:MET:HE2	2.17	0.75
1:A:1112:VAL:O	21:U:252:LYS:CB	2.34	0.75
26:2:53:LYS:HE3	26:2:95:ILE:HD11	1.67	0.75
1:A:1310:HIS:N	21:U:252:LYS:CE	2.49	0.75
2:B:160:TYR:CE1	20:T:144:GLN:NE2	2.54	0.75
23:W:608:ILE:HG23	23:W:614:TYR:CE2	2.22	0.75
26:2:100:LEU:CD1	26:2:119:ARG:HG3	2.16	0.75
13:M:179:GLU:N	20:T:154:LYS:HG2	2.02	0.74
18:R:127:ASN:ND2	18:R:140:LYS:HE2	1.98	0.74
18:R:154:LEU:HD23	18:R:162:GLY:O	1.86	0.74
23:W:52:LEU:HD23	23:W:72:TYR:CE2	2.22	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:2:208:THR:HG23	26:2:209:PRO:CD	2.16	0.74
1:A:539:GLN:HE21	2:B:970:HIS:HB2	1.52	0.74
2:B:134:LYS:HD3	2:B:138:GLU:HB2	1.68	0.74
2:B:817:GLN:HE21	2:B:916:TYR:HB2	1.52	0.74
2:B:924:ARG:NH1	3:C:62:GLU:OE1	2.19	0.74
3:C:100:GLU:OE2	3:C:162:ARG:NH2	2.20	0.74
26:2:28:PRO:CA	27:3:25:GLN:CA	2.61	0.74
1:A:612:ASP:OD2	1:A:614:ASP:O	2.05	0.74
1:A:700:GLN:OE1	1:A:703:GLN:NE2	2.20	0.74
22:V:415:HIS:HA	22:V:421:TRP:CD1	2.22	0.74
26:2:196:ILE:HD11	26:2:210:ALA:CB	2.17	0.74
27:3:8:LEU:HD23	27:3:54:SER:HB3	1.68	0.74
1:A:1310:HIS:HB3	21:U:252:LYS:HE3	0.78	0.74
18:R:140:LYS:O	18:R:143:TYR:CE1	2.41	0.74
23:W:430:ASN:HB3	23:W:431:PRO:CD	2.17	0.74
26:2:30:VAL:CG1	27:3:25:GLN:CB	2.65	0.74
27:3:38:ILE:O	27:3:41:VAL:HG12	1.87	0.74
27:3:59:VAL:CA	27:3:71:TYR:CE1	2.70	0.74
1:A:374:SER:OG	1:A:666:ARG:NH2	2.20	0.74
1:A:1310:HIS:CE1	1:A:1334:TRP:HE3	2.06	0.74
2:B:894:THR:HA	13:M:52:TRP:CH2	2.23	0.74
3:C:12:THR:H	3:C:21:PHE:HA	1.52	0.74
9:I:99:SER:HG	9:I:105:GLU:HB2	1.51	0.74
17:Q:107:LEU:CA	18:R:218:LYS:CE	2.62	0.74
18:R:224:THR:CG2	18:R:230:GLU:CB	2.64	0.74
20:T:47:LYS:HG2	20:T:52:THR:HG23	1.69	0.74
21:U:232:GLU:O	21:U:233:LEU:CB	2.28	0.74
1:A:958:ARG:NH1	1:A:962:ASP:OD1	2.21	0.74
2:B:79:GLU:HA	2:B:79:GLU:OE2	1.85	0.74
17:Q:187:ILE:CB	18:R:212:VAL:N	2.49	0.74
22:V:519:TYR:HE2	25:1:20:LEU:HG	1.52	0.74
26:2:132:ASP:O	26:2:135:GLN:HG2	1.88	0.74
27:3:11:LEU:HD22	27:3:160:ARG:CG	2.16	0.74
2:B:806:PHE:O	2:B:1050:ARG:NH1	2.21	0.74
5:E:27:LEU:HG	5:E:64:HIS:CG	2.21	0.74
18:R:195:PRO:CG	18:R:199:LYS:CA	2.65	0.74
22:V:412:MET:CA	22:V:417:THR:HG21	2.17	0.74
22:V:534:TYR:CE1	22:V:535:THR:OG1	2.40	0.74
26:2:234:LEU:CD2	26:2:237:LEU:HD12	2.14	0.74
1:A:320:ASN:HD21	1:A:329:MET:HE3	1.53	0.74
1:A:621:ILE:O	1:A:623:PRO:HD3	1.84	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:2:180:SER:O	26:2:184:LEU:HG	1.87	0.74
22:V:321:GLU:OE1	23:W:499:ASN:OD1	2.06	0.74
26:2:211:GLN:CG	26:2:257:SER:HB3	2.13	0.74
17:Q:113:ARG:HB2	18:R:221:ARG:HD3	1.68	0.74
18:R:195:PRO:HG2	18:R:199:LYS:H	1.53	0.74
22:V:674:THR:OG1	26:2:392:ARG:NE	2.21	0.74
25:1:1:MET:HG2	26:2:413:LEU:HB3	1.68	0.74
27:3:12:VAL:HG23	27:3:161:ILE:HG23	1.70	0.74
1:A:631:GLU:HG3	1:A:636:ILE:HD11	1.70	0.73
1:A:1307:VAL:CG1	1:A:1339:ASP:H	2.01	0.73
2:B:74:ALA:O	2:B:76:GLY:N	2.21	0.73
3:C:211:LEU:C	3:C:213:GLU:H	1.95	0.73
12:L:18:ILE:HA	12:L:25:GLU:HA	1.70	0.73
17:Q:112:ARG:HB3	18:R:221:ARG:NH2	2.03	0.73
23:W:73:CYS:HB2	23:W:209:TYR:CZ	2.22	0.73
27:3:111:ILE:HG13	27:3:112:VAL:N	2.03	0.73
5:E:52:ARG:HG3	5:E:53:PRO:N	2.03	0.73
26:2:237:LEU:O	26:2:240:LEU:HD13	1.88	0.73
26:2:243:SER:HB3	26:2:258:LEU:HD22	1.69	0.73
20:T:146:ASP:O	20:T:147:LYS:CB	2.37	0.73
22:V:523:VAL:HG21	25:1:20:LEU:CD2	2.17	0.73
25:1:1:MET:HE3	26:2:415:GLN:C	2.13	0.73
26:2:41:CYS:O	26:2:44:VAL:HG12	1.88	0.73
26:2:118:LEU:HD21	27:3:39:ASP:C	2.12	0.73
26:2:163:MET:CE	26:2:206:LEU:HD12	2.14	0.73
26:2:243:SER:HB2	26:2:258:LEU:HD22	1.71	0.73
22:V:516:PRO:CB	22:V:706:LYS:NZ	2.51	0.73
25:1:34:ILE:HD13	25:1:54:GLN:OE1	1.88	0.73
27:3:226:TYR:HA	27:3:230:VAL:HG23	1.71	0.73
2:B:242:ARG:O	2:B:252:ILE:HG22	1.82	0.73
3:C:101:PHE:HB2	3:C:163:ALA:HB3	1.71	0.73
25:1:28:ALA:HB3	25:1:31:LYS:HB2	1.71	0.73
27:3:214:TYR:HE2	27:3:216:LYS:HE2	1.53	0.73
2:B:759:VAL:HG12	2:B:999:ALA:HB2	1.71	0.73
3:C:200:PRO:HG3	3:C:217:GLN:CB	2.19	0.73
20:T:139:VAL:O	20:T:140:ARG:CB	2.37	0.73
22:V:516:PRO:HB3	25:1:15:ALA:CB	2.05	0.73
26:2:117:ASN:HB3	27:3:42:MET:CE	2.18	0.73
27:3:141:LEU:O	27:3:144:ILE:HG22	1.89	0.73
8:H:65:TYR:HE2	8:H:70:LEU:HB3	1.53	0.73
26:2:42:LEU:HD12	26:2:59:MET:HE1	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:2:175:LEU:HD22	26:2:216:MET:SD	2.29	0.73
2:B:1119:CYS:HB2	2:B:1137:CYS:SG	2.28	0.72
8:H:66:GLU:O	8:H:67:ASP:CB	2.35	0.72
12:L:17:TYR:O	12:L:18:ILE:CB	2.33	0.72
22:V:667:THR:HA	25:1:62:ASP:OD1	1.89	0.72
23:W:59:TYR:CD2	23:W:62:ALA:CB	2.71	0.72
26:2:172:SER:HA	26:2:175:LEU:CD2	2.19	0.72
1:A:831:LEU:HB2	2:B:715:ASP:HB2	1.70	0.72
2:B:92:TYR:C	20:T:145:LEU:HD23	2.12	0.72
12:L:37:ARG:O	12:L:39:CYS:N	2.22	0.72
16:P:297:LYS:HB2	16:P:298:PRO:HD2	1.71	0.72
2:B:92:TYR:C	20:T:145:LEU:HD22	2.13	0.72
14:N:26:ARG:NE	14:N:36:GLU:OE1	2.21	0.72
17:Q:32:LEU:HD13	18:R:203:PHE:CE2	2.24	0.72
17:Q:144:LEU:O	17:Q:153:ARG:N	2.23	0.72
2:B:100:GLU:OE2	2:B:116:ARG:NH1	2.22	0.72
19:S:126:ILE:HB	19:S:138:PHE:HB2	1.70	0.72
22:V:394:SER:HB3	22:V:416:THR:O	1.88	0.72
26:2:117:ASN:HB2	27:3:104:LEU:HD11	1.71	0.72
26:2:160:LEU:HA	26:2:206:LEU:HD11	1.70	0.72
27:3:165:LYS:HG3	27:3:203:LEU:CD1	2.20	0.72
1:A:625:ASP:N	1:A:637:MET:HB3	2.03	0.72
22:V:516:PRO:HG2	22:V:706:LYS:CE	2.19	0.72
24:0:76:LEU:O	24:0:77:LYS:O	2.07	0.72
26:2:60:LEU:HD11	26:2:95:ILE:HB	1.71	0.72
26:2:117:ASN:ND2	27:3:42:MET:HE1	2.04	0.72
2:B:57:ARG:NH1	2:B:60:GLU:OE1	2.23	0.72
14:N:318:ASP:CB	16:P:239:ARG:HH21	2.03	0.72
22:V:523:VAL:CG1	25:1:20:LEU:HD23	2.15	0.72
23:W:73:CYS:C	23:W:209:TYR:CE2	2.67	0.72
26:2:118:LEU:CD2	27:3:39:ASP:CA	2.68	0.72
26:2:134:SER:O	26:2:138:PRO:HD2	1.89	0.72
26:2:211:GLN:HA	26:2:261:PHE:HZ	1.49	0.72
1:A:257:PRO:HD2	1:A:260:VAL:HB	1.71	0.72
1:A:621:ILE:O	1:A:623:PRO:CD	2.36	0.72
9:I:94:ALA:HA	9:I:114:CYS:HA	1.72	0.72
23:W:209:TYR:OH	23:W:234:ASP:N	2.23	0.72
23:W:584:TYR:HD1	23:W:594:ALA:HB2	1.51	0.72
26:2:35:TYR:CG	26:2:62:LEU:HD12	2.25	0.72
2:B:205:VAL:O	2:B:371:ARG:NH1	2.23	0.72
9:I:101:SER:H	9:I:104:ALA:HA	1.55	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:145:LEU:HD11	20:T:148:VAL:HG22	1.72	0.72
25:1:2:VAL:HG12	26:2:422:LEU:HD13	1.71	0.72
1:A:1163:HIS:HA	1:A:1300:GLY:HA3	1.70	0.72
1:A:1314:THR:HG1	1:A:1332:GLN:NE2	1.85	0.72
2:B:878:ASP:O	2:B:879:GLU:O	2.07	0.72
2:B:1129:ASN:HA	2:B:1135:TYR:HA	1.71	0.72
26:2:118:LEU:HD22	27:3:39:ASP:CA	2.19	0.72
26:2:251:VAL:CG1	26:2:254:MET:HB2	2.20	0.72
27:3:217:VAL:HG13	27:3:226:TYR:CZ	2.25	0.72
1:A:546:ARG:HG3	1:A:639:ILE:HD11	1.72	0.71
1:A:621:ILE:CG2	1:A:623:PRO:CD	2.68	0.71
27:3:144:ILE:HG12	27:3:147:MET:HE3	1.70	0.71
1:A:611:ASP:OD2	1:A:617:PRO:HG3	1.91	0.71
1:A:612:ASP:O	1:A:613:GLU:C	2.33	0.71
1:A:790:GLN:NE2	1:A:820:ARG:O	2.22	0.71
1:A:1211:LEU:HD11	1:A:1258:ARG:HB2	1.71	0.71
14:N:311:GLU:HB3	16:P:251:LEU:HD23	1.72	0.71
17:Q:191:LEU:CD2	18:R:212:VAL:CG1	2.67	0.71
1:A:1308:TYR:CD1	1:A:1338:THR:CG2	2.73	0.71
1:A:1457:ASN:OD1	1:A:1462:GLN:NE2	2.22	0.71
13:M:10:LEU:C	13:M:12:ARG:H	1.99	0.71
27:3:222:SER:HB2	27:3:226:TYR:HE2	1.54	0.71
1:A:1303:GLN:HE22	1:A:1342:SER:HB3	1.55	0.71
22:V:355:CYS:HG	22:V:381:TRP:CD1	2.08	0.71
27:3:33:THR:HG23	27:3:36:LYS:N	1.98	0.71
27:3:33:THR:HG22	27:3:36:LYS:HB2	1.73	0.71
1:A:610:PRO:O	1:A:611:ASP:CB	2.28	0.71
1:A:621:ILE:HA	1:A:623:PRO:HD3	1.68	0.71
26:2:218:GLN:HE22	26:2:265:LEU:HA	1.55	0.71
1:A:1308:TYR:CD1	1:A:1338:THR:HG21	2.25	0.71
2:B:849:ASP:OD2	12:L:29:LYS:NZ	2.23	0.71
7:G:110:ARG:NH2	7:G:118:GLU:OE2	2.24	0.71
20:T:139:VAL:O	20:T:140:ARG:HB3	1.90	0.71
23:W:209:TYR:HE1	23:W:233:PHE:CD1	2.08	0.71
25:1:9:LEU:HD22	25:1:51:ASN:ND2	2.04	0.71
26:2:163:MET:O	26:2:167:PRO:HD2	1.91	0.71
26:2:189:GLU:HA	26:2:192:GLU:HG2	1.72	0.71
27:3:18:ASN:CG	27:3:20:ILE:HD13	2.15	0.71
27:3:69:PHE:CE1	27:3:139:LYS:HD2	2.25	0.71
17:Q:191:LEU:HD22	18:R:212:VAL:CG1	2.21	0.71
25:1:29:LEU:HD23	25:1:30:GLY:N	2.06	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:2:81:LYS:HD2	26:2:89:LEU:CD2	2.20	0.71
26:2:86:SER:CB	26:2:140:LYS:HE2	2.20	0.71
26:2:171:VAL:HG12	26:2:216:MET:SD	2.31	0.71
1:A:582:PRO:HD2	8:H:47:ILE:HD12	1.72	0.71
14:N:326:GLN:O	15:O:92:LYS:NZ	2.22	0.71
20:T:176:ALA:O	20:T:208:GLN:NE2	2.24	0.71
26:2:31:LEU:N	27:3:25:GLN:O	2.23	0.71
26:2:126:GLY:C	26:2:178:LEU:HD23	2.16	0.71
27:3:133:LEU:HD22	27:3:134:ALA:H	1.56	0.71
1:A:790:GLN:HA	1:A:822:PHE:HA	1.71	0.70
1:A:1451:MET:HE1	1:A:1460:LEU:HD22	1.73	0.70
2:B:743:ARG:O	2:B:922:ARG:NH1	2.24	0.70
2:B:803:ARG:NH1	10:J:8:PHE:O	2.24	0.70
3:C:47:ILE:HA	3:C:165:ALA:HA	1.72	0.70
17:Q:106:LYS:HG2	18:R:218:LYS:HG2	1.73	0.70
18:R:154:LEU:CD2	18:R:162:GLY:O	2.39	0.70
22:V:504:LYS:HB3	22:V:654:GLU:O	1.91	0.70
25:1:55:GLU:OE2	26:2:402:ARG:HG3	1.90	0.70
2:B:1067:ILE:HG22	2:B:1068:GLN:H	1.55	0.70
6:F:56:TYR:O	6:F:108:ARG:NH2	2.22	0.70
17:Q:67:LYS:HG3	17:Q:72:ILE:HD11	1.73	0.70
21:U:286:THR:HG21	21:U:299:LYS:HB3	1.72	0.70
12:L:25:GLU:CG	12:L:27:GLU:CD	2.61	0.70
26:2:185:MET:SD	26:2:232:GLU:HB2	2.32	0.70
3:C:154:ARG:HD3	10:J:65:LEU:CB	2.21	0.70
9:I:86:CYS:C	9:I:88:LYS:N	2.48	0.70
15:O:79:VAL:HG21	15:O:93:VAL:HG12	1.73	0.70
20:T:177:ARG:HG3	20:T:208:GLN:OE1	1.88	0.70
25:1:2:VAL:HG12	26:2:456:LYS:HE2	1.72	0.70
26:2:199:ALA:CB	26:2:202:GLN:HE22	2.02	0.70
27:3:177:PHE:CZ	27:3:203:LEU:HD23	2.27	0.70
13:M:297:PRO:HB3	13:M:310:VAL:HG21	1.73	0.70
16:P:271:GLU:OE1	16:P:271:GLU:N	2.23	0.70
26:2:117:ASN:HD21	27:3:108:ASN:CA	2.05	0.70
26:2:192:GLU:HG3	26:2:193:PRO:CD	2.18	0.70
1:A:611:ASP:OD2	1:A:617:PRO:CG	2.38	0.70
2:B:216:ALA:N	2:B:239:MET:O	2.25	0.70
25:1:2:VAL:CG1	26:2:456:LYS:CG	2.53	0.70
3:C:6:GLN:HG2	3:C:25:ASN:ND2	2.04	0.70
22:V:393:THR:HA	22:V:418:LYS:CD	2.21	0.70
25:1:34:ILE:HG12	25:1:50:VAL:CG1	2.18	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:2:30:VAL:HG13	27:3:25:GLN:O	1.88	0.70
1:A:625:ASP:OD1	1:A:637:MET:CE	2.39	0.70
22:V:531:ILE:CG2	22:V:534:TYR:CZ	2.64	0.70
26:2:117:ASN:HD21	27:3:108:ASN:HB3	1.47	0.70
2:B:497:LYS:N	2:B:498:PRO:HD2	2.04	0.70
3:C:10:ARG:NH2	3:C:24:GLU:OE2	2.23	0.70
17:Q:112:ARG:CB	18:R:221:ARG:HH22	2.03	0.70
23:W:696:TRP:CD1	23:W:697:ILE:HG13	2.26	0.70
25:1:18:GLN:CB	25:1:44:PHE:HE2	2.02	0.70
26:2:48:LEU:CB	26:2:49:PRO:HD3	2.19	0.70
2:B:93:LEU:C	20:T:145:LEU:HD23	2.17	0.70
10:J:63:ALA:N	10:J:64:PRO:CD	2.55	0.70
26:2:218:GLN:CD	26:2:265:LEU:HA	2.17	0.70
8:H:110:THR:O	8:H:111:ARG:CB	2.40	0.69
13:M:286:ARG:HG3	13:M:316:LEU:HG	1.74	0.69
22:V:648:LYS:O	22:V:650:MET:N	2.24	0.69
23:W:589:GLU:O	23:W:594:ALA:HB1	1.91	0.69
24:0:54:ARG:NE	27:3:182:PHE:CD1	2.60	0.69
25:1:1:MET:HB2	26:2:418:PHE:CB	2.21	0.69
1:A:121:SER:HA	1:A:126:ILE:HG21	1.73	0.69
1:A:1313:GLN:HB2	1:A:1333:GLU:HG2	1.74	0.69
14:N:353:LEU:HB2	14:N:370:ALA:HB3	1.74	0.69
18:R:90:GLN:NE2	18:R:172:GLU:OE2	2.25	0.69
25:1:8:VAL:HG11	25:1:45:VAL:HG12	1.74	0.69
26:2:218:GLN:OE1	26:2:265:LEU:HA	1.92	0.69
8:H:65:TYR:CD2	8:H:70:LEU:HD23	2.28	0.69
18:R:195:PRO:HG2	18:R:199:LYS:CA	2.22	0.69
26:2:181:GLN:HG3	26:2:229:ASP:CG	2.18	0.69
17:Q:25:PHE:HA	18:R:215:GLU:OE1	1.93	0.69
22:V:516:PRO:HB2	22:V:706:LYS:HZ1	1.55	0.69
25:1:1:MET:HG3	26:2:418:PHE:HB2	1.73	0.69
1:A:731:ASN:CG	21:U:253:THR:CG2	2.41	0.69
2:B:499:ARG:HB3	2:B:499:ARG:HH11	1.57	0.69
2:B:983:GLU:OE2	2:B:1047:TYR:N	2.19	0.69
25:1:53:LEU:HD12	25:1:53:LEU:H	1.57	0.69
27:3:69:PHE:CZ	27:3:139:LYS:HD2	2.27	0.69
2:B:777:ASN:O	10:J:47:ARG:NH1	2.25	0.69
5:E:80:PRO:HA	5:E:107:GLN:HB2	1.73	0.69
18:R:195:PRO:CG	18:R:199:LYS:O	2.40	0.69
25:1:1:MET:HE2	26:2:413:LEU:O	1.91	0.69
2:B:239:MET:HE1	2:B:256:ILE:CD1	2.08	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:499:ARG:HB3	2:B:499:ARG:CZ	2.20	0.69
8:H:113:SER:OG	8:H:126:GLN:NE2	2.26	0.69
17:Q:109:HIS:O	18:R:221:ARG:NH2	2.25	0.69
26:2:130:SER:O	26:2:133:THR:HG22	1.92	0.69
1:A:625:ASP:H	1:A:637:MET:HB3	1.56	0.69
2:B:109:MET:HE1	2:B:174:LEU:HB3	1.75	0.69
22:V:370:SER:OG	22:V:614:SER:OG	2.10	0.69
23:W:70:LEU:HD21	23:W:72:TYR:CZ	2.27	0.69
25:1:19:PHE:O	25:1:23:LEU:HG	1.92	0.69
26:2:117:ASN:CB	27:3:42:MET:HE3	2.22	0.69
27:3:34:LEU:O	27:3:34:LEU:HD13	1.92	0.69
5:E:27:LEU:H	5:E:64:HIS:HB3	1.51	0.69
26:2:31:LEU:CD1	27:3:33:THR:HG21	2.22	0.69
27:3:162:LEU:HA	27:3:192:ASP:OD1	1.92	0.69
1:A:529:GLN:HE22	1:A:1097:GLU:HB3	1.55	0.69
2:B:360:LYS:HG3	2:B:553:LEU:HD23	1.74	0.69
2:B:427:LYS:HE3	20:T:164:GLU:HG2	1.74	0.69
2:B:634:LEU:HD23	2:B:661:VAL:HA	1.75	0.69
17:Q:113:ARG:CD	18:R:217:GLN:O	2.41	0.69
19:S:157:ALA:HA	19:S:161:GLU:HB2	1.75	0.69
23:W:189:TRP:HE1	23:W:194:LEU:HB2	1.56	0.69
26:2:211:GLN:HA	26:2:261:PHE:CE1	2.28	0.69
27:3:51:MET:HE3	27:3:52:ASN:ND2	2.07	0.69
8:H:2:ALA:N	8:H:66:GLU:O	2.25	0.68
20:T:228:ILE:CA	28:X:30:DG:H5"	2.22	0.68
26:2:140:LYS:HD3	26:2:162:PHE:HE1	1.58	0.68
27:3:215:LEU:HD12	27:3:230:VAL:CG1	2.23	0.68
2:B:245:GLN:HE21	2:B:252:ILE:HD12	1.58	0.68
3:C:136:ASP:O	3:C:138:ASP:N	2.22	0.68
5:E:15:LYS:NZ	5:E:33:LEU:O	2.27	0.68
9:I:64:GLU:CD	9:I:103:ARG:HH21	2.01	0.68
26:2:117:ASN:CG	27:3:108:ASN:ND2	2.50	0.68
26:2:176:ALA:HB1	26:2:178:LEU:CD1	2.23	0.68
27:3:144:ILE:CG1	27:3:147:MET:HE3	2.23	0.68
20:T:8:ASP:HB3	20:T:105:SER:HA	1.75	0.68
22:V:523:VAL:HG21	25:1:20:LEU:CG	2.22	0.68
1:A:1310:HIS:H	21:U:252:LYS:NZ	1.90	0.68
2:B:36:GLU:OE1	2:B:652:SER:OG	2.11	0.68
12:L:22:CYS:HB3	12:L:39:CYS:HB2	1.75	0.68
13:M:106:THR:HG22	13:M:109:SER:OG	1.92	0.68
22:V:451:PHE:CZ	28:X:57:DC:H5"	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:926:ASN:HD21	1:A:931:ARG:HD2	1.58	0.68
6:F:47:ALA:HB1	6:F:51:ARG:HE	1.58	0.68
26:2:163:MET:CE	26:2:206:LEU:HB3	2.23	0.68
27:3:114:GLU:O	27:3:118:LEU:HD23	1.92	0.68
1:A:844:ARG:NH2	2:B:500:GLN:O	2.26	0.68
10:J:3:ILE:HG21	10:J:18:TRP:HB2	1.74	0.68
12:L:16:ILE:HD11	12:L:28:ILE:C	2.17	0.68
14:N:375:GLU:OE1	15:O:59:ARG:NH2	2.26	0.68
17:Q:32:LEU:CD1	18:R:203:PHE:CE2	2.76	0.68
26:2:118:LEU:HD13	27:3:39:ASP:OD1	1.93	0.68
1:A:71:CYS:H	1:A:75:ALA:HA	1.59	0.68
1:A:420:ILE:N	1:A:445:LYS:O	2.24	0.68
1:A:601:ASN:HD21	1:A:632:ASN:H	1.42	0.68
17:Q:110:MET:CG	18:R:218:LYS:HD2	2.24	0.68
1:A:67:ARG:HH22	13:M:48:VAL:HG23	1.59	0.68
1:A:653:VAL:HG23	1:A:669:TYR:CE2	2.27	0.68
1:A:1287:CYS:HA	2:B:250:SER:CB	2.23	0.68
2:B:201:ALA:O	2:B:222:ARG:NH2	2.26	0.68
2:B:830:GLU:OE2	2:B:870:THR:OG1	2.11	0.68
8:H:111:ARG:NE	8:H:126:GLN:OE1	2.26	0.68
25:1:39:ASP:OD1	25:1:43:VAL:HB	1.94	0.68
25:1:59:GLU:OE2	26:2:402:ARG:CZ	2.42	0.68
26:2:199:ALA:HB3	26:2:202:GLN:NE2	2.02	0.68
2:B:87:LYS:HB3	2:B:129:THR:HB	1.76	0.68
2:B:93:LEU:CA	20:T:145:LEU:CD2	2.67	0.68
2:B:894:THR:HA	13:M:52:TRP:HH2	1.56	0.68
3:C:253:LYS:NZ	11:K:102:GLU:OE1	2.27	0.68
11:K:44:ASN:OD1	11:K:45:ILE:N	2.27	0.68
13:M:134:ILE:HG12	13:M:171:GLU:HG3	1.76	0.68
21:U:206:LEU:HD11	21:U:228:MET:HB3	1.76	0.68
27:3:18:ASN:CG	27:3:64:ILE:HD11	2.19	0.68
27:3:130:GLU:HB2	27:3:173:GLN:NE2	2.09	0.68
27:3:159:SER:OG	27:3:189:ILE:HD12	1.94	0.68
1:A:826:SER:H	1:A:829:ALA:HB3	1.59	0.68
2:B:1106:ARG:HA	2:B:1110:ALA:HB3	1.76	0.68
12:L:17:TYR:CA	12:L:46:LYS:CA	2.64	0.68
26:2:56:VAL:O	26:2:60:LEU:HG	1.94	0.68
26:2:117:ASN:ND2	27:3:108:ASN:CA	2.57	0.68
27:3:66:GLU:CA	27:3:132:LEU:HD12	2.13	0.68
1:A:625:ASP:O	1:A:638:GLY:CA	2.41	0.67
5:E:170:LEU:HD23	5:E:208:LEU:HB2	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:163:PRO:HA	16:P:262:CYS:HB3	1.75	0.67
21:U:185:MET:HE3	21:U:192:ARG:HH22	1.58	0.67
1:A:552:ASP:HB3	8:H:24:ARG:HD3	1.76	0.67
1:A:1310:HIS:CA	21:U:252:LYS:CE	2.70	0.67
7:G:93:ASN:OD1	7:G:94:LYS:N	2.26	0.67
7:G:99:THR:HG21	7:G:143:ILE:HD11	1.76	0.67
17:Q:113:ARG:HD3	18:R:221:ARG:HD3	1.75	0.67
21:U:256:THR:O	21:U:257:GLN:C	2.38	0.67
2:B:483:ARG:NH2	2:B:527:ALA:O	2.27	0.67
7:G:153:ASP:O	7:G:155:ASN:N	2.27	0.67
9:I:105:GLU:O	9:I:107:ALA:CA	2.42	0.67
17:Q:106:LYS:CG	18:R:218:LYS:HE2	2.23	0.67
19:S:49:ARG:NH1	19:S:96:GLN:O	2.25	0.67
25:1:1:MET:CG	26:2:415:GLN:O	2.42	0.67
27:3:111:ILE:O	27:3:115:ILE:HD13	1.94	0.67
1:A:22:GLN:HB3	2:B:1170:ARG:HG3	1.77	0.67
1:A:65:ILE:HD12	1:A:263:ALA:HB3	1.76	0.67
17:Q:106:LYS:HZ3	18:R:219:LEU:HD13	1.58	0.67
19:S:166:ARG:HH11	19:S:166:ARG:HG3	1.59	0.67
26:2:160:LEU:HD12	26:2:160:LEU:H	1.60	0.67
26:2:181:GLN:CD	26:2:229:ASP:HB2	2.19	0.67
27:3:59:VAL:N	27:3:71:TYR:CD1	2.63	0.67
2:B:79:GLU:C	2:B:80:GLU:HG2	2.20	0.67
3:C:53:ASP:HB3	3:C:160:ARG:HB3	1.76	0.67
21:U:180:ILE:HG21	21:U:187:TYR:HB2	1.76	0.67
22:V:393:THR:HA	22:V:418:LYS:HE3	1.76	0.67
22:V:515:SER:HB3	22:V:539:ASN:ND2	2.04	0.67
10:J:63:ALA:H	10:J:64:PRO:HD2	1.60	0.67
22:V:516:PRO:HB2	22:V:706:LYS:NZ	2.10	0.67
26:2:118:LEU:HD11	27:3:43:VAL:HG23	1.75	0.67
26:2:211:GLN:HB3	26:2:261:PHE:HE1	1.59	0.67
1:A:874:LYS:HG3	1:A:880:ARG:HD2	1.77	0.67
9:I:99:SER:OG	9:I:105:GLU:HG3	1.84	0.67
14:N:353:LEU:N	14:N:370:ALA:O	2.17	0.67
18:R:195:PRO:HG2	18:R:199:LYS:N	2.08	0.67
21:U:218:ASP:O	21:U:222:ARG:HB2	1.95	0.67
25:1:1:MET:SD	26:2:419:GLU:HB2	2.34	0.67
27:3:137:LEU:HB3	27:3:180:VAL:CG1	2.20	0.67
1:A:1196:TYR:CD2	1:A:1246:ILE:HD11	2.29	0.67
2:B:63:PRO:HB3	2:B:408:PHE:HZ	1.59	0.67
8:H:17:PRO:HG3	8:H:27:ARG:H	1.58	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:1:34:ILE:CG1	25:1:50:VAL:HG11	2.21	0.67
18:R:224:THR:HG23	18:R:230:GLU:HB2	1.75	0.67
22:V:667:THR:HA	25:1:62:ASP:CG	2.19	0.67
26:2:170:ALA:HB1	26:2:213:TRP:CZ3	2.29	0.67
26:2:251:VAL:HG11	26:2:254:MET:HG3	1.77	0.67
2:B:892:CYS:HA	13:M:52:TRP:HE1	1.58	0.67
26:2:44:VAL:HG13	26:2:45:PHE:HD1	1.59	0.67
27:3:217:VAL:HG13	27:3:226:TYR:CE2	2.30	0.67
2:B:501:LEU:HD11	2:B:505:LEU:HD22	1.77	0.66
20:T:145:LEU:HD13	20:T:148:VAL:HG22	1.75	0.66
1:A:43:TYR:HD1	1:A:45:GLU:HG2	1.59	0.66
1:A:418:TYR:O	1:A:447:GLU:N	2.28	0.66
20:T:154:LYS:HD2	20:T:154:LYS:N	2.08	0.66
22:V:519:TYR:CE2	25:1:20:LEU:CG	2.73	0.66
23:W:52:LEU:HD23	23:W:72:TYR:CZ	2.29	0.66
1:A:642:LYS:HD3	21:U:284:PRO:HD3	1.77	0.66
1:A:1323:THR:HG23	1:A:1325:ASP:H	1.59	0.66
3:C:50:VAL:HB	12:L:55:PHE:HB2	1.77	0.66
10:J:21:TYR:HB2	10:J:38:LEU:HD11	1.77	0.66
14:N:46:TRP:HZ2	15:O:11:LEU:HD12	1.60	0.66
14:N:318:ASP:HB2	16:P:239:ARG:HH21	1.59	0.66
16:P:309:LYS:HD2	29:Y:82:DT:H3'	1.78	0.66
27:3:187:GLN:CG	27:3:189:ILE:HG12	2.24	0.66
2:B:842:HIS:HE1	13:M:27:TYR:HB3	1.61	0.66
27:3:130:GLU:HB2	27:3:173:GLN:HE22	1.61	0.66
27:3:184:ALA:CA	27:3:187:GLN:HG2	2.25	0.66
1:A:816:GLY:O	1:A:819:SER:OG	2.14	0.66
1:A:885:GLN:NE2	5:E:168:ASN:OD1	2.22	0.66
11:K:18:LYS:O	11:K:36:ASN:N	2.23	0.66
26:2:189:GLU:HA	26:2:192:GLU:CG	2.26	0.66
2:B:1029:TYR:OH	3:C:185:GLU:OE1	2.13	0.66
5:E:52:ARG:CB	5:E:53:PRO:CD	2.73	0.66
12:L:34:ILE:HG13	12:L:42:ARG:HD2	1.78	0.66
23:W:209:TYR:HH	23:W:233:PHE:CA	1.94	0.66
23:W:293:ARG:HG2	23:W:421:PHE:CZ	2.30	0.66
2:B:848:LEU:HD21	2:B:868:GLY:HA3	1.77	0.66
3:C:67:ARG:NH1	3:C:150:ILE:O	2.28	0.66
16:P:179:ASP:OD1	16:P:181:LYS:NZ	2.29	0.66
16:P:293:TYR:HD2	16:P:302:LEU:HD13	1.61	0.66
26:2:56:VAL:HG11	26:2:91:SER:HB2	1.77	0.66
27:3:45:GLY:O	27:3:49:LEU:HD23	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:191:PHE:CB	18:R:202:PHE:CD1	2.78	0.66
27:3:207:CYS:SG	27:3:214:TYR:HB2	2.34	0.66
28:X:52:DG:N2	29:Y:43:DG:C2	2.64	0.66
1:A:361:PHE:H	2:B:1063:ALA:HA	1.61	0.66
9:I:84:HIS:H	9:I:84:HIS:CD2	2.13	0.66
9:I:86:CYS:O	9:I:87:GLN:C	2.39	0.66
13:M:124:MET:HA	13:M:127:ARG:NH2	2.11	0.66
23:W:432:ILE:CD1	23:W:434:HIS:HE1	2.09	0.66
1:A:782:SER:O	1:A:787:VAL:N	2.29	0.66
3:C:99:VAL:HG13	3:C:124:SER:HB2	1.77	0.66
20:T:174:LYS:CB	28:X:20:DG:H4'	2.26	0.66
27:3:144:ILE:O	27:3:147:MET:HG3	1.96	0.66
3:C:200:PRO:CG	3:C:217:GLN:CB	2.74	0.65
18:R:191:PHE:CB	18:R:202:PHE:CE1	2.79	0.65
1:A:1112:VAL:O	21:U:252:LYS:CG	2.44	0.65
2:B:935:PHE:HE2	2:B:945:CYS:HB2	1.62	0.65
20:T:164:GLU:OE2	20:T:167:ARG:NH2	2.29	0.65
26:2:173:GLN:CD	26:2:179:LEU:HD21	2.22	0.65
26:2:218:GLN:CG	26:2:268:PHE:HB3	2.26	0.65
1:A:784:VAL:HG23	1:A:785:ILE:HG13	1.78	0.65
17:Q:105:TYR:CE1	18:R:234:GLU:CG	2.78	0.65
22:V:631:GLY:O	22:V:632:SER:HB3	1.95	0.65
25:1:8:VAL:HG12	25:1:9:LEU:N	2.10	0.65
26:2:172:SER:O	26:2:175:LEU:HD23	1.95	0.65
26:2:236:PHE:CZ	26:2:262:LEU:HD22	2.32	0.65
27:3:14:VAL:HG22	27:3:163:VAL:HA	1.78	0.65
1:A:73:THR:OG1	2:B:1130:THR:OG1	2.15	0.65
22:V:522:TYR:HE2	25:1:62:ASP:CG	1.96	0.65
17:Q:187:ILE:O	18:R:212:VAL:HA	1.97	0.65
22:V:531:ILE:CA	22:V:534:TYR:HE2	1.89	0.65
25:1:10:ILE:HG21	26:2:407:VAL:HG21	1.77	0.65
25:1:35:ILE:HG22	25:1:46:ILE:HD12	1.78	0.65
1:A:1172:ASN:O	1:A:1215:GLU:N	2.19	0.65
23:W:423:ASP:C	23:W:425:THR:H	2.04	0.65
26:2:57:MET:HA	26:2:60:LEU:HD11	1.76	0.65
26:2:171:VAL:HG13	26:2:216:MET:CB	2.26	0.65
1:A:434:LYS:HB2	1:A:437:ASP:HB3	1.79	0.65
1:A:604:ARG:O	1:A:606:HIS:N	2.28	0.65
1:A:1146:GLN:O	1:A:1150:ASP:N	2.27	0.65
5:E:65:ASN:O	5:E:67:ASP:CA	2.43	0.65
23:W:584:TYR:CZ	23:W:614:TYR:HB2	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:0:98:GLN:OE1	27:3:209:ILE:HA	1.96	0.65
26:2:117:ASN:CG	27:3:108:ASN:CG	2.65	0.65
26:2:117:ASN:ND2	27:3:42:MET:CE	2.60	0.65
1:A:113:PHE:CE1	18:R:229:ASP:N	2.62	0.65
1:A:611:ASP:OD2	1:A:617:PRO:CB	2.45	0.65
3:C:214:ASP:OD2	3:C:216:SER:OG	2.12	0.65
22:V:412:MET:HA	22:V:417:THR:HG21	1.77	0.65
23:W:410:TYR:C	23:W:412:LYS:N	2.52	0.65
24:0:54:ARG:CD	27:3:182:PHE:CE1	2.60	0.65
27:3:131:THR:O	27:3:133:LEU:HD13	1.97	0.65
27:3:146:ARG:O	27:3:149:LYS:HG2	1.95	0.65
1:A:275:ASP:HB2	1:A:342:ARG:NH2	2.10	0.65
2:B:65:ILE:HG21	2:B:412:LEU:HD11	1.76	0.65
22:V:520:ARG:HG3	25:1:23:LEU:HD11	1.79	0.65
26:2:159:VAL:HG11	26:2:161:HIS:HD2	1.62	0.65
26:2:266:ARG:O	26:2:270:LEU:HB2	1.97	0.65
27:3:70:LEU:CD1	27:3:115:ILE:HD11	2.27	0.65
1:A:1274:GLU:O	1:A:1275:VAL:C	2.40	0.65
2:B:93:LEU:HD12	2:B:123:PRO:O	1.97	0.65
5:E:62:VAL:HG23	5:E:72:MET:CB	2.22	0.65
26:2:45:PHE:HB2	26:2:51:LEU:CD1	2.26	0.65
1:A:1290:SER:HB3	2:B:250:SER:O	1.97	0.64
2:B:102:ASP:O	13:M:217:ARG:NE	2.27	0.64
17:Q:106:LYS:C	18:R:218:LYS:HE2	2.20	0.64
26:2:81:LYS:HE3	26:2:93:LEU:CD2	2.20	0.64
27:3:106:SER:O	27:3:110:VAL:HG23	1.97	0.64
7:G:91:GLN:HB2	7:G:98:PHE:HD2	1.62	0.64
13:M:178:LYS:C	20:T:154:LYS:HB2	2.21	0.64
27:3:33:THR:CG2	27:3:36:LYS:HB2	2.26	0.64
27:3:187:GLN:HG3	27:3:189:ILE:CG1	2.24	0.64
1:A:1147:SER:OG	1:A:1351:ASP:OD2	2.15	0.64
1:A:1310:HIS:HE1	1:A:1334:TRP:HA	1.61	0.64
2:B:242:ARG:C	2:B:244:GLY:H	2.06	0.64
3:C:211:LEU:C	3:C:213:GLU:N	2.52	0.64
20:T:138:PRO:C	20:T:140:ARG:H	2.05	0.64
23:W:581:LEU:HD21	23:W:608:ILE:HG21	1.78	0.64
26:2:270:LEU:HD23	26:2:273:GLN:HE21	1.62	0.64
1:A:370:ASP:HB2	1:A:483:ARG:HB3	1.80	0.64
1:A:1244:ASN:HB3	1:A:1260:ARG:HB2	1.79	0.64
2:B:874:PRO:O	2:B:876:ASN:N	2.27	0.64
25:1:35:ILE:HG22	25:1:46:ILE:CD1	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:2:270:LEU:HD23	26:2:270:LEU:O	1.97	0.64
27:3:192:ASP:HB2	27:3:231:PHE:CE1	2.32	0.64
1:A:425:ASP:HB3	13:M:39:LEU:CG	2.28	0.64
2:B:714:PRO:HD2	2:B:1001:PRO:HB3	1.77	0.64
3:C:13:GLU:O	3:C:20:LYS:N	2.30	0.64
26:2:202:GLN:HE21	26:2:202:GLN:H	1.44	0.64
11:K:29:ASN:ND2	11:K:78:THR:O	2.30	0.64
18:R:140:LYS:HG2	18:R:141:PRO:HD3	1.78	0.64
23:W:696:TRP:HD1	23:W:697:ILE:HG13	1.62	0.64
25:1:1:MET:HE3	26:2:415:GLN:CA	2.28	0.64
25:1:59:GLU:CD	26:2:402:ARG:NH1	2.56	0.64
27:3:17:ALA:CB	27:3:63:HIS:HD2	2.10	0.64
1:A:621:ILE:HG22	1:A:623:PRO:CD	2.28	0.64
1:A:1250:ASP:HA	1:A:1255:LEU:HD21	1.78	0.64
3:C:258:ASP:OD2	11:K:18:LYS:NZ	2.31	0.64
18:R:195:PRO:HB3	18:R:199:LYS:CD	2.27	0.64
23:W:59:TYR:CE1	23:W:62:ALA:HB2	2.26	0.64
1:A:1253:GLU:HG2	1:A:1254:LYS:HG2	1.79	0.64
17:Q:102:VAL:O	17:Q:105:TYR:N	2.31	0.64
18:R:161:ARG:NE	18:R:203:PHE:CE1	2.60	0.64
19:S:126:ILE:N	19:S:138:PHE:O	2.23	0.64
27:3:160:ARG:NH2	27:3:190:LEU:HD12	2.13	0.64
2:B:92:TYR:CB	20:T:145:LEU:HB3	2.26	0.64
2:B:1107:LEU:O	2:B:1111:SER:OG	2.15	0.64
18:R:129:LYS:CB	18:R:140:LYS:CB	2.69	0.64
20:T:145:LEU:C	20:T:147:LYS:H	2.03	0.64
22:V:426:VAL:HG13	22:V:427:MET:H	1.63	0.64
24:0:77:LYS:C	24:0:79:ASN:H	2.03	0.64
26:2:140:LYS:HG2	26:2:162:PHE:CE1	2.33	0.64
27:3:165:LYS:O	27:3:165:LYS:HD3	1.98	0.64
1:A:1036:ASN:HB2	5:E:202:ARG:HB3	1.78	0.64
1:A:1288:ILE:O	1:A:1292:MET:N	2.27	0.64
2:B:646:ARG:HD3	2:B:651:TYR:N	2.13	0.64
16:P:205:ARG:O	16:P:206:GLU:C	2.40	0.64
20:T:158:ASN:HB3	20:T:161:TYR:HB3	1.80	0.64
26:2:258:LEU:HG	26:2:262:LEU:CD2	2.28	0.64
27:3:214:TYR:CE2	27:3:216:LYS:HE2	2.32	0.64
1:A:621:ILE:C	1:A:623:PRO:HD2	2.18	0.63
8:H:10:PHE:N	8:H:56:PHE:O	2.28	0.63
17:Q:187:ILE:CB	18:R:212:VAL:H	2.09	0.63
1:A:629:VAL:HG13	1:A:636:ILE:HB	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:17:LEU:HD13	17:Q:194:THR:HB	1.80	0.63
17:Q:106:LYS:HG2	18:R:218:LYS:CE	2.27	0.63
27:3:59:VAL:HB	27:3:71:TYR:CD1	2.25	0.63
27:3:64:ILE:HB	27:3:123:ASP:OD2	1.98	0.63
27:3:144:ILE:HD13	27:3:147:MET:HE3	1.80	0.63
12:L:25:GLU:HB2	12:L:27:GLU:CG	2.25	0.63
12:L:26:ASN:HA	12:L:37:ARG:HH12	1.63	0.63
18:R:155:LEU:CB	18:R:204:ASN:ND2	2.59	0.63
20:T:174:LYS:HE3	28:X:20:DG:H1'	1.80	0.63
25:1:38:ILE:HB	25:1:44:PHE:HE1	1.63	0.63
27:3:133:LEU:HD22	27:3:134:ALA:N	2.14	0.63
2:B:692:THR:HB	9:I:76:PRO:HB2	1.79	0.63
2:B:829:PHE:HE1	2:B:869:LYS:HD3	1.63	0.63
26:2:30:VAL:CG1	27:3:25:GLN:CA	2.72	0.63
27:3:59:VAL:CB	27:3:71:TYR:HE1	1.94	0.63
1:A:514:GLU:OE2	2:B:1101:GLN:HB2	1.99	0.63
1:A:565:MET:HG2	11:K:61:TYR:C	2.24	0.63
2:B:840:MET:O	2:B:842:HIS:N	2.31	0.63
2:B:956:PHE:O	2:B:1029:TYR:N	2.23	0.63
23:W:419:GLU:HB3	23:W:420:PRO:CD	2.29	0.63
25:1:5:LEU:HD21	26:2:408:LEU:HD13	0.85	0.63
25:1:13:ASP:CG	25:1:14:PRO:HD2	2.24	0.63
26:2:123:LEU:O	26:2:123:LEU:HD23	1.99	0.63
26:2:220:LEU:O	26:2:220:LEU:HD13	1.98	0.63
2:B:1087:GLY:N	2:B:1090:GLU:OE1	2.28	0.63
14:N:333:ASN:HB3	14:N:359:ASN:O	1.99	0.63
26:2:173:GLN:HG2	26:2:179:LEU:HG	1.81	0.63
26:2:177:GLN:OE1	26:2:220:LEU:HD22	1.98	0.63
26:2:211:GLN:CB	26:2:261:PHE:HE1	2.11	0.63
27:3:190:LEU:H	27:3:190:LEU:CD2	2.11	0.63
24:0:77:LYS:C	24:0:79:ASN:N	2.56	0.63
1:A:485:ASN:HB3	1:A:488:VAL:HG23	1.79	0.63
1:A:497:ASP:HB2	2:B:942:LYS:HE3	1.80	0.63
17:Q:21:VAL:HA	18:R:210:PHE:HE2	1.64	0.63
17:Q:25:PHE:HD2	18:R:215:GLU:OE2	1.80	0.63
22:V:315:VAL:HG12	23:W:500:ASP:CB	2.17	0.63
26:2:31:LEU:CG	27:3:33:THR:HB	2.28	0.63
26:2:89:LEU:HD23	26:2:89:LEU:O	1.99	0.63
26:2:118:LEU:CD2	27:3:39:ASP:C	2.72	0.63
27:3:149:LYS:HG3	27:3:150:GLU:N	2.12	0.63
27:3:196:LEU:CD2	27:3:223:LEU:HD23	2.25	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1208:SER:O	1:A:1260:ARG:NH1	2.31	0.63
2:B:242:ARG:O	2:B:244:GLY:N	2.31	0.63
2:B:765:GLU:O	2:B:768:ARG:NH1	2.31	0.63
13:M:297:PRO:HA	13:M:310:VAL:HG11	1.81	0.63
14:N:368:SER:N	15:O:54:ASN:O	2.25	0.63
26:2:60:LEU:HD11	26:2:95:ILE:CB	2.29	0.63
1:A:191:ILE:HD12	1:A:216:LEU:HD11	1.81	0.62
1:A:734:ARG:HH21	9:I:105:GLU:C	2.07	0.62
9:I:92:LYS:NZ	9:I:93:GLU:OE2	2.32	0.62
25:1:18:GLN:NE2	25:1:44:PHE:HZ	1.96	0.62
25:1:47:ALA:HB1	25:1:50:VAL:HB	1.81	0.62
27:3:58:ALA:CA	27:3:71:TYR:OH	2.41	0.62
2:B:513:GLU:O	2:B:525:ASN:ND2	2.32	0.62
3:C:129:PRO:HG2	3:C:134:ASN:HD22	1.63	0.62
10:J:40:LEU:O	10:J:46:ARG:NE	2.32	0.62
17:Q:113:ARG:HE	18:R:217:GLN:C	2.06	0.62
22:V:316:LEU:HB2	22:V:321:GLU:CG	2.29	0.62
27:3:184:ALA:HA	27:3:187:GLN:CG	2.29	0.62
1:A:427:ILE:CD1	13:M:38:GLY:O	2.46	0.62
1:A:551:ARG:CD	1:A:637:MET:HE1	2.28	0.62
2:B:779:ILE:HA	2:B:1045:PRO:HA	1.80	0.62
22:V:451:PHE:CE2	28:X:57:DC:H5"	2.34	0.62
26:2:46:ARG:CD	26:2:85:GLU:HB2	2.30	0.62
1:A:612:ASP:C	1:A:614:ASP:N	2.55	0.62
2:B:133:ILE:C	2:B:134:LYS:HG2	2.25	0.62
3:C:35:ARG:HA	3:C:38:PHE:CD2	2.35	0.62
10:J:63:ALA:H	10:J:64:PRO:CD	2.12	0.62
18:R:210:PHE:HD1	18:R:210:PHE:O	1.82	0.62
22:V:516:PRO:CD	22:V:706:LYS:NZ	2.55	0.62
25:1:1:MET:HB3	26:2:413:LEU:HG	1.81	0.62
25:1:38:ILE:HB	25:1:44:PHE:CE1	2.35	0.62
26:2:35:TYR:CZ	26:2:62:LEU:HG	2.34	0.62
1:A:43:TYR:CD1	1:A:45:GLU:HG2	2.34	0.62
3:C:47:ILE:HG21	3:C:68:LEU:HD23	1.80	0.62
13:M:173:VAL:HB	13:M:175:ARG:HH12	1.63	0.62
17:Q:113:ARG:HE	18:R:217:GLN:HB3	1.64	0.62
25:1:4:VAL:CG1	26:2:411:GLN:O	2.40	0.62
25:1:35:ILE:HA	25:1:46:ILE:HG13	1.80	0.62
27:3:46:ASN:CG	27:3:104:LEU:HD22	2.25	0.62
1:A:934:LEU:O	1:A:936:GLU:N	2.30	0.62
1:A:1313:GLN:OE1	1:A:1335:ILE:HD13	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:838:GLN:OE1	2:B:886:ARG:NH1	2.33	0.62
9:I:86:CYS:C	9:I:88:LYS:H	2.08	0.62
12:L:25:GLU:CB	12:L:27:GLU:HG3	2.26	0.62
22:V:517:GLU:HB2	22:V:713:LEU:HD22	1.79	0.62
23:W:584:TYR:CG	23:W:594:ALA:HB2	2.34	0.62
27:3:17:ALA:HB1	27:3:63:HIS:HD2	1.63	0.62
1:A:1080:ILE:HD13	6:F:54:THR:HG21	1.82	0.62
1:A:1290:SER:CB	2:B:250:SER:O	2.48	0.62
1:A:1307:VAL:O	1:A:1308:TYR:CD2	2.52	0.62
2:B:87:LYS:O	2:B:129:THR:N	2.23	0.62
2:B:322:GLY:HA3	2:B:335:ARG:HB3	1.81	0.62
3:C:110:ASP:HA	3:C:155:LYS:HD2	1.82	0.62
13:M:107:MET:HE2	13:M:107:MET:CA	2.29	0.62
17:Q:22:ILE:HG22	17:Q:34:LEU:HD13	1.81	0.62
1:A:551:ARG:NH1	1:A:637:MET:HE1	2.15	0.62
1:A:939:VAL:HA	1:A:942:VAL:HG22	1.81	0.62
16:P:296:ILE:O	16:P:297:LYS:C	2.42	0.62
18:R:195:PRO:HB3	18:R:199:LYS:HD2	1.82	0.62
25:1:17:LYS:O	25:1:20:LEU:HB3	1.99	0.62
27:3:70:LEU:HD13	27:3:115:ILE:CD1	2.28	0.62
2:B:808:SER:OG	2:B:1050:ARG:NH1	2.33	0.62
5:E:107:GLN:HG2	5:E:132:GLN:NE2	2.15	0.62
8:H:9:ILE:O	8:H:33:GLU:HG2	1.99	0.62
9:I:95:VAL:N	9:I:113:VAL:O	2.24	0.62
13:M:107:MET:HB2	13:M:112:ARG:HH12	1.65	0.62
20:T:31:TRP:HD1	20:T:62:LEU:HD21	1.64	0.62
25:1:1:MET:HA	26:2:413:LEU:HA	1.80	0.62
25:1:13:ASP:OD1	25:1:14:PRO:HD2	2.00	0.62
1:A:948:ILE:HG13	1:A:1007:ILE:HD11	1.81	0.62
1:A:1204:VAL:HA	1:A:1207:ILE:HG23	1.81	0.62
2:B:194:LEU:HD11	2:B:466:VAL:HG12	1.81	0.62
2:B:226:GLU:OE1	2:B:227:ASN:ND2	2.33	0.62
2:B:801:VAL:HA	2:B:805:PHE:HB3	1.81	0.62
3:C:56:SER:OG	3:C:158:GLU:N	2.33	0.62
3:C:154:ARG:NE	10:J:65:LEU:HD12	2.15	0.62
5:E:149:VAL:HB	5:E:192:LYS:HB3	1.80	0.62
6:F:78:PRO:HD3	7:G:16:ARG:HA	1.82	0.62
14:N:344:ARG:NH2	29:Y:78:DT:OP1	2.23	0.62
25:1:10:ILE:HG22	26:2:407:VAL:HG21	1.80	0.62
1:A:931:ARG:O	1:A:933:THR:N	2.32	0.61
1:A:1307:VAL:HG13	1:A:1338:THR:HA	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:34:VAL:HG11	15:O:28:ILE:HG22	1.82	0.61
17:Q:23:ARG:CZ	18:R:207:SER:H	2.13	0.61
17:Q:110:MET:CA	18:R:218:LYS:HG3	2.29	0.61
27:3:9:ASN:O	27:3:56:LYS:HD3	1.99	0.61
8:H:74:GLU:C	8:H:76:ASN:N	2.39	0.61
23:W:250:ASN:CB	23:W:434:HIS:CG	2.82	0.61
26:2:189:GLU:O	26:2:193:PRO:HD2	2.00	0.61
26:2:218:GLN:HG2	26:2:268:PHE:HB3	1.82	0.61
1:A:85:PHE:CD1	1:A:257:PRO:HD3	2.35	0.61
2:B:50:PHE:HA	2:B:54:SER:HB2	1.82	0.61
2:B:131:THR:O	2:B:132:VAL:HG12	1.99	0.61
3:C:1:MET:HG3	3:C:2:PRO:HD2	1.82	0.61
26:2:160:LEU:HB3	26:2:206:LEU:CD1	2.27	0.61
7:G:58:VAL:HB	7:G:67:LEU:HB3	1.82	0.61
9:I:87:GLN:HE21	9:I:121:HIS:HB3	1.65	0.61
14:N:314:LEU:HD11	16:P:238:ALA:HB1	1.82	0.61
17:Q:187:ILE:O	18:R:212:VAL:CA	2.47	0.61
23:W:209:TYR:OH	23:W:233:PHE:C	2.42	0.61
1:A:208:ASP:OD2	1:A:212:LYS:NZ	2.33	0.61
2:B:788:TYR:HB2	2:B:795:ILE:HD11	1.81	0.61
6:F:100:ARG:HB2	6:F:120:VAL:HG12	1.83	0.61
8:H:96:VAL:HB	8:H:136:GLU:HA	1.83	0.61
15:O:59:ARG:O	15:O:80:GLU:N	2.32	0.61
25:1:1:MET:HG2	26:2:414:SER:N	2.16	0.61
25:1:10:ILE:C	25:1:10:ILE:HD13	2.26	0.61
26:2:31:LEU:HG	27:3:25:GLN:O	2.00	0.61
26:2:83:GLN:OE1	26:2:83:GLN:HA	2.01	0.61
26:2:197:THR:HG21	26:2:239:GLN:CD	2.24	0.61
27:3:16:ASP:O	27:3:21:TRP:NE1	2.27	0.61
27:3:134:ALA:HB2	27:3:176:ASN:OD1	1.99	0.61
1:A:784:VAL:HA	1:A:827:TYR:HB2	1.83	0.61
10:J:63:ALA:N	10:J:64:PRO:HD2	2.15	0.61
16:P:161:ILE:O	16:P:161:ILE:HG22	1.99	0.61
16:P:192:TYR:HB2	16:P:200:VAL:HG22	1.83	0.61
22:V:516:PRO:CB	22:V:706:LYS:HZ1	2.11	0.61
27:3:8:LEU:HA	27:3:54:SER:HB3	1.83	0.61
27:3:18:ASN:O	27:3:21:TRP:HD1	1.83	0.61
1:A:475:ARG:NH2	11:K:68:GLU:OE2	2.26	0.61
1:A:637:MET:HG3	8:H:122:LEU:HD21	1.83	0.61
3:C:136:ASP:HB2	3:C:145:GLN:CD	2.22	0.61
20:T:20:LEU:O	20:T:114:ALA:N	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:611:GLY:O	22:V:615:PHE:HB3	2.01	0.61
1:A:275:ASP:HA	1:A:278:HIS:ND1	2.16	0.61
1:A:1290:SER:OG	2:B:250:SER:O	2.19	0.61
2:B:713:PHE:HB3	2:B:716:HIS:ND1	2.15	0.61
8:H:65:TYR:CD2	8:H:70:LEU:CD2	2.84	0.61
16:P:167:ASN:HB2	29:Y:80:DT:C4'	2.30	0.61
18:R:142:LYS:HE2	18:R:144:ASN:HB3	1.83	0.61
18:R:195:PRO:CG	18:R:199:LYS:C	2.73	0.61
26:2:60:LEU:CD1	26:2:95:ILE:HB	2.31	0.61
26:2:93:LEU:HA	26:2:96:TRP:HD1	1.64	0.61
27:3:64:ILE:CG1	27:3:123:ASP:HB3	2.29	0.61
1:A:72:GLN:HE22	1:A:84:HIS:CD2	2.19	0.61
1:A:935:GLN:HA	1:A:1001:PRO:HA	1.81	0.61
5:E:104:ILE:O	5:E:129:GLN:NE2	2.33	0.61
8:H:66:GLU:O	8:H:67:ASP:HB2	1.99	0.61
23:W:37:HIS:ND1	23:W:454:VAL:HG13	2.15	0.61
1:A:693:ILE:HG13	2:B:1023:ARG:HE	1.63	0.61
1:A:1347:LEU:HB3	5:E:137:ILE:HG12	1.83	0.61
2:B:67:LEU:HD22	2:B:419:ALA:HB1	1.83	0.61
8:H:66:GLU:O	8:H:67:ASP:CG	2.44	0.61
8:H:105:SER:O	8:H:106:THR:CB	2.48	0.61
12:L:15:MET:HG3	12:L:47:LYS:HB2	1.83	0.61
13:M:279:GLY:HA2	20:T:153:TYR:CE1	2.35	0.61
18:R:195:PRO:HG3	18:R:199:LYS:CA	2.28	0.61
2:B:242:ARG:HB3	2:B:252:ILE:CG2	2.30	0.60
2:B:405:ARG:O	2:B:409:LYS:HG3	2.01	0.60
14:N:341:LYS:HB3	14:N:352:HIS:HB2	1.80	0.60
23:W:209:TYR:CE1	23:W:233:PHE:CD1	2.89	0.60
27:3:24:LYS:HE2	27:3:220:MET:SD	2.41	0.60
28:X:17:DA:H2"	28:X:18:DG:C8	2.36	0.60
1:A:18:ILE:HG21	2:B:1171:MET:HG3	1.83	0.60
2:B:37:LYS:HE2	2:B:653:TRP:CD1	2.36	0.60
17:Q:25:PHE:HE2	18:R:215:GLU:HG3	1.61	0.60
25:1:50:VAL:HA	25:1:53:LEU:HD13	1.82	0.60
26:2:100:LEU:HG	26:2:119:ARG:NE	2.13	0.60
27:3:58:ALA:CA	27:3:71:TYR:CE2	2.80	0.60
27:3:100:LYS:HG3	27:3:101:TYR:N	2.16	0.60
1:A:1143:LEU:HB3	1:A:1147:SER:HB2	1.83	0.60
2:B:85:LEU:H	2:B:132:VAL:HG12	1.64	0.60
8:H:107:GLU:O	8:H:108:ALA:C	2.44	0.60
12:L:36:CYS:HB2	12:L:44:MET:HE1	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:423:ASP:O	23:W:425:THR:N	2.34	0.60
24:O:55:LEU:HD12	27:3:178:MET:CE	2.31	0.60
26:2:164:VAL:HG13	26:2:209:PRO:HG2	1.83	0.60
26:2:202:GLN:NE2	26:2:202:GLN:H	2.00	0.60
1:A:426:ARG:O	13:M:40:VAL:N	2.34	0.60
1:A:459:ASN:HB3	1:A:469:MET:HE3	1.83	0.60
1:A:625:ASP:CA	1:A:637:MET:HE3	2.30	0.60
2:B:225:LEU:HD13	2:B:228:SER:HB2	1.83	0.60
2:B:568:PHE:O	2:B:614:ILE:N	2.34	0.60
8:H:31:GLU:HA	8:H:38:ASP:HA	1.82	0.60
20:T:138:PRO:O	20:T:140:ARG:N	2.34	0.60
20:T:224:ASN:HB3	20:T:226:LYS:HG2	1.82	0.60
23:W:37:HIS:CE1	23:W:454:VAL:CG1	2.82	0.60
23:W:584:TYR:HB2	23:W:594:ALA:HB2	1.81	0.60
26:2:30:VAL:HG22	26:2:34:LEU:CD2	2.31	0.60
2:B:737:ILE:HD11	2:B:743:ARG:HG3	1.83	0.60
4:D:103:LEU:HD22	7:G:144:ARG:HH12	1.65	0.60
26:2:171:VAL:HG13	26:2:216:MET:HB2	1.83	0.60
1:A:1248:ASN:ND2	1:A:1254:LYS:O	2.28	0.60
2:B:75:SER:O	2:B:78:VAL:HG22	2.00	0.60
2:B:257:VAL:HG23	2:B:257:VAL:O	2.00	0.60
2:B:873:LEU:HB3	2:B:874:PRO:HD3	1.79	0.60
2:B:876:ASN:OD1	2:B:879:GLU:CD	2.44	0.60
6:F:96:GLU:O	6:F:100:ARG:N	2.34	0.60
9:I:22:ASN:OD1	9:I:41:ASN:ND2	2.35	0.60
11:K:77:THR:OG1	11:K:81:TYR:O	2.14	0.60
13:M:106:THR:CG2	13:M:109:SER:OG	2.49	0.60
16:P:297:LYS:CB	16:P:298:PRO:HD2	2.22	0.60
20:T:228:ILE:HD12	20:T:230:LYS:HD3	1.83	0.60
22:V:368:ALA:O	22:V:371:VAL:HG22	2.00	0.60
23:W:59:TYR:OH	23:W:63:TYR:CE2	2.52	0.60
25:1:8:VAL:O	26:2:407:VAL:HG12	2.00	0.60
26:2:236:PHE:CE2	26:2:262:LEU:HD13	2.36	0.60
3:C:200:PRO:CG	3:C:217:GLN:CD	2.57	0.60
4:D:108:ALA:N	4:D:128:GLN:OE1	2.32	0.60
7:G:11:ILE:O	7:G:68:TYR:N	2.25	0.60
8:H:98:ARG:HD3	8:H:115:TYR:HD2	1.66	0.60
12:L:22:CYS:SG	12:L:24:THR:OG1	2.56	0.60
15:O:86:GLU:HG3	15:O:88:ILE:HD11	1.82	0.60
18:R:195:PRO:CB	18:R:199:LYS:HD2	2.31	0.60
19:S:47:LEU:HD22	20:T:7:LEU:HD22	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:628:VAL:HA	1:A:638:GLY:HA3	1.84	0.60
1:A:1313:GLN:HB2	1:A:1333:GLU:CG	2.31	0.60
2:B:117:ASN:HA	2:B:189:GLY:HA3	1.84	0.60
2:B:655:ASP:O	2:B:659:SER:N	2.35	0.60
13:M:289:TYR:OH	13:M:314:PRO:O	2.17	0.60
3:C:154:ARG:HD3	10:J:65:LEU:HD13	1.71	0.60
14:N:308:GLN:NE2	14:N:310:GLU:O	2.28	0.60
18:R:155:LEU:HG	18:R:204:ASN:HD22	0.77	0.60
20:T:155:PRO:O	20:T:157:ALA:N	2.27	0.60
23:W:410:TYR:HE2	23:W:413:GLY:HA3	1.65	0.60
25:1:1:MET:HB2	26:2:418:PHE:HB3	1.84	0.60
1:A:611:ASP:CB	1:A:617:PRO:HG3	2.32	0.60
2:B:600:GLU:O	2:B:620:ARG:NH2	2.30	0.60
23:W:73:CYS:CB	23:W:209:TYR:CZ	2.84	0.60
26:2:259:LEU:HD12	26:2:259:LEU:C	2.27	0.60
1:A:1028:PRO:O	1:A:1032:GLN:N	2.34	0.59
5:E:63:ALA:O	5:E:64:HIS:CG	2.54	0.59
26:2:44:VAL:HG13	26:2:45:PHE:N	2.17	0.59
1:A:1212:LEU:HD23	1:A:1259:ILE:HD11	1.83	0.59
2:B:56:GLN:O	2:B:60:GLU:N	2.30	0.59
3:C:183:ALA:HB3	3:C:232:ASN:HB3	1.84	0.59
9:I:105:GLU:O	9:I:107:ALA:C	2.45	0.59
11:K:20:THR:N	11:K:34:THR:O	2.28	0.59
25:1:1:MET:HA	26:2:414:SER:N	2.14	0.59
26:2:42:LEU:HD12	26:2:59:MET:HE3	1.83	0.59
26:2:217:LEU:HD23	26:2:233:ILE:CD1	2.32	0.59
1:A:1394:ASN:HB3	1:A:1397:HIS:ND1	2.17	0.59
3:C:146:ASP:O	3:C:148:ILE:N	2.36	0.59
3:C:154:ARG:HD3	10:J:65:LEU:HB2	1.82	0.59
4:D:26:PHE:HZ	7:G:42:TYR:HA	1.66	0.59
8:H:14:ASP:HB3	8:H:29:HIS:HB2	1.85	0.59
18:R:129:LYS:HB2	18:R:140:LYS:HB2	1.75	0.59
20:T:20:LEU:N	20:T:112:GLN:O	2.28	0.59
26:2:203:PHE:HD2	26:2:205:LEU:HD23	1.64	0.59
9:I:86:CYS:SG	9:I:119:CYS:SG	3.00	0.59
19:S:102:VAL:O	19:S:108:ARG:N	2.35	0.59
21:U:221:ALA:C	21:U:223:MET:H	2.10	0.59
27:3:143:TYR:O	27:3:146:ARG:HG2	2.01	0.59
1:A:612:ASP:O	1:A:614:ASP:CA	2.50	0.59
3:C:106:ARG:NE	3:C:108:ASN:OD1	2.35	0.59
6:F:51:ARG:NH1	6:F:122:GLU:OE1	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:222:VAL:HG22	20:T:223:GLN:H	1.67	0.59
26:2:42:LEU:CD2	26:2:55:TRP:HB2	2.13	0.59
26:2:196:ILE:HA	26:2:202:GLN:OE1	2.02	0.59
26:2:215:PHE:CD2	26:2:264:HIS:HB2	2.38	0.59
27:3:131:THR:HG23	27:3:133:LEU:CD1	2.33	0.59
27:3:174:TYR:CE1	27:3:178:MET:HE3	2.37	0.59
27:3:213:LEU:HD23	27:3:230:VAL:HG12	1.84	0.59
27:3:216:LYS:H	27:3:216:LYS:CD	2.13	0.59
1:A:544:ALA:HB2	1:A:680:LEU:HD13	1.83	0.59
1:A:593:SER:HB3	1:A:634:GLU:HA	1.84	0.59
2:B:131:THR:O	2:B:132:VAL:CG1	2.50	0.59
6:F:44:ARG:H	6:F:45:PRO:HD2	1.66	0.59
9:I:112:TYR:N	9:I:123:TRP:O	2.34	0.59
18:R:129:LYS:C	18:R:140:LYS:CB	2.72	0.59
20:T:177:ARG:HG2	20:T:208:GLN:CG	2.29	0.59
22:V:520:ARG:NE	22:V:521:GLU:OE2	2.28	0.59
27:3:42:MET:HE2	27:3:108:ASN:CG	2.27	0.59
1:A:880:ARG:NH1	1:A:884:ASN:O	2.35	0.59
8:H:3:GLY:N	8:H:67:ASP:OD1	2.34	0.59
9:I:119:CYS:SG	9:I:120:GLY:N	2.76	0.59
11:K:21:ILE:HG23	11:K:33:PHE:CE1	2.38	0.59
12:L:16:ILE:HG22	12:L:16:ILE:O	2.03	0.59
14:N:318:ASP:CA	16:P:239:ARG:HE	2.16	0.59
26:2:35:TYR:CB	26:2:62:LEU:HD12	2.33	0.59
26:2:206:LEU:HD22	26:2:206:LEU:N	2.17	0.59
27:3:110:VAL:O	27:3:114:GLU:HG2	2.02	0.59
1:A:479:TRP:N	11:K:2:ASN:O	2.35	0.59
13:M:107:MET:HE2	13:M:107:MET:HA	1.84	0.59
14:N:21:VAL:HG11	15:O:40:PHE:HD1	1.68	0.59
16:P:261:SER:HB3	29:Y:81:DA:H4'	1.85	0.59
17:Q:105:TYR:OH	18:R:222:SER:HA	2.03	0.59
25:1:29:LEU:HD23	25:1:29:LEU:C	2.27	0.59
26:2:159:VAL:HG22	26:2:160:LEU:N	2.16	0.59
1:A:686:THR:HG21	2:B:1041:ILE:HG13	1.84	0.59
1:A:1168:LYS:HG3	1:A:1220:HIS:CE1	2.37	0.59
2:B:248:LYS:C	2:B:249:LYS:HG2	2.27	0.59
22:V:609:LYS:NZ	29:Y:38:DT:OP1	2.34	0.59
22:V:703:PHE:CZ	22:V:712:LEU:CD2	2.86	0.59
24:0:77:LYS:H	24:0:77:LYS:HD2	1.68	0.59
25:1:38:ILE:H	25:1:38:ILE:CD1	2.16	0.59
26:2:177:GLN:HE22	26:2:220:LEU:HA	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:93:LEU:C	20:T:145:LEU:HD21	2.27	0.59
2:B:175:ASN:O	2:B:739:ASN:ND2	2.32	0.59
2:B:556:ILE:HD12	2:B:561:ILE:HG21	1.84	0.59
2:B:897:ARG:NH1	2:B:1079:SER:OG	2.35	0.59
5:E:13:ILE:HG22	5:E:136:LEU:HA	1.85	0.59
13:M:182:ALA:HB2	20:T:154:LYS:HA	1.84	0.59
17:Q:131:VAL:HG21	17:Q:159:THR:HG21	1.85	0.59
23:W:175:TYR:HD1	23:W:175:TYR:H	1.46	0.59
23:W:584:TYR:HB2	23:W:594:ALA:CB	2.32	0.59
25:1:34:ILE:O	25:1:46:ILE:HG13	2.03	0.59
26:2:56:VAL:HG11	26:2:91:SER:CB	2.32	0.59
1:A:622:SER:N	1:A:623:PRO:CD	2.21	0.58
1:A:1264:SER:O	1:A:1266:GLU:N	2.33	0.58
2:B:88:PHE:CD2	2:B:128:ILE:HG12	2.37	0.58
2:B:542:LEU:HA	2:B:545:LEU:HD12	1.85	0.58
3:C:217:GLN:O	3:C:218:ALA:HB2	1.99	0.58
22:V:321:GLU:HA	23:W:499:ASN:HD21	1.65	0.58
26:2:203:PHE:CE2	26:2:205:LEU:HD23	2.38	0.58
27:3:169:ASP:CB	27:3:202:LEU:HD23	2.33	0.58
28:X:64:DC:O2	29:Y:31:DG:N2	2.36	0.58
1:A:1307:VAL:O	1:A:1308:TYR:CG	2.56	0.58
17:Q:113:ARG:CD	18:R:221:ARG:HG3	2.29	0.58
18:R:225:VAL:HG13	18:R:226:ASP:CG	2.17	0.58
24:0:109:THR:HB	24:0:144:SER:H	1.67	0.58
26:2:160:LEU:HD12	26:2:160:LEU:N	2.18	0.58
27:3:215:LEU:HD12	27:3:230:VAL:HG13	1.85	0.58
1:A:426:ARG:HB3	13:M:40:VAL:HG21	1.84	0.58
2:B:63:PRO:HB3	2:B:408:PHE:CZ	2.38	0.58
2:B:430:ASN:HB2	20:T:159:HIS:HE1	1.67	0.58
2:B:1022:LEU:HD12	2:B:1023:ARG:HG2	1.85	0.58
8:H:110:THR:O	8:H:110:THR:HG22	2.02	0.58
17:Q:104:LYS:NZ	18:R:238:LYS:HD2	2.18	0.58
26:2:118:LEU:HD12	26:2:118:LEU:C	2.29	0.58
28:X:47:DC:H2"	28:X:48:DG:C8	2.39	0.58
1:A:625:ASP:H	1:A:637:MET:CB	2.17	0.58
2:B:131:THR:C	2:B:132:VAL:CG1	2.76	0.58
2:B:171:LEU:HD22	2:B:176:GLU:HG2	1.83	0.58
2:B:866:ILE:H	2:B:895:PHE:HA	1.67	0.58
14:N:49:LYS:NZ	15:O:17:GLU:OE1	2.25	0.58
16:P:207:PRO:HB2	16:P:229:GLN:OE1	2.03	0.58
25:1:34:ILE:HG22	25:1:46:ILE:CD1	2.32	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:2:62:LEU:HD13	26:2:62:LEU:C	2.28	0.58
26:2:159:VAL:HG13	26:2:160:LEU:N	2.17	0.58
27:3:131:THR:CG2	27:3:133:LEU:HD12	2.33	0.58
27:3:215:LEU:CD1	27:3:230:VAL:HG13	2.32	0.58
27:3:222:SER:HB2	27:3:226:TYR:CE2	2.36	0.58
29:Y:30:DG:C2	29:Y:31:DG:C4	2.92	0.58
1:A:555:LEU:HD22	1:A:591:ILE:HG13	1.84	0.58
2:B:1115:GLN:HB2	2:B:1148:LEU:HD11	1.84	0.58
3:C:205:LYS:NZ	3:C:213:GLU:OE2	2.34	0.58
18:R:196:ASP:O	18:R:197:LYS:CB	2.50	0.58
25:1:53:LEU:HD12	25:1:53:LEU:N	2.18	0.58
2:B:548:TRP:CD1	2:B:583:LEU:HD13	2.38	0.58
2:B:573:TRP:CZ2	2:B:576:ILE:HG23	2.38	0.58
2:B:1036:LYS:HB2	3:C:194:HIS:HB3	1.85	0.58
5:E:65:ASN:O	5:E:67:ASP:C	2.47	0.58
7:G:6:SER:HA	7:G:73:LYS:HA	1.85	0.58
10:J:12:LYS:HE2	10:J:40:LEU:HA	1.86	0.58
14:N:318:ASP:HA	16:P:239:ARG:NE	2.18	0.58
21:U:143:LYS:NZ	21:U:147:MET:SD	2.75	0.58
24:O:54:ARG:C	27:3:209:ILE:HD11	2.26	0.58
1:A:47:THR:HG23	1:A:53:LYS:HA	1.86	0.58
1:A:286:ILE:HD13	1:A:313:HIS:CD2	2.38	0.58
1:A:1164:THR:N	1:A:1299:GLN:O	2.34	0.58
7:G:98:PHE:HZ	17:Q:152:PHE:CE1	2.22	0.58
17:Q:25:PHE:HB3	18:R:215:GLU:OE2	2.04	0.58
17:Q:110:MET:CE	18:R:213:ASP:HA	2.27	0.58
21:U:200:ASP:OD2	21:U:203:ASN:ND2	2.30	0.58
27:3:14:VAL:HG23	27:3:163:VAL:HG13	1.86	0.58
27:3:144:ILE:HG12	27:3:147:MET:CE	2.34	0.58
1:A:381:PRO:HB3	11:K:2:ASN:HD21	1.68	0.58
1:A:423:ASN:ND2	1:A:425:ASP:OD2	2.30	0.58
1:A:611:ASP:HB3	1:A:617:PRO:HG3	1.86	0.58
1:A:734:ARG:NH2	9:I:105:GLU:O	2.36	0.58
2:B:936:ALA:HB2	2:B:1051:LEU:HD11	1.86	0.58
22:V:534:TYR:CD1	22:V:535:THR:N	2.71	0.58
25:1:2:VAL:CG1	26:2:456:LYS:CD	2.81	0.58
1:A:1223:ASP:OD2	1:A:1224:ARG:NE	2.36	0.58
1:A:1308:TYR:CD1	1:A:1338:THR:HG22	2.37	0.58
4:D:23:PRO:O	4:D:27:GLU:N	2.35	0.58
5:E:52:ARG:HB2	5:E:53:PRO:CD	2.33	0.58
11:K:11:LEU:O	11:K:37:LYS:NZ	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:106:LYS:HZ1	18:R:219:LEU:HD13	1.67	0.58
18:R:140:LYS:HA	18:R:143:TYR:CZ	2.39	0.58
18:R:195:PRO:HG3	18:R:199:LYS:O	2.00	0.58
27:3:21:TRP:CD2	27:3:34:LEU:HD23	2.39	0.58
1:A:607:SER:HB2	1:A:641:CYS:SG	2.44	0.58
2:B:755:GLN:HB2	2:B:776:ILE:HA	1.85	0.58
2:B:831:LYS:NZ	2:B:845:TYR:O	2.27	0.58
5:E:52:ARG:CG	5:E:53:PRO:N	2.60	0.58
7:G:55:GLY:N	7:G:69:PRO:O	2.35	0.58
7:G:78:ARG:NH1	7:G:79:PRO:O	2.37	0.58
19:S:112:GLY:HA2	19:S:145:ASN:O	2.04	0.58
23:W:584:TYR:CB	23:W:594:ALA:HB2	2.33	0.58
25:1:2:VAL:HB	26:2:456:LYS:HD3	1.86	0.58
26:2:236:PHE:CZ	26:2:258:LEU:HD11	2.39	0.58
27:3:172:LEU:HD13	27:3:172:LEU:C	2.29	0.58
1:A:66:GLU:HB2	1:A:265:VAL:HG21	1.86	0.57
2:B:224:CYS:HB2	2:B:230:ARG:HA	1.86	0.57
2:B:718:GLN:NE2	2:B:975:ARG:O	2.32	0.57
9:I:98:GLN:NE2	9:I:108:MET:HG3	2.17	0.57
27:3:44:LEU:HD13	27:3:44:LEU:C	2.29	0.57
1:A:44:PRO:HG3	1:A:284:VAL:HB	1.85	0.57
1:A:734:ARG:NH2	9:I:105:GLU:C	2.62	0.57
1:A:1187:ALA:HA	1:A:1190:GLN:HB2	1.84	0.57
2:B:552:ASN:OD1	2:B:553:LEU:N	2.37	0.57
2:B:897:ARG:HD2	2:B:1079:SER:HA	1.85	0.57
2:B:1072:ARG:HE	2:B:1113:PRO:HD2	1.68	0.57
3:C:77:ASP:HB2	3:C:128:ILE:HG22	1.85	0.57
9:I:105:GLU:HB3	9:I:107:ALA:HB3	1.86	0.57
12:L:16:ILE:O	12:L:17:TYR:CD2	2.57	0.57
18:R:140:LYS:CG	18:R:141:PRO:HD3	2.34	0.57
26:2:423:ALA:HA	26:2:426:ARG:HE	1.70	0.57
1:A:797:ARG:HB3	1:A:820:ARG:HB3	1.85	0.57
5:E:44:SER:OG	5:E:46:ASP:HB2	2.04	0.57
8:H:65:TYR:CD2	8:H:70:LEU:HB3	2.39	0.57
14:N:318:ASP:HB3	16:P:239:ARG:HE	1.68	0.57
16:P:180:LEU:HB3	16:P:200:VAL:HG23	1.86	0.57
17:Q:25:PHE:CD2	18:R:215:GLU:OE2	2.56	0.57
17:Q:32:LEU:HD13	18:R:161:ARG:NH2	2.19	0.57
18:R:202:PHE:C	18:R:203:PHE:CG	2.82	0.57
27:3:169:ASP:CG	27:3:202:LEU:HD23	2.28	0.57
2:B:131:THR:C	2:B:132:VAL:HG13	2.28	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:411:LEU:HD12	2:B:440:ILE:HD11	1.86	0.57
5:E:27:LEU:HD12	5:E:64:HIS:CG	2.20	0.57
11:K:7:PHE:HA	11:K:10:PHE:CE2	2.39	0.57
13:M:295:ARG:HG2	13:M:299:LEU:HG	1.86	0.57
14:N:354:LYS:HA	14:N:369:LYS:HA	1.86	0.57
19:S:31:PHE:HB2	20:T:92:THR:HB	1.86	0.57
23:W:70:LEU:CG	23:W:72:TYR:CE1	2.87	0.57
26:2:28:PRO:C	27:3:25:GLN:O	2.47	0.57
26:2:117:ASN:HD22	27:3:42:MET:HE1	1.70	0.57
1:A:1037:ALA:HA	5:E:200:ALA:HB1	1.86	0.57
1:A:1308:TYR:CE1	1:A:1338:THR:HG21	2.40	0.57
5:E:63:ALA:O	5:E:64:HIS:CB	2.53	0.57
10:J:43:TYR:HA	10:J:46:ARG:HB2	1.86	0.57
16:P:297:LYS:HB2	16:P:298:PRO:CD	2.24	0.57
22:V:415:HIS:CD2	22:V:416:THR:CG2	2.88	0.57
25:1:4:VAL:HG11	26:2:412:PHE:CD2	2.28	0.57
27:3:19:PRO:HG2	27:3:123:ASP:O	2.05	0.57
1:A:642:LYS:HZ3	21:U:283:GLU:HA	1.69	0.57
5:E:110:MET:HB2	5:E:115:LYS:HE3	1.87	0.57
9:I:23:MET:HE3	9:I:25:TYR:HE1	1.69	0.57
17:Q:23:ARG:CZ	18:R:207:SER:CB	2.76	0.57
17:Q:129:CYS:SG	17:Q:159:THR:OG1	2.62	0.57
20:T:12:ALA:HA	20:T:109:ILE:HD11	1.85	0.57
20:T:174:LYS:HE3	28:X:21:DG:H5'	1.87	0.57
22:V:523:VAL:HG21	25:1:20:LEU:HD23	1.86	0.57
26:2:220:LEU:HD13	26:2:220:LEU:C	2.28	0.57
27:3:14:VAL:HG23	27:3:163:VAL:HA	1.84	0.57
3:C:193:ARG:NH2	3:C:218:ALA:O	2.38	0.57
3:C:212:ASP:C	3:C:213:GLU:O	2.43	0.57
17:Q:187:ILE:O	18:R:212:VAL:N	2.38	0.57
22:V:520:ARG:HD3	25:1:19:PHE:HB3	1.85	0.57
26:2:192:GLU:CG	26:2:193:PRO:HD2	2.23	0.57
27:3:195:VAL:HG21	27:3:214:TYR:OH	2.05	0.57
2:B:1114:TYR:CE1	2:B:1153:TYR:HD2	2.22	0.57
8:H:17:PRO:HB3	8:H:27:ARG:HB3	1.87	0.57
17:Q:202:GLU:O	17:Q:203:ILE:HB	2.05	0.57
25:1:59:GLU:CD	26:2:402:ARG:HH12	2.12	0.57
26:2:30:VAL:N	27:3:25:GLN:CB	2.48	0.57
26:2:181:GLN:HA	26:2:181:GLN:HE21	1.70	0.57
27:3:223:LEU:HD11	27:3:227:LEU:HD11	1.87	0.57
1:A:21:VAL:HB	1:A:1449:ASP:HB3	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:66:GLU:O	1:A:68:THR:N	2.38	0.57
3:C:6:GLN:CG	3:C:25:ASN:HD22	2.17	0.57
3:C:115:VAL:O	3:C:150:ILE:N	2.36	0.57
16:P:293:TYR:HB3	16:P:302:LEU:HB2	1.87	0.57
19:S:8:SER:HB3	20:T:49:GLN:HA	1.86	0.57
26:2:60:LEU:HD11	26:2:95:ILE:CG2	2.35	0.57
1:A:1307:VAL:HG12	1:A:1339:ASP:H	1.70	0.57
1:A:1309:MET:CG	21:U:252:LYS:HD2	2.34	0.57
2:B:242:ARG:C	2:B:244:GLY:N	2.62	0.57
15:O:66:ARG:NE	16:P:185:LEU:O	2.37	0.57
2:B:851:ASP:OD2	12:L:17:TYR:OH	2.11	0.56
5:E:148:HIS:HB2	5:E:183:PHE:CZ	2.40	0.56
13:M:169:ARG:NH1	13:M:207:ASP:O	2.37	0.56
18:R:140:LYS:N	18:R:141:PRO:CD	2.39	0.56
22:V:413:LEU:HD11	28:X:55:DC:C4'	2.35	0.56
23:W:410:TYR:CE2	23:W:413:GLY:HA3	2.40	0.56
25:1:9:LEU:CB	25:1:51:ASN:HD21	2.14	0.56
26:2:211:GLN:HB3	26:2:261:PHE:CE1	2.40	0.56
1:A:202:TRP:HB2	1:A:212:LYS:HE2	1.87	0.56
1:A:769:MET:HE1	1:A:775:LYS:HB2	1.87	0.56
1:A:1246:ILE:HG23	1:A:1258:ARG:HG3	1.86	0.56
2:B:490:GLY:O	2:B:491:ARG:O	2.23	0.56
2:B:823:PHE:HD1	13:M:140:ASN:HB3	1.69	0.56
3:C:205:LYS:HB3	3:C:209:SER:OG	2.05	0.56
13:M:173:VAL:O	13:M:175:ARG:NH1	2.38	0.56
15:O:66:ARG:HD3	16:P:185:LEU:HA	1.87	0.56
17:Q:113:ARG:CB	18:R:221:ARG:HD3	2.31	0.56
22:V:550:PHE:CZ	22:V:554:ARG:CZ	2.88	0.56
1:A:275:ASP:HB2	1:A:342:ARG:HH22	1.70	0.56
1:A:621:ILE:CD1	1:A:623:PRO:HB3	2.27	0.56
1:A:891:TYR:CZ	1:A:1087:VAL:HG21	2.40	0.56
1:A:1305:SER:O	1:A:1306:LYS:HB3	2.05	0.56
2:B:488:PRO:O	2:B:489:ILE:HG13	2.04	0.56
2:B:544:PHE:O	2:B:548:TRP:N	2.39	0.56
2:B:803:ARG:HD3	10:J:8:PHE:HA	1.88	0.56
3:C:48:ASP:HB3	3:C:166:LYS:HD2	1.86	0.56
3:C:154:ARG:HH11	10:J:65:LEU:HB2	1.68	0.56
13:M:214:PHE:HB3	13:M:218:PHE:CE2	2.40	0.56
17:Q:128:LYS:NZ	17:Q:133:SER:O	2.37	0.56
25:1:3:ASN:CB	26:2:412:PHE:O	2.52	0.56
26:2:82:ALA:HA	26:2:89:LEU:HD11	1.85	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:2:185:MET:HB2	26:2:229:ASP:OD1	2.05	0.56
27:3:57:LEU:HD23	27:3:58:ALA:C	2.31	0.56
27:3:210:THR:HG22	27:3:210:THR:O	2.04	0.56
1:A:47:THR:HG22	1:A:49:GLY:H	1.70	0.56
8:H:7:GLU:HG3	8:H:59:VAL:HG22	1.87	0.56
12:L:33:PRO:HG2	12:L:35:ARG:HG2	1.87	0.56
23:W:143:ARG:HG2	23:W:143:ARG:NH1	2.19	0.56
26:2:47:GLU:HG3	26:2:48:LEU:N	2.20	0.56
1:A:53:LYS:HE3	1:A:58:MET:HE2	1.88	0.56
4:D:15:GLU:HG2	4:D:23:PRO:HD3	1.87	0.56
17:Q:113:ARG:HE	18:R:217:GLN:CA	2.18	0.56
18:R:155:LEU:CD2	18:R:204:ASN:HD21	2.11	0.56
23:W:209:TYR:CZ	23:W:233:PHE:HA	2.38	0.56
23:W:423:ASP:C	23:W:425:THR:N	2.63	0.56
25:1:8:VAL:HG12	25:1:9:LEU:H	1.69	0.56
25:1:18:GLN:CD	25:1:44:PHE:HZ	2.13	0.56
25:1:52:VAL:HG22	25:1:53:LEU:HD12	1.87	0.56
26:2:130:SER:HB2	26:2:173:GLN:OE1	2.06	0.56
27:3:165:LYS:HD3	27:3:165:LYS:C	2.31	0.56
28:X:57:DC:H2"	28:X:58:DT:H72	1.86	0.56
1:A:357:LYS:O	2:B:1086:PHE:N	2.36	0.56
1:A:740:GLN:O	1:A:743:ARG:HG2	2.05	0.56
13:M:11:PRO:O	13:M:12:ARG:CB	2.47	0.56
27:3:173:GLN:CA	27:3:176:ASN:HD21	2.10	0.56
27:3:187:GLN:NE2	27:3:189:ILE:HG13	2.20	0.56
1:A:1196:TYR:HD2	1:A:1246:ILE:HD11	1.68	0.56
2:B:626:LEU:HD22	2:B:633:LEU:HD11	1.87	0.56
8:H:65:TYR:CZ	8:H:70:LEU:HD22	2.41	0.56
27:3:44:LEU:HD13	27:3:44:LEU:O	2.06	0.56
27:3:178:MET:SD	27:3:181:ILE:HD12	2.46	0.56
1:A:375:ILE:HD11	1:A:666:ARG:HE	1.69	0.56
7:G:63:ARG:NH2	7:G:65:PHE:O	2.38	0.56
26:2:117:ASN:HB2	27:3:104:LEU:CD1	2.35	0.56
1:A:181:HIS:ND1	1:A:181:HIS:O	2.38	0.56
2:B:225:LEU:H	2:B:231:PRO:HD2	1.71	0.56
6:F:79:VAL:HG12	6:F:81:VAL:H	1.71	0.56
19:S:126:ILE:O	19:S:138:PHE:N	2.35	0.56
20:T:229:HIS:CD2	28:X:28:DG:H21	2.24	0.56
1:A:85:PHE:HD1	1:A:257:PRO:HD3	1.70	0.56
1:A:924:TYR:N	1:A:924:TYR:CD1	2.74	0.56
3:C:63:PHE:O	3:C:67:ARG:HG3	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:214:PHE:O	13:M:218:PHE:HD2	1.89	0.56
17:Q:104:LYS:HZ1	18:R:238:LYS:HE3	1.70	0.56
17:Q:141:ALA:HB1	17:Q:152:PHE:CE1	2.40	0.56
19:S:166:ARG:HH11	19:S:166:ARG:CG	2.19	0.56
24:0:54:ARG:CB	27:3:209:ILE:HG23	2.25	0.56
27:3:71:TYR:CG	27:3:72:PRO:HD2	2.18	0.56
1:A:47:THR:HA	1:A:54:LEU:HG	1.87	0.55
1:A:686:THR:HG21	2:B:1041:ILE:HA	1.88	0.55
2:B:156:LEU:HB2	2:B:183:GLY:H	1.71	0.55
2:B:591:ARG:HA	2:B:596:ILE:HB	1.88	0.55
2:B:676:ALA:N	2:B:695:HIS:O	2.33	0.55
14:N:318:ASP:HB3	16:P:239:ARG:HH21	1.71	0.55
22:V:519:TYR:CD2	25:1:20:LEU:HB2	2.42	0.55
26:2:160:LEU:H	26:2:160:LEU:CD1	2.18	0.55
1:A:1209:PRO:HB3	9:I:33:ARG:NH1	2.19	0.55
2:B:268:PRO:HB2	2:B:271:ILE:HG12	1.88	0.55
2:B:485:LEU:HB2	2:B:524:LYS:HB2	1.88	0.55
2:B:633:LEU:HG	2:B:635:LEU:H	1.71	0.55
2:B:829:PHE:CE1	2:B:869:LYS:HD3	2.40	0.55
5:E:30:GLN:O	5:E:34:ASP:N	2.34	0.55
13:M:17:ASN:OD1	13:M:18:HIS:ND1	2.39	0.55
25:1:18:GLN:HB2	25:1:44:PHE:CZ	2.38	0.55
25:1:36:GLN:HB3	25:1:45:VAL:HG12	1.88	0.55
26:2:28:PRO:C	27:3:25:GLN:C	2.74	0.55
26:2:81:LYS:HG3	26:2:82:ALA:N	2.21	0.55
2:B:837:CYS:HB2	2:B:889:LYS:HD2	1.89	0.55
9:I:68:ILE:HG23	9:I:122:ARG:HD2	1.88	0.55
16:P:288:PHE:CD1	16:P:289:PRO:HD2	2.41	0.55
22:V:531:ILE:CB	22:V:534:TYR:CE2	2.89	0.55
25:1:31:LYS:O	25:1:32:LYS:HB2	2.06	0.55
27:3:160:ARG:HB3	27:3:190:LEU:CD2	2.32	0.55
27:3:223:LEU:HD13	27:3:227:LEU:HG	1.89	0.55
1:A:46:THR:HA	1:A:57:LEU:HD13	1.89	0.55
1:A:364:ARG:NH1	1:A:461:GLN:OE1	2.39	0.55
1:A:408:ARG:NH1	1:A:414:PRO:HB2	2.21	0.55
1:A:551:ARG:HH12	8:H:120:GLY:C	2.14	0.55
4:D:79:THR:HG23	4:D:137:LYS:HG2	1.89	0.55
19:S:119:THR:HG22	19:S:123:SER:HA	1.89	0.55
19:S:127:PHE:HB2	20:T:19:TRP:HB2	1.87	0.55
20:T:217:LEU:HB3	20:T:233:TRP:CE3	2.40	0.55
27:3:22:TRP:O	27:3:25:GLN:NE2	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:372:ASN:O	1:A:372:ASN:ND2	2.38	0.55
5:E:54:ARG:O	5:E:58:LEU:N	2.35	0.55
15:O:67:PHE:HB2	15:O:72:TRP:CE3	2.41	0.55
22:V:519:TYR:HD2	25:1:20:LEU:HB2	1.72	0.55
26:2:222:THR:HG23	26:2:222:THR:O	2.07	0.55
27:3:223:LEU:HD13	27:3:223:LEU:O	2.06	0.55
1:A:43:TYR:CD2	1:A:44:PRO:HD2	2.42	0.55
1:A:516:GLN:HA	1:A:520:MET:HG2	1.89	0.55
1:A:1280:ASP:HB3	1:A:1283:VAL:HG22	1.87	0.55
2:B:242:ARG:C	2:B:252:ILE:HG23	2.21	0.55
2:B:566:LYS:HA	2:B:576:ILE:HG22	1.89	0.55
2:B:814:TYR:N	2:B:921:ILE:O	2.32	0.55
3:C:101:PHE:O	3:C:163:ALA:N	2.28	0.55
14:N:360:LEU:HD11	15:O:81:PHE:CD2	2.41	0.55
23:W:408:SER:O	23:W:409:THR:CG2	2.54	0.55
27:3:190:LEU:HD23	27:3:190:LEU:N	2.18	0.55
1:A:65:ILE:HG22	1:A:66:GLU:H	1.72	0.55
1:A:489:THR:O	1:A:493:ASN:N	2.39	0.55
1:A:1027:ASP:OD2	5:E:162:ARG:NE	2.25	0.55
1:A:1150:ASP:OD2	1:A:1153:ARG:N	2.39	0.55
16:P:270:LEU:HD22	16:P:291:LEU:HD13	1.89	0.55
18:R:88:ARG:NH1	18:R:97:LEU:HD23	2.22	0.55
23:W:143:ARG:HG2	23:W:143:ARG:HH11	1.71	0.55
25:1:34:ILE:HG21	25:1:54:GLN:CD	2.31	0.55
26:2:251:VAL:HG12	26:2:254:MET:HB2	1.85	0.55
1:A:43:TYR:CG	1:A:44:PRO:HD2	2.41	0.55
1:A:426:ARG:NE	1:A:447:GLU:OE2	2.33	0.55
1:A:910:LYS:HD2	1:A:911:PRO:HD2	1.88	0.55
1:A:1162:GLU:HA	1:A:1308:TYR:HE2	1.71	0.55
1:A:1304:ILE:O	1:A:1306:LYS:N	2.40	0.55
2:B:829:PHE:HD1	2:B:869:LYS:HB3	1.72	0.55
2:B:934:LYS:HG2	2:B:1051:LEU:HD12	1.88	0.55
13:M:107:MET:HE2	13:M:107:MET:N	2.21	0.55
16:P:167:ASN:ND2	29:Y:79:DT:H1'	2.21	0.55
16:P:171:THR:HG23	16:P:256:GLN:HG3	1.89	0.55
16:P:205:ARG:O	16:P:206:GLU:O	2.25	0.55
21:U:205:ASN:HB3	21:U:231:ASP:OD2	2.06	0.55
22:V:516:PRO:HD2	22:V:706:LYS:HZ3	1.68	0.55
26:2:214:TYR:CD2	26:2:261:PHE:CD2	2.95	0.55
27:3:42:MET:SD	27:3:111:ILE:HD13	2.46	0.55
1:A:551:ARG:HH11	1:A:637:MET:HE1	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:113:ARG:NE	18:R:217:GLN:HB3	2.21	0.55
17:Q:187:ILE:CG2	18:R:211:SER:C	2.79	0.55
20:T:31:TRP:CD1	20:T:62:LEU:HD21	2.41	0.55
25:1:25:GLU:HG2	25:1:32:LYS:HA	1.89	0.55
26:2:53:LYS:CE	26:2:95:ILE:HD11	2.36	0.55
26:2:123:LEU:CD2	26:2:178:LEU:HD11	2.37	0.55
26:2:208:THR:O	26:2:212:LEU:HG	2.07	0.55
1:A:21:VAL:HG21	1:A:1427:LEU:HD11	1.88	0.55
1:A:515:ILE:HG23	1:A:519:ALA:HB3	1.89	0.55
1:A:926:ASN:OD1	1:A:931:ARG:CG	2.55	0.55
1:A:928:ARG:O	1:A:930:LEU:N	2.40	0.55
1:A:935:GLN:O	1:A:1002:SER:N	2.40	0.55
2:B:751:LEU:HD11	2:B:806:PHE:HA	1.89	0.55
2:B:810:PHE:HB2	2:B:927:ARG:HG2	1.89	0.55
12:L:17:TYR:OH	12:L:46:LYS:NZ	2.39	0.55
13:M:179:GLU:HG2	20:T:154:LYS:HE3	1.89	0.55
14:N:332:GLU:HB2	15:O:93:VAL:HA	1.88	0.55
21:U:230:SER:O	21:U:231:ASP:HB3	2.07	0.55
21:U:266:CYS:O	21:U:268:LYS:N	2.32	0.55
25:1:4:VAL:HG12	26:2:411:GLN:C	2.30	0.55
1:A:625:ASP:OD1	1:A:637:MET:HE1	2.05	0.54
1:A:1121:VAL:HA	1:A:1124:LEU:HB3	1.89	0.54
1:A:1146:GLN:HG2	1:A:1150:ASP:HB2	1.88	0.54
1:A:1463:LEU:HD21	6:F:64:ARG:HH22	1.71	0.54
2:B:552:ASN:HB3	2:B:555:GLU:HB3	1.89	0.54
2:B:1040:GLN:NE2	3:C:195:THR:OG1	2.40	0.54
8:H:65:TYR:CE2	8:H:70:LEU:HB2	2.41	0.54
18:R:163:LEU:C	18:R:164:GLY:O	2.49	0.54
22:V:251:PHE:O	22:V:257:LYS:HA	2.06	0.54
2:B:953:ASP:HA	3:C:36:ARG:HH12	1.72	0.54
10:J:14:VAL:HG23	10:J:17:LYS:HB2	1.90	0.54
17:Q:69:ASP:HA	18:R:225:VAL:CG2	2.37	0.54
22:V:514:MET:SD	22:V:537:ASN:ND2	2.80	0.54
1:A:880:ARG:HG2	1:A:886:VAL:HA	1.88	0.54
2:B:778:SER:O	2:B:1046:THR:N	2.37	0.54
5:E:10:LEU:HB3	5:E:58:LEU:HD11	1.89	0.54
7:G:98:PHE:HE2	17:Q:145:PHE:CG	2.25	0.54
16:P:214:PHE:HD2	16:P:218:LYS:HB2	1.73	0.54
22:V:667:THR:HA	25:1:62:ASP:OD2	2.07	0.54
23:W:408:SER:O	23:W:409:THR:HG22	2.08	0.54
27:3:71:TYR:HD2	27:3:72:PRO:HD2	1.70	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:320:ASN:HB2	1:A:336:LEU:HD23	1.90	0.54
3:C:68:LEU:HD12	3:C:71:ILE:HD12	1.90	0.54
6:F:81:VAL:HG12	6:F:101:LYS:HD3	1.88	0.54
10:J:67:LYS:HB2	12:L:23:HIS:CD2	2.35	0.54
14:N:360:LEU:HB2	14:N:365:TYR:HE2	1.72	0.54
22:V:609:LYS:CE	29:Y:38:DT:OP1	2.55	0.54
23:W:52:LEU:CD2	23:W:72:TYR:OH	2.55	0.54
26:2:123:LEU:HD21	26:2:178:LEU:CD1	2.38	0.54
26:2:138:PRO:O	26:2:139:ASP:HB2	2.08	0.54
1:A:608:THR:HG21	1:A:639:ILE:HG23	1.89	0.54
2:B:512:ALA:HA	2:B:723:THR:HG22	1.89	0.54
2:B:1094:GLN:HA	2:B:1097:HIS:HB2	1.88	0.54
3:C:44:ILE:N	3:C:168:GLY:O	2.31	0.54
5:E:105:VAL:HG12	5:E:132:GLN:HG3	1.88	0.54
9:I:59:THR:O	9:I:59:THR:HG22	2.08	0.54
16:P:165:LEU:HA	16:P:260:GLY:HA2	1.89	0.54
20:T:139:VAL:O	20:T:139:VAL:HG12	2.06	0.54
25:1:13:ASP:OD1	25:1:14:PRO:CD	2.56	0.54
26:2:138:PRO:HG3	26:2:189:GLU:CG	2.35	0.54
1:A:1309:MET:O	1:A:1336:LEU:HA	2.07	0.54
2:B:440:ILE:H	2:B:440:ILE:HD12	1.71	0.54
2:B:836:THR:HG22	2:B:885:ARG:HB3	1.90	0.54
3:C:125:PRO:O	3:C:127:VAL:N	2.40	0.54
5:E:149:VAL:O	5:E:192:LYS:N	2.23	0.54
11:K:35:ILE:HB	11:K:71:ILE:HG13	1.89	0.54
15:O:28:ILE:HB	15:O:32:LEU:HD23	1.88	0.54
18:R:103:LEU:HB3	18:R:109:LEU:HA	1.90	0.54
19:S:110:PHE:CD1	19:S:148:PRO:HA	2.42	0.54
20:T:146:ASP:C	20:T:147:LYS:CG	2.75	0.54
22:V:321:GLU:CA	23:W:499:ASN:ND2	2.58	0.54
27:3:223:LEU:HD13	27:3:223:LEU:C	2.32	0.54
1:A:526:VAL:HA	1:A:533:PRO:HA	1.88	0.54
2:B:573:TRP:CZ3	2:B:575:GLY:HA2	2.43	0.54
9:I:110:LEU:O	9:I:124:THR:OG1	2.26	0.54
13:M:267:GLU:OE1	13:M:269:ARG:NH2	2.41	0.54
20:T:30:GLN:HG2	20:T:62:LEU:HG	1.89	0.54
25:1:34:ILE:HG23	25:1:50:VAL:HG11	1.89	0.54
26:2:177:GLN:NE2	26:2:220:LEU:HA	2.22	0.54
1:A:43:TYR:OH	1:A:285:LYS:HE2	2.06	0.54
1:A:378:VAL:O	1:A:475:ARG:N	2.41	0.54
1:A:1372:GLU:CD	5:E:195:ARG:HH21	2.15	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:248:LYS:O	2:B:249:LYS:HG2	2.08	0.54
2:B:1117:HIS:HA	2:B:1147:SER:O	2.07	0.54
2:B:1135:TYR:HB2	2:B:1146:ILE:HG13	1.90	0.54
3:C:23:ILE:HB	3:C:231:TYR:HE2	1.72	0.54
5:E:166:ARG:HB2	5:E:169:GLN:HG3	1.90	0.54
8:H:8:ASP:OD1	8:H:9:ILE:N	2.41	0.54
9:I:17:CYS:N	9:I:22:ASN:O	2.35	0.54
18:R:210:PHE:CD1	18:R:210:PHE:C	2.86	0.54
22:V:325:ARG:HH22	23:W:499:ASN:HB3	0.72	0.54
22:V:531:ILE:C	22:V:534:TYR:CE2	2.85	0.54
25:1:52:VAL:HG23	25:1:53:LEU:N	2.21	0.54
27:3:64:ILE:HG23	27:3:128:HIS:CG	2.42	0.54
27:3:160:ARG:NH2	27:3:192:ASP:HB3	2.23	0.54
1:A:910:LYS:O	1:A:963:ARG:NH2	2.37	0.54
1:A:927:GLU:O	1:A:931:ARG:CB	2.56	0.54
1:A:936:GLU:HB2	1:A:939:VAL:HG23	1.89	0.54
2:B:568:PHE:N	2:B:612:ILE:O	2.33	0.54
3:C:46:ALA:HB3	3:C:176:TRP:NE1	2.23	0.54
25:1:1:MET:HA	26:2:413:LEU:CA	2.38	0.54
27:3:105:THR:HG23	27:3:106:SER:N	2.23	0.54
1:A:1305:SER:O	1:A:1306:LYS:CB	2.55	0.54
2:B:670:GLU:HA	2:B:673:VAL:HG22	1.90	0.54
2:B:813:SER:HA	2:B:922:ARG:HA	1.89	0.54
3:C:109:GLU:H	3:C:109:GLU:CD	2.17	0.54
5:E:73:PHE:O	5:E:103:LEU:N	2.28	0.54
14:N:38:VAL:HG13	15:O:22:LEU:HD22	1.89	0.54
19:S:48:GLU:O	19:S:99:LEU:N	2.38	0.54
22:V:534:TYR:CD1	22:V:534:TYR:C	2.86	0.54
27:3:34:LEU:HD13	27:3:34:LEU:C	2.33	0.54
1:A:871:VAL:HG23	1:A:1088:GLY:HA3	1.90	0.53
2:B:874:PRO:C	2:B:876:ASN:H	2.17	0.53
3:C:177:ASN:ND2	3:C:179:THR:O	2.41	0.53
8:H:6:PHE:HB3	8:H:60:ILE:HB	1.90	0.53
12:L:25:GLU:O	12:L:37:ARG:NH2	2.39	0.53
15:O:71:VAL:HG22	15:O:98:CYS:HA	1.90	0.53
18:R:191:PHE:CB	18:R:202:PHE:HD1	2.21	0.53
22:V:504:LYS:HD2	22:V:654:GLU:O	2.08	0.53
22:V:516:PRO:HD2	22:V:706:LYS:NZ	2.22	0.53
26:2:28:PRO:HB3	27:3:33:THR:OG1	2.08	0.53
1:A:1005:HIS:CE1	1:A:1007:ILE:HB	2.43	0.53
1:A:1235:ILE:HA	1:A:1296:MET:HE1	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:752:TYR:HE1	2:B:809:VAL:HG23	1.72	0.53
5:E:172:ARG:O	5:E:207:ARG:NE	2.36	0.53
12:L:17:TYR:CB	12:L:46:LYS:HA	2.38	0.53
13:M:107:MET:HA	13:M:107:MET:CE	2.32	0.53
14:N:32:ASP:OD1	15:O:29:THR:OG1	2.23	0.53
14:N:318:ASP:CB	16:P:239:ARG:HE	2.20	0.53
20:T:155:PRO:C	20:T:157:ALA:H	2.14	0.53
22:V:638:GLN:O	22:V:642:ARG:HG2	2.08	0.53
25:1:1:MET:CB	26:2:418:PHE:HB2	2.38	0.53
26:2:31:LEU:HD13	27:3:33:THR:HG22	1.86	0.53
26:2:211:GLN:HE21	26:2:257:SER:CB	2.21	0.53
1:A:46:THR:HG23	1:A:57:LEU:HD22	1.88	0.53
1:A:875:TYR:HA	1:A:1083:PRO:HB2	1.91	0.53
2:B:242:ARG:HB3	2:B:252:ILE:HG21	1.90	0.53
2:B:868:GLY:HA2	2:B:893:SER:HB2	1.89	0.53
8:H:88:PHE:HD1	8:H:146:LYS:HD2	1.73	0.53
13:M:40:VAL:C	13:M:42:GLY:H	2.17	0.53
17:Q:34:LEU:HA	17:Q:37:LEU:HD12	1.90	0.53
20:T:177:ARG:HD3	20:T:209:PRO:HD2	1.90	0.53
21:U:132:ARG:N	21:U:167:GLU:OE2	2.41	0.53
22:V:523:VAL:CG2	25:1:20:LEU:HD23	2.37	0.53
23:W:419:GLU:CB	23:W:420:PRO:CD	2.81	0.53
25:1:2:VAL:HG12	26:2:422:LEU:CD1	2.27	0.53
26:2:37:HIS:HB3	26:2:38:PRO:CD	2.35	0.53
26:2:234:LEU:HD23	26:2:234:LEU:C	2.34	0.53
2:B:51:ILE:HD12	2:B:160:TYR:CE2	2.44	0.53
2:B:935:PHE:CE2	2:B:945:CYS:HB2	2.42	0.53
4:D:112:LYS:HE2	4:D:124:ASP:OD2	2.09	0.53
17:Q:20:TYR:O	18:R:210:PHE:CE2	2.61	0.53
20:T:30:GLN:NE2	20:T:62:LEU:O	2.28	0.53
27:3:15:VAL:HG23	27:3:15:VAL:O	2.08	0.53
27:3:106:SER:O	27:3:109:GLU:HG3	2.08	0.53
1:A:1123:ARG:NH1	1:A:1126:GLU:OE1	2.40	0.53
3:C:74:ILE:HG13	3:C:76:ASP:H	1.74	0.53
13:M:225:PRO:HG2	13:M:228:VAL:HG23	1.90	0.53
17:Q:187:ILE:O	18:R:212:VAL:HG12	2.08	0.53
18:R:210:PHE:HD1	18:R:210:PHE:C	2.16	0.53
25:1:1:MET:HB2	26:2:418:PHE:HB2	1.90	0.53
27:3:191:ILE:N	27:3:210:THR:HG21	2.23	0.53
1:A:225:PHE:HA	1:A:228:ILE:HG12	1.91	0.53
1:A:579:ILE:O	1:A:584:PRO:HA	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:309:PHE:HE2	9:I:25:TYR:HE2	1.57	0.53
2:B:591:ARG:NH2	2:B:669:GLU:OE1	2.42	0.53
4:D:73:ARG:NH1	4:D:103:LEU:O	2.41	0.53
16:P:325:PHE:CZ	16:P:329:TYR:HD2	2.26	0.53
22:V:366:ASN:ND2	22:V:613:THR:HG21	2.16	0.53
23:W:189:TRP:NE1	23:W:194:LEU:HB2	2.22	0.53
25:1:21:LEU:O	25:1:24:ASP:HB3	2.09	0.53
26:2:241:SER:O	26:2:245:LEU:HD23	2.09	0.53
1:A:124:PRO:HA	1:A:127:LYS:HB2	1.91	0.53
1:A:272:ASN:ND2	1:A:278:HIS:HD2	2.07	0.53
1:A:602:CYS:HB2	1:A:655:ILE:HD11	1.91	0.53
1:A:986:MET:HE1	1:A:1072:ILE:HA	1.91	0.53
2:B:471:ASN:OD1	2:B:473:LEU:HG	2.09	0.53
2:B:733:MET:HE3	2:B:1052:LYS:HA	1.91	0.53
3:C:77:ASP:OD2	3:C:81:LYS:NZ	2.41	0.53
16:P:297:LYS:HA	16:P:297:LYS:NZ	2.23	0.53
17:Q:187:ILE:C	18:R:212:VAL:CA	2.80	0.53
20:T:229:HIS:HA	28:X:29:DC:H4'	1.90	0.53
26:2:141:HIS:HA	26:2:162:PHE:CE2	2.44	0.53
26:2:208:THR:HG23	26:2:209:PRO:HD2	1.91	0.53
1:A:1308:TYR:HA	1:A:1338:THR:HG22	1.90	0.53
2:B:956:PHE:HB2	2:B:960:GLY:HA2	1.90	0.53
4:D:26:PHE:CZ	7:G:42:TYR:HA	2.44	0.53
24:0:54:ARG:CB	27:3:209:ILE:CG2	2.87	0.53
25:1:35:ILE:O	25:1:35:ILE:HG13	2.08	0.53
1:A:579:ILE:HB	1:A:585:LEU:HB2	1.91	0.53
1:A:1313:GLN:C	1:A:1315:ASP:N	2.66	0.53
2:B:152:ILE:HG23	2:B:154:ILE:HD11	1.90	0.53
2:B:182:GLY:HA2	2:B:184:TYR:CE1	2.44	0.53
2:B:792:ASP:OD1	2:B:975:ARG:NH2	2.42	0.53
18:R:89:HIS:ND1	18:R:139:PHE:HE1	2.06	0.53
22:V:516:PRO:CA	25:1:15:ALA:C	2.76	0.53
23:W:70:LEU:HD21	23:W:72:TYR:OH	2.08	0.53
26:2:159:VAL:CG1	26:2:161:HIS:H	2.06	0.53
27:3:10:LEU:HD21	27:3:143:TYR:CE2	2.44	0.53
27:3:14:VAL:HG23	27:3:14:VAL:O	2.09	0.53
27:3:100:LYS:O	27:3:103:LEU:HB2	2.08	0.53
1:A:568:SER:N	1:A:671:ASN:OD1	2.29	0.53
2:B:623:ARG:O	2:B:665:ILE:N	2.37	0.53
2:B:753:TYR:CZ	10:J:4:PRO:HB3	2.44	0.53
17:Q:71:PHE:HD1	17:Q:72:ILE:HG23	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:77:ARG:N	17:Q:93:PHE:O	2.35	0.53
22:V:413:LEU:HD11	28:X:55:DC:H4'	1.91	0.53
22:V:426:VAL:C	22:V:427:MET:O	2.51	0.53
2:B:71:ALA:HA	2:B:81:PRO:HB3	1.90	0.52
3:C:14:LEU:HD23	11:K:112:LYS:HE2	1.91	0.52
3:C:19:VAL:HG12	3:C:233:VAL:HB	1.90	0.52
3:C:63:PHE:HE2	10:J:2:ILE:HG21	1.73	0.52
5:E:27:LEU:CB	5:E:64:HIS:CG	2.74	0.52
7:G:119:PHE:HB2	7:G:128:TYR:CE1	2.44	0.52
7:G:119:PHE:HB2	7:G:128:TYR:HE1	1.74	0.52
8:H:24:ARG:HG2	8:H:46:GLN:HE22	1.73	0.52
8:H:108:ALA:O	8:H:109:ALA:C	2.52	0.52
17:Q:105:TYR:CE2	18:R:222:SER:HB2	2.44	0.52
19:S:46:ARG:HB2	19:S:101:ARG:HB2	1.91	0.52
26:2:206:LEU:HD22	26:2:206:LEU:H	1.71	0.52
26:2:221:GLN:CD	26:2:230:LEU:HB2	2.34	0.52
1:A:152:ASN:O	1:A:152:ASN:ND2	2.41	0.52
1:A:403:GLN:HG3	1:A:440:LEU:HD21	1.92	0.52
1:A:621:ILE:O	1:A:623:PRO:HD2	2.07	0.52
2:B:83:ARG:O	2:B:134:LYS:HA	2.08	0.52
7:G:22:LEU:HD21	7:G:68:TYR:CE2	2.44	0.52
8:H:74:GLU:O	8:H:76:ASN:CA	2.54	0.52
15:O:9:THR:O	15:O:13:ASN:N	2.30	0.52
17:Q:113:ARG:CD	18:R:221:ARG:CG	2.62	0.52
26:2:160:LEU:CG	26:2:206:LEU:HD21	2.39	0.52
26:2:171:VAL:CG2	26:2:213:TRP:HA	2.20	0.52
27:3:10:LEU:HD21	27:3:143:TYR:CD2	2.45	0.52
27:3:21:TRP:O	27:3:24:LYS:HB2	2.09	0.52
27:3:70:LEU:HD22	27:3:114:GLU:HB3	1.91	0.52
2:B:1068:GLN:N	2:B:1073:GLN:O	2.43	0.52
20:T:94:THR:HG22	20:T:109:ILE:HG23	1.91	0.52
21:U:194:ARG:HD2	21:U:220:PHE:CE2	2.44	0.52
23:W:52:LEU:HD23	23:W:72:TYR:HE2	1.71	0.52
26:2:30:VAL:O	26:2:34:LEU:HD23	2.09	0.52
1:A:457:ILE:HG21	2:B:1102:PHE:CZ	2.44	0.52
1:A:914:LYS:O	1:A:918:LYS:N	2.38	0.52
1:A:998:PRO:HA	1:A:1059:ARG:NE	2.24	0.52
2:B:1021:HIS:CE1	2:B:1023:ARG:HB2	2.44	0.52
8:H:28:LEU:HD11	8:H:50:VAL:HG21	1.91	0.52
8:H:40:ILE:HB	8:H:124:ARG:HG2	1.91	0.52
9:I:66:THR:HA	9:I:122:ARG:NH2	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:127:ARG:HG3	13:M:127:ARG:HH21	1.74	0.52
14:N:360:LEU:HD11	15:O:81:PHE:HD2	1.73	0.52
21:U:230:SER:O	21:U:231:ASP:CB	2.56	0.52
23:W:584:TYR:HB2	23:W:591:GLY:HA3	1.92	0.52
25:1:1:MET:CG	26:2:418:PHE:HB2	2.38	0.52
1:A:1219:LYS:O	1:A:1222:THR:OG1	2.22	0.52
2:B:24:GLU:HA	2:B:27:TRP:HD1	1.74	0.52
2:B:455:ASP:O	2:B:457:LYS:N	2.37	0.52
2:B:566:LYS:NZ	2:B:609:GLU:O	2.43	0.52
6:F:56:TYR:HE1	6:F:124:ILE:HD12	1.74	0.52
13:M:214:PHE:HB3	13:M:218:PHE:HE2	1.75	0.52
16:P:297:LYS:HA	16:P:297:LYS:HE2	1.87	0.52
20:T:138:PRO:C	20:T:140:ARG:N	2.68	0.52
24:O:77:LYS:HG2	24:O:225:GLU:OE2	2.09	0.52
1:A:641:CYS:SG	1:A:644:SER:OG	2.52	0.52
1:A:876:ASP:HA	6:F:52:ILE:HD13	1.92	0.52
1:A:1243:LEU:HD11	1:A:1259:ILE:HD12	1.91	0.52
2:B:21:LEU:HD21	2:B:635:LEU:HD23	1.90	0.52
2:B:1026:GLU:N	2:B:1041:ILE:O	2.39	0.52
14:N:25:VAL:HB	15:O:36:VAL:HG22	1.91	0.52
17:Q:18:ALA:HA	17:Q:21:VAL:HG22	1.90	0.52
18:R:195:PRO:CB	18:R:199:LYS:CG	2.88	0.52
26:2:86:SER:O	26:2:90:LEU:HD13	2.08	0.52
1:A:410:ASN:OD1	1:A:417:LYS:NZ	2.35	0.52
1:A:817:PRO:HB2	1:A:822:PHE:HB3	1.92	0.52
2:B:75:SER:OG	2:B:78:VAL:CG2	2.50	0.52
2:B:239:MET:SD	2:B:256:ILE:HD13	2.49	0.52
2:B:613:ARG:HD3	2:B:615:TYR:HE2	1.74	0.52
8:H:65:TYR:CE2	8:H:70:LEU:CD2	2.92	0.52
14:N:15:ARG:HA	14:N:18:ILE:HD12	1.91	0.52
17:Q:72:ILE:HD12	17:Q:96:TYR:CD1	2.45	0.52
17:Q:110:MET:SD	18:R:218:LYS:HB2	2.49	0.52
25:1:3:ASN:HB2	26:2:412:PHE:O	2.10	0.52
13:M:23:LEU:HD21	13:M:41:VAL:HG21	1.92	0.52
22:V:520:ARG:CG	25:1:23:LEU:HD11	2.39	0.52
24:O:77:LYS:HD2	24:O:77:LYS:N	2.23	0.52
26:2:199:ALA:HB1	26:2:201:PHE:CD2	2.43	0.52
2:B:40:VAL:HA	2:B:42:GLN:HE22	1.75	0.52
2:B:345:LYS:O	2:B:349:PRO:HG3	2.10	0.52
2:B:711:ILE:HD12	2:B:939:HIS:HA	1.90	0.52
2:B:780:VAL:HG13	2:B:965:ILE:HB	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:100:GLU:N	3:C:124:SER:OG	2.43	0.52
23:W:428:ILE:HA	23:W:430:ASN:ND2	2.23	0.52
27:3:100:LYS:HG3	27:3:101:TYR:H	1.74	0.52
27:3:165:LYS:HE3	27:3:200:SER:OG	2.09	0.52
1:A:138:LYS:HE3	1:A:1441:GLU:HG3	1.91	0.52
1:A:405:LEU:HD23	1:A:448:ARG:HB2	1.92	0.52
1:A:600:ILE:HD12	1:A:659:GLU:HB2	1.92	0.52
1:A:1416:ARG:NH2	1:A:1434:GLU:OE2	2.43	0.52
2:B:249:LYS:O	2:B:251:ALA:N	2.42	0.52
2:B:867:ILE:O	2:B:894:THR:N	2.43	0.52
3:C:101:PHE:N	3:C:163:ALA:O	2.27	0.52
14:N:317:GLU:OE2	16:P:235:ARG:HD2	2.10	0.52
17:Q:187:ILE:HG22	18:R:212:VAL:O	2.08	0.52
27:3:42:MET:CG	27:3:111:ILE:HD11	2.40	0.52
1:A:433:PRO:HD3	13:M:35:PRO:O	2.10	0.51
1:A:529:GLN:NE2	1:A:1098:PRO:HD3	2.25	0.51
3:C:151:VAL:HG22	3:C:152:LYS:H	1.75	0.51
8:H:75:TYR:CZ	8:H:77:PRO:HG3	2.44	0.51
8:H:103:GLU:HG2	8:H:109:ALA:HB2	1.92	0.51
14:N:42:LEU:HD11	15:O:15:LEU:HD12	1.91	0.51
14:N:312:GLU:O	14:N:314:LEU:N	2.37	0.51
16:P:167:ASN:HD21	29:Y:79:DT:H1'	1.75	0.51
22:V:321:GLU:CB	23:W:499:ASN:CG	2.32	0.51
22:V:531:ILE:O	22:V:534:TYR:CZ	2.63	0.51
22:V:689:VAL:CB	26:2:391:ILE:HD11	2.36	0.51
27:3:204:GLN:HG2	27:3:214:TYR:CZ	2.44	0.51
1:A:432:HIS:HD2	13:M:38:GLY:HA3	1.76	0.51
1:A:674:THR:O	1:A:678:ASN:ND2	2.41	0.51
1:A:879:VAL:O	1:A:887:VAL:N	2.29	0.51
1:A:1139:LEU:N	1:A:1338:THR:O	2.42	0.51
1:A:1162:GLU:OE2	1:A:1224:ARG:NH1	2.42	0.51
2:B:92:TYR:HB2	20:T:145:LEU:HD22	1.90	0.51
2:B:273:PHE:HA	2:B:276:LEU:HD12	1.92	0.51
2:B:331:THR:HG21	2:B:334:LYS:HE2	1.92	0.51
3:C:7:PRO:O	3:C:8:THR:C	2.52	0.51
7:G:12:LEU:HG	7:G:63:ARG:NH1	2.26	0.51
13:M:124:MET:HA	13:M:127:ARG:HH22	1.75	0.51
13:M:218:PHE:HD1	13:M:277:ILE:HG22	1.74	0.51
16:P:199:ALA:HB2	16:P:214:PHE:HD1	1.74	0.51
17:Q:113:ARG:HE	18:R:217:GLN:CB	2.23	0.51
17:Q:146:ASP:HB3	17:Q:149:THR:HG22	1.90	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:412:MET:N	22:V:417:THR:HG21	2.25	0.51
23:W:116:CYS:SG	23:W:191:PRO:HD2	2.51	0.51
26:2:257:SER:O	26:2:261:PHE:HD1	1.93	0.51
1:A:381:PRO:HB3	11:K:2:ASN:ND2	2.25	0.51
1:A:604:ARG:HD3	1:A:604:ARG:N	2.25	0.51
1:A:1290:SER:OG	2:B:250:SER:C	2.53	0.51
1:A:1453:GLY:O	1:A:1457:ASN:ND2	2.44	0.51
2:B:222:ARG:HB3	2:B:232:THR:O	2.09	0.51
2:B:258:ALA:HB2	2:B:269:ILE:HG22	1.93	0.51
2:B:347:MET:O	2:B:361:LYS:NZ	2.39	0.51
2:B:551:GLU:OE1	2:B:551:GLU:N	2.42	0.51
9:I:88:LYS:HD2	9:I:121:HIS:CE1	2.46	0.51
11:K:19:ILE:HA	11:K:35:ILE:HA	1.93	0.51
13:M:263:GLN:HA	13:M:268:LYS:HG2	1.91	0.51
14:N:358:MET:HB2	14:N:365:TYR:HB2	1.92	0.51
20:T:146:ASP:O	20:T:147:LYS:HB3	2.09	0.51
20:T:206:THR:HG21	20:T:213:LEU:HD13	1.92	0.51
22:V:428:GLU:OE1	22:V:460:ALA:HA	2.11	0.51
25:1:8:VAL:CG1	25:1:45:VAL:HG13	2.35	0.51
27:3:10:LEU:HD22	27:3:147:MET:HG2	1.92	0.51
27:3:133:LEU:HD13	27:3:133:LEU:N	2.14	0.51
27:3:222:SER:HB3	27:3:225:GLN:HG2	1.92	0.51
1:A:696:SER:O	1:A:700:GLN:N	2.36	0.51
1:A:1175:ILE:HB	9:I:54:TYR:HB3	1.93	0.51
2:B:125:TYR:HE1	2:B:148:PHE:HB2	1.76	0.51
2:B:842:HIS:ND1	13:M:25:GLU:O	2.43	0.51
2:B:1137:CYS:HB3	2:B:1142:ASN:HB3	1.91	0.51
3:C:5:ASN:C	3:C:7:PRO:CD	2.69	0.51
5:E:99:ILE:HD11	5:E:102:ALA:HB2	1.93	0.51
13:M:231:ALA:HA	13:M:301:PRO:HG3	1.93	0.51
18:R:89:HIS:CG	18:R:139:PHE:CZ	2.98	0.51
20:T:184:LEU:HA	20:T:187:LEU:HD12	1.92	0.51
22:V:523:VAL:CG2	25:1:20:LEU:CD2	2.86	0.51
22:V:531:ILE:O	22:V:534:TYR:CE2	2.63	0.51
22:V:612:ASP:OD2	22:V:635:GLN:OE1	2.27	0.51
23:W:419:GLU:HB3	23:W:420:PRO:HD2	1.92	0.51
26:2:215:PHE:CE2	26:2:264:HIS:HB2	2.46	0.51
27:3:64:ILE:HG21	27:3:128:HIS:CB	2.40	0.51
1:A:21:VAL:HG23	1:A:1451:MET:SD	2.51	0.51
2:B:108:MET:SD	2:B:120:TYR:HA	2.51	0.51
2:B:455:ASP:C	2:B:457:LYS:H	2.18	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:10:PHE:CE1	8:H:32:SER:HB2	2.46	0.51
8:H:65:TYR:CD1	8:H:65:TYR:N	2.79	0.51
14:N:312:GLU:HB2	14:N:313:PRO:HD3	1.93	0.51
14:N:356:GLY:HA3	14:N:367:PHE:CZ	2.46	0.51
15:O:3:TYR:OH	15:O:99:ASP:O	2.24	0.51
23:W:408:SER:C	23:W:409:THR:HG22	2.35	0.51
26:2:28:PRO:HG3	27:3:33:THR:OG1	2.11	0.51
1:A:583:ARG:NH2	3:C:223:ASN:OD1	2.34	0.51
1:A:926:ASN:ND2	1:A:931:ARG:CD	2.57	0.51
1:A:1204:VAL:O	1:A:1207:ILE:HG12	2.11	0.51
2:B:934:LYS:HE3	2:B:1053:HIS:CG	2.44	0.51
16:P:167:ASN:HB3	16:P:259:VAL:HB	1.92	0.51
17:Q:105:TYR:CZ	18:R:234:GLU:OE2	2.63	0.51
26:2:160:LEU:HB3	26:2:206:LEU:HD21	1.93	0.51
1:A:1127:LEU:HD21	1:A:1378:LEU:HD11	1.93	0.51
2:B:85:LEU:HB3	2:B:131:THR:O	2.10	0.51
2:B:1062:ARG:NH1	2:B:1066:PRO:O	2.43	0.51
4:D:72:SER:O	4:D:142:TYR:OH	2.23	0.51
8:H:65:TYR:HE2	8:H:70:LEU:CB	2.17	0.51
16:P:167:ASN:HB2	29:Y:80:DT:H4'	1.92	0.51
18:R:103:LEU:HD12	18:R:116:LYS:HE3	1.92	0.51
23:W:581:LEU:C	23:W:581:LEU:HD13	2.36	0.51
26:2:57:MET:HA	26:2:60:LEU:CG	2.41	0.51
26:2:77:LYS:CD	26:2:78:GLU:HG3	2.41	0.51
26:2:193:PRO:HB2	26:2:194:PRO:HD3	1.92	0.51
27:3:141:LEU:HG	27:3:187:GLN:HE22	1.75	0.51
1:A:426:ARG:NH1	13:M:40:VAL:HG11	2.26	0.51
1:A:478:PRO:HB3	11:K:4:PRO:CD	2.40	0.51
2:B:1079:SER:O	13:M:53:ARG:NH2	2.44	0.51
26:2:231:VAL:O	26:2:234:LEU:HB3	2.11	0.51
27:3:12:VAL:HG12	27:3:58:ALA:HB3	1.92	0.51
1:A:909:LEU:HB2	1:A:975:SER:OG	2.11	0.51
1:A:987:ILE:HG12	1:A:1068:LEU:HD21	1.91	0.51
1:A:1435:THR:OG1	1:A:1436:VAL:N	2.42	0.51
2:B:519:ALA:HB1	2:B:523:VAL:HG23	1.93	0.51
3:C:43:PRO:HA	3:C:169:PHE:HB3	1.91	0.51
3:C:101:PHE:HB3	3:C:120:LEU:HD11	1.92	0.51
8:H:65:TYR:CE2	8:H:70:LEU:HD22	2.45	0.51
12:L:38:GLU:O	13:M:226:LYS:NZ	2.43	0.51
16:P:277:HIS:O	16:P:281:SER:N	2.42	0.51
17:Q:183:GLN:O	17:Q:186:PRO:HD2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:315:VAL:CG1	23:W:500:ASP:HB3	2.26	0.51
26:2:251:VAL:CG1	26:2:254:MET:CB	2.89	0.51
27:3:131:THR:HG23	27:3:133:LEU:HD12	1.92	0.51
1:A:564:LEU:HD22	1:A:570:TRP:CE2	2.45	0.51
1:A:722:ASN:HB2	1:A:724:GLU:HG2	1.93	0.51
1:A:923:ASP:C	1:A:925:THR:H	2.19	0.51
2:B:92:TYR:HB3	20:T:145:LEU:CG	2.40	0.51
2:B:425:ARG:HH11	2:B:425:ARG:HG3	1.75	0.51
3:C:20:LYS:HE2	3:C:232:ASN:ND2	2.25	0.51
3:C:58:VAL:CG1	10:J:65:LEU:HD22	2.41	0.51
4:D:86:LEU:O	4:D:89:GLN:HG2	2.10	0.51
5:E:59:THR:HG23	5:E:75:PHE:HA	1.92	0.51
5:E:103:LEU:HA	5:E:128:GLU:HB2	1.93	0.51
16:P:167:ASN:O	16:P:259:VAL:N	2.41	0.51
16:P:291:LEU:N	16:P:304:ILE:O	2.31	0.51
19:S:31:PHE:O	20:T:92:THR:N	2.44	0.51
20:T:142:SER:C	20:T:144:GLN:H	2.19	0.51
22:V:393:THR:CA	22:V:418:LYS:HE3	2.41	0.51
26:2:81:LYS:CE	26:2:89:LEU:HD21	2.42	0.51
26:2:236:PHE:CE1	26:2:261:PHE:CB	2.94	0.51
27:3:58:ALA:C	27:3:71:TYR:OH	2.52	0.51
1:A:456:VAL:HG21	1:A:503:LEU:HD11	1.92	0.50
1:A:613:GLU:HG3	21:U:261:PHE:HD1	1.76	0.50
1:A:721:HIS:HA	9:I:108:MET:O	2.11	0.50
1:A:1290:SER:HG	2:B:250:SER:C	2.16	0.50
2:B:278:PHE:HZ	2:B:359:THR:HG23	1.77	0.50
5:E:27:LEU:N	5:E:64:HIS:HB3	2.18	0.50
6:F:75:MET:HE1	7:G:65:PHE:CE1	2.46	0.50
12:L:26:ASN:HA	12:L:37:ARG:NH1	2.26	0.50
17:Q:106:LYS:O	18:R:218:LYS:HE3	2.11	0.50
20:T:27:LEU:HD11	20:T:58:LEU:HD21	1.93	0.50
21:U:276:VAL:HG22	21:U:277:GLN:H	1.76	0.50
22:V:516:PRO:CB	25:1:15:ALA:O	2.59	0.50
22:V:689:VAL:CG2	26:2:391:ILE:CD1	2.88	0.50
27:3:121:LYS:HD3	27:3:121:LYS:N	2.25	0.50
1:A:371:PRO:HD2	2:B:788:TYR:CE1	2.46	0.50
2:B:264:LYS:HE3	2:B:326:ALA:HA	1.93	0.50
2:B:520:VAL:C	2:B:522:LEU:H	2.19	0.50
6:F:70:ALA:HB1	6:F:89:PRO:HB2	1.93	0.50
17:Q:105:TYR:CE1	18:R:234:GLU:HG3	2.45	0.50
25:1:1:MET:HE1	26:2:440:LEU:CD1	2.28	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:75:ALA:C	2:B:1131:ARG:HH21	2.19	0.50
1:A:595:ILE:HG22	1:A:668:PHE:CE1	2.46	0.50
2:B:797:ASN:ND2	2:B:954:MET:SD	2.85	0.50
2:B:1028:LEU:HD13	2:B:1041:ILE:HB	1.94	0.50
7:G:11:ILE:HB	7:G:68:TYR:HB2	1.93	0.50
20:T:159:HIS:CG	20:T:160:GLN:N	2.79	0.50
22:V:504:LYS:CB	22:V:654:GLU:O	2.59	0.50
23:W:73:CYS:O	23:W:209:TYR:CE2	2.64	0.50
26:2:35:TYR:CD1	26:2:35:TYR:N	2.79	0.50
26:2:199:ALA:HB1	26:2:201:PHE:CE2	2.47	0.50
27:3:64:ILE:CG2	27:3:128:HIS:HB3	2.41	0.50
27:3:107:ALA:O	27:3:111:ILE:HG23	2.11	0.50
27:3:226:TYR:O	27:3:230:VAL:HB	2.10	0.50
1:A:489:THR:HG23	1:A:494:ALA:HB3	1.92	0.50
1:A:500:GLU:OE2	2:B:1058:LYS:HB3	2.12	0.50
2:B:281:ASP:CG	9:I:22:ASN:HD22	2.20	0.50
2:B:1123:GLY:HA3	2:B:1170:ARG:HB2	1.93	0.50
5:E:150:VAL:HG12	5:E:185:ILE:HD13	1.93	0.50
9:I:56:ASN:CG	9:I:57:LYS:H	2.20	0.50
16:P:161:ILE:O	16:P:162:VAL:C	2.55	0.50
20:T:93:LEU:HB2	20:T:110:VAL:HB	1.93	0.50
25:1:2:VAL:HG23	25:1:2:VAL:O	2.11	0.50
26:2:28:PRO:HA	27:3:33:THR:HB	1.92	0.50
26:2:51:LEU:CD2	26:2:55:TRP:CD1	2.94	0.50
26:2:236:PHE:CZ	26:2:262:LEU:CD2	2.94	0.50
26:2:245:LEU:HD22	26:2:245:LEU:N	2.27	0.50
27:3:12:VAL:HG23	27:3:12:VAL:O	2.10	0.50
1:A:66:GLU:HB2	1:A:265:VAL:CG2	2.40	0.50
1:A:292:ARG:NH1	1:A:295:GLN:OE1	2.45	0.50
1:A:452:ASP:CG	1:A:476:ILE:HG12	2.36	0.50
2:B:36:GLU:OE1	2:B:654:GLN:N	2.34	0.50
2:B:568:PHE:CZ	2:B:573:TRP:HD1	2.28	0.50
2:B:884:ASN:OD1	2:B:885:ARG:N	2.44	0.50
2:B:1094:GLN:HG2	2:B:1103:LEU:HB2	1.93	0.50
3:C:172:GLU:HG2	12:L:58:ARG:HH22	1.77	0.50
6:F:44:ARG:HD3	6:F:113:GLY:O	2.12	0.50
8:H:98:ARG:HB3	8:H:115:TYR:HB2	1.93	0.50
9:I:23:MET:HE3	9:I:25:TYR:CE1	2.47	0.50
11:K:12:LEU:HD21	11:K:18:LYS:HA	1.92	0.50
12:L:25:GLU:CG	12:L:27:GLU:OE2	2.40	0.50
22:V:393:THR:HA	22:V:418:LYS:CG	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:3:12:VAL:CG2	27:3:161:ILE:HA	2.42	0.50
1:A:427:ILE:HG23	13:M:38:GLY:C	2.37	0.50
1:A:923:ASP:C	1:A:925:THR:N	2.68	0.50
1:A:1317:LYS:HB2	21:U:295:GLY:HA3	1.93	0.50
2:B:205:VAL:HG21	2:B:368:MET:HG3	1.92	0.50
2:B:713:PHE:CD1	2:B:1001:PRO:HA	2.46	0.50
3:C:11:ILE:HG12	11:K:108:ALA:HB1	1.93	0.50
5:E:54:ARG:HA	5:E:57:ASP:HB2	1.93	0.50
13:M:105:ARG:NH1	29:Y:64:DC:O5'	2.43	0.50
17:Q:25:PHE:CD1	18:R:210:PHE:HZ	2.30	0.50
21:U:175:ALA:CB	21:U:222:ARG:NH2	2.63	0.50
26:2:140:LYS:CG	26:2:162:PHE:CE1	2.94	0.50
27:3:202:LEU:HD22	27:3:202:LEU:N	2.27	0.50
1:A:551:ARG:NH1	1:A:637:MET:SD	2.84	0.50
1:A:731:ASN:ND2	21:U:253:THR:CG2	2.70	0.50
2:B:988:LYS:O	2:B:992:ASN:ND2	2.43	0.50
3:C:6:GLN:HG3	3:C:25:ASN:CG	2.37	0.50
4:D:76:ASN:HB3	4:D:79:THR:HB	1.92	0.50
13:M:222:LEU:HD22	13:M:269:ARG:HG3	1.94	0.50
14:N:333:ASN:HB3	14:N:360:LEU:HA	1.93	0.50
16:P:289:PRO:HB3	29:Y:84:DG:C5'	2.29	0.50
17:Q:106:LYS:HG2	18:R:218:LYS:CG	2.41	0.50
17:Q:113:ARG:HD3	18:R:217:GLN:O	2.10	0.50
17:Q:120:ASP:HB3	17:Q:174:ARG:HG3	1.94	0.50
21:U:188:LYS:O	21:U:192:ARG:HG3	2.11	0.50
23:W:494:ILE:HD11	23:W:680:ALA:HB2	1.93	0.50
26:2:199:ALA:CB	26:2:201:PHE:CE2	2.95	0.50
27:3:216:LYS:O	27:3:216:LYS:HG2	2.12	0.50
1:A:233:CYS:O	1:A:238:MET:N	2.45	0.50
2:B:157:ARG:HB2	2:B:181:PRO:O	2.12	0.50
2:B:1072:ARG:HD3	2:B:1112:ASP:OD1	2.12	0.50
23:W:325:THR:HG22	23:W:329:PHE:CE2	2.47	0.50
26:2:211:GLN:CA	26:2:261:PHE:CE1	2.95	0.50
27:3:174:TYR:HE1	27:3:178:MET:HE3	1.77	0.50
27:3:215:LEU:HD12	27:3:230:VAL:CG2	2.42	0.50
1:A:432:HIS:CE1	1:A:438:LEU:HB2	2.47	0.50
1:A:618:TYR:O	1:A:620:HIS:N	2.44	0.50
2:B:1030:ASN:ND2	2:B:1033:THR:OG1	2.45	0.50
2:B:1075:MET:HB2	2:B:1082:GLY:HA2	1.94	0.50
7:G:12:LEU:HG	7:G:63:ARG:HH11	1.77	0.50
20:T:229:HIS:ND1	28:X:29:DC:O4'	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:0:55:LEU:HD12	27:3:178:MET:HE3	1.93	0.50
26:2:118:LEU:HD21	27:3:39:ASP:OD1	1.95	0.50
26:2:214:TYR:CB	26:2:261:PHE:CE2	2.95	0.50
27:3:10:LEU:CD2	27:3:143:TYR:HE2	2.25	0.50
27:3:18:ASN:O	27:3:21:TRP:CD1	2.63	0.50
1:A:16:ARG:HD2	2:B:1147:SER:HB3	1.93	0.49
1:A:510:GLU:HA	6:F:67:GLY:HA3	1.94	0.49
1:A:922:PHE:CD1	1:A:1052:ARG:HB2	2.47	0.49
2:B:10:TYR:CE2	2:B:12:GLU:HB3	2.47	0.49
2:B:591:ARG:HG2	2:B:598:VAL:HG12	1.93	0.49
5:E:14:ARG:O	5:E:18:MET:HG2	2.11	0.49
7:G:93:ASN:HD21	17:Q:151:THR:HA	1.76	0.49
13:M:118:PHE:HE1	13:M:142:PHE:HB3	1.77	0.49
17:Q:105:TYR:CB	18:R:234:GLU:HG2	2.41	0.49
18:R:191:PHE:CB	18:R:202:PHE:HE1	2.23	0.49
18:R:195:PRO:HG3	18:R:199:LYS:HB3	1.87	0.49
23:W:624:PRO:O	23:W:656:ALA:HB1	2.12	0.49
25:1:43:VAL:HG12	25:1:44:PHE:N	2.27	0.49
26:2:35:TYR:CD1	26:2:62:LEU:CD1	2.95	0.49
26:2:170:ALA:CB	26:2:213:TRP:CZ3	2.95	0.49
26:2:181:GLN:HE21	26:2:181:GLN:CA	2.23	0.49
26:2:236:PHE:CZ	26:2:258:LEU:CD1	2.95	0.49
27:3:137:LEU:CD1	27:3:177:PHE:CE1	2.95	0.49
27:3:190:LEU:HA	27:3:210:THR:HG21	1.91	0.49
1:A:380:VAL:N	1:A:475:ARG:O	2.37	0.49
1:A:389:THR:HG22	1:A:449:HIS:HA	1.94	0.49
1:A:926:ASN:OD1	1:A:927:GLU:N	2.45	0.49
9:I:88:LYS:HD2	9:I:121:HIS:HE1	1.77	0.49
10:J:7:CYS:HB3	10:J:10:CYS:SG	2.52	0.49
12:L:19:CYS:HB2	12:L:36:CYS:SG	2.53	0.49
18:R:88:ARG:NH2	18:R:93:ASP:HB3	2.27	0.49
22:V:516:PRO:HG2	22:V:706:LYS:HE2	1.92	0.49
26:2:223:ALA:O	26:2:224:GLN:HB3	2.12	0.49
26:2:236:PHE:CE2	26:2:262:LEU:CD1	2.94	0.49
1:A:33:ARG:O	2:B:1138:ARG:HG2	2.11	0.49
1:A:286:ILE:HD13	1:A:313:HIS:HD2	1.77	0.49
1:A:525:ILE:O	1:A:534:VAL:N	2.36	0.49
1:A:625:ASP:OD1	1:A:637:MET:HE3	2.12	0.49
2:B:166:LEU:HB3	2:B:170:ASP:HB2	1.94	0.49
2:B:1066:PRO:HD3	13:M:30:GLY:HA3	1.94	0.49
3:C:94:CYS:O	3:C:98:SER:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:96:GLU:OE2	4:D:117:SER:OG	2.22	0.49
8:H:106:THR:C	8:H:108:ALA:H	2.15	0.49
13:M:279:GLY:CA	20:T:153:TYR:HE1	2.25	0.49
14:N:310:GLU:HB3	14:N:313:PRO:HD2	1.93	0.49
14:N:345:SER:N	14:N:348:LYS:O	2.43	0.49
15:O:11:LEU:HG	15:O:40:PHE:HZ	1.77	0.49
18:R:194:ARG:N	18:R:195:PRO:CD	2.54	0.49
20:T:135:SER:O	20:T:137:LYS:HG3	2.12	0.49
22:V:315:VAL:CG1	23:W:500:ASP:CG	2.80	0.49
26:2:35:TYR:CD1	26:2:62:LEU:CG	2.92	0.49
26:2:90:LEU:CD2	26:2:140:LYS:HD3	2.42	0.49
26:2:189:GLU:CA	26:2:192:GLU:HG2	2.41	0.49
26:2:251:VAL:HG11	26:2:254:MET:HB2	1.94	0.49
27:3:177:PHE:CZ	27:3:203:LEU:CD2	2.95	0.49
2:B:89:GLU:OE2	20:T:140:ARG:NH1	2.46	0.49
2:B:936:ALA:O	2:B:1049:GLN:N	2.29	0.49
4:D:19:GLN:HB2	4:D:21:ILE:HG12	1.94	0.49
5:E:134:GLU:CD	5:E:181:ARG:HH12	2.20	0.49
11:K:109:ILE:HA	11:K:112:LYS:NZ	2.27	0.49
16:P:293:TYR:CD2	16:P:302:LEU:HD13	2.44	0.49
17:Q:105:TYR:CE1	18:R:234:GLU:OE2	2.65	0.49
22:V:667:THR:CA	25:1:62:ASP:OD1	2.59	0.49
23:W:596:LEU:HG	23:W:597:LEU:N	2.27	0.49
26:2:163:MET:HE1	26:2:206:LEU:HB3	1.94	0.49
27:3:165:LYS:HZ1	27:3:200:SER:H	1.61	0.49
1:A:97:VAL:HG21	1:A:322:LEU:HD11	1.94	0.49
1:A:1086:MET:HE2	1:A:1466:ALA:HB3	1.94	0.49
1:A:1223:ASP:OD2	1:A:1224:ARG:NH2	2.44	0.49
2:B:342:VAL:HG13	2:B:346:GLU:HB2	1.94	0.49
6:F:45:PRO:HD3	6:F:115:TYR:CZ	2.48	0.49
17:Q:188:TYR:N	18:R:212:VAL:HA	2.27	0.49
18:R:177:ASN:HD21	18:R:202:PHE:HE2	1.61	0.49
20:T:162:ASN:O	20:T:165:TYR:HB3	2.13	0.49
26:2:46:ARG:HD3	26:2:85:GLU:HB2	1.93	0.49
26:2:57:MET:HA	26:2:60:LEU:HG	1.94	0.49
27:3:33:THR:CG2	27:3:36:LYS:H	2.04	0.49
1:A:456:VAL:O	1:A:472:HIS:N	2.35	0.49
1:A:535:MET:HE1	1:A:669:TYR:HB3	1.95	0.49
1:A:581:LYS:HB2	8:H:91:VAL:H	1.77	0.49
1:A:614:ASP:C	1:A:616:GLY:N	2.71	0.49
1:A:1143:LEU:HB3	1:A:1147:SER:CB	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:133:ILE:O	2:B:134:LYS:HG3	2.09	0.49
2:B:1142:ASN:ND2	2:B:1145:GLN:HG2	2.28	0.49
8:H:70:LEU:O	8:H:72:ASP:N	2.39	0.49
9:I:28:GLU:OE2	9:I:33:ARG:NH1	2.46	0.49
13:M:169:ARG:HD3	13:M:207:ASP:H	1.77	0.49
23:W:419:GLU:HG3	23:W:432:ILE:CG2	2.42	0.49
25:1:1:MET:CE	26:2:415:GLN:C	2.84	0.49
26:2:118:LEU:HD23	27:3:42:MET:CB	2.35	0.49
26:2:176:ALA:O	26:2:177:GLN:HB2	2.12	0.49
27:3:21:TRP:CG	27:3:34:LEU:HD23	2.48	0.49
27:3:108:ASN:O	27:3:111:ILE:HG12	2.12	0.49
1:A:364:ARG:HG3	1:A:501:MET:O	2.12	0.49
1:A:764:ASN:OD1	1:A:766:PHE:N	2.36	0.49
1:A:1169:VAL:HG22	1:A:1220:HIS:NE2	2.28	0.49
1:A:1319:LYS:HE3	1:A:1331:LEU:HD23	1.95	0.49
2:B:89:GLU:HG3	2:B:90:GLN:H	1.77	0.49
3:C:27:ASP:HB3	3:C:30:VAL:HG23	1.95	0.49
7:G:95:VAL:HG11	17:Q:127:PHE:CZ	2.48	0.49
11:K:56:VAL:HA	11:K:77:THR:HG22	1.95	0.49
11:K:81:TYR:HE2	11:K:86:ALA:HB2	1.78	0.49
12:L:16:ILE:CG1	12:L:27:GLU:C	2.79	0.49
24:0:55:LEU:N	27:3:209:ILE:HD11	2.28	0.49
26:2:51:LEU:HD23	26:2:51:LEU:C	2.37	0.49
26:2:93:LEU:CD2	26:2:96:TRP:HE1	2.25	0.49
26:2:181:GLN:HE22	26:2:220:LEU:HD12	1.76	0.49
26:2:188:THR:HG23	26:2:189:GLU:N	2.27	0.49
1:A:903:PHE:HA	1:A:978:VAL:HA	1.95	0.49
2:B:418:TYR:OH	2:B:433:LEU:HD23	2.12	0.49
5:E:18:MET:HE1	5:E:60:VAL:HG11	1.94	0.49
8:H:105:SER:HB2	8:H:108:ALA:HB2	1.93	0.49
25:1:38:ILE:HG22	25:1:44:PHE:CE1	2.48	0.49
26:2:30:VAL:CB	27:3:25:GLN:CB	2.83	0.49
27:3:12:VAL:HG22	27:3:161:ILE:HA	1.94	0.49
27:3:187:GLN:O	27:3:188:ASN:HB2	2.12	0.49
27:3:220:MET:N	27:3:221:PRO:HD2	2.28	0.49
1:A:781:ILE:HA	1:A:784:VAL:HG22	1.95	0.49
1:A:802:PHE:HZ	2:B:670:GLU:O	1.96	0.49
1:A:821:GLY:HA2	1:A:838:PHE:CD2	2.48	0.49
1:A:931:ARG:C	1:A:933:THR:H	2.19	0.49
1:A:1189:ASP:HA	1:A:1192:TRP:HD1	1.77	0.49
1:A:1310:HIS:CE1	1:A:1334:TRP:HA	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:763:SER:HA	2:B:766:TYR:CD2	2.47	0.49
2:B:798:ARG:O	2:B:801:VAL:HB	2.13	0.49
2:B:915:GLY:HA3	13:M:133:ASN:OD1	2.13	0.49
3:C:45:ILE:CG1	3:C:79:VAL:HB	2.37	0.49
18:R:196:ASP:OD2	18:R:198:LYS:NZ	2.46	0.49
22:V:370:SER:O	22:V:374:TRP:HD1	1.96	0.49
22:V:634:ARG:HG2	22:V:679:PHE:CZ	2.48	0.49
23:W:608:ILE:O	23:W:614:TYR:OH	2.21	0.49
24:O:209:THR:HA	24:O:219:TYR:CD1	2.48	0.49
26:2:159:VAL:N	26:2:162:PHE:HB3	2.28	0.49
26:2:211:GLN:HE21	26:2:257:SER:HB3	1.78	0.49
26:2:426:ARG:HD2	26:2:444:THR:CG2	2.43	0.49
27:3:166:ALA:O	27:3:198:SER:HB2	2.13	0.49
27:3:178:MET:HE2	27:3:202:LEU:HD13	1.92	0.49
1:A:85:PHE:HE2	2:B:1163:MET:HE2	1.78	0.49
1:A:527:THR:N	1:A:532:ARG:O	2.36	0.49
1:A:540:ASP:HB3	1:A:680:LEU:HD21	1.94	0.49
1:A:922:PHE:HB3	1:A:1052:ARG:HD2	1.95	0.49
2:B:835:GLU:OE1	2:B:835:GLU:N	2.45	0.49
3:C:210:GLU:O	3:C:213:GLU:HB2	2.13	0.49
4:D:44:ARG:HD2	4:D:47:GLN:OE1	2.12	0.49
8:H:62:SER:HA	8:H:141:VAL:HA	1.93	0.49
13:M:279:GLY:CA	20:T:153:TYR:CE1	2.96	0.49
18:R:192:VAL:HG12	18:R:201:LEU:O	2.13	0.49
18:R:195:PRO:CB	18:R:199:LYS:CD	2.89	0.49
22:V:516:PRO:HB3	25:1:15:ALA:O	2.13	0.49
22:V:523:VAL:HB	25:1:20:LEU:HD23	1.92	0.49
23:W:608:ILE:HG23	23:W:614:TYR:CZ	2.48	0.49
26:2:77:LYS:HD3	26:2:78:GLU:HG3	1.94	0.49
27:3:12:VAL:CG2	27:3:161:ILE:HG23	2.43	0.49
1:A:432:HIS:HE2	1:A:438:LEU:HD13	1.77	0.48
1:A:642:LYS:NZ	21:U:283:GLU:HA	2.28	0.48
2:B:133:ILE:C	2:B:134:LYS:CG	2.84	0.48
2:B:249:LYS:HE3	2:B:249:LYS:HB3	1.46	0.48
2:B:956:PHE:HD2	2:B:960:GLY:HA2	1.77	0.48
8:H:105:SER:O	8:H:106:THR:HB	2.12	0.48
13:M:107:MET:HB2	13:M:112:ARG:NH1	2.28	0.48
17:Q:124:ARG:HG2	17:Q:126:SER:H	1.76	0.48
23:W:285:TYR:CE1	23:W:403:PHE:CZ	3.01	0.48
27:3:10:LEU:CD2	27:3:143:TYR:CE2	2.95	0.48
1:A:65:ILE:HD11	1:A:258:LEU:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:987:ILE:HG23	1:A:1060:LEU:HD11	1.95	0.48
1:A:1162:GLU:HA	1:A:1308:TYR:CE2	2.47	0.48
1:A:1304:ILE:HG22	1:A:1340:GLY:HA3	1.95	0.48
1:A:1372:GLU:OE1	5:E:193:ILE:HG21	2.13	0.48
2:B:57:ARG:O	2:B:61:ASP:N	2.46	0.48
2:B:867:ILE:HB	2:B:894:THR:HB	1.94	0.48
2:B:1003:ASN:ND2	2:B:1007:ASN:OD1	2.42	0.48
12:L:17:TYR:CB	12:L:46:LYS:CA	2.90	0.48
18:R:160:GLN:C	18:R:162:GLY:H	2.21	0.48
23:W:37:HIS:NE2	23:W:454:VAL:CG1	2.76	0.48
25:1:38:ILE:CG2	25:1:44:PHE:CE1	2.96	0.48
26:2:89:LEU:HD23	26:2:93:LEU:HG	1.94	0.48
26:2:159:VAL:HG22	26:2:160:LEU:HD13	1.95	0.48
26:2:179:LEU:CB	26:2:184:LEU:HD11	2.40	0.48
27:3:60:ILE:HG22	27:3:61:ALA:N	2.26	0.48
27:3:217:VAL:CG1	27:3:226:TYR:CE2	2.95	0.48
1:A:908:THR:C	1:A:910:LYS:H	2.21	0.48
1:A:1031:ARG:HA	1:A:1034:GLN:HB3	1.94	0.48
2:B:573:TRP:HZ2	2:B:576:ILE:HG23	1.78	0.48
2:B:848:LEU:HD23	2:B:852:GLY:HA2	1.95	0.48
2:B:1163:MET:HA	2:B:1167:ILE:O	2.13	0.48
3:C:105:VAL:HG12	3:C:159:LEU:HB3	1.95	0.48
3:C:266:GLU:O	3:C:270:ASP:HB2	2.14	0.48
5:E:149:VAL:HB	5:E:192:LYS:HE2	1.95	0.48
9:I:57:LYS:HE2	9:I:60:HIS:CE1	2.48	0.48
11:K:40:HIS:CE1	11:K:63:VAL:H	2.31	0.48
13:M:117:ALA:O	13:M:121:ILE:N	2.46	0.48
13:M:295:ARG:NH2	13:M:298:ASP:OD2	2.45	0.48
17:Q:123:ASN:O	17:Q:123:ASN:ND2	2.45	0.48
26:2:178:LEU:HD12	26:2:178:LEU:N	2.28	0.48
26:2:198:SER:OG	26:2:238:PHE:HE2	1.96	0.48
26:2:218:GLN:HG2	26:2:268:PHE:CB	2.44	0.48
27:3:59:VAL:HG13	27:3:59:VAL:O	2.12	0.48
27:3:160:ARG:HE	27:3:190:LEU:HG	1.78	0.48
27:3:174:TYR:HD1	27:3:202:LEU:HD11	1.78	0.48
1:A:14:PRO:HG2	1:A:16:ARG:NH1	2.29	0.48
1:A:613:GLU:CG	21:U:261:PHE:HD1	2.26	0.48
1:A:798:ILE:O	1:A:820:ARG:NE	2.46	0.48
1:A:1220:HIS:HA	1:A:1223:ASP:HB3	1.94	0.48
2:B:209:ALA:HB1	2:B:211:LYS:HG3	1.96	0.48
2:B:249:LYS:C	2:B:251:ALA:H	2.21	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:294:ASP:OD2	2:B:379:ARG:NH2	2.44	0.48
3:C:134:ASN:OD1	3:C:135:ARG:N	2.46	0.48
5:E:28:VAL:HG13	5:E:32:GLU:OE1	2.13	0.48
13:M:108:SER:O	13:M:110:SER:OG	2.28	0.48
18:R:163:LEU:O	18:R:164:GLY:C	2.56	0.48
19:S:49:ARG:HB3	19:S:96:GLN:HB3	1.95	0.48
21:U:225:ALA:HB3	21:U:228:MET:HG2	1.95	0.48
23:W:73:CYS:HB2	23:W:209:TYR:CE1	2.48	0.48
26:2:166:SER:HB3	26:2:167:PRO:CD	2.43	0.48
2:B:26:CYS:O	2:B:29:VAL:HB	2.13	0.48
3:C:262:GLN:O	3:C:266:GLU:HG2	2.14	0.48
13:M:178:LYS:O	20:T:154:LYS:HB2	1.94	0.48
16:P:206:GLU:OE2	16:P:206:GLU:HA	2.12	0.48
17:Q:106:LYS:CB	18:R:218:LYS:HE2	2.43	0.48
24:0:55:LEU:HD12	27:3:178:MET:HE1	1.95	0.48
1:A:345:GLY:O	1:A:351:ARG:HB3	2.13	0.48
1:A:1191:GLU:HG2	9:I:1:MET:SD	2.54	0.48
2:B:75:SER:O	2:B:78:VAL:N	2.47	0.48
2:B:675:LEU:HD21	2:B:697:GLU:OE2	2.13	0.48
2:B:970:HIS:C	2:B:973:PRO:HD2	2.39	0.48
2:B:1068:GLN:O	2:B:1072:ARG:N	2.45	0.48
6:F:108:ARG:HB2	6:F:116:GLU:HG3	1.96	0.48
8:H:106:THR:C	8:H:108:ALA:N	2.71	0.48
17:Q:25:PHE:CD1	18:R:210:PHE:CZ	3.01	0.48
17:Q:71:PHE:HA	17:Q:100:VAL:CG2	2.40	0.48
19:S:127:PHE:HB2	20:T:19:TRP:CB	2.43	0.48
21:U:145:ARG:NE	21:U:173:GLU:OE1	2.34	0.48
25:1:38:ILE:CG2	25:1:44:PHE:CD1	2.94	0.48
26:2:35:TYR:CE2	26:2:62:LEU:CB	2.96	0.48
26:2:89:LEU:CD2	26:2:93:LEU:HG	2.44	0.48
26:2:203:PHE:CE2	26:2:205:LEU:CD2	2.96	0.48
1:A:20:ARG:HE	2:B:1174:VAL:C	2.22	0.48
1:A:140:ARG:NH1	1:A:234:PHE:O	2.47	0.48
1:A:156:GLY:HA2	1:A:181:HIS:CE1	2.49	0.48
2:B:562:ALA:O	2:B:610:ARG:NH2	2.38	0.48
6:F:86:GLU:N	6:F:86:GLU:OE1	2.47	0.48
7:G:97:LEU:HD13	7:G:128:TYR:CD2	2.48	0.48
12:L:38:GLU:HG2	12:L:39:CYS:N	2.27	0.48
15:O:76:LEU:HD13	15:O:95:ILE:HD12	1.95	0.48
17:Q:166:SER:OG	17:Q:170:LYS:HB3	2.14	0.48
18:R:89:HIS:ND1	18:R:139:PHE:CE1	2.81	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:1:38:ILE:HA	25:1:44:PHE:CD1	2.37	0.48
1:A:330:GLN:CB	13:M:107:MET:SD	2.88	0.48
1:A:927:GLU:O	1:A:931:ARG:HB2	2.14	0.48
1:A:981:CYS:SG	1:A:1075:LYS:HB3	2.54	0.48
2:B:97:THR:HG22	2:B:107:PRO:HA	1.95	0.48
4:D:124:ASP:HA	4:D:127:LEU:HB3	1.96	0.48
5:E:106:VAL:HG23	5:E:129:GLN:HE22	1.78	0.48
24:0:77:LYS:HA	24:0:77:LYS:HE3	1.94	0.48
25:1:5:LEU:HD11	26:2:408:LEU:CB	2.11	0.48
25:1:34:ILE:HG22	25:1:46:ILE:CG1	2.44	0.48
25:1:38:ILE:HD13	25:1:38:ILE:N	2.26	0.48
25:1:57:VAL:CG2	25:1:61:MET:HE3	2.44	0.48
27:3:42:MET:HE2	27:3:108:ASN:CB	2.42	0.48
1:A:71:CYS:O	1:A:75:ALA:N	2.47	0.48
1:A:253:LEU:HD12	1:A:254:PRO:HD2	1.96	0.48
1:A:660:MET:HB3	1:A:664:ILE:HB	1.94	0.48
1:A:817:PRO:HB2	1:A:822:PHE:CB	2.42	0.48
2:B:546:GLU:C	2:B:546:GLU:CD	2.82	0.48
2:B:932:GLY:N	2:B:945:CYS:O	2.37	0.48
5:E:41:LYS:O	5:E:46:ASP:N	2.42	0.48
8:H:107:GLU:OE1	8:H:107:GLU:HA	2.13	0.48
10:J:30:THR:HG22	10:J:33:ASP:H	1.78	0.48
12:L:22:CYS:HB3	12:L:39:CYS:CB	2.40	0.48
16:P:169:VAL:HB	16:P:257:ASN:HB3	1.96	0.48
16:P:261:SER:CB	29:Y:81:DA:H4'	2.43	0.48
24:0:98:GLN:OE1	27:3:209:ILE:CA	2.60	0.48
26:2:60:LEU:CD1	26:2:95:ILE:CG2	2.91	0.48
26:2:251:VAL:HG11	26:2:254:MET:CB	2.43	0.48
1:A:198:LEU:HB3	1:A:216:LEU:HD12	1.95	0.48
1:A:618:TYR:C	1:A:620:HIS:N	2.70	0.48
1:A:921:ARG:HB2	1:A:956:PHE:CZ	2.48	0.48
1:A:1310:HIS:N	21:U:252:LYS:NZ	2.59	0.48
1:A:1310:HIS:H	21:U:252:LYS:HZ2	1.62	0.48
1:A:1430:CYS:HB2	1:A:1435:THR:HA	1.96	0.48
2:B:10:TYR:HE2	2:B:12:GLU:HB3	1.79	0.48
2:B:198:GLU:O	2:B:488:PRO:HD3	2.14	0.48
2:B:438:ARG:HA	2:B:441:SER:HB2	1.96	0.48
2:B:1029:TYR:CE1	2:B:1036:LYS:HG2	2.48	0.48
3:C:33:SER:O	3:C:37:VAL:HG23	2.14	0.48
7:G:14:HIS:HB3	7:G:17:TYR:CD2	2.49	0.48
7:G:97:LEU:HD13	7:G:128:TYR:HD2	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:345:SER:O	14:N:347:ASN:N	2.43	0.48
22:V:519:TYR:HE2	25:1:20:LEU:CG	2.19	0.48
23:W:70:LEU:HG	23:W:72:TYR:CE1	2.49	0.48
23:W:73:CYS:HB3	23:W:209:TYR:CG	2.48	0.48
23:W:430:ASN:CB	23:W:431:PRO:CD	2.85	0.48
24:O:165:ARG:HB2	24:O:193:LYS:O	2.14	0.48
25:1:22:TYR:CD1	25:1:22:TYR:C	2.92	0.48
27:3:216:LYS:O	27:3:218:PRO:HD3	2.14	0.48
1:A:913:ASN:OD1	1:A:967:ARG:NH2	2.47	0.47
2:B:956:PHE:CD2	2:B:960:GLY:HA2	2.49	0.47
2:B:1130:THR:HB	2:B:1134:THR:N	2.29	0.47
3:C:16:ASP:HA	3:C:240:ARG:HG3	1.96	0.47
6:F:45:PRO:HA	6:F:115:TYR:O	2.14	0.47
13:M:244:LEU:HD11	13:M:295:ARG:HD3	1.95	0.47
17:Q:55:ASP:HB3	17:Q:58:GLN:HB2	1.96	0.47
20:T:138:PRO:O	20:T:141:LEU:HG	2.13	0.47
22:V:394:SER:CB	22:V:416:THR:O	2.59	0.47
23:W:28:LEU:HD13	23:W:28:LEU:C	2.38	0.47
26:2:30:VAL:CG2	26:2:34:LEU:HD23	2.41	0.47
27:3:195:VAL:HG23	27:3:214:TYR:CE1	2.48	0.47
1:A:101:VAL:O	1:A:105:LYS:HG3	2.14	0.47
1:A:702:ILE:HG23	1:A:752:THR:HB	1.96	0.47
5:E:39:GLU:O	5:E:43:GLN:N	2.40	0.47
13:M:178:LYS:C	20:T:154:LYS:CG	2.87	0.47
17:Q:126:SER:HB2	17:Q:136:PHE:O	2.14	0.47
18:R:224:THR:HG23	18:R:230:GLU:CB	2.41	0.47
22:V:361:CYS:HB3	22:V:405:VAL:HG21	1.96	0.47
22:V:428:GLU:OE1	22:V:428:GLU:HA	2.13	0.47
23:W:73:CYS:HB3	23:W:209:TYR:CD1	2.50	0.47
25:1:9:LEU:N	25:1:9:LEU:HD12	2.29	0.47
27:3:34:LEU:HD13	27:3:38:ILE:HG12	1.96	0.47
27:3:124:ILE:HD13	27:3:124:ILE:C	2.38	0.47
27:3:131:THR:HG23	27:3:133:LEU:HD13	1.95	0.47
1:A:376:ASP:OD2	1:A:473:ARG:NE	2.47	0.47
1:A:465:HIS:CE1	1:A:467:MET:HB2	2.50	0.47
1:A:551:ARG:CG	1:A:625:ASP:OD1	2.62	0.47
1:A:637:MET:CG	8:H:122:LEU:HD21	2.44	0.47
1:A:1313:GLN:C	1:A:1315:ASP:H	2.22	0.47
1:A:1313:GLN:HB3	1:A:1333:GLU:HG2	1.95	0.47
2:B:780:VAL:HG21	2:B:1048:TYR:CE2	2.50	0.47
2:B:1040:GLN:HG2	3:C:203:TRP:CZ2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:52:ARG:HA	5:E:53:PRO:HD3	1.69	0.47
9:I:25:TYR:N	9:I:38:ALA:O	2.40	0.47
12:L:18:ILE:HB	12:L:45:TYR:HB3	1.96	0.47
16:P:180:LEU:HA	16:P:183:ILE:HD12	1.96	0.47
16:P:299:ARG:HA	16:P:299:ARG:HD2	1.49	0.47
21:U:218:ASP:O	21:U:222:ARG:NE	2.35	0.47
22:V:413:LEU:HA	28:X:56:DA:C5'	2.44	0.47
22:V:528:LYS:HD3	29:Y:36:DA:H4'	1.96	0.47
23:W:419:GLU:HG3	23:W:432:ILE:HG23	1.96	0.47
25:1:18:GLN:CD	25:1:44:PHE:CZ	2.93	0.47
26:2:30:VAL:CG2	26:2:34:LEU:CD2	2.91	0.47
26:2:42:LEU:HD22	26:2:52:ALA:HA	1.95	0.47
27:3:226:TYR:CA	27:3:230:VAL:HG23	2.42	0.47
28:X:15:DA:H2''	28:X:16:DA:C8	2.49	0.47
1:A:775:LYS:HB3	2:B:974:SER:HB3	1.95	0.47
1:A:1085:GLU:OE1	6:F:60:TYR:OH	2.28	0.47
2:B:309:PHE:HE2	9:I:25:TYR:CE2	2.32	0.47
2:B:860:VAL:HG12	2:B:902:GLY:C	2.38	0.47
5:E:20:LEU:HD12	5:E:182:TYR:CE1	2.49	0.47
7:G:52:ASP:H	7:G:72:TYR:HA	1.79	0.47
15:O:64:THR:OG1	15:O:75:VAL:HB	2.14	0.47
16:P:207:PRO:CB	16:P:229:GLN:OE1	2.62	0.47
21:U:174:GLU:O	21:U:178:GLN:N	2.42	0.47
26:2:203:PHE:CD2	26:2:204:LEU:N	2.82	0.47
29:Y:59:DG:H2''	29:Y:60:DA:C8	2.50	0.47
1:A:204:HIS:CD2	1:A:207:GLU:HG2	2.50	0.47
1:A:592:PHE:CE2	1:A:596:ILE:HD11	2.49	0.47
2:B:273:PHE:CD1	2:B:284:ILE:HG23	2.49	0.47
2:B:388:TYR:HE1	2:B:502:HIS:HB3	1.80	0.47
5:E:173:ILE:N	5:E:208:LEU:O	2.41	0.47
11:K:35:ILE:HB	11:K:71:ILE:CG1	2.44	0.47
17:Q:109:HIS:O	18:R:221:ARG:NE	2.35	0.47
17:Q:187:ILE:C	18:R:212:VAL:H	2.23	0.47
25:1:53:LEU:H	25:1:53:LEU:CD1	2.26	0.47
26:2:85:GLU:O	26:2:89:LEU:HB2	2.14	0.47
26:2:133:THR:HG23	26:2:134:SER:N	2.28	0.47
27:3:10:LEU:HA	27:3:56:LYS:HG2	1.96	0.47
27:3:160:ARG:HB2	27:3:190:LEU:HG	1.96	0.47
29:Y:30:DG:N2	29:Y:31:DG:N3	2.62	0.47
1:A:111:CYS:HA	1:A:188:GLN:NE2	2.29	0.47
1:A:478:PRO:HB3	11:K:4:PRO:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:621:ILE:HA	1:A:623:PRO:CD	2.41	0.47
2:B:497:LYS:H	2:B:498:PRO:CD	1.85	0.47
2:B:1028:LEU:HB2	2:B:1041:ILE:HD13	1.95	0.47
5:E:62:VAL:HG21	5:E:72:MET:HE2	1.97	0.47
6:F:52:ILE:HG21	6:F:110:LEU:HD21	1.97	0.47
8:H:112:LEU:HB3	8:H:131:ASN:HD21	1.80	0.47
25:1:13:ASP:CG	25:1:14:PRO:CD	2.88	0.47
27:3:70:LEU:HD22	27:3:114:GLU:CB	2.44	0.47
29:Y:34:DC:H2'	29:Y:35:DG:C8	2.50	0.47
1:A:245:PRO:HA	1:A:248:MET:HE2	1.96	0.47
1:A:616:GLY:O	1:A:619:LYS:HB2	2.15	0.47
1:A:662:HIS:NE2	6:F:127:ASP:OD2	2.28	0.47
1:A:868:MET:HB2	1:A:1092:ALA:HB2	1.95	0.47
1:A:880:ARG:HH12	5:E:169:GLN:CD	2.22	0.47
2:B:274:ARG:NH2	2:B:312:GLN:OE1	2.45	0.47
2:B:626:LEU:HG	2:B:698:ILE:HD13	1.95	0.47
2:B:936:ALA:HA	2:B:942:LYS:HA	1.95	0.47
3:C:169:PHE:HZ	11:K:10:PHE:CZ	2.32	0.47
5:E:188:GLY:HA2	5:E:208:LEU:HD21	1.97	0.47
6:F:80:MET:HG3	6:F:103:PRO:HD3	1.97	0.47
6:F:99:ALA:O	6:F:100:ARG:HG2	2.15	0.47
12:L:25:GLU:O	12:L:37:ARG:NH1	2.47	0.47
17:Q:69:ASP:CA	18:R:225:VAL:CG2	2.92	0.47
17:Q:154:CYS:SG	17:Q:155:THR:N	2.88	0.47
23:W:73:CYS:CB	23:W:209:TYR:CE1	2.97	0.47
24:0:54:ARG:CG	27:3:182:PHE:CZ	2.80	0.47
25:1:45:VAL:HG21	26:2:409:TYR:CE2	2.50	0.47
26:2:46:ARG:CD	26:2:85:GLU:CB	2.93	0.47
26:2:84:GLU:OE1	26:2:84:GLU:HA	2.15	0.47
26:2:236:PHE:HE2	26:2:262:LEU:CD1	2.27	0.47
27:3:8:LEU:HD23	27:3:54:SER:CB	2.42	0.47
27:3:34:LEU:HD22	27:3:37:CYS:SG	2.54	0.47
27:3:53:ARG:HA	27:3:101:TYR:HE1	1.78	0.47
27:3:56:LYS:HD3	27:3:56:LYS:N	2.30	0.47
1:A:391:ALA:HB2	1:A:447:GLU:HG2	1.97	0.47
1:A:927:GLU:C	1:A:931:ARG:HG3	2.35	0.47
2:B:551:GLU:HB3	2:B:556:ILE:HD13	1.96	0.47
2:B:604:ILE:O	2:B:613:ARG:N	2.44	0.47
3:C:200:PRO:C	3:C:217:GLN:OE1	2.58	0.47
9:I:96:PHE:HD2	9:I:110:LEU:HD22	1.79	0.47
14:N:332:GLU:HB3	15:O:92:LYS:HE2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:191:LEU:HD21	18:R:212:VAL:CG1	2.32	0.47
19:S:42:TRP:CD1	19:S:102:VAL:HG11	2.50	0.47
23:W:37:HIS:CG	23:W:454:VAL:HG13	2.50	0.47
25:1:38:ILE:O	25:1:38:ILE:HG12	2.15	0.47
26:2:35:TYR:CD2	26:2:62:LEU:CB	2.95	0.47
26:2:205:LEU:HD22	26:2:205:LEU:N	2.29	0.47
26:2:236:PHE:CD1	26:2:261:PHE:HB3	2.49	0.47
27:3:15:VAL:HG12	27:3:164:ILE:HD12	1.97	0.47
27:3:137:LEU:HD11	27:3:177:PHE:CE1	2.50	0.47
2:B:539:SER:HA	2:B:542:LEU:HB3	1.97	0.47
2:B:1036:LYS:HB2	3:C:194:HIS:CB	2.43	0.47
3:C:8:THR:H	3:C:25:ASN:HB3	1.80	0.47
5:E:71:GLN:O	5:E:100:THR:OG1	2.25	0.47
17:Q:110:MET:HB3	18:R:218:LYS:CG	2.24	0.47
17:Q:191:LEU:HD22	18:R:212:VAL:HB	1.97	0.47
19:S:10:ASN:O	20:T:47:LYS:HB2	2.15	0.47
20:T:161:TYR:O	20:T:164:GLU:HB3	2.15	0.47
21:U:184:ASP:O	21:U:188:LYS:HG3	2.14	0.47
21:U:218:ASP:C	21:U:218:ASP:OD1	2.58	0.47
25:1:59:GLU:CD	26:2:402:ARG:CZ	2.88	0.47
26:2:217:LEU:CD2	26:2:233:ILE:HD11	2.45	0.47
1:A:931:ARG:C	1:A:933:THR:N	2.73	0.47
2:B:685:LYS:HA	2:B:688:ALA:HB2	1.97	0.47
3:C:24:GLU:HG2	3:C:228:ARG:HA	1.97	0.47
6:F:108:ARG:HB2	6:F:116:GLU:CG	2.45	0.47
16:P:168:ILE:HG13	16:P:226:SER:C	2.40	0.47
17:Q:188:TYR:CD2	17:Q:192:ARG:HB2	2.49	0.47
18:R:195:PRO:HG2	18:R:199:LYS:CB	2.17	0.47
25:1:22:TYR:O	25:1:25:GLU:HB3	2.14	0.47
26:2:93:LEU:CA	26:2:96:TRP:CD1	2.94	0.47
1:A:426:ARG:O	13:M:39:LEU:CA	2.55	0.46
1:A:427:ILE:HG23	13:M:38:GLY:CA	2.45	0.46
1:A:601:ASN:ND2	1:A:632:ASN:H	2.09	0.46
1:A:848:ILE:HD13	2:B:499:ARG:HG3	1.97	0.46
3:C:53:ASP:N	3:C:160:ARG:O	2.48	0.46
10:J:67:LYS:NZ	12:L:23:HIS:O	2.47	0.46
11:K:99:SER:O	11:K:103:GLU:HG3	2.15	0.46
15:O:4:GLN:OE1	15:O:4:GLN:N	2.43	0.46
16:P:297:LYS:CE	16:P:297:LYS:CA	2.88	0.46
17:Q:104:LYS:HZ2	18:R:238:LYS:CD	2.25	0.46
17:Q:104:LYS:NZ	18:R:238:LYS:CE	2.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:263:LEU:C	23:W:263:LEU:HD23	2.39	0.46
23:W:584:TYR:CD1	23:W:594:ALA:CB	2.87	0.46
23:W:623:VAL:HG23	23:W:681:ASP:HB2	1.98	0.46
25:1:10:ILE:HG12	25:1:43:VAL:CG1	2.45	0.46
25:1:53:LEU:O	25:1:57:VAL:HG12	2.15	0.46
26:2:51:LEU:HD21	26:2:55:TRP:CD1	2.50	0.46
27:3:24:LYS:HE2	27:3:196:LEU:HB3	1.97	0.46
1:A:74:CYS:HA	2:B:1129:ASN:O	2.15	0.46
1:A:924:TYR:CD1	1:A:949:GLN:NE2	2.81	0.46
2:B:242:ARG:HB3	2:B:252:ILE:HG23	1.96	0.46
2:B:499:ARG:C	2:B:500:GLN:O	2.53	0.46
8:H:81:ARG:C	8:H:83:SER:H	2.24	0.46
20:T:137:LYS:HB3	20:T:138:PRO:HD2	1.97	0.46
22:V:366:ASN:HD22	22:V:613:THR:CG2	2.14	0.46
22:V:413:LEU:HD11	28:X:55:DC:O4'	2.15	0.46
25:1:11:GLU:HG2	26:2:404:THR:OG1	2.14	0.46
25:1:45:VAL:CG2	26:2:409:TYR:CE2	2.98	0.46
26:2:96:TRP:CZ2	26:2:97:HIS:NE2	2.83	0.46
26:2:189:GLU:CB	26:2:190:PRO:HD3	2.43	0.46
27:3:124:ILE:O	27:3:127:GLN:HB2	2.14	0.46
27:3:177:PHE:O	27:3:181:ILE:HG13	2.15	0.46
1:A:520:MET:HB3	1:A:522:PRO:HD2	1.97	0.46
1:A:621:ILE:CA	1:A:623:PRO:CD	2.71	0.46
1:A:1371:ILE:HD11	1:A:1406:THR:HG22	1.98	0.46
2:B:46:SER:HB2	2:B:395:LEU:HD23	1.96	0.46
2:B:294:ASP:CG	2:B:379:ARG:HH22	2.24	0.46
2:B:487:SER:C	2:B:489:ILE:H	2.24	0.46
2:B:1132:THR:HG23	2:B:1133:HIS:CD2	2.50	0.46
9:I:12:VAL:HG11	9:I:15:ARG:NH2	2.31	0.46
13:M:15:CYS:HB2	13:M:18:HIS:O	2.15	0.46
13:M:48:VAL:O	13:M:52:TRP:N	2.48	0.46
14:N:32:ASP:HB3	14:N:34:VAL:HG23	1.98	0.46
14:N:349:TRP:HH2	16:P:191:GLU:OE2	1.98	0.46
18:R:89:HIS:CG	18:R:139:PHE:HZ	2.34	0.46
25:1:38:ILE:CB	25:1:44:PHE:CE1	2.98	0.46
1:A:18:ILE:HD11	1:A:1460:LEU:CD2	2.46	0.46
1:A:60:PRO:HG2	1:A:62:GLN:HB3	1.97	0.46
1:A:76:GLY:HA3	2:B:1131:ARG:NH2	2.31	0.46
1:A:452:ASP:HA	1:A:474:VAL:HG23	1.97	0.46
1:A:467:MET:HE1	1:A:527:THR:HA	1.97	0.46
1:A:609:HIS:N	1:A:610:PRO:HD2	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1061:SER:HA	2:B:1084:LEU:HD11	1.96	0.46
2:B:1114:TYR:CD1	2:B:1153:TYR:HB2	2.51	0.46
3:C:4:ALA:HB1	11:K:97:GLU:OE1	2.14	0.46
6:F:56:TYR:HD1	6:F:124:ILE:HB	1.81	0.46
8:H:50:VAL:HG13	8:H:56:PHE:CZ	2.51	0.46
10:J:35:LEU:HB3	10:J:46:ARG:HD2	1.98	0.46
17:Q:25:PHE:CB	18:R:215:GLU:OE2	2.63	0.46
20:T:174:LYS:CG	28:X:20:DG:H4'	2.45	0.46
25:1:54:GLN:O	25:1:57:VAL:HG12	2.16	0.46
26:2:29:GLY:N	27:3:25:GLN:CB	2.76	0.46
27:3:64:ILE:CG2	27:3:128:HIS:CG	2.99	0.46
1:A:384:ILE:O	1:A:388:MET:N	2.43	0.46
1:A:1468:THR:O	6:F:64:ARG:NH2	2.42	0.46
2:B:172:CYS:HB2	10:J:62:TYR:CG	2.51	0.46
2:B:386:ASP:HB3	2:B:502:HIS:HD2	1.80	0.46
2:B:1130:THR:N	2:B:1134:THR:O	2.48	0.46
7:G:95:VAL:HG11	17:Q:127:PHE:HZ	1.79	0.46
13:M:10:LEU:H	13:M:11:PRO:HD3	1.36	0.46
13:M:118:PHE:CE1	13:M:142:PHE:HB3	2.51	0.46
14:N:318:ASP:HB2	16:P:239:ARG:NH2	2.28	0.46
16:P:268:ILE:HD13	16:P:332:LEU:HG	1.98	0.46
18:R:205:ASP:HA	18:R:206:LYS:HB2	1.96	0.46
23:W:657:MET:O	23:W:660:ALA:HB3	2.15	0.46
25:1:1:MET:CG	26:2:413:LEU:CB	2.68	0.46
25:1:18:GLN:OE1	25:1:19:PHE:CD1	2.68	0.46
26:2:90:LEU:HD21	26:2:140:LYS:HD3	1.98	0.46
26:2:100:LEU:HD11	26:2:119:ARG:CG	2.31	0.46
26:2:201:PHE:CD1	26:2:202:GLN:N	2.83	0.46
26:2:214:TYR:CE1	26:2:233:ILE:HG23	2.51	0.46
27:3:10:LEU:CD1	27:3:56:LYS:HG2	2.44	0.46
1:A:408:ARG:HH11	1:A:414:PRO:HB2	1.79	0.46
2:B:75:SER:HG	2:B:78:VAL:HG22	1.76	0.46
2:B:752:TYR:HE1	2:B:809:VAL:CG2	2.29	0.46
2:B:836:THR:C	2:B:886:ARG:HA	2.41	0.46
2:B:910:THR:HB	12:L:43:ILE:HD13	1.98	0.46
3:C:14:LEU:HB3	3:C:19:VAL:HG23	1.98	0.46
3:C:54:ALA:HB3	3:C:160:ARG:HB2	1.97	0.46
17:Q:185:GLU:O	17:Q:189:ALA:N	2.48	0.46
17:Q:187:ILE:HG23	18:R:212:VAL:O	1.96	0.46
22:V:615:PHE:O	22:V:642:ARG:NH2	2.48	0.46
26:2:138:PRO:HD3	26:2:189:GLU:CD	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:2:211:GLN:CD	26:2:261:PHE:CE1	2.94	0.46
27:3:165:LYS:NZ	27:3:200:SER:H	2.12	0.46
27:3:228:LEU:HD23	27:3:228:LEU:C	2.41	0.46
1:A:357:LYS:HE3	2:B:1073:GLN:HG2	1.98	0.46
1:A:432:HIS:NE2	1:A:438:LEU:HD13	2.31	0.46
1:A:994:PHE:CZ	1:A:1064:ALA:HA	2.50	0.46
2:B:425:ARG:HD3	2:B:427:LYS:HD2	1.98	0.46
2:B:451:GLY:HA2	2:B:467:SER:HB3	1.97	0.46
2:B:1066:PRO:HB2	2:B:1075:MET:HG3	1.98	0.46
2:B:1130:THR:C	2:B:1132:THR:H	2.21	0.46
6:F:116:GLU:HG3	6:F:118:TRP:HE1	1.81	0.46
19:S:26:TYR:HB2	19:S:139:PRO:O	2.16	0.46
20:T:227:GLY:C	28:X:30:DG:H5''	2.40	0.46
21:U:291:CYS:N	21:U:296:ASN:O	2.36	0.46
26:2:187:SER:OG	26:2:190:PRO:HD2	2.16	0.46
27:3:21:TRP:HA	27:3:24:LYS:CG	2.45	0.46
27:3:125:LYS:C	27:3:127:GLN:H	2.24	0.46
1:A:527:THR:HG22	1:A:532:ARG:O	2.16	0.46
1:A:788:VAL:HB	1:A:823:VAL:HB	1.98	0.46
2:B:939:HIS:CD2	2:B:980:HIS:HA	2.50	0.46
5:E:122:ALA:HB3	5:E:125:TYR:HB3	1.98	0.46
9:I:73:SER:HB2	9:I:115:THR:OG1	2.15	0.46
17:Q:110:MET:O	17:Q:113:ARG:HB3	2.16	0.46
19:S:109:LYS:HD2	19:S:149:LEU:HD23	1.97	0.46
22:V:519:TYR:HA	22:V:522:TYR:HB3	1.98	0.46
27:3:121:LYS:HD3	27:3:121:LYS:H	1.81	0.46
1:A:364:ARG:HB2	1:A:502:ASN:OD1	2.16	0.46
2:B:29:VAL:HG22	2:B:643:LEU:HD11	1.98	0.46
2:B:63:PRO:HG2	2:B:64:PRO:HD3	1.97	0.46
2:B:1093:CYS:O	2:B:1097:HIS:N	2.48	0.46
3:C:6:GLN:HG2	3:C:25:ASN:HD21	1.76	0.46
3:C:117:SER:HB2	3:C:130:VAL:HG11	1.98	0.46
18:R:190:LEU:O	18:R:203:PHE:N	2.49	0.46
20:T:172:ASP:OD1	20:T:173:GLY:N	2.48	0.46
22:V:609:LYS:HD2	29:Y:38:DT:OP1	2.16	0.46
26:2:96:TRP:CH2	26:2:97:HIS:CE1	3.03	0.46
27:3:10:LEU:HB2	27:3:56:LYS:HE3	1.98	0.46
1:A:63:GLY:HA3	1:A:258:LEU:HD23	1.98	0.46
2:B:26:CYS:O	2:B:30:ILE:HG13	2.16	0.46
2:B:89:GLU:HB3	2:B:127:ASP:HB3	1.98	0.46
2:B:550:MET:HE2	2:B:550:MET:HB3	1.86	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:573:TRP:CH2	2:B:575:GLY:HA2	2.51	0.46
8:H:117:SER:HA	8:H:121:LEU:O	2.16	0.46
9:I:81:THR:HG22	9:I:94:ALA:O	2.16	0.46
13:M:177:PHE:O	13:M:181:CYS:N	2.38	0.46
13:M:185:ARG:HA	20:T:158:ASN:HB2	1.98	0.46
16:P:237:TYR:O	16:P:240:VAL:CG2	2.64	0.46
17:Q:69:ASP:CA	18:R:225:VAL:HG22	2.46	0.46
20:T:30:GLN:O	20:T:62:LEU:HD11	2.16	0.46
22:V:408:SER:HB3	22:V:418:LYS:HB3	1.98	0.46
25:1:2:VAL:HG12	26:2:456:LYS:CE	2.43	0.46
1:A:385:ALA:HB2	1:A:476:ILE:HD12	1.97	0.45
1:A:909:LEU:HD13	1:A:973:GLY:HA2	1.98	0.45
2:B:175:ASN:HA	10:J:62:TYR:CD2	2.51	0.45
2:B:1062:ARG:NH2	2:B:1074:PRO:HB3	2.31	0.45
21:U:133:ALA:HB2	21:U:167:GLU:HG3	1.98	0.45
25:1:22:TYR:HD1	25:1:23:LEU:HD23	1.80	0.45
29:Y:66:DC:H2"	29:Y:67:DC:C6	2.50	0.45
1:A:51:ARG:H	1:A:52:PRO:HD2	1.81	0.45
1:A:721:HIS:O	9:I:109:ARG:HA	2.16	0.45
1:A:930:LEU:HD11	8:H:107:GLU:OE2	2.16	0.45
1:A:1036:ASN:OD1	1:A:1037:ALA:N	2.49	0.45
2:B:254:GLN:NE2	2:B:300:MET:SD	2.74	0.45
2:B:834:ARG:HA	2:B:840:MET:SD	2.55	0.45
5:E:72:MET:HG3	5:E:101:ARG:HB2	1.97	0.45
7:G:165:ASP:HB2	7:G:168:LEU:HD11	1.98	0.45
9:I:25:TYR:HD2	9:I:40:ARG:HG3	1.81	0.45
17:Q:12:ALA:O	17:Q:15:LYS:HB2	2.15	0.45
17:Q:18:ALA:O	17:Q:22:ILE:HG23	2.15	0.45
17:Q:106:LYS:CG	18:R:218:LYS:HG2	2.44	0.45
21:U:185:MET:HE3	21:U:192:ARG:NH2	2.27	0.45
25:1:57:VAL:HG13	25:1:58:GLY:N	2.31	0.45
26:2:130:SER:HB2	26:2:179:LEU:HD23	1.99	0.45
27:3:10:LEU:N	27:3:56:LYS:HE3	2.31	0.45
27:3:69:PHE:HE1	27:3:139:LYS:HD2	1.77	0.45
2:B:125:TYR:HE2	20:T:148:VAL:O	1.99	0.45
2:B:128:ILE:HB	2:B:145:GLN:HB2	1.98	0.45
2:B:295:PRO:O	2:B:299:GLU:HG2	2.16	0.45
2:B:845:TYR:OH	2:B:891:ASP:OD1	2.33	0.45
6:F:44:ARG:HB3	6:F:114:SER:HA	1.97	0.45
13:M:268:LYS:O	13:M:269:ARG:NH1	2.37	0.45
14:N:343:HIS:O	14:N:350:LYS:N	2.36	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:197:TYR:HB2	20:T:202:LEU:HD21	1.98	0.45
20:T:198:ASN:OD1	20:T:199:LEU:N	2.50	0.45
22:V:550:PHE:CZ	22:V:554:ARG:NH2	2.84	0.45
26:2:35:TYR:HB2	26:2:62:LEU:HD12	1.98	0.45
26:2:203:PHE:CD2	26:2:205:LEU:CD2	2.95	0.45
27:3:60:ILE:HG23	27:3:68:ARG:O	2.17	0.45
27:3:69:PHE:HZ	27:3:139:LYS:HB3	1.73	0.45
1:A:956:PHE:HA	1:A:959:MET:HB2	1.99	0.45
2:B:68:GLN:HA	2:B:83:ARG:HA	1.98	0.45
2:B:631:GLN:O	2:B:683:GLN:HG2	2.16	0.45
8:H:2:ALA:O	8:H:4:ILE:N	2.50	0.45
8:H:10:PHE:CE2	8:H:58:LEU:HD13	2.52	0.45
11:K:64:PRO:HD2	11:K:70:LYS:O	2.16	0.45
14:N:315:ASN:C	14:N:317:GLU:H	2.23	0.45
20:T:145:LEU:C	20:T:147:LYS:N	2.64	0.45
23:W:37:HIS:CD2	23:W:454:VAL:CG1	3.00	0.45
25:1:4:VAL:CG1	26:2:412:PHE:HD2	2.19	0.45
25:1:40:ASP:HB2	25:1:43:VAL:H	1.81	0.45
26:2:211:GLN:CB	26:2:261:PHE:CE1	2.95	0.45
26:2:219:TYR:CD1	26:2:219:TYR:C	2.95	0.45
27:3:196:LEU:HB3	27:3:220:MET:SD	2.56	0.45
1:A:478:PRO:HB2	1:A:479:TRP:CE3	2.52	0.45
1:A:551:ARG:NH1	1:A:637:MET:CE	2.79	0.45
1:A:611:ASP:HB3	1:A:617:PRO:CG	2.47	0.45
1:A:1137:PRO:HA	1:A:1360:ASN:HD21	1.80	0.45
2:B:384:ASP:OD2	2:B:387:HIS:N	2.49	0.45
2:B:588:ARG:NH2	2:B:603:MET:HE2	2.31	0.45
7:G:116:GLU:O	7:G:130:THR:HA	2.16	0.45
7:G:120:ASP:OD2	7:G:123:SER:OG	2.28	0.45
13:M:105:ARG:NH1	29:Y:64:DC:H3'	2.31	0.45
13:M:123:THR:O	13:M:127:ARG:NH2	2.50	0.45
14:N:25:VAL:HG11	15:O:36:VAL:HG13	1.99	0.45
14:N:318:ASP:CA	16:P:239:ARG:NE	2.79	0.45
16:P:264:VAL:HG23	16:P:266:PHE:H	1.81	0.45
20:T:23:VAL:HG21	20:T:31:TRP:CZ3	2.51	0.45
21:U:136:THR:OG1	21:U:141:ARG:NH1	2.49	0.45
22:V:321:GLU:CG	23:W:499:ASN:ND2	2.76	0.45
22:V:514:MET:SD	22:V:537:ASN:CG	2.99	0.45
22:V:514:MET:HE2	22:V:667:THR:HG21	1.99	0.45
26:2:30:VAL:CG1	27:3:24:LYS:C	2.83	0.45
27:3:64:ILE:HG21	27:3:128:HIS:HB3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:3:69:PHE:HZ	27:3:139:LYS:HD2	1.81	0.45
1:A:320:ASN:ND2	1:A:329:MET:HE3	2.27	0.45
1:A:431:PHE:HD2	13:M:33:ILE:HG21	1.82	0.45
1:A:1030:SER:O	1:A:1034:GLN:N	2.41	0.45
1:A:1310:HIS:NE2	1:A:1334:TRP:HE3	2.14	0.45
2:B:795:ILE:HG12	2:B:947:ILE:HG22	1.99	0.45
2:B:1029:TYR:CD1	2:B:1036:LYS:HG2	2.51	0.45
19:S:172:ASN:OD1	19:S:173:HIS:N	2.50	0.45
21:U:299:LYS:HB2	21:U:301:CYS:O	2.17	0.45
26:2:100:LEU:CG	26:2:119:ARG:HE	2.22	0.45
26:2:117:ASN:HB2	27:3:104:LEU:CG	2.47	0.45
26:2:217:LEU:CD2	26:2:233:ILE:CD1	2.95	0.45
26:2:240:LEU:HD12	26:2:240:LEU:N	2.30	0.45
27:3:148:ASN:CG	27:3:157:MET:HE2	2.42	0.45
1:A:84:HIS:N	1:A:257:PRO:HB3	2.32	0.45
1:A:514:GLU:OE1	2:B:1099:ALA:HB1	2.17	0.45
1:A:902:GLU:O	1:A:979:LEU:N	2.34	0.45
1:A:1191:GLU:H	9:I:1:MET:HE1	1.81	0.45
1:A:1301:ILE:O	1:A:1304:ILE:HG12	2.17	0.45
1:A:1479:LYS:HD3	6:F:103:PRO:HA	1.99	0.45
2:B:738:THR:OG1	10:J:62:TYR:OH	2.23	0.45
2:B:881:GLU:HA	2:B:883:THR:OG1	2.16	0.45
3:C:11:ILE:HA	3:C:21:PHE:CB	2.46	0.45
7:G:60:GLN:HB2	7:G:63:ARG:NE	2.32	0.45
7:G:107:PHE:O	7:G:160:ILE:HG13	2.17	0.45
8:H:57:ARG:O	8:H:145:MET:HA	2.17	0.45
8:H:98:ARG:HD3	8:H:115:TYR:CD2	2.48	0.45
10:J:3:ILE:HD13	10:J:18:TRP:CB	2.47	0.45
16:P:329:TYR:N	16:P:330:PRO:HD2	2.32	0.45
18:R:202:PHE:O	18:R:203:PHE:CE1	2.63	0.45
25:1:2:VAL:HG12	26:2:456:LYS:HG2	1.81	0.45
26:2:117:ASN:CA	27:3:104:LEU:HD21	2.47	0.45
26:2:170:ALA:C	26:2:213:TRP:CZ3	2.94	0.45
26:2:223:ALA:C	26:2:225:SER:H	2.24	0.45
1:A:426:ARG:CB	13:M:40:VAL:HG22	2.38	0.45
2:B:75:SER:C	2:B:78:VAL:HG22	2.41	0.45
2:B:856:PRO:HD3	12:L:46:LYS:HD3	1.98	0.45
7:G:46:ILE:HD11	7:G:77:PHE:HB2	1.99	0.45
16:P:297:LYS:HE2	16:P:297:LYS:CA	2.46	0.45
17:Q:145:PHE:HA	17:Q:152:PHE:HA	1.98	0.45
18:R:156:ASP:O	18:R:158:HIS:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:95:VAL:O	20:T:106:LEU:HD12	2.17	0.45
27:3:64:ILE:CG2	27:3:128:HIS:CB	2.94	0.45
27:3:148:ASN:ND2	27:3:157:MET:HG3	2.32	0.45
2:B:66:ASP:HB3	2:B:85:LEU:HD13	1.99	0.45
2:B:75:SER:O	2:B:78:VAL:CG2	2.65	0.45
2:B:193:VAL:HG11	2:B:481:HIS:CD2	2.52	0.45
2:B:201:ALA:HA	2:B:392:ARG:HG2	1.98	0.45
2:B:626:LEU:HA	2:B:662:VAL:HG12	1.98	0.45
2:B:640:ILE:HA	2:B:643:LEU:HD12	1.98	0.45
20:T:199:LEU:HD13	20:T:233:TRP:NE1	2.31	0.45
22:V:426:VAL:O	22:V:427:MET:C	2.52	0.45
22:V:689:VAL:CG2	26:2:391:ILE:HD13	2.46	0.45
23:W:37:HIS:NE2	23:W:454:VAL:HG11	2.32	0.45
26:2:203:PHE:CG	26:2:204:LEU:N	2.84	0.45
27:3:219:GLN:OE1	27:3:219:GLN:HA	2.17	0.45
1:A:548:PHE:HE2	1:A:592:PHE:HB2	1.81	0.45
1:A:909:LEU:HD22	1:A:1328:PHE:CZ	2.51	0.45
1:A:1178:ASP:OD1	1:A:1184:THR:HA	2.16	0.45
1:A:1241:ASP:O	1:A:1262:MET:HG3	2.17	0.45
1:A:1307:VAL:C	1:A:1308:TYR:CD2	2.95	0.45
2:B:876:ASN:OD1	2:B:879:GLU:OE2	2.35	0.45
21:U:229:ALA:HB1	21:U:234:LYS:HB3	1.99	0.45
26:2:94:ARG:HD2	26:2:95:ILE:CD1	2.47	0.45
26:2:117:ASN:ND2	27:3:108:ASN:N	2.65	0.45
26:2:236:PHE:CD1	26:2:239:GLN:CD	2.95	0.45
26:2:251:VAL:HG11	26:2:254:MET:SD	2.56	0.45
26:2:258:LEU:HG	26:2:262:LEU:HD21	1.99	0.45
27:3:42:MET:CG	27:3:111:ILE:CD1	2.95	0.45
27:3:100:LYS:HB3	27:3:103:LEU:CD1	2.38	0.45
1:A:902:GLU:N	1:A:979:LEU:O	2.48	0.44
2:B:369:VAL:O	2:B:373:LEU:N	2.41	0.44
2:B:674:MET:HB2	9:I:77:THR:HG22	1.98	0.44
2:B:862:GLY:O	2:B:898:THR:HA	2.18	0.44
3:C:74:ILE:HD12	3:C:238:SER:C	2.42	0.44
11:K:57:LEU:HD13	11:K:77:THR:C	2.42	0.44
16:P:301:VAL:HG11	28:X:14:DA:H5"	1.98	0.44
17:Q:55:ASP:O	17:Q:59:LEU:N	2.42	0.44
19:S:29:MET:HB2	20:T:96:PHE:CD1	2.52	0.44
25:1:1:MET:SD	26:2:413:LEU:CB	3.03	0.44
26:2:123:LEU:CD2	26:2:178:LEU:CD1	2.95	0.44
27:3:9:ASN:C	27:3:56:LYS:HE3	2.41	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:404:GLU:OE1	1:A:407:ARG:HD2	2.17	0.44
1:A:431:PHE:HB2	13:M:33:ILE:HG21	1.99	0.44
1:A:556:GLU:HG3	1:A:559:GLU:H	1.82	0.44
1:A:1022:ILE:HG12	1:A:1034:GLN:OE1	2.17	0.44
1:A:1361:ASP:OD2	1:A:1364:GLU:HG2	2.16	0.44
2:B:84:TYR:HA	2:B:132:VAL:CG1	2.47	0.44
2:B:93:LEU:HD23	2:B:160:TYR:CE2	2.52	0.44
2:B:385:ARG:HD2	2:B:497:LYS:HE3	1.99	0.44
2:B:780:VAL:HG21	2:B:1048:TYR:HE2	1.81	0.44
2:B:1117:HIS:CE1	2:B:1148:LEU:HD13	2.51	0.44
4:D:83:VAL:HG13	4:D:134:ILE:HG12	1.99	0.44
5:E:104:ILE:HG23	5:E:129:GLN:NE2	2.32	0.44
8:H:71:ASP:OD1	8:H:71:ASP:N	2.50	0.44
10:J:63:ALA:CB	10:J:64:PRO:HD3	2.32	0.44
12:L:13:GLN:O	12:L:29:LYS:HD3	2.17	0.44
18:R:123:ALA:C	18:R:125:VAL:H	2.25	0.44
18:R:155:LEU:HD11	18:R:203:PHE:HA	1.98	0.44
18:R:155:LEU:C	18:R:204:ASN:ND2	2.76	0.44
19:S:143:TRP:C	19:S:143:TRP:CD1	2.95	0.44
20:T:164:GLU:CD	20:T:167:ARG:HH21	2.25	0.44
20:T:165:TYR:O	20:T:169:LYS:HG2	2.17	0.44
21:U:177:TYR:CE1	21:U:181:ARG:HA	2.52	0.44
22:V:370:SER:O	22:V:374:TRP:CD1	2.71	0.44
26:2:159:VAL:HG12	26:2:161:HIS:HB2	1.99	0.44
28:X:57:DC:H2"	28:X:58:DT:C7	2.46	0.44
1:A:361:PHE:N	2:B:1062:ARG:O	2.50	0.44
1:A:894:ASP:OD1	1:A:1396:ARG:NH2	2.50	0.44
1:A:972:THR:O	1:A:1317:LYS:HD3	2.17	0.44
2:B:99:TRP:HB2	13:M:129:ASN:ND2	2.32	0.44
2:B:249:LYS:C	2:B:251:ALA:N	2.75	0.44
11:K:105:PHE:O	11:K:109:ILE:HG12	2.17	0.44
16:P:212:LEU:O	16:P:219:MET:HA	2.18	0.44
17:Q:135:THR:HG23	17:Q:164:ASP:OD1	2.18	0.44
20:T:44:ARG:HH22	20:T:80:GLU:CD	2.25	0.44
26:2:61:PHE:CE1	26:2:99:GLN:NE2	2.85	0.44
26:2:81:LYS:CG	26:2:82:ALA:N	2.79	0.44
26:2:171:VAL:HG13	26:2:216:MET:HB3	1.98	0.44
26:2:206:LEU:CD2	26:2:206:LEU:H	2.31	0.44
26:2:236:PHE:HZ	26:2:258:LEU:HD11	1.82	0.44
1:A:283:ILE:HA	1:A:286:ILE:HG12	2.00	0.44
1:A:578:ALA:N	1:A:585:LEU:O	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:636:ILE:O	1:A:637:MET:SD	2.76	0.44
2:B:629:GLU:N	2:B:632:LYS:O	2.41	0.44
5:E:192:LYS:HA	5:E:206:TYR:HD1	1.82	0.44
7:G:60:GLN:HB2	7:G:63:ARG:HE	1.82	0.44
9:I:96:PHE:HA	9:I:111:TYR:O	2.18	0.44
13:M:138:THR:HG23	13:M:163:CYS:HB3	1.99	0.44
14:N:29:PHE:CE1	15:O:36:VAL:HG21	2.52	0.44
16:P:294:ARG:HH21	16:P:294:ARG:HG3	1.82	0.44
20:T:223:GLN:HB3	20:T:233:TRP:CE3	2.52	0.44
22:V:321:GLU:OE2	23:W:500:ASP:CA	2.59	0.44
22:V:514:MET:HE2	22:V:664:SER:HB3	2.00	0.44
26:2:28:PRO:CB	27:3:33:THR:OG1	2.65	0.44
26:2:89:LEU:HD23	26:2:89:LEU:C	2.42	0.44
26:2:214:TYR:OH	26:2:265:LEU:HD13	2.18	0.44
27:3:144:ILE:O	27:3:144:ILE:HD13	2.18	0.44
27:3:160:ARG:CB	27:3:190:LEU:CD2	2.95	0.44
1:A:267:GLN:NE2	1:A:267:GLN:HA	2.27	0.44
1:A:579:ILE:HD12	1:A:585:LEU:HD12	1.99	0.44
1:A:1317:LYS:NZ	21:U:294:CYS:O	2.45	0.44
2:B:11:ASP:HB2	2:B:638:ARG:HD3	2.00	0.44
2:B:21:LEU:HD23	2:B:633:LEU:HD23	2.00	0.44
2:B:134:LYS:HG3	2:B:136:GLY:H	1.83	0.44
2:B:627:ILE:HA	2:B:695:HIS:CD2	2.53	0.44
2:B:888:THR:O	2:B:890:ARG:HG2	2.17	0.44
2:B:905:ASP:OD2	2:B:922:ARG:NE	2.44	0.44
3:C:37:VAL:HG12	3:C:248:ALA:HB1	1.99	0.44
5:E:71:GLN:NE2	5:E:97:GLU:HG3	2.32	0.44
6:F:53:THR:HB	6:F:108:ARG:HH11	1.83	0.44
8:H:76:ASN:OD1	8:H:78:THR:OG1	2.33	0.44
22:V:519:TYR:CE2	22:V:523:VAL:HG21	2.53	0.44
23:W:73:CYS:CB	23:W:209:TYR:CE2	3.00	0.44
26:2:117:ASN:CB	27:3:42:MET:HE1	2.42	0.44
27:3:22:TRP:O	27:3:25:GLN:CG	2.55	0.44
27:3:33:THR:CG2	27:3:36:LYS:CB	2.95	0.44
27:3:141:LEU:C	27:3:144:ILE:HG22	2.41	0.44
2:B:318:LEU:HD13	2:B:336:ILE:HG23	1.99	0.44
2:B:655:ASP:HA	2:B:658:ALA:HB3	2.00	0.44
2:B:663:GLU:OE2	2:B:695:HIS:NE2	2.51	0.44
2:B:888:THR:O	2:B:890:ARG:N	2.50	0.44
3:C:101:PHE:HA	3:C:121:ILE:O	2.18	0.44
3:C:211:LEU:O	3:C:213:GLU:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:44:ARG:HB2	4:D:61:PHE:CZ	2.53	0.44
7:G:84:VAL:HG12	7:G:144:ARG:HD3	1.98	0.44
8:H:65:TYR:CE1	8:H:70:LEU:HD22	2.53	0.44
9:I:17:CYS:O	9:I:21:ASN:N	2.46	0.44
16:P:174:LEU:O	16:P:249:LYS:N	2.51	0.44
18:R:154:LEU:HD21	18:R:162:GLY:O	2.15	0.44
22:V:534:TYR:HE1	22:V:535:THR:OG1	2.00	0.44
22:V:612:ASP:CG	22:V:635:GLN:CD	2.86	0.44
23:W:73:CYS:HB3	23:W:209:TYR:CD2	2.52	0.44
24:0:60:HIS:CE1	24:0:159:MET:SD	3.11	0.44
25:1:1:MET:HG2	26:2:413:LEU:CB	2.44	0.44
26:2:56:VAL:HG23	26:2:57:MET:N	2.32	0.44
26:2:127:LYS:CA	26:2:178:LEU:HD23	2.48	0.44
26:2:140:LYS:CD	26:2:162:PHE:HE1	2.29	0.44
27:3:222:SER:HB3	27:3:225:GLN:CD	2.43	0.44
1:A:607:SER:O	21:U:301:CYS:HA	2.17	0.44
1:A:1199:MET:O	1:A:1201:ASP:N	2.51	0.44
2:B:198:GLU:OE1	2:B:487:SER:OG	2.33	0.44
2:B:508:MET:HE3	2:B:667:THR:HG23	1.98	0.44
8:H:94:GLY:HA3	8:H:118:TYR:HA	1.98	0.44
21:U:225:ALA:CB	21:U:228:MET:HG2	2.48	0.44
22:V:405:VAL:HG12	22:V:406:ALA:H	1.82	0.44
23:W:143:ARG:HH11	23:W:143:ARG:CG	2.31	0.44
26:2:35:TYR:CD1	26:2:62:LEU:HD12	2.52	0.44
26:2:164:VAL:HG13	26:2:209:PRO:CG	2.45	0.44
26:2:189:GLU:HB2	26:2:190:PRO:CD	2.43	0.44
27:3:187:GLN:CD	27:3:189:ILE:HG13	2.43	0.44
1:A:129:ILE:CD1	1:A:140:ARG:HA	2.48	0.44
1:A:367:ILE:HD13	1:A:494:ALA:HB1	1.99	0.44
1:A:395:THR:OG1	1:A:398:ASN:OD1	2.31	0.44
3:C:74:ILE:HG22	3:C:129:PRO:O	2.17	0.44
6:F:68:THR:O	6:F:72:GLN:HG3	2.17	0.44
8:H:39:LEU:HA	8:H:124:ARG:O	2.17	0.44
9:I:97:PHE:O	9:I:111:TYR:N	2.47	0.44
9:I:99:SER:OG	9:I:105:GLU:HG2	2.08	0.44
9:I:102:ALA:O	9:I:104:ALA:N	2.50	0.44
14:N:337:CYS:O	15:O:97:ALA:HA	2.17	0.44
15:O:64:THR:HG22	16:P:188:ARG:HB3	2.00	0.44
16:P:289:PRO:CB	29:Y:84:DG:H5'	2.32	0.44
17:Q:45:GLU:OE1	17:Q:94:ILE:N	2.43	0.44
17:Q:188:TYR:HD1	18:R:212:VAL:HB	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:17:GLY:HA2	20:T:109:ILE:O	2.17	0.44
21:U:216:PRO:HD2	21:U:219:LEU:HD23	1.99	0.44
22:V:531:ILE:CG1	22:V:534:TYR:HE2	2.31	0.44
23:W:59:TYR:CE2	23:W:62:ALA:HB2	2.22	0.44
23:W:189:TRP:CE3	23:W:190:CYS:N	2.86	0.44
25:1:25:GLU:OE2	25:1:35:ILE:HG12	2.18	0.44
27:3:154:ASN:CG	27:3:155:GLN:H	2.26	0.44
1:A:349:ARG:O	1:A:353:ASN:HB2	2.17	0.44
1:A:875:TYR:HE1	1:A:1470:CYS:SG	2.40	0.44
1:A:1014:LYS:O	1:A:1018:LYS:HG3	2.18	0.44
2:B:280:SER:HB3	9:I:21:ASN:HB2	1.99	0.44
3:C:241:PRO:HA	3:C:244:ILE:HD12	2.00	0.44
20:T:223:GLN:HB3	20:T:233:TRP:CD2	2.52	0.44
21:U:150:ALA:HA	21:U:153:ARG:NH1	2.33	0.44
21:U:176:ILE:HG22	21:U:187:TYR:CD2	2.53	0.44
22:V:518:PHE:CD1	22:V:713:LEU:HD13	2.53	0.44
22:V:519:TYR:HB3	25:1:16:MET:HG3	2.00	0.44
26:2:34:LEU:N	26:2:34:LEU:HD22	2.33	0.44
26:2:140:LYS:HD3	26:2:162:PHE:CE1	2.47	0.44
26:2:172:SER:C	26:2:175:LEU:HD23	2.43	0.44
26:2:203:PHE:HD2	26:2:205:LEU:H	1.65	0.44
26:2:270:LEU:HD23	26:2:270:LEU:C	2.43	0.44
1:A:30:GLU:O	1:A:34:MET:N	2.35	0.43
1:A:64:VAL:HB	1:A:70:ARG:O	2.18	0.43
1:A:345:GLY:C	1:A:348:GLY:H	2.26	0.43
1:A:636:ILE:O	1:A:637:MET:HG2	2.17	0.43
1:A:1031:ARG:O	1:A:1035:GLU:N	2.42	0.43
1:A:1310:HIS:CA	21:U:252:LYS:CD	2.95	0.43
2:B:602:SER:O	2:B:614:ILE:HG23	2.18	0.43
2:B:746:THR:O	2:B:812:ARG:HA	2.18	0.43
2:B:954:MET:HE2	2:B:954:MET:HB3	1.82	0.43
6:F:51:ARG:HD3	6:F:118:TRP:CZ2	2.53	0.43
8:H:50:VAL:HG13	8:H:56:PHE:HZ	1.83	0.43
15:O:48:LEU:HD23	15:O:52:VAL:HG21	2.00	0.43
17:Q:106:LYS:HG2	18:R:218:LYS:CD	2.48	0.43
17:Q:123:ASN:O	17:Q:125:ALA:N	2.50	0.43
17:Q:202:GLU:O	17:Q:203:ILE:CB	2.65	0.43
19:S:47:LEU:HG	19:S:98:TRP:CE3	2.53	0.43
20:T:225:VAL:HG23	20:T:227:GLY:H	1.83	0.43
22:V:409:THR:H	22:V:418:LYS:CB	2.31	0.43
22:V:446:ILE:HD12	22:V:451:PHE:HB3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:647:LYS:O	22:V:648:LYS:O	2.35	0.43
26:2:123:LEU:HD23	26:2:123:LEU:C	2.41	0.43
26:2:215:PHE:CE2	26:2:264:HIS:ND1	2.86	0.43
27:3:71:TYR:CG	27:3:71:TYR:O	2.70	0.43
1:A:932:ARG:HA	1:A:932:ARG:HD2	1.61	0.43
2:B:37:LYS:HE2	2:B:653:TRP:HD1	1.80	0.43
2:B:169:ARG:HA	2:B:172:CYS:SG	2.57	0.43
2:B:488:PRO:C	2:B:489:ILE:HG12	2.41	0.43
2:B:654:GLN:O	2:B:658:ALA:N	2.39	0.43
2:B:979:GLY:HA2	2:B:982:ILE:HD12	2.00	0.43
2:B:1030:ASN:OD1	2:B:1031:GLY:N	2.51	0.43
4:D:51:ALA:C	4:D:53:ASP:H	2.25	0.43
5:E:192:LYS:HG3	5:E:206:TYR:CE1	2.54	0.43
7:G:49:THR:H	7:G:74:ALA:HA	1.82	0.43
9:I:84:HIS:CD2	9:I:84:HIS:N	2.84	0.43
17:Q:191:LEU:HD22	18:R:212:VAL:HG12	1.97	0.43
18:R:141:PRO:HG2	18:R:142:LYS:H	1.83	0.43
18:R:158:HIS:CE1	18:R:206:LYS:HD3	2.53	0.43
19:S:46:ARG:N	19:S:101:ARG:O	2.38	0.43
19:S:143:TRP:NE1	19:S:145:ASN:OD1	2.37	0.43
24:0:106:ILE:HD11	24:0:127:HIS:HB3	2.00	0.43
25:1:18:GLN:HG3	25:1:19:PHE:H	1.83	0.43
25:1:34:ILE:CG2	25:1:50:VAL:HG11	2.48	0.43
1:A:43:TYR:O	1:A:45:GLU:N	2.51	0.43
1:A:219:GLU:O	1:A:223:GLU:HG2	2.18	0.43
1:A:1184:THR:HG22	1:A:1190:GLN:HA	2.00	0.43
2:B:161:CYS:O	2:B:164:ASN:ND2	2.51	0.43
2:B:309:PHE:CD2	9:I:40:ARG:HD2	2.54	0.43
2:B:845:TYR:CE2	2:B:865:VAL:HG11	2.53	0.43
9:I:86:CYS:O	9:I:88:LYS:C	2.61	0.43
9:I:97:PHE:HD1	9:I:98:GLN:O	2.00	0.43
14:N:327:GLU:OE1	16:P:188:ARG:NH1	2.51	0.43
14:N:363:ARG:NH2	15:O:86:GLU:OE2	2.51	0.43
16:P:174:LEU:HD22	16:P:248:ALA:HB1	2.00	0.43
20:T:196:TYR:HD1	20:T:232:THR:HG21	1.83	0.43
25:1:20:LEU:C	25:1:20:LEU:HD13	2.43	0.43
26:2:117:ASN:HD21	27:3:108:ASN:N	2.16	0.43
26:2:270:LEU:HA	26:2:273:GLN:HG3	2.00	0.43
27:3:160:ARG:HE	27:3:160:ARG:HB2	1.58	0.43
27:3:184:ALA:C	27:3:187:GLN:HG2	2.43	0.43
1:A:28:PRO:HB3	1:A:251:THR:OG1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:PRO:HB3	1:A:237:GLY:CA	2.45	0.43
1:A:456:VAL:HG12	1:A:505:LEU:HD13	2.00	0.43
1:A:621:ILE:CG2	1:A:623:PRO:HD3	2.44	0.43
2:B:68:GLN:HG3	2:B:82:PRO:O	2.19	0.43
2:B:84:TYR:HA	2:B:132:VAL:HG12	1.99	0.43
2:B:431:LEU:O	2:B:435:ILE:HG12	2.17	0.43
8:H:56:PHE:CE1	8:H:148:LEU:HA	2.54	0.43
9:I:84:HIS:CG	9:I:85:PRO:CD	2.84	0.43
13:M:279:GLY:CA	20:T:153:TYR:OH	2.67	0.43
15:O:57:ASN:OD1	15:O:58:PHE:N	2.51	0.43
17:Q:32:LEU:HD11	18:R:203:PHE:HD2	1.68	0.43
21:U:266:CYS:O	21:U:267:LYS:HG2	2.18	0.43
22:V:282:LYS:HE3	22:V:482:PHE:CD1	2.54	0.43
26:2:35:TYR:CG	26:2:62:LEU:CD1	2.99	0.43
26:2:47:GLU:HG3	26:2:48:LEU:H	1.83	0.43
26:2:117:ASN:ND2	27:3:104:LEU:O	2.52	0.43
1:A:457:ILE:CG2	1:A:504:HIS:HB2	2.48	0.43
1:A:910:LYS:HB3	1:A:963:ARG:HH12	1.83	0.43
1:A:1018:LYS:O	1:A:1021:VAL:HG23	2.17	0.43
1:A:1151:ALA:HB2	1:A:1334:TRP:CZ2	2.53	0.43
1:A:1345:ARG:O	1:A:1349:GLU:HG2	2.19	0.43
1:A:1369:LEU:HD23	5:E:139:ILE:HB	2.00	0.43
2:B:360:LYS:HA	2:B:363:TYR:HD2	1.82	0.43
2:B:454:GLY:HA3	2:B:459:ALA:O	2.18	0.43
2:B:736:TYR:CD2	2:B:737:ILE:HG12	2.54	0.43
2:B:1036:LYS:HG3	3:C:186:TYR:OH	2.18	0.43
6:F:51:ARG:HH12	6:F:122:GLU:CD	2.26	0.43
15:O:60:GLY:O	15:O:76:LEU:HD23	2.18	0.43
16:P:303:LEU:O	16:P:310:VAL:HA	2.18	0.43
20:T:191:PHE:CD2	20:T:235:LEU:HG	2.54	0.43
20:T:198:ASN:HD21	20:T:200:LYS:HE2	1.83	0.43
22:V:615:PHE:CD1	22:V:616:ASP:N	2.86	0.43
22:V:689:VAL:CG2	26:2:391:ILE:HD11	2.48	0.43
25:1:7:GLY:C	25:1:8:VAL:HG23	2.43	0.43
26:2:159:VAL:CG2	26:2:160:LEU:H	2.16	0.43
26:2:201:PHE:CD1	26:2:201:PHE:C	2.96	0.43
26:2:221:GLN:HG2	26:2:268:PHE:HZ	1.75	0.43
1:A:367:ILE:CD1	1:A:494:ALA:HB1	2.47	0.43
1:A:391:ALA:HA	1:A:446:VAL:O	2.19	0.43
1:A:535:MET:HE2	1:A:537:ILE:HD11	2.00	0.43
1:A:1167:ARG:HA	1:A:1293:LEU:HD22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1301:ILE:HD13	1:A:1342:SER:OG	2.19	0.43
2:B:240:LEU:HD13	2:B:242:ARG:NE	2.33	0.43
3:C:235:SER:HB2	3:C:241:PRO:HG3	1.99	0.43
5:E:62:VAL:HG21	5:E:72:MET:CE	2.48	0.43
5:E:76:PHE:HA	5:E:77:PRO:HD2	1.81	0.43
8:H:90:TYR:O	8:H:144:LEU:HA	2.18	0.43
10:J:21:TYR:CZ	10:J:25:LEU:HD21	2.54	0.43
11:K:109:ILE:HA	11:K:112:LYS:HZ3	1.83	0.43
13:M:148:GLN:C	13:M:150:SER:H	2.27	0.43
14:N:46:TRP:CZ2	15:O:11:LEU:HD12	2.48	0.43
14:N:337:CYS:SG	14:N:353:LEU:HD13	2.58	0.43
20:T:21:VAL:HA	20:T:114:ALA:O	2.18	0.43
26:2:230:LEU:C	26:2:230:LEU:HD13	2.44	0.43
27:3:64:ILE:HB	27:3:123:ASP:CG	2.43	0.43
27:3:121:LYS:H	27:3:121:LYS:CD	2.32	0.43
27:3:124:ILE:O	27:3:124:ILE:HG23	2.18	0.43
27:3:178:MET:HA	27:3:181:ILE:HD12	1.99	0.43
1:A:19:LYS:N	2:B:1173:SER:HA	2.34	0.43
1:A:272:ASN:C	1:A:278:HIS:HE2	2.26	0.43
1:A:312:PHE:HE2	1:A:326:PRO:HB2	1.82	0.43
1:A:425:ASP:HB3	13:M:39:LEU:HD11	1.99	0.43
1:A:874:LYS:HD2	6:F:111:PRO:HB3	2.00	0.43
1:A:967:ARG:HH11	1:A:967:ARG:HG3	1.84	0.43
1:A:1013:VAL:HG22	1:A:1049:LEU:HD23	2.00	0.43
1:A:1274:GLU:OE1	1:A:1274:GLU:HA	2.16	0.43
1:A:1308:TYR:CB	1:A:1336:LEU:HD13	2.36	0.43
2:B:109:MET:HE3	2:B:111:ASN:HB2	2.01	0.43
10:J:20:ALA:O	10:J:24:LEU:HG	2.19	0.43
15:O:20:ASP:OD1	15:O:24:GLN:NE2	2.52	0.43
16:P:165:LEU:HD13	16:P:318:ARG:HG3	2.00	0.43
17:Q:34:LEU:HD23	17:Q:37:LEU:HD12	2.00	0.43
21:U:266:CYS:C	21:U:268:LYS:H	2.24	0.43
23:W:293:ARG:HG2	23:W:421:PHE:HE1	1.76	0.43
25:1:4:VAL:HG22	25:1:5:LEU:N	2.32	0.43
25:1:50:VAL:HG12	25:1:50:VAL:O	2.18	0.43
26:2:202:GLN:HE21	26:2:202:GLN:N	2.15	0.43
26:2:214:TYR:HB3	26:2:261:PHE:CE2	2.53	0.43
26:2:223:ALA:H	26:2:268:PHE:HE1	1.64	0.43
26:2:236:PHE:CD2	26:2:236:PHE:C	2.95	0.43
27:3:137:LEU:HD12	27:3:177:PHE:CE1	2.54	0.43
27:3:184:ALA:O	27:3:187:GLN:HG2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:807:LEU:HB2	1:A:810:PHE:CD2	2.54	0.43
1:A:877:ALA:O	1:A:890:ARG:HA	2.19	0.43
1:A:945:ASN:HB3	1:A:948:ILE:HG22	2.00	0.43
1:A:1027:ASP:OD1	1:A:1027:ASP:N	2.52	0.43
1:A:1310:HIS:CE1	1:A:1334:TRP:CE3	2.96	0.43
2:B:442:ASP:HA	2:B:445:LYS:HD2	1.99	0.43
3:C:173:HIS:HB3	3:C:176:TRP:CE3	2.53	0.43
3:C:211:LEU:HD12	3:C:230:TYR:OH	2.18	0.43
5:E:112:PRO:HA	5:E:115:LYS:HD2	2.00	0.43
13:M:169:ARG:HD3	13:M:206:VAL:HB	1.99	0.43
15:O:60:GLY:HA3	15:O:79:VAL:HA	2.01	0.43
15:O:64:THR:HG21	16:P:188:ARG:CZ	2.49	0.43
16:P:289:PRO:HB2	29:Y:83:DA:H4'	2.00	0.43
17:Q:19:LYS:O	17:Q:22:ILE:HG13	2.19	0.43
17:Q:106:LYS:HG3	18:R:222:SER:OG	2.18	0.43
17:Q:183:GLN:C	17:Q:186:PRO:HD2	2.43	0.43
19:S:53:ASN:HB2	19:S:96:GLN:OE1	2.19	0.43
19:S:127:PHE:CB	20:T:19:TRP:HB2	2.48	0.43
21:U:184:ASP:OD1	21:U:185:MET:N	2.52	0.43
21:U:262:THR:HA	21:U:269:LYS:HG2	2.00	0.43
21:U:276:VAL:HG13	21:U:277:GLN:HG3	2.00	0.43
22:V:514:MET:HE3	25:1:16:MET:CE	2.48	0.43
24:O:165:ARG:HD3	24:O:194:ILE:HG12	2.01	0.43
25:1:3:ASN:HB3	26:2:412:PHE:O	2.18	0.43
26:2:409:TYR:CD2	26:2:443:VAL:HG22	2.54	0.43
27:3:229:TRP:CD1	27:3:229:TRP:C	2.96	0.43
1:A:18:ILE:HD13	2:B:1171:MET:HB2	2.00	0.43
1:A:805:ARG:NH2	2:B:671:GLU:O	2.52	0.43
1:A:907:ALA:H	1:A:975:SER:HB3	1.82	0.43
1:A:1209:PRO:CB	9:I:33:ARG:HH12	2.23	0.43
1:A:1309:MET:HG3	21:U:252:LYS:HD2	1.99	0.43
3:C:9:VAL:HG11	11:K:105:PHE:HA	1.99	0.43
4:D:74:PHE:CD2	4:D:80:ILE:HG12	2.54	0.43
7:G:94:LYS:O	7:G:110:ARG:HD2	2.18	0.43
13:M:14:THR:N	13:M:20:ASP:HB3	2.34	0.43
13:M:18:HIS:NE2	13:M:36:GLU:OE2	2.52	0.43
14:N:332:GLU:HB3	15:O:92:LYS:CE	2.49	0.43
17:Q:104:LYS:NZ	18:R:238:LYS:HE3	2.34	0.43
20:T:212:TYR:O	20:T:215:GLU:HB2	2.19	0.43
20:T:228:ILE:HA	28:X:30:DG:C5'	2.41	0.43
26:2:118:LEU:CD1	27:3:43:VAL:HG22	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:3:14:VAL:CG2	27:3:163:VAL:HG13	2.48	0.43
27:3:65:GLN:O	27:3:132:LEU:HD11	2.18	0.43
28:X:11:DT:H2"	28:X:12:DA:H8	1.83	0.43
1:A:460:ARG:HA	1:A:501:MET:SD	2.59	0.43
1:A:601:ASN:HB2	1:A:988:TRP:CZ3	2.54	0.43
1:A:826:SER:OG	1:A:829:ALA:N	2.47	0.43
2:B:198:GLU:OE1	2:B:524:LYS:NZ	2.50	0.43
2:B:508:MET:C	2:B:527:ALA:HB2	2.44	0.43
2:B:777:ASN:O	10:J:47:ARG:HD2	2.19	0.43
2:B:838:GLN:HE21	2:B:890:ARG:HD3	1.83	0.43
3:C:151:VAL:HG22	3:C:152:LYS:N	2.34	0.43
5:E:81:LYS:HG3	5:E:109:GLY:C	2.44	0.43
13:M:178:LYS:O	20:T:154:LYS:CG	2.58	0.43
17:Q:22:ILE:HG21	17:Q:34:LEU:HB3	2.00	0.43
26:2:243:SER:HB3	26:2:258:LEU:CD2	2.45	0.43
27:3:105:THR:CG2	27:3:106:SER:N	2.82	0.43
27:3:165:LYS:HZ1	27:3:200:SER:N	2.16	0.43
28:X:18:DG:O6	29:Y:75:DC:N4	2.52	0.43
1:A:1175:ILE:HG12	1:A:1212:LEU:HD13	1.99	0.42
1:A:1317:LYS:HE2	21:U:295:GLY:HA3	2.00	0.42
1:A:1365:ILE:O	1:A:1370:GLY:N	2.47	0.42
1:A:1372:GLU:HG3	5:E:148:HIS:HE1	1.84	0.42
1:A:1470:CYS:O	6:F:109:TYR:HD2	2.02	0.42
2:B:94:SER:O	2:B:122:ALA:HB1	2.19	0.42
2:B:805:PHE:O	2:B:929:PRO:HG2	2.19	0.42
7:G:120:ASP:OD2	7:G:129:LYS:NZ	2.41	0.42
8:H:9:ILE:HA	8:H:57:ARG:HA	2.01	0.42
15:O:42:LYS:HE3	15:O:42:LYS:HB3	1.75	0.42
24:O:97:ASP:OD1	27:3:208:ASP:CG	2.61	0.42
26:2:87:THR:C	26:2:89:LEU:H	2.27	0.42
26:2:181:GLN:HA	26:2:181:GLN:NE2	2.34	0.42
26:2:224:GLN:N	26:2:268:PHE:HZ	2.16	0.42
27:3:9:ASN:OD1	27:3:158:LYS:HB3	2.19	0.42
27:3:141:LEU:HA	27:3:144:ILE:HG22	2.01	0.42
27:3:221:PRO:C	27:3:223:LEU:H	2.27	0.42
1:A:364:ARG:NH2	1:A:500:GLU:O	2.52	0.42
1:A:368:THR:O	1:A:483:ARG:HA	2.19	0.42
2:B:23:GLN:OE1	2:B:23:GLN:N	2.51	0.42
2:B:132:VAL:O	2:B:132:VAL:HG23	2.18	0.42
2:B:757:PRO:HD3	2:B:769:PHE:CE2	2.55	0.42
2:B:1028:LEU:HD13	2:B:1041:ILE:HD13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1030:ASN:HB3	2:B:1034:GLY:N	2.34	0.42
3:C:11:ILE:HA	3:C:21:PHE:HB2	2.01	0.42
3:C:40:ALA:HB1	3:C:171:LYS:HB2	2.00	0.42
5:E:26:TYR:HA	5:E:64:HIS:O	2.18	0.42
5:E:58:LEU:HB3	5:E:76:PHE:CD2	2.54	0.42
10:J:35:LEU:HB3	10:J:46:ARG:CD	2.49	0.42
22:V:415:HIS:HD2	22:V:416:THR:CG2	2.31	0.42
25:1:1:MET:SD	26:2:419:GLU:N	2.92	0.42
25:1:43:VAL:CG1	25:1:44:PHE:N	2.83	0.42
27:3:137:LEU:HB2	27:3:180:VAL:HG11	1.96	0.42
27:3:165:LYS:CG	27:3:203:LEU:HD12	2.36	0.42
27:3:228:LEU:HD23	27:3:228:LEU:O	2.17	0.42
1:A:64:VAL:HG21	1:A:68:THR:HG23	2.00	0.42
1:A:88:ILE:HD13	1:A:284:VAL:HG22	2.01	0.42
1:A:875:TYR:HA	1:A:1083:PRO:CB	2.49	0.42
1:A:1166:LEU:HD12	1:A:1296:MET:SD	2.59	0.42
2:B:53:MET:O	2:B:57:ARG:N	2.49	0.42
2:B:255:ARG:NH2	2:B:307:GLU:OE2	2.52	0.42
2:B:1056:ASP:OD1	2:B:1056:ASP:N	2.51	0.42
5:E:82:VAL:HG23	5:E:106:VAL:HG13	2.00	0.42
8:H:24:ARG:HG2	8:H:46:GLN:NE2	2.33	0.42
9:I:98:GLN:HB2	9:I:100:HIS:CE1	2.55	0.42
11:K:57:LEU:H	11:K:77:THR:HA	1.84	0.42
16:P:223:GLY:CA	29:Y:79:DT:H4'	2.49	0.42
21:U:191:VAL:O	21:U:195:ILE:N	2.46	0.42
22:V:674:THR:HG23	26:2:392:ARG:HH22	1.66	0.42
26:2:236:PHE:CE1	26:2:239:GLN:NE2	2.87	0.42
1:A:540:ASP:OD2	2:B:968:ASN:ND2	2.53	0.42
2:B:65:ILE:CG2	2:B:412:LEU:HD11	2.44	0.42
2:B:1102:PHE:O	2:B:1106:ARG:HG2	2.19	0.42
5:E:177:ASP:OD2	5:E:179:VAL:HB	2.19	0.42
9:I:37:TYR:N	9:I:46:GLN:O	2.35	0.42
11:K:13:PHE:HB2	11:K:16:GLU:HG3	2.00	0.42
11:K:37:LYS:HA	11:K:69:HIS:HB3	2.01	0.42
16:P:227:GLU:HG2	16:P:228:GLU:H	1.84	0.42
16:P:284:GLU:HB3	16:P:287:LEU:HB3	2.01	0.42
18:R:158:HIS:HE1	18:R:206:LYS:HD3	1.84	0.42
25:1:8:VAL:CG1	25:1:9:LEU:N	2.80	0.42
1:A:10:ASP:N	2:B:1132:THR:HA	2.34	0.42
1:A:114:CYS:C	1:A:116:LYS:H	2.27	0.42
1:A:371:PRO:HD2	2:B:788:TYR:CD1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:551:ARG:HD3	1:A:637:MET:CE	2.37	0.42
1:A:903:PHE:CZ	1:A:976:LYS:HB3	2.55	0.42
1:A:1274:GLU:O	1:A:1276:VAL:CG2	2.62	0.42
2:B:69:ALA:N	2:B:82:PRO:O	2.46	0.42
2:B:588:ARG:O	2:B:592:ARG:N	2.41	0.42
2:B:862:GLY:N	2:B:900:GLU:O	2.53	0.42
2:B:1130:THR:HB	2:B:1134:THR:H	1.84	0.42
6:F:45:PRO:HB3	6:F:115:TYR:CE1	2.54	0.42
10:J:1:MET:SD	10:J:55:LEU:N	2.81	0.42
13:M:12:ARG:HG3	13:M:13:VAL:HG13	2.01	0.42
13:M:158:ALA:HA	13:M:186:ILE:HG13	2.01	0.42
13:M:214:PHE:HA	13:M:217:ARG:NH1	2.34	0.42
17:Q:106:LYS:O	18:R:218:LYS:CE	2.66	0.42
26:2:77:LYS:HD3	26:2:78:GLU:CG	2.49	0.42
26:2:93:LEU:HA	26:2:93:LEU:HD23	1.77	0.42
27:3:11:LEU:CD1	27:3:48:HIS:NE2	2.82	0.42
1:A:72:GLN:HG2	1:A:74:CYS:H	1.83	0.42
1:A:319:ASP:O	1:A:322:LEU:HG	2.19	0.42
1:A:606:HIS:HB3	1:A:627:LYS:HA	2.01	0.42
1:A:609:HIS:HB2	21:U:300:PHE:CZ	2.54	0.42
1:A:775:LYS:CB	2:B:974:SER:HB3	2.50	0.42
1:A:909:LEU:HD22	1:A:1328:PHE:CE2	2.55	0.42
2:B:240:LEU:HD23	2:B:257:VAL:HG13	2.01	0.42
2:B:442:ASP:OD1	2:B:445:LYS:HD2	2.19	0.42
2:B:527:ALA:HB3	2:B:530:ALA:HB2	2.01	0.42
2:B:1116:VAL:HG11	2:B:1125:MET:SD	2.59	0.42
4:D:32:LEU:HD11	7:G:75:ILE:HG22	2.02	0.42
5:E:130:PHE:HB3	5:E:135:LEU:HD11	2.02	0.42
7:G:55:GLY:HA3	7:G:69:PRO:HB2	2.00	0.42
7:G:117:MET:HE1	7:G:163:LEU:HD22	2.02	0.42
10:J:20:ALA:O	10:J:24:LEU:N	2.45	0.42
12:L:16:ILE:CG1	12:L:28:ILE:O	2.63	0.42
13:M:135:VAL:HG12	13:M:139:ASN:ND2	2.34	0.42
19:S:13:GLU:HG3	20:T:44:ARG:HA	2.00	0.42
20:T:225:VAL:HG11	28:X:29:DC:H5"	2.02	0.42
21:U:175:ALA:HB1	21:U:222:ARG:HH22	1.73	0.42
22:V:315:VAL:HG13	23:W:500:ASP:HB2	0.42	0.42
22:V:524:ALA:HB2	25:1:23:LEU:HD13	2.01	0.42
26:2:89:LEU:CD2	26:2:89:LEU:C	2.93	0.42
26:2:185:MET:SD	26:2:232:GLU:CB	3.07	0.42
27:3:128:HIS:NE2	27:3:130:GLU:CG	2.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:908:THR:O	1:A:963:ARG:NH1	2.53	0.42
1:A:930:LEU:HD11	8:H:107:GLU:CD	2.45	0.42
1:A:939:VAL:O	1:A:943:LEU:HG	2.18	0.42
2:B:972:ILE:O	2:B:976:MET:N	2.51	0.42
2:B:1015:LEU:HD21	2:B:1024:GLY:HA2	2.02	0.42
3:C:61:ASP:OD1	3:C:61:ASP:N	2.52	0.42
5:E:52:ARG:HB2	5:E:53:PRO:HD2	2.00	0.42
5:E:55:ARG:HH11	5:E:107:GLN:HE22	1.68	0.42
14:N:38:VAL:CG1	15:O:22:LEU:HD22	2.49	0.42
14:N:329:PHE:HB3	14:N:331:THR:HG23	2.01	0.42
22:V:514:MET:HB3	25:1:16:MET:SD	2.59	0.42
26:2:221:GLN:CG	26:2:268:PHE:CZ	2.95	0.42
1:A:419:ILE:O	1:A:426:ARG:HA	2.19	0.42
1:A:484:LEU:HD21	1:A:496:PHE:HE1	1.83	0.42
1:A:540:ASP:CG	2:B:968:ASN:HD21	2.28	0.42
2:B:109:MET:HB3	2:B:112:GLU:HB2	2.02	0.42
2:B:411:LEU:HD12	2:B:440:ILE:CD1	2.49	0.42
2:B:837:CYS:SG	2:B:838:GLN:N	2.93	0.42
2:B:849:ASP:HB3	2:B:851:ASP:OD1	2.20	0.42
2:B:896:LEU:HD21	2:B:900:GLU:HB2	2.00	0.42
3:C:81:LYS:HG3	3:C:82:LEU:HD12	2.01	0.42
5:E:26:TYR:HA	5:E:64:HIS:CB	2.50	0.42
5:E:27:LEU:HD13	5:E:64:HIS:HE2	1.77	0.42
11:K:24:ASP:H	11:K:31:CYS:HA	1.84	0.42
18:R:131:GLU:HB3	18:R:138:ALA:HB3	2.01	0.42
22:V:325:ARG:HH21	23:W:499:ASN:CB	1.95	0.42
22:V:444:HIS:O	22:V:447:PRO:CD	2.61	0.42
26:2:123:LEU:CD2	26:2:123:LEU:C	2.93	0.42
27:3:42:MET:SD	27:3:111:ILE:CD1	3.07	0.42
27:3:109:GLU:HG3	27:3:110:VAL:N	2.35	0.42
27:3:146:ARG:HG3	27:3:147:MET:N	2.35	0.42
27:3:178:MET:O	27:3:182:PHE:HD2	2.01	0.42
1:A:13:CYS:HB2	2:B:1135:TYR:CE2	2.55	0.42
1:A:71:CYS:N	1:A:75:ALA:HA	2.31	0.42
1:A:1454:VAL:HG11	1:A:1466:ALA:HB3	2.02	0.42
1:A:1460:LEU:O	2:B:1152:PRO:HD3	2.20	0.42
2:B:800:ALA:O	2:B:805:PHE:HB2	2.20	0.42
9:I:57:LYS:HE2	9:I:60:HIS:NE2	2.35	0.42
12:L:21:GLU:OE1	12:L:21:GLU:N	2.53	0.42
21:U:215:ILE:HG22	21:U:220:PHE:HB2	2.01	0.42
21:U:286:THR:CG2	21:U:299:LYS:HB3	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:25:MET:SD	23:W:58:ALA:HB2	2.59	0.42
26:2:236:PHE:CE1	26:2:261:PHE:HB3	2.54	0.42
1:A:266:MET:HE3	1:A:266:MET:HB2	1.96	0.42
1:A:546:ARG:CG	1:A:639:ILE:HD11	2.47	0.42
1:A:1217:ASP:OD2	1:A:1220:HIS:N	2.53	0.42
1:A:1302:GLU:O	1:A:1303:GLN:HB3	2.20	0.42
2:B:67:LEU:CD2	2:B:419:ALA:HB1	2.48	0.42
2:B:92:TYR:O	2:B:125:TYR:N	2.30	0.42
2:B:798:ARG:N	2:B:949:TYR:O	2.48	0.42
2:B:1080:ARG:HG2	13:M:53:ARG:CZ	2.50	0.42
3:C:75:SER:N	3:C:238:SER:O	2.42	0.42
3:C:266:GLU:CD	11:K:19:ILE:HG23	2.45	0.42
5:E:158:GLU:OE2	5:E:162:ARG:NH2	2.53	0.42
7:G:158:PHE:CZ	17:Q:139:LEU:HA	2.55	0.42
9:I:7:TYR:CZ	9:I:9:PRO:HG3	2.55	0.42
11:K:1:MET:SD	11:K:3:ALA:HB3	2.59	0.42
13:M:154:ARG:HD3	13:M:154:ARG:HA	1.88	0.42
17:Q:75:ARG:N	17:Q:95:ASN:O	2.41	0.42
21:U:283:GLU:CD	21:U:284:PRO:HD2	2.45	0.42
22:V:411:SER:O	22:V:417:THR:HB	2.19	0.42
22:V:517:GLU:CB	22:V:713:LEU:HD22	2.46	0.42
25:1:10:ILE:C	25:1:10:ILE:CD1	2.93	0.42
26:2:118:LEU:HD22	27:3:39:ASP:CB	2.50	0.42
26:2:176:ALA:HB3	26:2:178:LEU:HD13	1.98	0.42
26:2:211:GLN:HE21	26:2:257:SER:HB2	1.84	0.42
26:2:251:VAL:HG12	26:2:254:MET:N	2.28	0.42
27:3:160:ARG:CZ	27:3:190:LEU:CD1	2.97	0.42
27:3:217:VAL:HG12	27:3:218:PRO:O	2.20	0.42
1:A:1096:GLY:O	1:A:1100:THR:HG23	2.20	0.41
2:B:109:MET:CE	2:B:174:LEU:HB3	2.47	0.41
2:B:552:ASN:O	2:B:556:ILE:HG12	2.19	0.41
2:B:934:LYS:HA	2:B:944:THR:HG22	2.01	0.41
3:C:20:LYS:HA	3:C:232:ASN:HA	2.00	0.41
5:E:31:ASP:O	5:E:35:GLN:N	2.53	0.41
7:G:40:GLY:HA2	7:G:152:VAL:HG11	2.02	0.41
9:I:101:SER:N	9:I:104:ALA:HA	2.29	0.41
14:N:318:ASP:CB	16:P:239:ARG:NH2	2.76	0.41
15:O:18:SER:O	15:O:22:LEU:HG	2.20	0.41
16:P:227:GLU:HG2	16:P:228:GLU:N	2.35	0.41
16:P:231:ARG:O	16:P:235:ARG:HG3	2.20	0.41
18:R:188:GLN:HG3	18:R:189:ILE:HG13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:37:VAL:HG11	19:S:42:TRP:CZ2	2.55	0.41
21:U:161:ILE:HG21	21:U:211:LEU:HB3	2.01	0.41
22:V:448:ALA:HB1	28:X:58:DT:OP1	2.19	0.41
26:2:166:SER:HB3	26:2:167:PRO:HD3	2.00	0.41
27:3:185:GLN:HE21	27:3:185:GLN:CA	2.18	0.41
27:3:197:ASP:O	27:3:198:SER:HB3	2.20	0.41
28:X:11:DT:H2'	28:X:12:DA:C8	2.55	0.41
1:A:65:ILE:HG22	1:A:66:GLU:N	2.34	0.41
1:A:202:TRP:O	1:A:211:GLU:HA	2.21	0.41
1:A:378:VAL:N	1:A:473:ARG:O	2.52	0.41
1:A:478:PRO:HB3	11:K:4:PRO:HD3	2.01	0.41
1:A:606:HIS:HB3	1:A:628:VAL:H	1.85	0.41
1:A:632:ASN:OD1	1:A:992:LYS:NZ	2.52	0.41
1:A:1171:ALA:O	9:I:57:LYS:HD3	2.21	0.41
2:B:192:LYS:HE3	2:B:192:LYS:HB3	1.87	0.41
2:B:505:LEU:HG	2:B:509:VAL:HB	2.02	0.41
3:C:214:ASP:CG	3:C:216:SER:OG	2.63	0.41
7:G:63:ARG:HH22	7:G:67:LEU:N	2.18	0.41
7:G:79:PRO:HG3	7:G:104:MET:SD	2.60	0.41
8:H:105:SER:HB2	8:H:108:ALA:CB	2.50	0.41
13:M:283:VAL:O	13:M:287:GLN:HG2	2.21	0.41
16:P:166:GLN:HG3	29:Y:81:DA:C5'	2.39	0.41
16:P:206:GLU:HB2	16:P:207:PRO:HD2	1.96	0.41
18:R:155:LEU:HB3	18:R:204:ASN:HD21	1.80	0.41
18:R:194:ARG:H	18:R:195:PRO:HD3	1.69	0.41
26:2:89:LEU:O	26:2:93:LEU:HG	2.21	0.41
26:2:163:MET:HE3	26:2:206:LEU:HB3	2.00	0.41
27:3:18:ASN:ND2	27:3:64:ILE:HD11	2.35	0.41
1:A:275:ASP:N	1:A:275:ASP:OD1	2.52	0.41
1:A:419:ILE:HA	1:A:446:VAL:HA	2.02	0.41
1:A:504:HIS:HB3	2:B:1106:ARG:NH2	2.35	0.41
1:A:630:VAL:HG23	1:A:634:GLU:C	2.45	0.41
1:A:963:ARG:HG2	1:A:967:ARG:NH1	2.35	0.41
1:A:1151:ALA:C	1:A:1155:LYS:HZ3	2.28	0.41
1:A:1207:ILE:HD12	1:A:1260:ARG:CB	2.51	0.41
2:B:374:LEU:O	2:B:378:GLY:N	2.51	0.41
2:B:473:LEU:HD22	2:B:1052:LYS:HD3	2.02	0.41
2:B:874:PRO:C	2:B:876:ASN:N	2.77	0.41
3:C:6:GLN:HB2	11:K:104:ARG:HH12	1.85	0.41
7:G:146:LYS:HD3	7:G:165:ASP:OD2	2.21	0.41
8:H:88:PHE:CD1	8:H:146:LYS:HD2	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:279:GLY:HA2	20:T:153:TYR:CZ	2.54	0.41
16:P:167:ASN:HB2	29:Y:80:DT:O4'	2.20	0.41
21:U:193:SER:OG	21:U:194:ARG:NH1	2.53	0.41
21:U:223:MET:HB2	21:U:224:THR:H	1.68	0.41
26:2:170:ALA:C	26:2:213:TRP:HZ3	2.27	0.41
27:3:12:VAL:HG22	27:3:161:ILE:HG12	2.00	0.41
1:A:349:ARG:HB3	2:B:1158:LEU:HD12	2.02	0.41
1:A:374:SER:HB3	1:A:377:GLN:HG3	2.02	0.41
1:A:1355:VAL:HA	5:E:142:HIS:HA	2.02	0.41
2:B:75:SER:OG	2:B:75:SER:O	2.35	0.41
2:B:92:TYR:CB	20:T:145:LEU:CD2	2.79	0.41
2:B:166:LEU:HB3	2:B:170:ASP:CB	2.49	0.41
2:B:302:LYS:HB3	2:B:303:PRO:HD3	2.02	0.41
2:B:453:TRP:HB3	2:B:463:ARG:CB	2.49	0.41
2:B:531:TYR:HD2	2:B:622:CYS:SG	2.44	0.41
2:B:720:PRO:HG2	2:B:721:ARG:NH1	2.35	0.41
2:B:865:VAL:HA	2:B:895:PHE:HB3	2.02	0.41
4:D:52:GLU:O	4:D:54:GLU:N	2.52	0.41
5:E:41:LYS:HA	5:E:46:ASP:HB3	2.02	0.41
6:F:53:THR:HB	6:F:108:ARG:NH1	2.36	0.41
7:G:154:LYS:HG3	7:G:155:ASN:H	1.86	0.41
13:M:118:PHE:HA	13:M:121:ILE:HB	2.03	0.41
13:M:182:ALA:HB2	20:T:154:LYS:HG3	2.02	0.41
14:N:25:VAL:HG12	15:O:39:GLN:HB3	2.02	0.41
16:P:180:LEU:HD12	16:P:183:ILE:HD12	2.02	0.41
23:W:584:TYR:CB	23:W:591:GLY:HA3	2.48	0.41
25:1:52:VAL:CG2	25:1:53:LEU:N	2.83	0.41
26:2:44:VAL:CG1	26:2:45:PHE:N	2.82	0.41
26:2:133:THR:CG2	26:2:134:SER:N	2.83	0.41
1:A:1167:ARG:HE	1:A:1293:LEU:HB3	1.86	0.41
1:A:1173:THR:HB	9:I:56:ASN:CB	2.49	0.41
1:A:1175:ILE:H	9:I:54:TYR:HB3	1.86	0.41
2:B:258:ALA:HB2	2:B:269:ILE:CG2	2.49	0.41
2:B:1126:ALA:HB3	2:B:1137:CYS:SG	2.61	0.41
4:D:23:PRO:HG2	4:D:26:PHE:HB2	2.03	0.41
6:F:93:ALA:O	6:F:97:LEU:N	2.52	0.41
7:G:142:GLU:O	7:G:170:LEU:HA	2.20	0.41
13:M:216:SER:HA	13:M:229:GLN:NE2	2.35	0.41
14:N:10:VAL:HB	14:N:11:PRO:HD3	2.02	0.41
14:N:39:LEU:HD12	14:N:42:LEU:HD23	2.01	0.41
15:O:62:LEU:HA	15:O:76:LEU:HG	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:207:PRO:HG2	16:P:209:THR:HG23	2.03	0.41
17:Q:101:ASN:C	17:Q:103:VAL:N	2.78	0.41
17:Q:201:TYR:CD1	17:Q:201:TYR:C	2.98	0.41
20:T:202:LEU:HD11	20:T:233:TRP:HB2	2.03	0.41
22:V:427:MET:HA	22:V:435:TRP:HB2	2.01	0.41
25:1:50:VAL:CG1	25:1:54:GLN:HG2	2.41	0.41
27:3:51:MET:HE3	27:3:52:ASN:HD22	1.84	0.41
27:3:64:ILE:CB	27:3:123:ASP:HB3	2.49	0.41
27:3:144:ILE:HG13	27:3:159:SER:OG	2.20	0.41
27:3:165:LYS:HE3	27:3:200:SER:N	2.36	0.41
27:3:202:LEU:N	27:3:202:LEU:CD2	2.82	0.41
29:Y:85:DG:C2	29:Y:86:DC:C2	3.08	0.41
1:A:37:THR:OG1	1:A:86:GLY:HA3	2.20	0.41
1:A:1000:LEU:HD12	1:A:1001:PRO:HD2	2.02	0.41
1:A:1456:GLU:HG2	1:A:1457:ASN:N	2.35	0.41
2:B:78:VAL:O	2:B:79:GLU:CB	2.48	0.41
2:B:724:TYR:HB3	2:B:728:MET:HE3	2.02	0.41
2:B:764:MET:HG2	2:B:767:LEU:HD12	2.01	0.41
2:B:790:GLN:HA	2:B:968:ASN:HD22	1.86	0.41
2:B:799:SER:O	2:B:802:ASP:HB2	2.21	0.41
9:I:69:ILE:O	9:I:72:VAL:HG22	2.21	0.41
20:T:23:VAL:HG13	20:T:27:LEU:HD23	2.01	0.41
23:W:175:TYR:CD1	23:W:175:TYR:N	2.76	0.41
26:2:30:VAL:HG13	26:2:31:LEU:N	2.35	0.41
27:3:172:LEU:C	27:3:172:LEU:CD1	2.94	0.41
1:A:120:ASP:OD1	1:A:121:SER:N	2.51	0.41
1:A:201:GLU:HA	1:A:212:LYS:O	2.21	0.41
1:A:375:ILE:HG12	1:A:666:ARG:HB2	2.03	0.41
1:A:1080:ILE:CD1	6:F:54:THR:HG21	2.50	0.41
2:B:471:ASN:HD22	2:B:730:LYS:HE3	1.85	0.41
2:B:488:PRO:C	2:B:489:ILE:CG1	2.92	0.41
2:B:1040:GLN:NE2	3:C:197:TYR:H	2.18	0.41
3:C:199:LYS:NZ	3:C:201:GLU:OE1	2.46	0.41
8:H:39:LEU:HD12	8:H:124:ARG:O	2.21	0.41
12:L:38:GLU:HG2	12:L:39:CYS:H	1.86	0.41
15:O:19:LEU:HD23	15:O:22:LEU:HD12	2.03	0.41
17:Q:21:VAL:O	17:Q:25:PHE:HD1	2.04	0.41
23:W:157:PHE:HA	23:W:189:TRP:CZ3	2.55	0.41
26:2:42:LEU:HD23	26:2:42:LEU:HA	1.78	0.41
26:2:57:MET:CA	26:2:60:LEU:HG	2.49	0.41
26:2:60:LEU:CD1	26:2:95:ILE:CB	2.95	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:3:18:ASN:OD1	27:3:19:PRO:HD2	2.21	0.41
27:3:133:LEU:CD2	27:3:134:ALA:N	2.82	0.41
27:3:187:GLN:CG	27:3:189:ILE:CG1	2.94	0.41
27:3:222:SER:HB3	27:3:225:GLN:OE1	2.21	0.41
27:3:228:LEU:C	27:3:228:LEU:CD2	2.93	0.41
1:A:61:ARG:O	1:A:72:GLN:HB3	2.19	0.41
1:A:516:GLN:O	1:A:523:ARG:NH1	2.41	0.41
1:A:916:PHE:CD1	1:A:963:ARG:HD2	2.55	0.41
1:A:1017:SER:HA	1:A:1020:LEU:HG	2.03	0.41
1:A:1479:LYS:HB3	6:F:103:PRO:HB3	2.03	0.41
2:B:22:TRP:HD1	2:B:24:GLU:HB2	1.85	0.41
2:B:63:PRO:HB2	2:B:88:PHE:CD1	2.56	0.41
2:B:236:TRP:HB2	2:B:259:THR:HB	2.03	0.41
2:B:602:SER:OG	2:B:620:ARG:NH1	2.54	0.41
2:B:669:GLU:O	2:B:673:VAL:HG13	2.21	0.41
2:B:821:LYS:N	2:B:825:GLN:O	2.39	0.41
2:B:1137:CYS:HB3	2:B:1142:ASN:CB	2.51	0.41
3:C:1:MET:SD	11:K:52:LYS:HE3	2.61	0.41
3:C:190:ASN:ND2	3:C:193:ARG:HA	2.36	0.41
8:H:64:LEU:O	8:H:83:SER:HB3	2.21	0.41
11:K:82:SER:HA	11:K:83:PRO:HD3	1.81	0.41
12:L:16:ILE:O	12:L:17:TYR:HD2	2.02	0.41
13:M:218:PHE:CD1	13:M:277:ILE:HG22	2.55	0.41
17:Q:170:LYS:HG3	17:Q:173:ALA:H	1.86	0.41
25:1:52:VAL:O	25:1:56:ARG:HG2	2.21	0.41
26:2:117:ASN:HB3	26:2:118:LEU:H	1.66	0.41
26:2:171:VAL:CG1	26:2:216:MET:SD	3.06	0.41
26:2:259:LEU:HD12	26:2:260:ASN:CA	2.50	0.41
27:3:14:VAL:HG22	27:3:162:LEU:O	2.21	0.41
1:A:16:ARG:N	2:B:1148:LEU:O	2.32	0.41
1:A:33:ARG:HB3	2:B:1139:GLY:HA2	2.02	0.41
1:A:204:HIS:O	1:A:206:ASN:N	2.43	0.41
1:A:549:THR:OG1	1:A:639:ILE:HG13	2.20	0.41
1:A:720:ALA:HB2	1:A:725:LEU:HD13	2.02	0.41
1:A:731:ASN:HD21	21:U:253:THR:HG22	1.78	0.41
1:A:1218:ARG:HA	1:A:1221:MET:HG2	2.03	0.41
2:B:68:GLN:OE1	2:B:135:GLU:HG3	2.21	0.41
2:B:194:LEU:HD13	2:B:467:SER:HB2	2.03	0.41
2:B:916:TYR:OH	13:M:136:ASP:OD2	2.30	0.41
2:B:956:PHE:HB2	2:B:960:GLY:C	2.45	0.41
2:B:1123:GLY:HA3	2:B:1171:MET:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:64:THR:HG21	7:G:46:ILE:HG23	2.02	0.41
9:I:29:ASP:O	9:I:33:ARG:N	2.53	0.41
9:I:80:ARG:HE	9:I:115:THR:HG21	1.85	0.41
10:J:3:ILE:HD13	10:J:18:TRP:HB2	2.03	0.41
11:K:32:LEU:HD21	11:K:72:ILE:HB	2.02	0.41
11:K:35:ILE:N	11:K:35:ILE:HD12	2.36	0.41
12:L:17:TYR:O	12:L:45:TYR:CD2	2.74	0.41
13:M:10:LEU:C	13:M:12:ARG:N	2.64	0.41
13:M:40:VAL:C	13:M:42:GLY:N	2.76	0.41
13:M:128:ILE:HG13	13:M:130:LEU:HG	2.02	0.41
13:M:259:TYR:HD1	13:M:274:ILE:HD12	1.86	0.41
14:N:39:LEU:O	14:N:42:LEU:HB3	2.21	0.41
14:N:314:LEU:HD12	16:P:248:ALA:O	2.21	0.41
17:Q:37:LEU:HD13	17:Q:71:PHE:CE1	2.55	0.41
17:Q:106:LYS:NZ	18:R:219:LEU:CD1	2.76	0.41
17:Q:191:LEU:HD22	18:R:212:VAL:CB	2.50	0.41
20:T:143:GLN:HA	20:T:143:GLN:HE21	1.86	0.41
20:T:198:ASN:O	20:T:202:LEU:HG	2.21	0.41
20:T:224:ASN:CG	20:T:226:LYS:H	2.28	0.41
22:V:353:ALA:O	22:V:357:VAL:HG23	2.21	0.41
22:V:518:PHE:HB2	25:1:16:MET:SD	2.61	0.41
23:W:73:CYS:O	23:W:209:TYR:HE2	2.04	0.41
23:W:492:PRO:HG2	23:W:678:VAL:HG22	2.03	0.41
25:1:1:MET:N	26:2:418:PHE:CB	2.84	0.41
25:1:10:ILE:HG22	26:2:407:VAL:CG2	2.50	0.41
25:1:31:LYS:C	25:1:33:PHE:H	2.28	0.41
25:1:38:ILE:CB	25:1:44:PHE:CD1	3.04	0.41
26:2:93:LEU:CA	26:2:96:TRP:HD1	2.31	0.41
26:2:93:LEU:HD23	26:2:96:TRP:HE1	1.85	0.41
26:2:94:ARG:HD2	26:2:95:ILE:HD13	2.02	0.41
26:2:123:LEU:HD21	26:2:178:LEU:HD11	2.02	0.41
26:2:204:LEU:CD2	26:2:254:MET:HG3	2.50	0.41
26:2:270:LEU:C	26:2:270:LEU:CD2	2.94	0.41
27:3:8:LEU:CD2	27:3:54:SER:HB3	2.45	0.41
27:3:33:THR:HG22	27:3:36:LYS:CB	2.44	0.41
27:3:34:LEU:C	27:3:34:LEU:CD1	2.94	0.41
27:3:41:VAL:HG13	27:3:42:MET:N	2.35	0.41
27:3:100:LYS:HE2	27:3:100:LYS:HB2	1.89	0.41
27:3:222:SER:HB3	27:3:225:GLN:CG	2.51	0.41
28:X:57:DC:C2'	28:X:58:DT:H72	2.50	0.41
1:A:42:LYS:HD3	1:A:55:GLY:H	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:47:THR:C	1:A:49:GLY:N	2.76	0.41
1:A:338:SER:O	1:A:342:ARG:HG3	2.21	0.41
1:A:470:MET:SD	1:A:521:VAL:HG23	2.61	0.41
1:A:702:ILE:O	1:A:706:ILE:HG12	2.21	0.41
1:A:1054:MET:O	1:A:1059:ARG:N	2.54	0.41
1:A:1165:THR:O	1:A:1169:VAL:HG23	2.21	0.41
1:A:1173:THR:HB	9:I:56:ASN:HB3	2.02	0.41
1:A:1198:GLU:H	1:A:1198:GLU:CD	2.29	0.41
3:C:190:ASN:ND2	3:C:195:THR:O	2.51	0.41
5:E:142:HIS:HB3	5:E:145:VAL:HG23	2.02	0.41
6:F:44:ARG:H	6:F:45:PRO:CD	2.34	0.41
11:K:81:TYR:CE2	11:K:86:ALA:HB2	2.55	0.41
12:L:16:ILE:C	12:L:17:TYR:CD2	2.99	0.41
16:P:193:ASN:HA	16:P:194:PRO:HD2	1.92	0.41
17:Q:129:CYS:HB2	17:Q:154:CYS:HB2	2.02	0.41
22:V:297:PHE:CG	22:V:298:ARG:N	2.89	0.41
22:V:409:THR:H	22:V:418:LYS:HG3	1.86	0.41
25:1:10:ILE:O	25:1:10:ILE:HG23	2.21	0.41
27:3:60:ILE:CG2	27:3:61:ALA:N	2.83	0.41
27:3:174:TYR:CZ	27:3:178:MET:HG3	2.56	0.41
1:A:404:GLU:OE1	1:A:407:ARG:NH1	2.45	0.40
1:A:432:HIS:CG	1:A:433:PRO:HD2	2.56	0.40
1:A:864:LEU:HD22	1:A:1095:LEU:HD23	2.02	0.40
1:A:915:ALA:O	1:A:919:LYS:N	2.45	0.40
1:A:1053:ARG:NE	1:A:1057:GLU:OE1	2.53	0.40
1:A:1218:ARG:HH12	1:A:1253:GLU:C	2.29	0.40
2:B:474:THR:H	2:B:477:SER:HB2	1.85	0.40
2:B:761:THR:H	2:B:764:MET:CE	2.33	0.40
5:E:11:TRP:CZ2	5:E:15:LYS:HE3	2.56	0.40
5:E:17:ILE:O	5:E:20:LEU:HB3	2.21	0.40
8:H:97:TYR:CZ	8:H:115:TYR:HB3	2.56	0.40
9:I:24:LEU:HD11	9:I:44:TYR:HE2	1.86	0.40
12:L:34:ILE:HD12	12:L:42:ARG:HB3	2.03	0.40
14:N:332:GLU:HA	15:O:92:LYS:O	2.21	0.40
15:O:70:ASN:HB3	15:O:99:ASP:HB3	2.02	0.40
16:P:200:VAL:HG12	16:P:213:ILE:HD13	2.02	0.40
18:R:195:PRO:HB2	18:R:199:LYS:CG	2.51	0.40
19:S:48:GLU:OE1	19:S:101:ARG:NH2	2.54	0.40
19:S:108:ARG:HA	19:S:108:ARG:HD3	1.97	0.40
22:V:413:LEU:H	22:V:417:THR:CG2	2.34	0.40
23:W:144:ALA:O	23:W:149:ASP:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:0:54:ARG:HA	27:3:209:ILE:HD13	1.06	0.40
26:2:236:PHE:HZ	26:2:258:LEU:CD1	2.34	0.40
27:3:217:VAL:HA	27:3:218:PRO:HD2	1.96	0.40
27:3:229:TRP:HD1	27:3:229:TRP:O	2.04	0.40
1:A:32:LYS:HG2	1:A:87:HIS:NE2	2.36	0.40
1:A:63:GLY:HA2	1:A:71:CYS:SG	2.62	0.40
1:A:240:PRO:HB3	1:A:244:ARG:HH11	1.87	0.40
1:A:337:LYS:O	1:A:341:GLN:HB3	2.21	0.40
1:A:416:ALA:HA	1:A:448:ARG:HA	2.03	0.40
1:A:587:THR:O	1:A:591:ILE:HG12	2.21	0.40
1:A:625:ASP:H	1:A:637:MET:CG	2.33	0.40
1:A:802:PHE:CZ	1:A:808:PRO:HB3	2.57	0.40
1:A:1161:LEU:HB3	1:A:1308:TYR:OH	2.21	0.40
2:B:607:ILE:HG21	9:I:72:VAL:N	2.36	0.40
2:B:1080:ARG:HG2	13:M:53:ARG:NH1	2.36	0.40
3:C:6:GLN:CD	3:C:25:ASN:HD22	2.29	0.40
3:C:47:ILE:HG22	12:L:57:ALA:HB2	2.04	0.40
7:G:89:VAL:HA	7:G:99:THR:HA	2.03	0.40
7:G:163:LEU:HD23	7:G:163:LEU:O	2.21	0.40
9:I:27:LYS:HE3	9:I:38:ALA:HB2	2.03	0.40
16:P:203:ARG:HG3	16:P:203:ARG:HH21	1.87	0.40
18:R:195:PRO:HB2	18:R:199:LYS:HD2	2.02	0.40
19:S:49:ARG:HD2	19:S:96:GLN:HB2	2.03	0.40
23:W:428:ILE:HA	23:W:430:ASN:HD21	1.85	0.40
23:W:428:ILE:C	23:W:430:ASN:HD22	2.30	0.40
25:1:1:MET:CA	26:2:413:LEU:HA	2.48	0.40
26:2:34:LEU:CD2	26:2:34:LEU:N	2.84	0.40
26:2:159:VAL:HG11	26:2:161:HIS:CD2	2.49	0.40
26:2:221:GLN:O	26:2:268:PHE:CE1	2.74	0.40
26:2:236:PHE:CE1	26:2:258:LEU:HD12	2.57	0.40
27:3:17:ALA:CB	27:3:63:HIS:CD2	2.99	0.40
27:3:131:THR:CG2	27:3:133:LEU:CD1	2.95	0.40
1:A:309:LEU:HG	1:A:313:HIS:CD2	2.57	0.40
1:A:336:LEU:HG	1:A:338:SER:H	1.86	0.40
1:A:340:LYS:HG3	1:A:1436:VAL:HG21	2.03	0.40
1:A:452:ASP:OD1	1:A:476:ILE:HG12	2.21	0.40
1:A:550:LYS:HG2	1:A:552:ASP:H	1.86	0.40
1:A:790:GLN:OE1	1:A:822:PHE:HB2	2.22	0.40
1:A:962:ASP:OD2	1:A:1046:ARG:HD2	2.21	0.40
1:A:1173:THR:HA	1:A:1214:VAL:HA	2.03	0.40
2:B:481:HIS:HA	2:B:484:ARG:NH1	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:19:VAL:CG1	3:C:233:VAL:HB	2.51	0.40
5:E:71:GLN:CD	5:E:99:ILE:HA	2.47	0.40
5:E:120:ASP:O	5:E:122:ALA:N	2.54	0.40
6:F:99:ALA:HB1	6:F:101:LYS:HG3	2.01	0.40
10:J:2:ILE:O	10:J:3:ILE:C	2.65	0.40
13:M:179:GLU:HG2	20:T:154:LYS:CE	2.51	0.40
13:M:195:PHE:CZ	13:M:199:LEU:HD11	2.56	0.40
13:M:279:GLY:HA2	20:T:153:TYR:OH	2.21	0.40
13:M:289:TYR:HA	13:M:292:ILE:HG12	2.03	0.40
17:Q:104:LYS:HE3	18:R:238:LYS:NZ	2.36	0.40
21:U:191:VAL:O	21:U:195:ILE:HG13	2.22	0.40
23:W:212:LEU:C	23:W:212:LEU:HD13	2.46	0.40
25:1:7:GLY:C	25:1:8:VAL:CG2	2.94	0.40
25:1:13:ASP:OD2	25:1:17:LYS:HB2	2.16	0.40
26:2:61:PHE:HE1	26:2:99:GLN:NE2	2.19	0.40
27:3:44:LEU:C	27:3:44:LEU:CD1	2.94	0.40
27:3:222:SER:O	27:3:226:TYR:CD2	2.75	0.40
1:A:15:LEU:HA	2:B:1148:LEU:HB3	2.02	0.40
1:A:312:PHE:CE2	1:A:326:PRO:HB2	2.55	0.40
2:B:74:ALA:C	2:B:76:GLY:N	2.79	0.40
2:B:225:LEU:O	2:B:230:ARG:HG2	2.20	0.40
2:B:834:ARG:HD2	2:B:840:MET:SD	2.61	0.40
3:C:54:ALA:O	3:C:160:ARG:N	2.36	0.40
5:E:82:VAL:HG21	5:E:106:VAL:HG22	2.03	0.40
5:E:172:ARG:NE	5:E:208:LEU:HD22	2.36	0.40
6:F:70:ALA:O	6:F:74:ALA:N	2.48	0.40
6:F:110:LEU:N	6:F:114:SER:O	2.55	0.40
9:I:27:LYS:O	9:I:35:LEU:HD12	2.22	0.40
17:Q:109:HIS:HB3	18:R:221:ARG:HB3	2.04	0.40
17:Q:124:ARG:HD3	17:Q:168:MET:SD	2.62	0.40
22:V:666:ASP:CB	25:1:17:LYS:HZ3	2.34	0.40
23:W:233:PHE:HB2	23:W:456:ILE:HG22	2.02	0.40
26:2:195:CYS:SG	26:2:196:ILE:N	2.95	0.40
26:2:201:PHE:CZ	26:2:202:GLN:OE1	2.74	0.40
27:3:68:ARG:HG2	27:3:69:PHE:N	2.36	0.40
29:Y:89:DC:H2"	29:Y:90:DC:C5	2.57	0.40
1:A:364:ARG:HH12	1:A:461:GLN:HB3	1.86	0.40
1:A:420:ILE:HB	1:A:445:LYS:HB2	2.03	0.40
1:A:746:ASN:HA	1:A:749:ARG:HE	1.86	0.40
1:A:1323:THR:HG23	1:A:1325:ASP:N	2.31	0.40
2:B:88:PHE:CE2	2:B:128:ILE:HG12	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:990:SER:O	2:B:994:GLY:N	2.53	0.40
4:D:105:PRO:O	4:D:135:GLN:NE2	2.47	0.40
6:F:116:GLU:CD	6:F:118:TRP:HE1	2.30	0.40
7:G:11:ILE:N	7:G:68:TYR:O	2.49	0.40
10:J:35:LEU:HB3	10:J:46:ARG:CZ	2.51	0.40
16:P:211:ALA:HA	16:P:220:VAL:O	2.21	0.40
16:P:237:TYR:O	16:P:240:VAL:HG23	2.22	0.40
16:P:295:MET:N	16:P:300:ILE:O	2.54	0.40
17:Q:104:LYS:NZ	18:R:238:LYS:CD	2.82	0.40
19:S:54:LYS:HE2	19:S:54:LYS:HB2	1.84	0.40
20:T:20:LEU:O	20:T:113:ARG:HA	2.21	0.40
20:T:154:LYS:HA	20:T:155:PRO:HD3	1.97	0.40
26:2:219:TYR:N	26:2:264:HIS:NE2	2.69	0.40
27:3:64:ILE:CG2	27:3:123:ASP:CG	2.95	0.40
27:3:64:ILE:HD12	27:3:128:HIS:HB3	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	1450/1970 (74%)	1305 (90%)	97 (7%)	48 (3%)	3	21
2	B	1163/1174 (99%)	1049 (90%)	76 (6%)	38 (3%)	3	21
3	C	273/275 (99%)	241 (88%)	18 (7%)	14 (5%)	1	15
4	D	127/142 (89%)	118 (93%)	8 (6%)	1 (1%)	16	54
5	E	208/210 (99%)	195 (94%)	7 (3%)	6 (3%)	3	23
6	F	84/127 (66%)	78 (93%)	4 (5%)	2 (2%)	4	27
7	G	169/172 (98%)	158 (94%)	10 (6%)	1 (1%)	21	59
8	H	148/150 (99%)	123 (83%)	13 (9%)	12 (8%)	1	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	123/125 (98%)	100 (81%)	14 (11%)	9 (7%)	1	10
10	J	65/67 (97%)	53 (82%)	9 (14%)	3 (5%)	2	17
11	K	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
12	L	44/58 (76%)	37 (84%)	3 (7%)	4 (9%)	0	8
13	M	256/316 (81%)	236 (92%)	12 (5%)	8 (3%)	3	22
14	N	109/376 (29%)	100 (92%)	5 (5%)	4 (4%)	2	20
15	O	97/109 (89%)	90 (93%)	7 (7%)	0	100	100
16	P	183/339 (54%)	170 (93%)	8 (4%)	5 (3%)	4	25
17	Q	176/439 (40%)	159 (90%)	11 (6%)	6 (3%)	3	21
18	R	163/291 (56%)	128 (78%)	22 (14%)	13 (8%)	1	9
19	S	134/517 (26%)	123 (92%)	7 (5%)	4 (3%)	3	22
20	T	218/249 (88%)	191 (88%)	17 (8%)	10 (5%)	2	17
21	U	168/301 (56%)	136 (81%)	21 (12%)	11 (6%)	1	12
22	V	473/782 (60%)	400 (85%)	46 (10%)	27 (6%)	1	14
23	W	661/760 (87%)	567 (86%)	69 (10%)	25 (4%)	2	19
24	0	186/395 (47%)	168 (90%)	13 (7%)	5 (3%)	4	25
25	1	60/71 (84%)	53 (88%)	5 (8%)	2 (3%)	3	21
26	2	264/462 (57%)	246 (93%)	14 (5%)	4 (2%)	8	40
27	3	187/308 (61%)	175 (94%)	9 (5%)	3 (2%)	7	38
All	All	7304/10302 (71%)	6511 (89%)	528 (7%)	265 (4%)	4	20

All (265) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	67	ARG
1	A	205	VAL
1	A	266	MET
1	A	267	GLN
1	A	531	ASN
1	A	605	THR
1	A	611	ASP
1	A	613	GLU
1	A	615	SER
1	A	623	PRO
1	A	911	PRO

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Mol	Chain	Res	Type
1	A	929	ALA
1	A	932	ARG
1	A	1117	VAL
1	A	1275	VAL
1	A	1303	GLN
1	A	1306	LYS
2	B	61	ASP
2	B	79	GLU
2	B	232	THR
2	B	250	SER
2	B	491	ARG
2	B	498	PRO
2	B	500	GLN
2	B	549	SER
2	B	841	ARG
2	B	879	GLU
3	C	7	PRO
3	C	89	THR
3	C	126	ARG
3	C	147	ASP
3	C	213	GLU
3	C	218	ALA
5	E	52	ARG
5	E	53	PRO
5	E	66	ASP
7	G	154	LYS
8	H	67	ASP
8	H	74	GLU
8	H	75	TYR
8	H	86	ASP
8	H	108	ALA
8	H	111	ARG
9	I	57	LYS
9	I	85	PRO
9	I	87	GLN
9	I	104	ALA
9	I	106	ASP
12	L	16	ILE
12	L	38	GLU
13	M	10	LEU
13	M	11	PRO
13	M	12	ARG

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Mol	Chain	Res	Type
13	M	44	ARG
13	M	109	SER
16	P	160	GLY
16	P	161	ILE
16	P	206	GLU
18	R	134	ASP
18	R	163	LEU
18	R	195	PRO
18	R	206	LYS
20	T	139	VAL
20	T	147	LYS
20	T	156	VAL
21	U	251	ALA
21	U	257	GLN
22	V	385	ASP
22	V	427	MET
22	V	461	HIS
22	V	491	ALA
22	V	499	ASN
22	V	632	SER
22	V	648	LYS
22	V	649	GLY
23	W	67	VAL
23	W	409	THR
23	W	411	ALA
23	W	419	GLU
23	W	420	PRO
23	W	421	PHE
23	W	424	ARG
23	W	430	ASN
23	W	504	ILE
23	W	573	ASP
23	W	595	ILE
23	W	630	SER
24	0	77	LYS
24	0	78	PRO
25	1	48	GLU
26	2	49	PRO
27	3	120	THR
27	3	209	ILE
1	A	44	PRO
1	A	273	GLN

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Mol	Chain	Res	Type
1	A	338	SER
1	A	346	LYS
1	A	625	ASP
1	A	930	LEU
1	A	935	GLN
1	A	1101	GLN
1	A	1264	SER
1	A	1273	GLU
1	A	1282	ASP
1	A	1435	THR
2	B	76	GLY
2	B	243	GLY
2	B	428	ASP
2	B	460	HIS
2	B	649	ASN
2	B	791	GLU
2	B	875	GLU
2	B	881	GLU
2	B	882	SER
2	B	883	THR
2	B	889	LYS
3	C	91	GLU
3	C	143	VAL
3	C	211	LEU
4	D	57	LEU
5	E	65	ASN
5	E	121	MET
8	H	3	GLY
8	H	21	LYS
8	H	107	GLU
10	J	14	VAL
12	L	17	TYR
12	L	18	ILE
17	Q	103	VAL
17	Q	169	PRO
18	R	157	GLN
18	R	164	GLY
18	R	212	VAL
20	T	146	ASP
20	T	181	GLN
21	U	227	GLU
21	U	233	LEU

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Mol	Chain	Res	Type
21	U	267	LYS
22	V	254	GLN
22	V	404	SER
23	W	124	LEU
23	W	408	SER
23	W	646	ILE
26	2	223	ALA
26	2	231	VAL
1	A	156	GLY
1	A	1200	PRO
1	A	1305	SER
1	A	1417	HIS
2	B	73	HIS
2	B	75	SER
2	B	229	SER
2	B	456	GLN
2	B	497	LYS
2	B	651	TYR
2	B	863	ASP
2	B	898	THR
2	B	1129	ASN
2	B	1132	THR
3	C	144	GLU
8	H	106	THR
9	I	92	LYS
9	I	119	CYS
13	M	106	THR
14	N	346	LYS
17	Q	163	GLU
18	R	196	ASP
19	S	170	VAL
20	T	124	TYR
21	U	222	ARG
21	U	226	GLU
21	U	256	THR
22	V	343	GLY
22	V	418	LYS
22	V	460	ALA
23	W	155	CYS
23	W	509	GLU
27	3	198	SER
1	A	72	GLN

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Mol	Chain	Res	Type
1	A	184	CYS
1	A	461	GLN
1	A	479	TRP
1	A	981	CYS
2	B	257	VAL
2	B	495	LEU
2	B	873	LEU
2	B	1136	GLU
3	C	137	ASN
5	E	64	HIS
6	F	85	GLY
8	H	70	LEU
8	H	71	ASP
9	I	20	CYS
10	J	3	ILE
13	M	149	LYS
14	N	355	ASP
17	Q	124	ARG
17	Q	165	GLU
18	R	197	LYS
20	T	38	GLY
20	T	135	SER
20	T	140	ARG
22	V	310	LEU
22	V	428	GLU
22	V	470	LEU
22	V	475	ASP
22	V	502	ILE
22	V	629	HIS
1	A	75	ALA
1	A	300	ALA
1	A	1106	THR
1	A	1265	ASP
1	A	1266	GLU
1	A	1342	SER
3	C	151	VAL
10	J	6	ARG
16	P	297	LYS
18	R	140	LYS
18	R	174	ALA
19	S	153	ARG
19	S	154	THR

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Mol	Chain	Res	Type
19	S	160	ALA
21	U	229	ALA
21	U	266	CYS
21	U	295	GLY
22	V	650	MET
23	W	152	LEU
23	W	551	SER
24	O	79	ASN
26	2	430	VAL
1	A	1281	ASP
2	B	737	ILE
6	F	44	ARG
9	I	105	GLU
13	M	247	GLY
14	N	312	GLU
18	R	141	PRO
18	R	225	VAL
22	V	436	GLY
22	V	582	GLY
23	W	36	GLY
23	W	345	ARG
23	W	697	ILE
1	A	50	GLY
2	B	493	GLY
22	V	311	LYS
22	V	651	VAL
1	A	51	ARG
1	A	498	GLY
22	V	426	VAL
22	V	457	ILE
23	W	495	ILE
24	O	216	GLY
3	C	6	GLN
3	C	78	ILE
17	Q	100	VAL
20	T	138	PRO
22	V	405	VAL
23	W	174	ILE
25	1	2	VAL
16	P	207	PRO
2	B	1008	VAL
14	N	313	PRO

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Mol	Chain	Res	Type
23	W	45	GLY
24	0	56	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1279/1748 (73%)	1249 (98%)	30 (2%)	44	64
2	B	1020/1028 (99%)	997 (98%)	23 (2%)	44	64
3	C	252/252 (100%)	248 (98%)	4 (2%)	55	70
4	D	119/126 (94%)	118 (99%)	1 (1%)	73	80
5	E	192/192 (100%)	187 (97%)	5 (3%)	40	62
6	F	74/111 (67%)	74 (100%)	0	100	100
7	G	152/153 (99%)	149 (98%)	3 (2%)	48	66
8	H	131/131 (100%)	128 (98%)	3 (2%)	44	64
9	I	112/112 (100%)	107 (96%)	5 (4%)	24	46
10	J	56/56 (100%)	56 (100%)	0	100	100
11	K	106/106 (100%)	103 (97%)	3 (3%)	38	59
12	L	43/55 (78%)	43 (100%)	0	100	100
13	M	222/268 (83%)	213 (96%)	9 (4%)	27	48
14	N	105/324 (32%)	105 (100%)	0	100	100
15	O	90/98 (92%)	88 (98%)	2 (2%)	45	64
16	P	159/293 (54%)	153 (96%)	6 (4%)	29	50
17	Q	164/373 (44%)	159 (97%)	5 (3%)	36	57
18	R	150/261 (58%)	139 (93%)	11 (7%)	13	34
19	S	121/448 (27%)	118 (98%)	3 (2%)	42	63
20	T	196/218 (90%)	185 (94%)	11 (6%)	19	40
21	U	148/266 (56%)	139 (94%)	9 (6%)	17	38
22	V	422/688 (61%)	403 (96%)	19 (4%)	24	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	W	577/664 (87%)	544 (94%)	33 (6%)	18	40
24	0	171/352 (49%)	163 (95%)	8 (5%)	23	45
25	1	56/64 (88%)	51 (91%)	5 (9%)	9	28
26	2	238/399 (60%)	229 (96%)	9 (4%)	29	50
27	3	171/272 (63%)	162 (95%)	9 (5%)	20	41
All	All	6526/9058 (72%)	6310 (97%)	216 (3%)	34	55

All (216) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	ASP
1	A	57	LEU
1	A	117	LEU
1	A	147	LEU
1	A	264	VAL
1	A	267	GLN
1	A	339	LEU
1	A	472	HIS
1	A	489	THR
1	A	611	ASP
1	A	613	GLU
1	A	615	SER
1	A	620	HIS
1	A	625	ASP
1	A	630	VAL
1	A	644	SER
1	A	647	THR
1	A	659	GLU
1	A	669	TYR
1	A	750	ASP
1	A	932	ARG
1	A	964	GLU
1	A	1117	VAL
1	A	1152	GLU
1	A	1289	GLU
1	A	1306	LYS
1	A	1307	VAL
1	A	1311	LEU
1	A	1314	THR
1	A	1386	ILE

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Mol	Chain	Res	Type
2	B	79	GLU
2	B	97	THR
2	B	125	TYR
2	B	131	THR
2	B	133	ILE
2	B	169	ARG
2	B	249	LYS
2	B	250	SER
2	B	256	ILE
2	B	442	ASP
2	B	499	ARG
2	B	546	GLU
2	B	588	ARG
2	B	604	ILE
2	B	664	TYR
2	B	666	ASP
2	B	782	ILE
2	B	814	TYR
2	B	879	GLU
2	B	880	LEU
2	B	881	GLU
2	B	1080	ARG
2	B	1127	ILE
3	C	61	ASP
3	C	212	ASP
3	C	215	GLU
3	C	217	GLN
4	D	45	LYS
5	E	50	GLU
5	E	62	VAL
5	E	64	HIS
5	E	134	GLU
5	E	172	ARG
7	G	63	ARG
7	G	144	ARG
7	G	163	LEU
8	H	65	TYR
8	H	84	ARG
8	H	107	GLU
9	I	27	LYS
9	I	58	ILE
9	I	72	VAL

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Mol	Chain	Res	Type
9	I	84	HIS
9	I	103	ARG
11	K	8	GLU
11	K	22	ASN
11	K	35	ILE
13	M	7	LEU
13	M	10	LEU
13	M	31	ASP
13	M	39	LEU
13	M	53	ARG
13	M	107	MET
13	M	114	MET
13	M	120	GLU
13	M	126	ASP
15	O	10	THR
15	O	24	GLN
16	P	161	ILE
16	P	206	GLU
16	P	271	GLU
16	P	297	LYS
16	P	299	ARG
16	P	301	VAL
17	Q	45	GLU
17	Q	100	VAL
17	Q	101	ASN
17	Q	139	LEU
17	Q	142	ASN
18	R	140	LYS
18	R	159	ASP
18	R	163	LEU
18	R	175	LEU
18	R	194	ARG
18	R	206	LYS
18	R	209	GLN
18	R	210	PHE
18	R	212	VAL
18	R	223	VAL
18	R	225	VAL
19	S	7	SER
19	S	163	GLU
19	S	166	ARG
20	T	143	GLN

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Mol	Chain	Res	Type
20	T	144	GLN
20	T	145	LEU
20	T	149	VAL
20	T	154	LYS
20	T	156	VAL
20	T	159	HIS
20	T	160	GLN
20	T	162	ASN
20	T	177	ARG
20	T	180	LYS
21	U	179	GLU
21	U	194	ARG
21	U	218	ASP
21	U	222	ARG
21	U	223	MET
21	U	234	LYS
21	U	252	LYS
21	U	253	THR
21	U	274	THR
22	V	246	MET
22	V	271	GLU
22	V	332	ARG
22	V	362	LEU
22	V	371	VAL
22	V	418	LYS
22	V	427	MET
22	V	429	TRP
22	V	458	VAL
22	V	471	VAL
22	V	479	ASP
22	V	482	PHE
22	V	492	ASN
22	V	517	GLU
22	V	568	LEU
22	V	581	TYR
22	V	590	MET
22	V	613	THR
22	V	614	SER
23	W	37	HIS
23	W	64	PRO
23	W	87	LEU
23	W	95	GLU

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Mol	Chain	Res	Type
23	W	101	LYS
23	W	112	ARG
23	W	122	THR
23	W	123	PRO
23	W	152	LEU
23	W	166	ARG
23	W	175	TYR
23	W	196	ARG
23	W	263	LEU
23	W	283	ASP
23	W	288	LEU
23	W	307	ASN
23	W	309	VAL
23	W	327	GLU
23	W	333	LEU
23	W	346	VAL
23	W	425	THR
23	W	461	LEU
23	W	523	LEU
23	W	533	ASP
23	W	554	GLU
23	W	581	LEU
23	W	596	LEU
23	W	610	PHE
23	W	620	MET
23	W	647	ARG
23	W	664	VAL
23	W	669	ARG
23	W	676	LEU
24	0	77	LYS
24	0	103	GLN
24	0	125	ARG
24	0	174	LEU
24	0	202	SER
24	0	218	THR
24	0	222	ILE
24	0	223	LEU
25	1	10	ILE
25	1	16	MET
25	1	18	GLN
25	1	21	LEU
25	1	38	ILE

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Mol	Chain	Res	Type
26	2	77	LYS
26	2	181	GLN
26	2	202	GLN
26	2	402	ARG
26	2	407	VAL
26	2	421	LEU
26	2	426	ARG
26	2	430	VAL
26	2	452	LYS
27	3	24	LYS
27	3	56	LYS
27	3	109	GLU
27	3	124	ILE
27	3	133	LEU
27	3	144	ILE
27	3	185	GLN
27	3	190	LEU
27	3	216	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (104) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	267	GLN
1	A	387	ASN
1	A	412	GLN
1	A	439	HIS
1	A	441	GLN
1	A	516	GLN
1	A	529	GLN
1	A	539	GLN
1	A	700	GLN
1	A	703	GLN
1	A	740	GLN
1	A	783	GLN
1	A	1082	HIS
1	A	1220	HIS
1	A	1310	HIS
1	A	1332	GLN
1	A	1422	GLN
2	B	98	HIS
2	B	197	GLN
2	B	227	ASN

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Mol	Chain	Res	Type
2	B	245	GLN
2	B	452	ASN
2	B	456	GLN
2	B	486	ASN
2	B	817	GLN
2	B	913	GLN
2	B	970	HIS
2	B	1003	ASN
2	B	1007	ASN
2	B	1040	GLN
2	B	1101	GLN
2	B	1117	HIS
2	B	1133	HIS
3	C	5	ASN
3	C	25	ASN
3	C	123	ASN
3	C	137	ASN
3	C	190	ASN
5	E	19	GLN
5	E	30	GLN
5	E	64	HIS
5	E	71	GLN
5	E	129	GLN
5	E	132	GLN
7	G	24	ASN
8	H	46	GLN
9	I	74	GLN
9	I	84	HIS
9	I	87	GLN
9	I	98	GLN
9	I	121	HIS
12	L	23	HIS
13	M	116	ASN
13	M	229	GLN
16	P	189	ASN
16	P	277	HIS
17	Q	123	ASN
18	R	177	ASN
18	R	204	ASN
18	R	209	GLN
19	S	152	HIS
20	T	14	GLN

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Mol	Chain	Res	Type
20	T	160	GLN
21	U	239	ASN
21	U	292	ASN
22	V	281	GLN
22	V	286	HIS
22	V	366	ASN
22	V	377	GLN
22	V	415	HIS
22	V	459	GLN
22	V	537	ASN
22	V	539	ASN
22	V	599	ASN
22	V	621	ASN
22	V	665	GLN
22	V	677	GLN
23	W	187	GLN
23	W	203	ASN
23	W	316	GLN
23	W	328	HIS
23	W	430	ASN
23	W	434	HIS
23	W	700	HIS
24	0	60	HIS
25	1	27	ASN
25	1	42	HIS
25	1	51	ASN
26	2	97	HIS
26	2	161	HIS
26	2	181	GLN
26	2	202	GLN
26	2	221	GLN
26	2	239	GLN
26	2	263	GLN
26	2	273	GLN
26	2	411	GLN
26	2	458	GLN
27	3	63	HIS
27	3	148	ASN
27	3	155	GLN
27	3	185	GLN
27	3	187	GLN
27	3	225	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 13 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

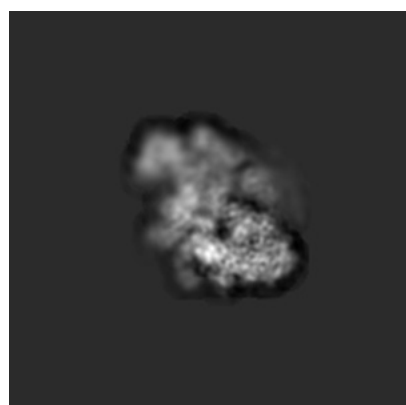
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3307. These allow visual inspection of the internal detail of the map and identification of artifacts.

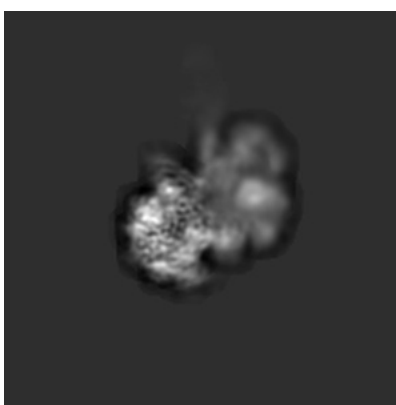
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

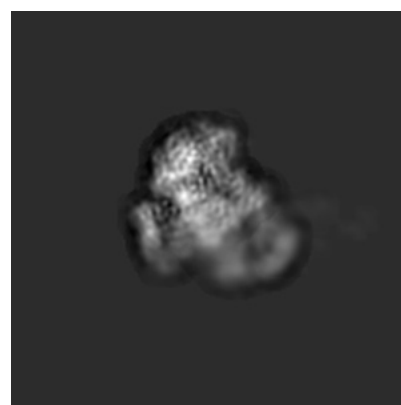
6.1.1 Primary map



X



Y

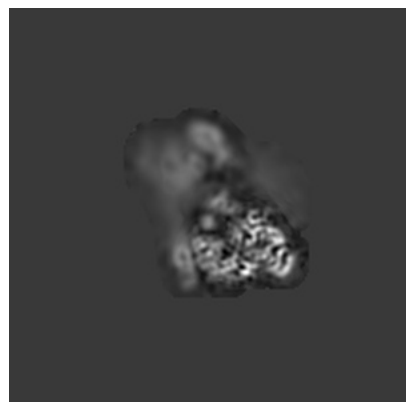


Z

The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

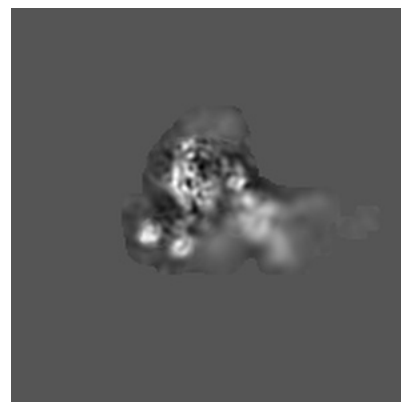
6.2.1 Primary map



X Index: 96



Y Index: 96

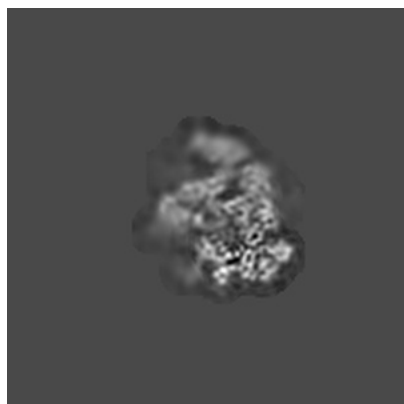


Z Index: 96

The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

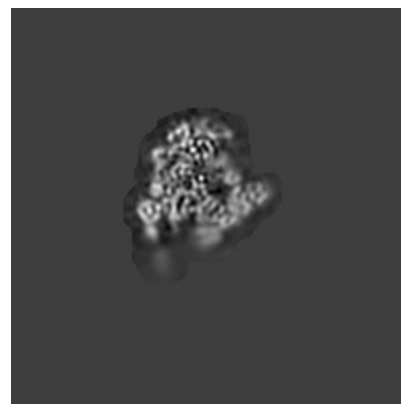
6.3.1 Primary map



X Index: 83



Y Index: 96



Z Index: 75

The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

6.4.1 Primary map



X



Y

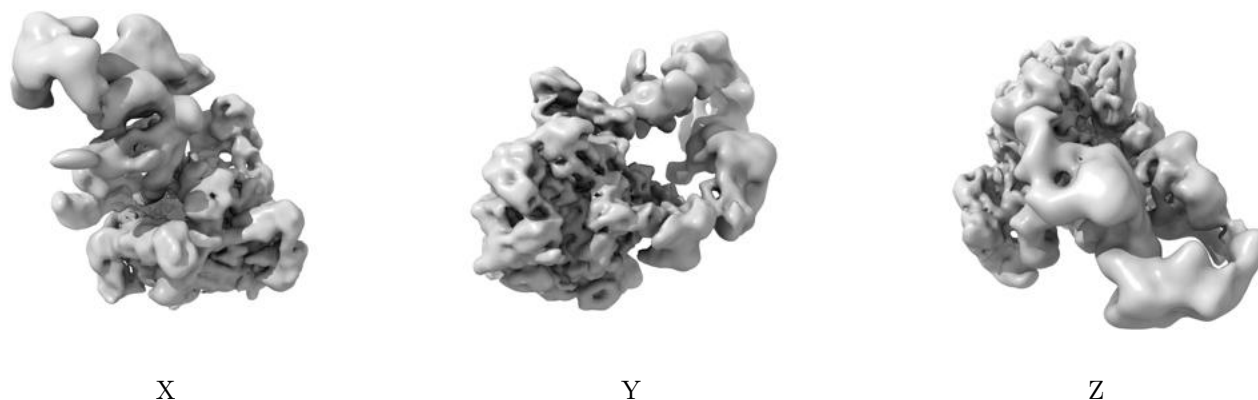


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.045. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

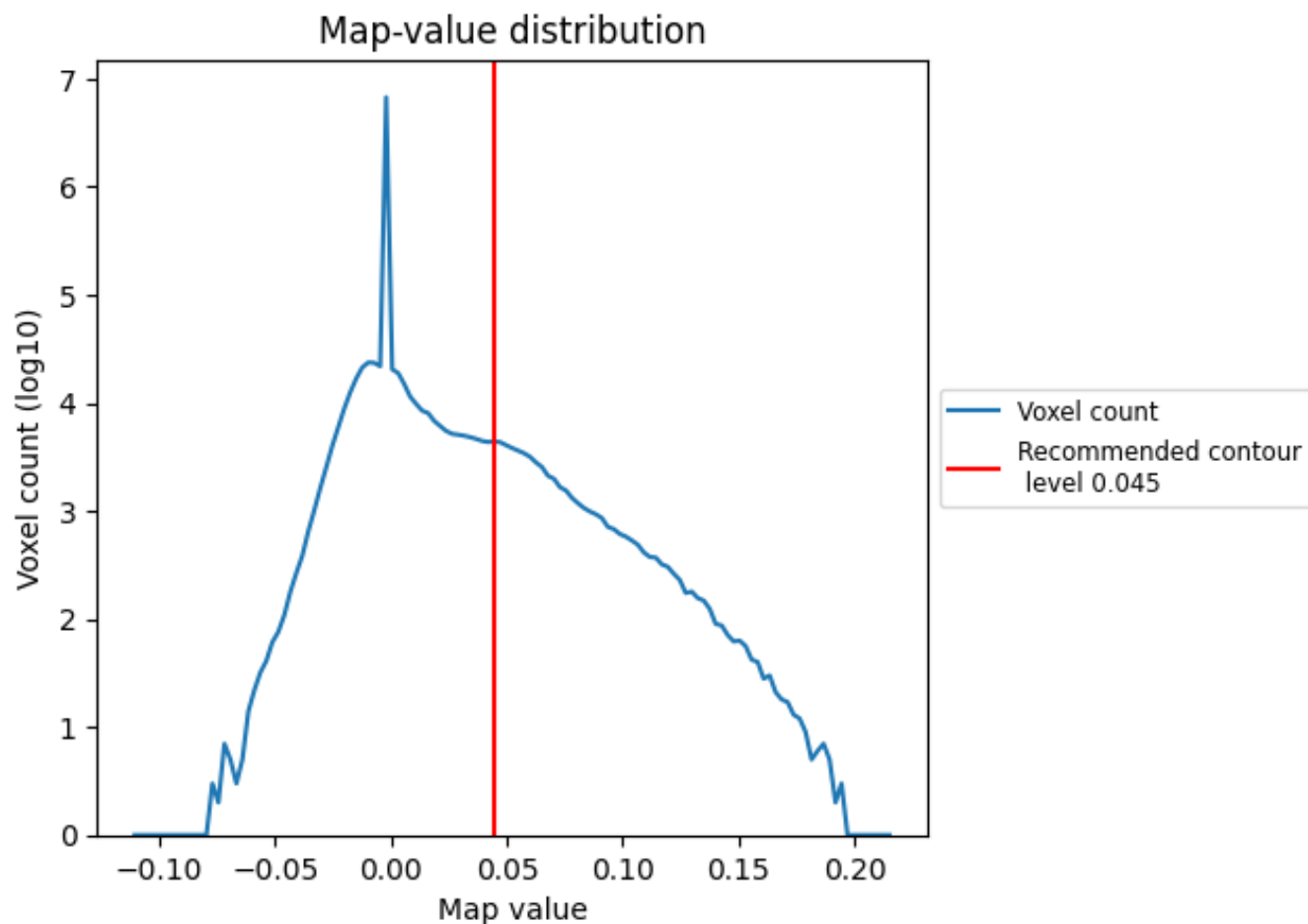
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

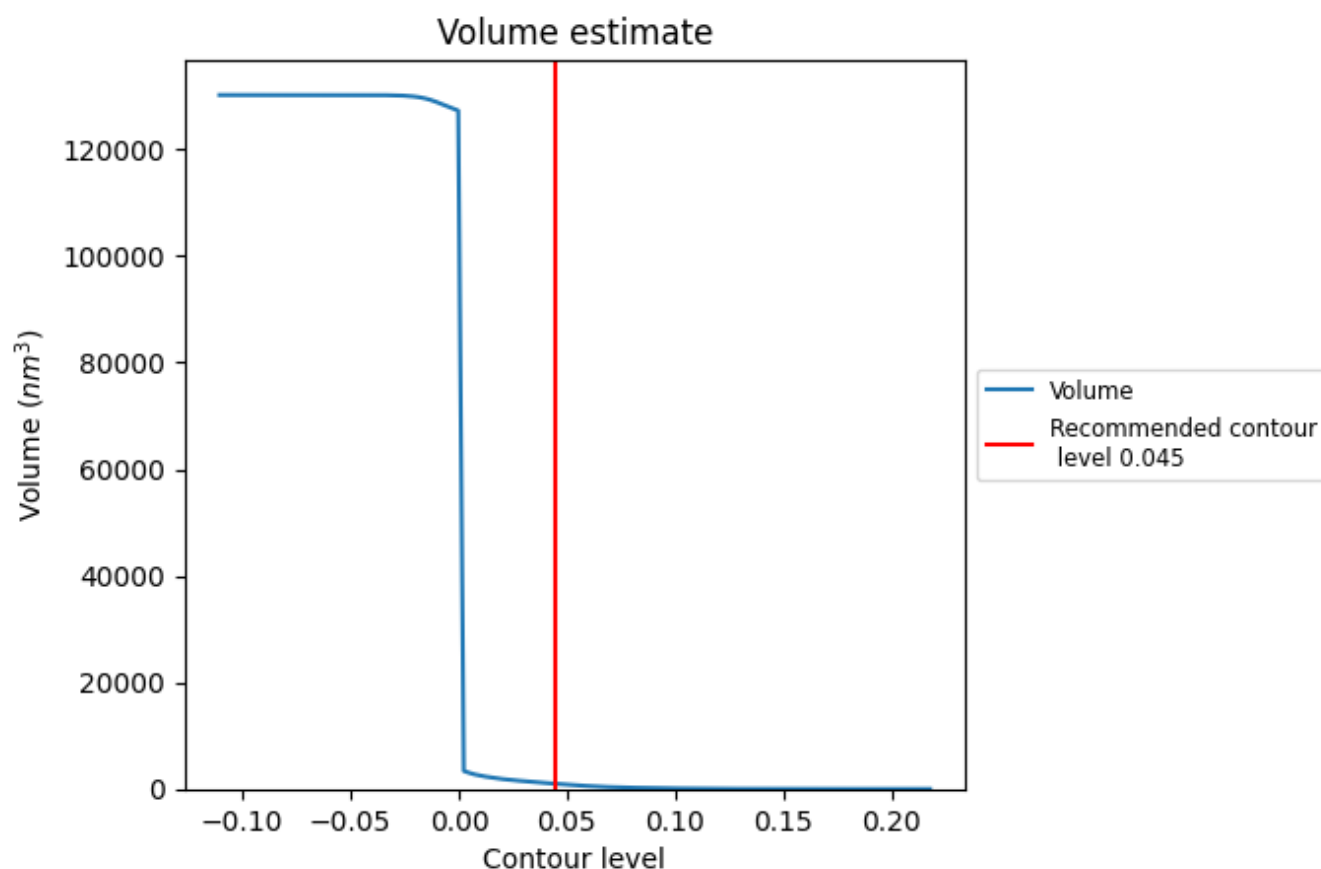
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

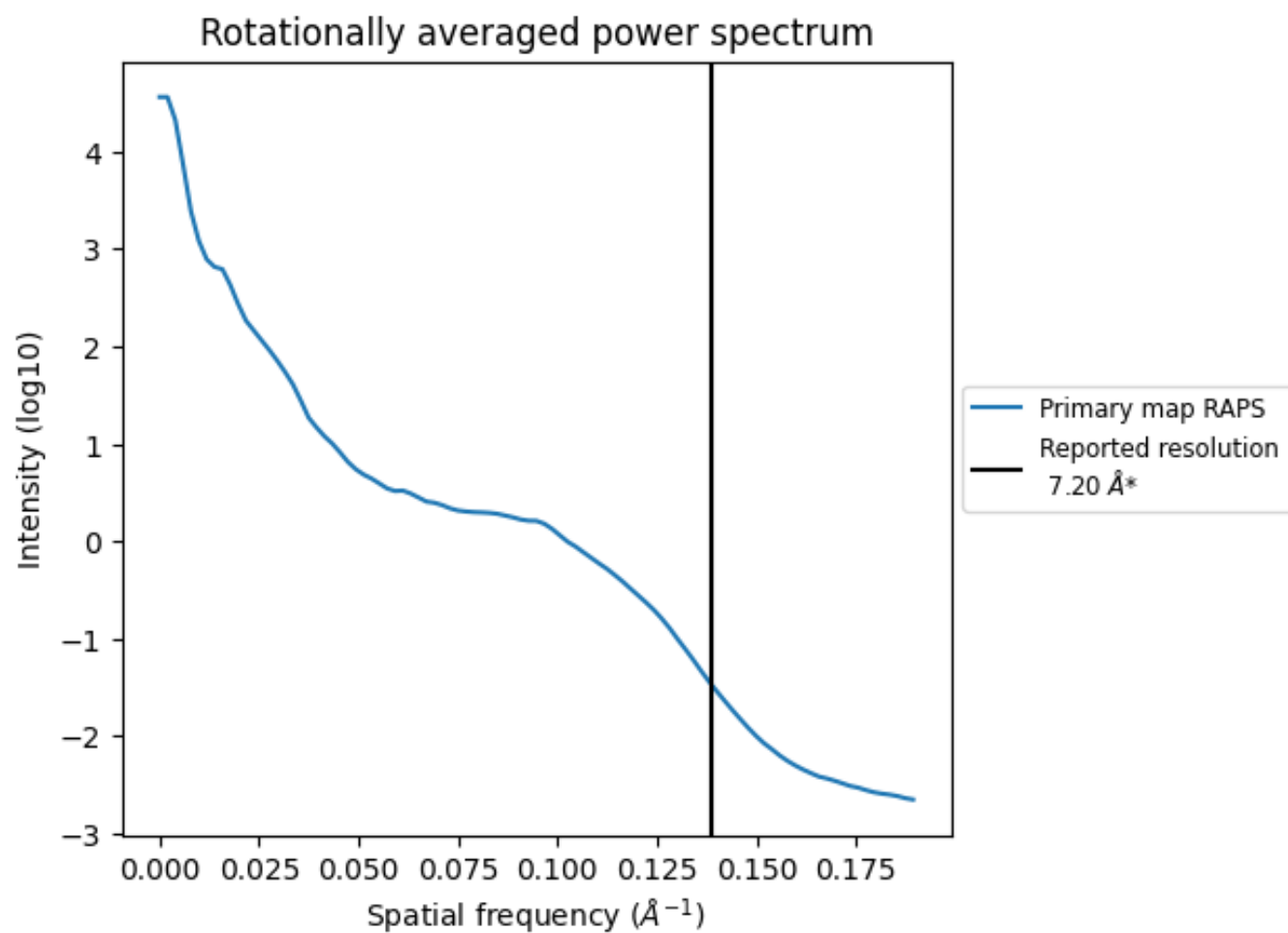
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 965 nm³; this corresponds to an approximate mass of 872 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

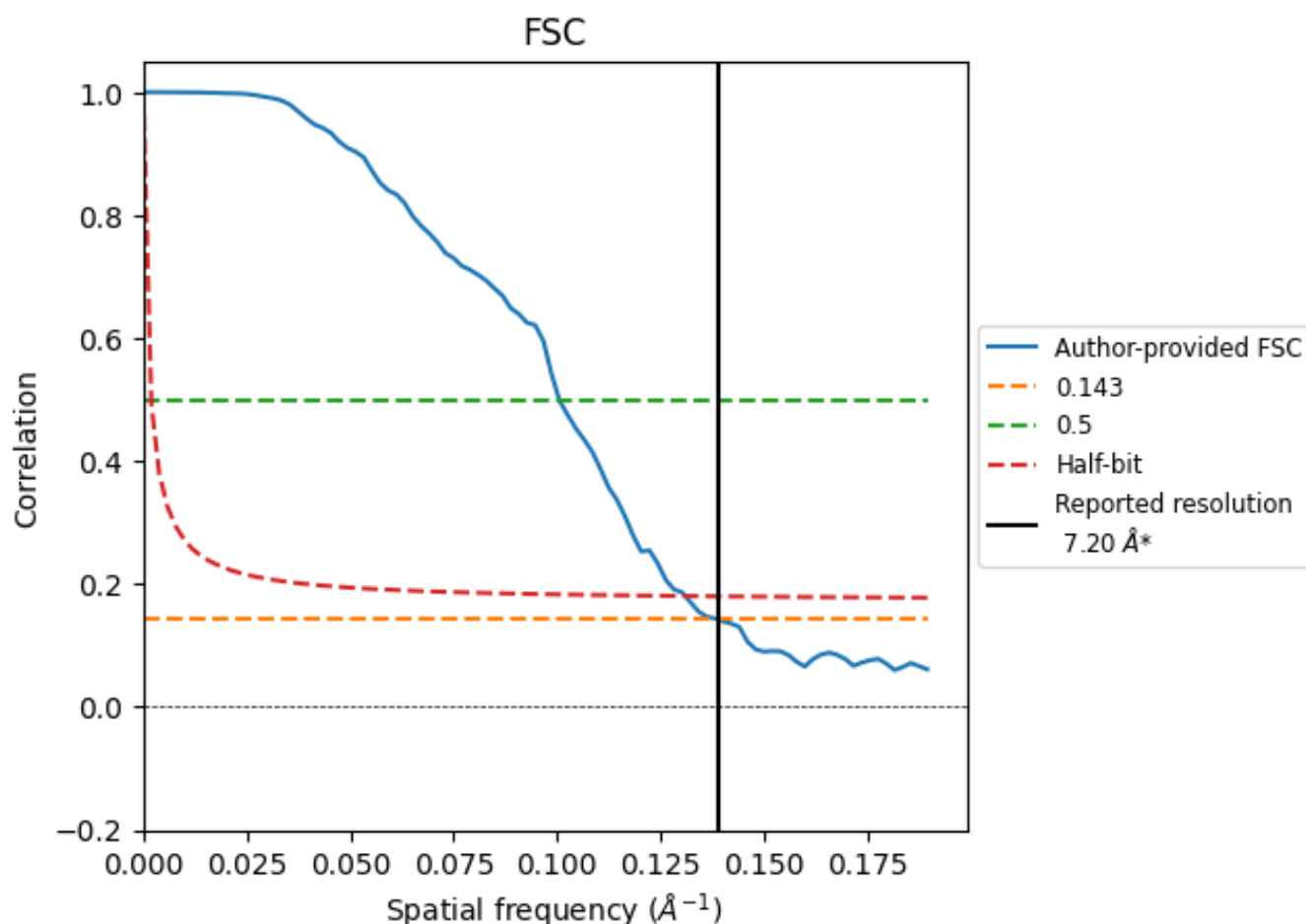


*Reported resolution corresponds to spatial frequency of 0.139 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.139 Å⁻¹

8.2 Resolution estimates [i](#)

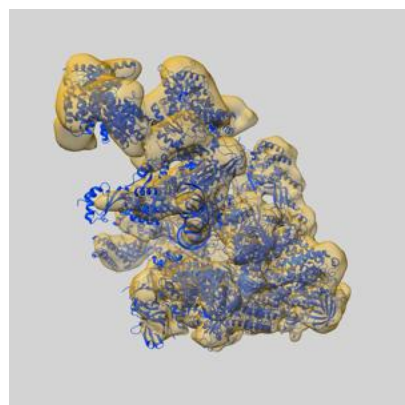
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.20	-	-
Author-provided FSC curve	7.23	9.95	7.64
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

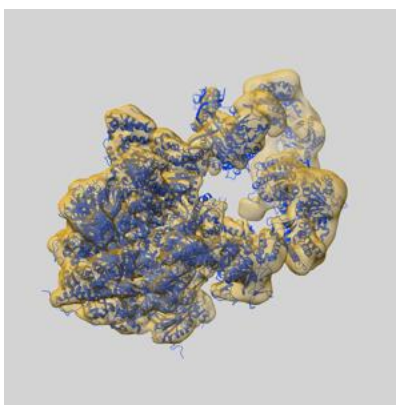
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3307 and PDB model 5IY6. Per-residue inclusion information can be found in section 3 on page 9.

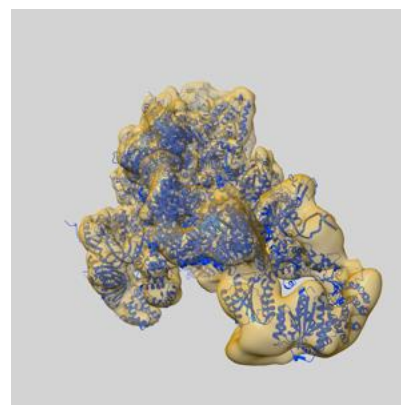
9.1 Map-model overlay [i](#)



X



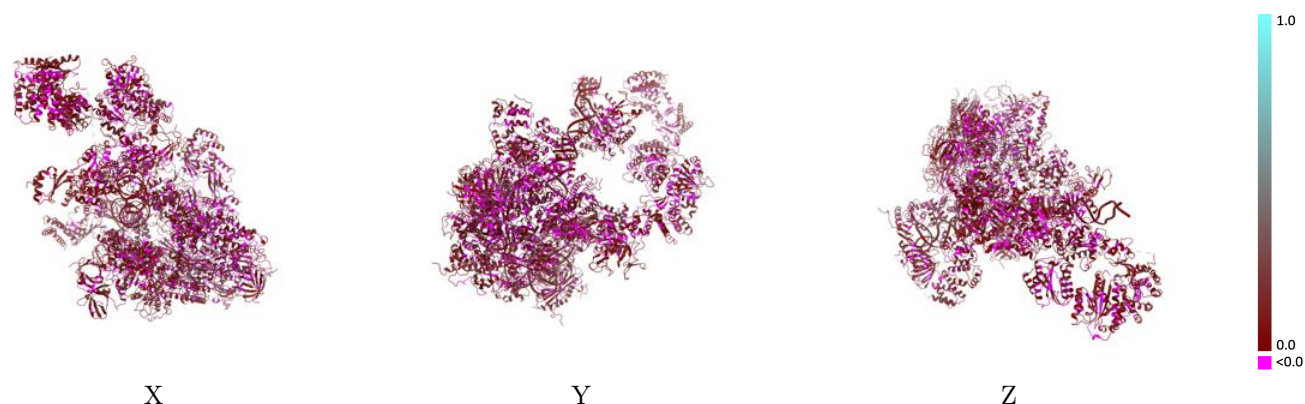
Y



Z

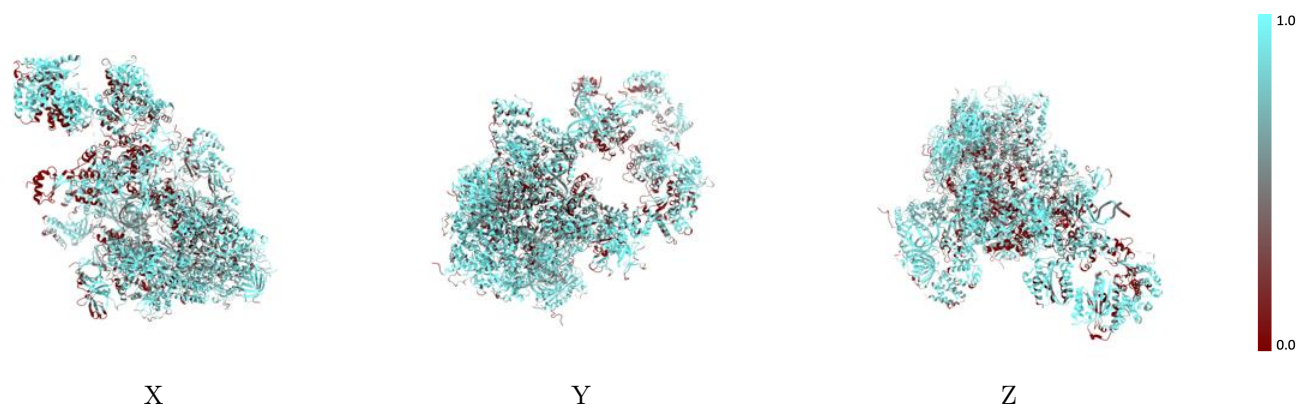
The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



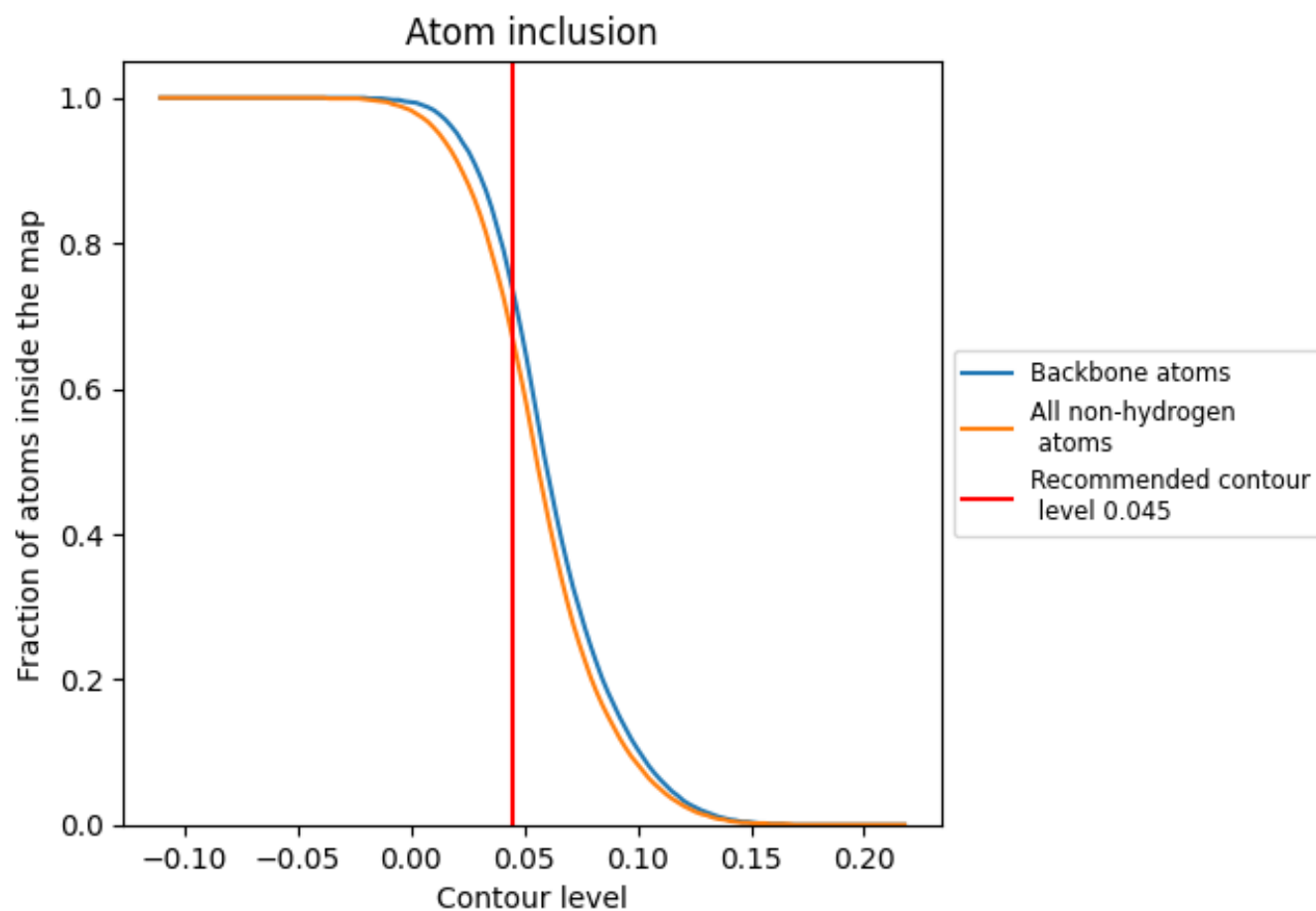
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.045).

9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 67% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6680	 0.0820
0	 0.7470	 0.0510
1	 0.3220	 0.0670
2	 0.5650	 0.0700
3	 0.6770	 0.0530
A	 0.6120	 0.0730
B	 0.6800	 0.0860
C	 0.8020	 0.1000
D	 0.7200	 0.0820
E	 0.6920	 0.0870
F	 0.6720	 0.0400
G	 0.7400	 0.0860
H	 0.7670	 0.0850
I	 0.7150	 0.1000
J	 0.7350	 0.0790
K	 0.7930	 0.1260
L	 0.8520	 0.1250
M	 0.7330	 0.1110
N	 0.7180	 0.1030
O	 0.8380	 0.0950
P	 0.8440	 0.0960
Q	 0.6610	 0.0940
R	 0.6830	 0.0970
S	 0.5540	 0.0750
T	 0.6240	 0.0950
U	 0.6100	 0.0840
V	 0.5560	 0.0630
W	 0.6280	 0.0530
X	 0.7800	 0.1280
Y	 0.7360	 0.1290

