



Full wwPDB EM Validation Report ⓘ

Sep 19, 2026 – 01:56 PM EDT

PDB ID : 9YIX / pdb_00009yix
EMDB ID : EMD-73001
Title : Cryo-EM structure of SeAvs7 MCP EFTu1 tetrameric complex
Authors : Zhang, J.; Feng, L.
Deposited on : 2025-10-02
Resolution : 3.43 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.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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) : 2.50

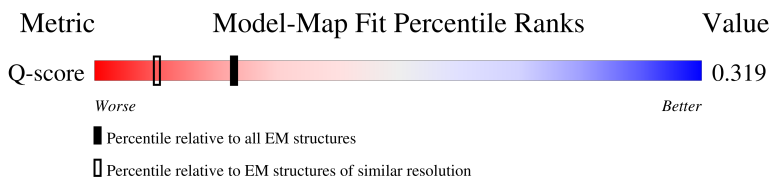
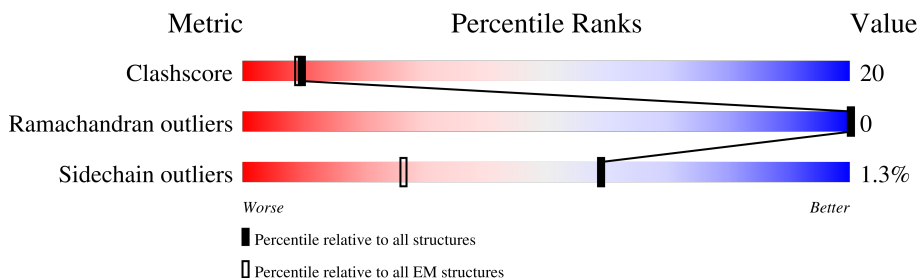
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.43 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.



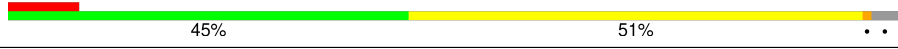
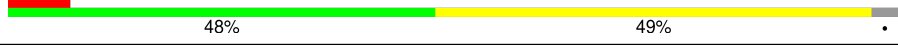
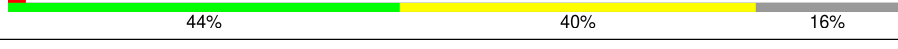
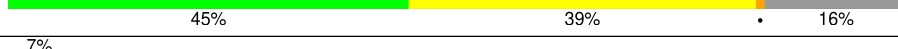
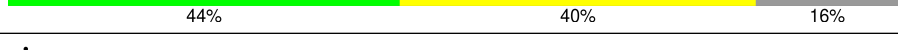
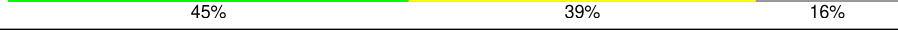
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13927 (2.93 - 3.93)

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	1523	 5% 69% 29% .
1	D	1523	 11% 68% 29% ..
1	G	1523	 34% 65% 33% ..
1	J	1523	 14% 68% 29% ..

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Mol	Chain	Length	Quality of chain
2	C	394	
2	F	394	
2	I	394	
2	L	394	
3	B	314	
3	E	314	
3	H	314	
3	K	314	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 67828 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 AAA family ATPase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1498	Total	C	N	O	S	0	0
			11960	7572	2126	2215	47		
1	G	1498	Total	C	N	O	S	0	0
			11960	7572	2126	2215	47		
1	D	1479	Total	C	N	O	S	0	0
			11824	7494	2097	2187	46		
1	J	1479	Total	C	N	O	S	0	0
			11824	7494	2097	2187	46		

- Molecule 2 is a protein called Elongation factor Tu 1.

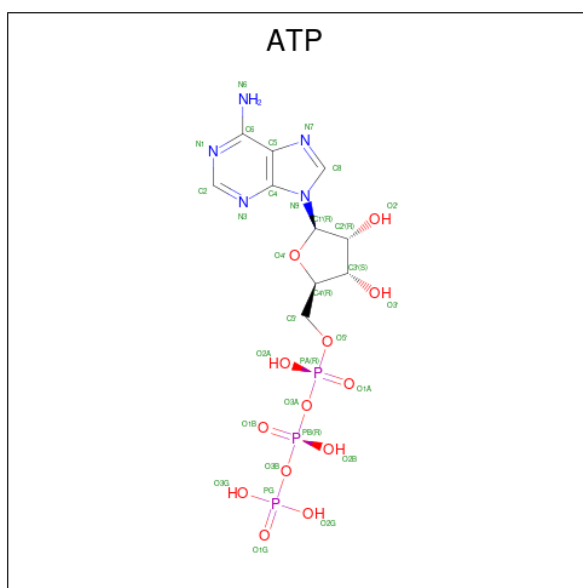
Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	384	Total	C	N	O	S	0	0
			2954	1867	508	566	13		
2	C	384	Total	C	N	O	S	0	0
			2954	1867	508	566	13		
2	F	384	Total	C	N	O	S	0	0
			2954	1867	508	566	13		
2	L	384	Total	C	N	O	S	0	0
			2954	1867	508	566	13		

- Molecule 3 is a protein called Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	265	Total	C	N	O	S	0	0
			2047	1310	343	387	7		
3	B	265	Total	C	N	O	S	0	0
			2047	1310	343	387	7		
3	E	265	Total	C	N	O	S	0	0
			2047	1310	343	387	7		
3	K	265	Total	C	N	O	S	0	0
			2047	1310	343	387	7		

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$)

(labeled as "Ligand of Interest" by depositor).

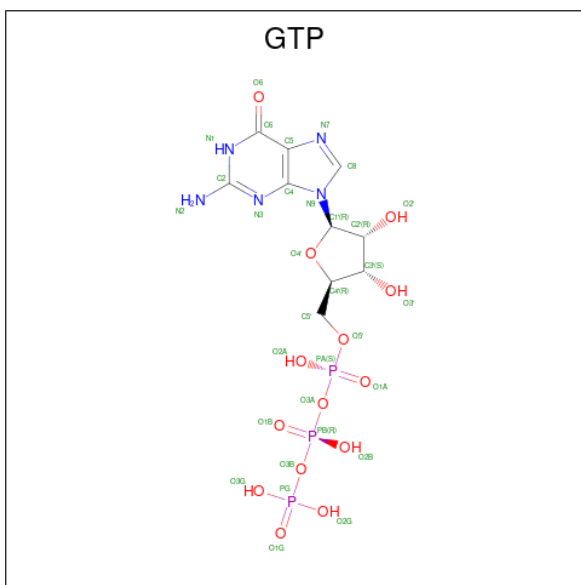


Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	G	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	D	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	J	1	Total	C	N	O	P	0
			31	10	5	13	3	

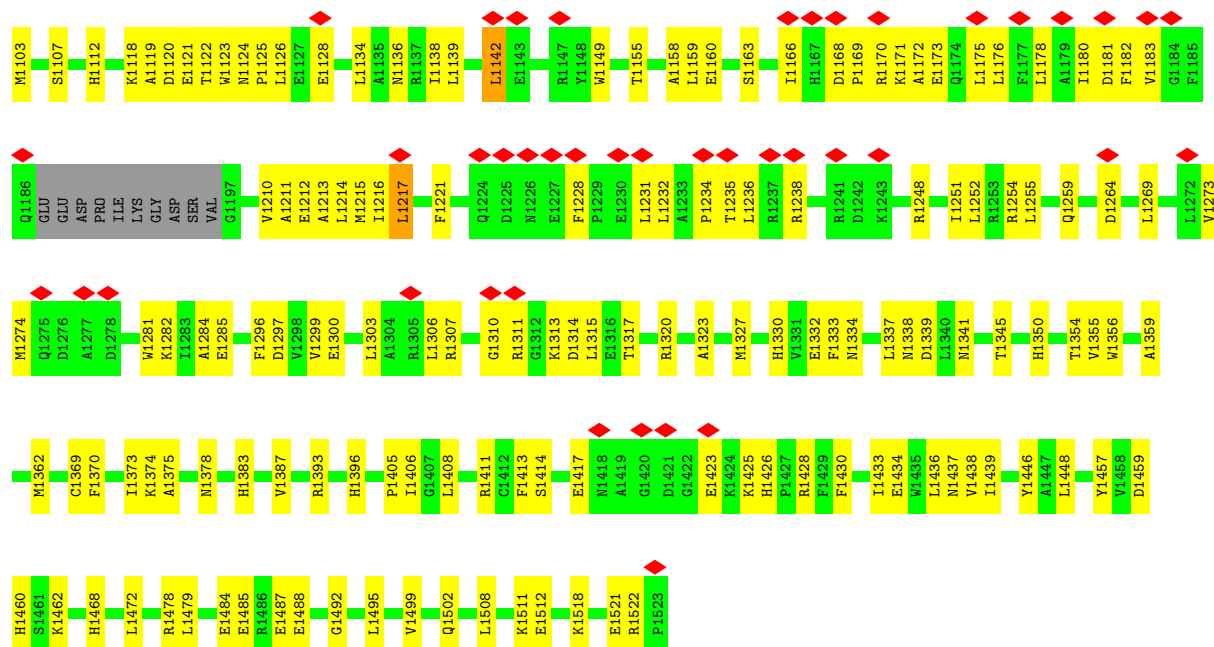
- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
5	A	1	Total	Mg	0
			1	1	
5	G	1	Total	Mg	0
			1	1	
5	D	1	Total	Mg	0
			1	1	
5	J	1	Total	Mg	0
			1	1	

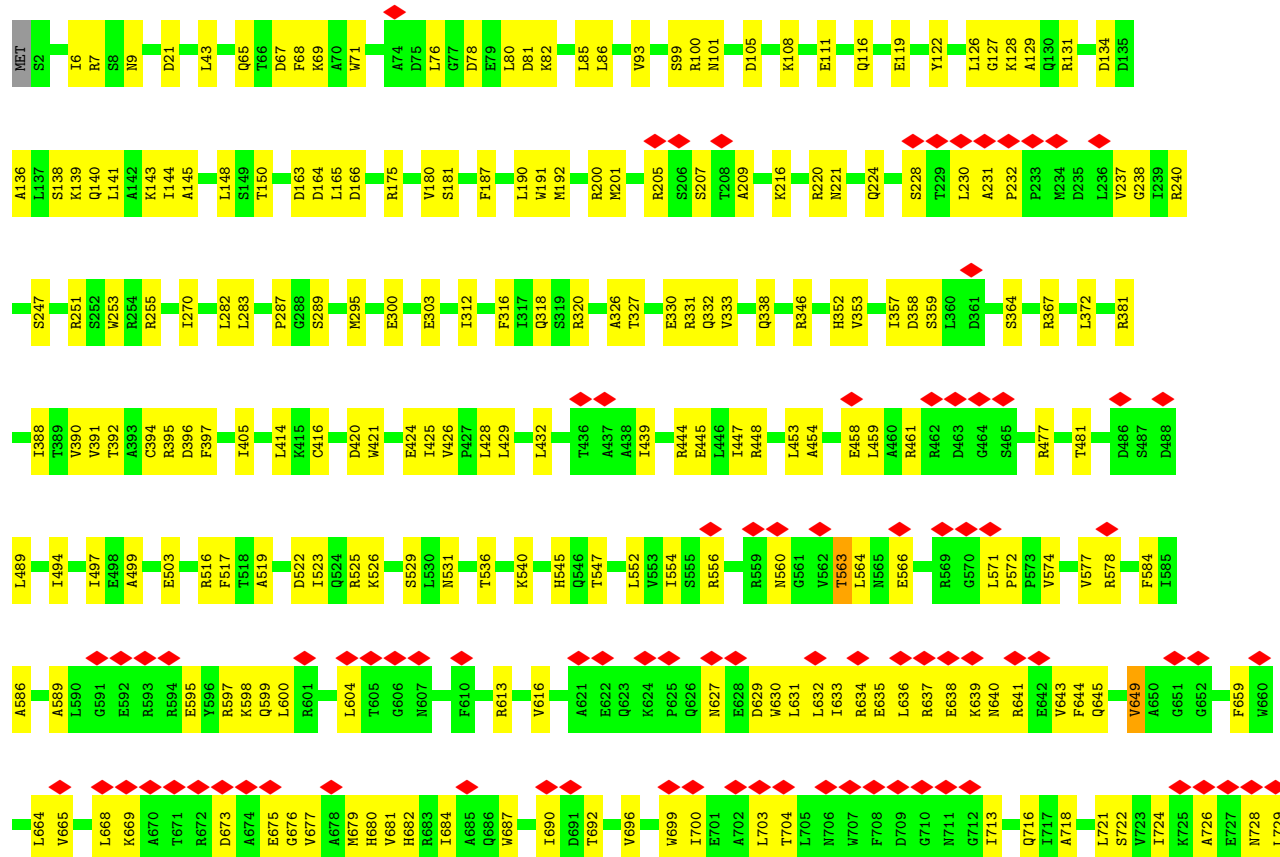
- Molecule 6 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃) (labeled as "Ligand of Interest" by depositor).

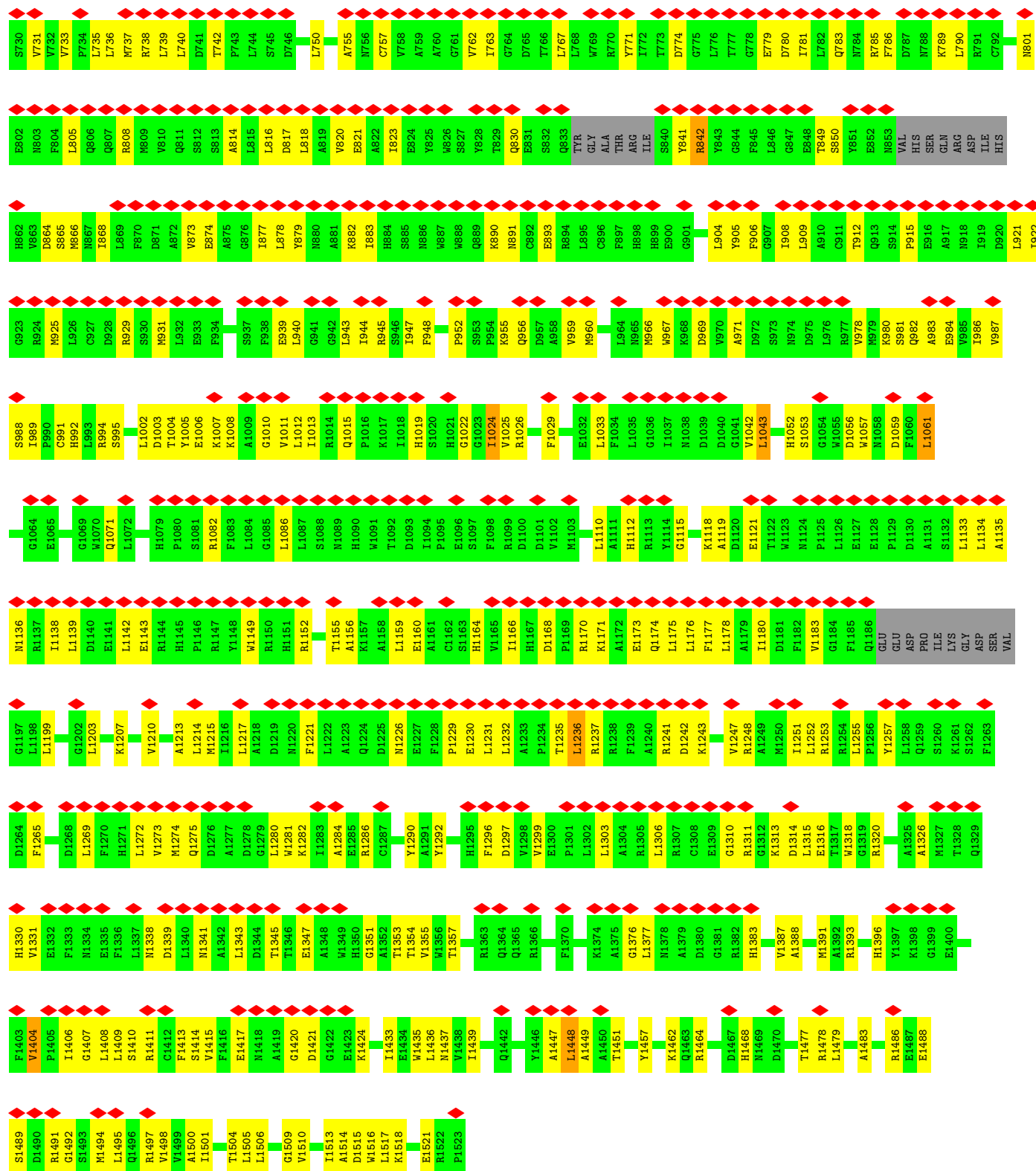


Mol	Chain	Residues	Atoms					AltConf
6	I	1	Total 32	C 10	N 5	O 14	P 3	0
6	C	1	Total 32	C 10	N 5	O 14	P 3	0
6	F	1	Total 32	C 10	N 5	O 14	P 3	0
6	L	1	Total 32	C 10	N 5	O 14	P 3	0



• Molecule 1: AAA family ATPase

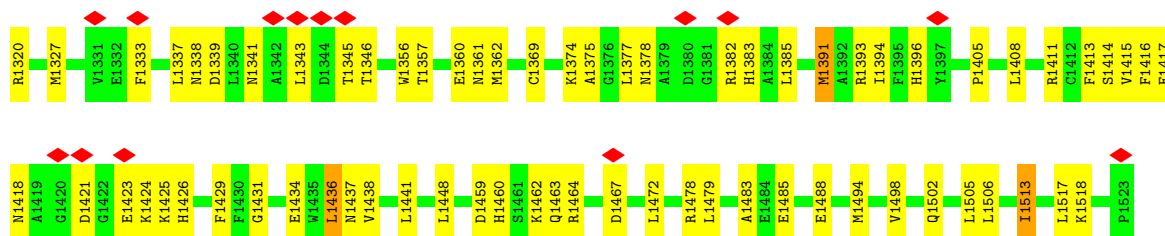




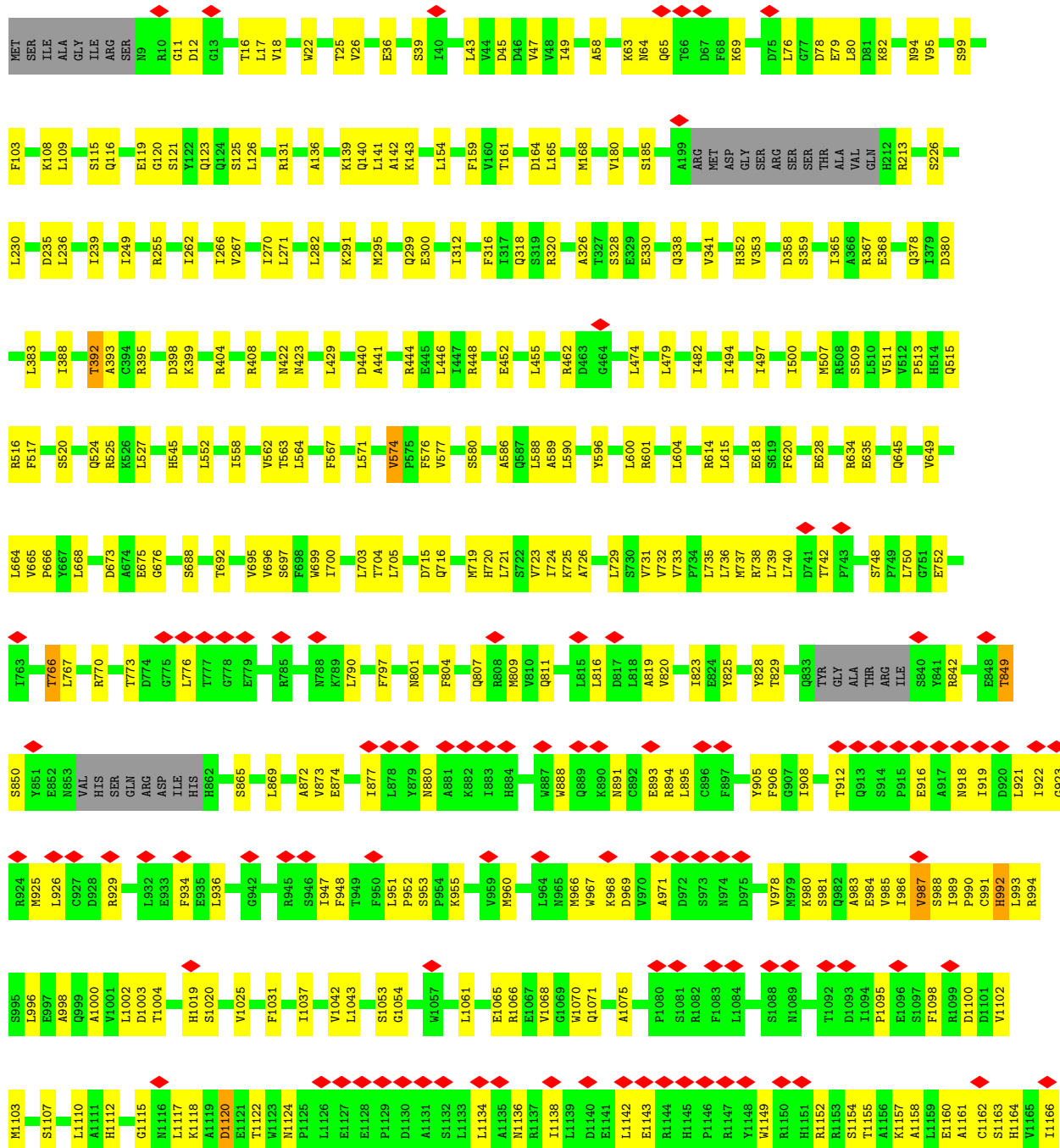
• Molecule 1: AAA family ATPase

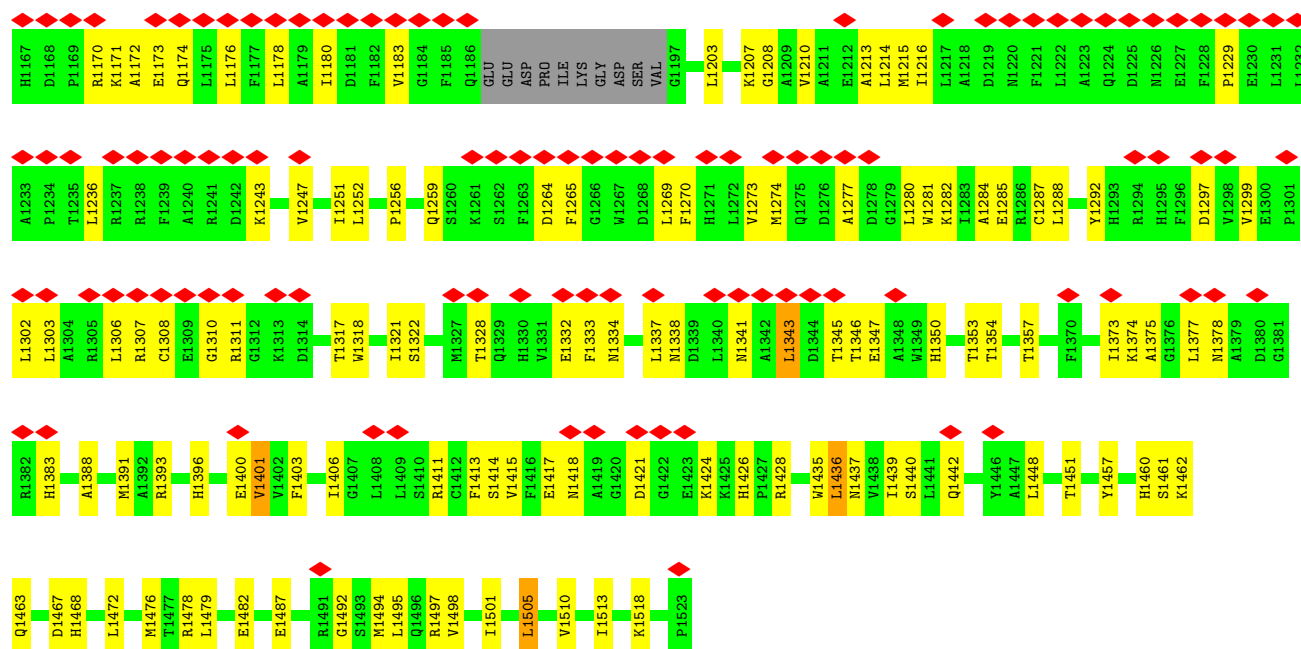


R1238	P1169	Q1071	Q982	P915	Q833	T742	V665	Q537	L347	K193	A88	MET
R1241	R1170	R1078	A983	E916	TTR	P743	P666	Q537	S359	L194	E89	SER
D1242	K1171	H1079	E984	A917	GLY	S748	P667	H545	S360	D195	N90	ILE
K1243	A1172	P1080	E985	N918	ALA	P748	L668	Q546	L361	Q196	P91	ALA
H1244	E1173	S1081	I886	I919	THR	G748	K669	T547	S364	G198	V93	GLY
M1250	Q1174	R1082	I887	D920	ILE	G751	A670	L548	S365	A199	F97	ILE
L1251	L1175	F1083	S988	L921	S840	L752	T671	L552	A365	ARG	R100	ARG
L1252	F1177	L1084	E997	R923	G844	N756	R672	V562	R367	ASP	R100	SER
R1253	A1178	M1103	A998	R924	T849	C757	D673	T563	L372	GLY	K108	N9
R1254	A1179	S1104	E999	N925	S850	A678	V677	E566	Q373	SER	K109	G11
S1260	I1180	G1105	E997	L926	N853	V759	M679	E566	Y374	ARG	K110	G12
K1261	V1106	V1107	C927	R928	VAL	V762	R683	R569	Q378	SER	Q116	G13
D1264	F1182	T1108	D928	R929	HIS	I763	R683	L571	R381	ALA	Q116	T16
F1265	V1183	L1117	D928	R929	SER	G764	Q686	V577	Y374	VAL	E119	F20
L1269	G1184	L1117	D928	R929	GLN	T766	S688	E592	I385	GLN	G120	D21
L1272	F1185	D1120	E933	F934	ASP	T773	T692	E592	I388	L214	Y122	V22
V1273	Q1186	E1121	F934	E935	ILE	D774	A693	R594	V391	R213	Q123	V26
M1274	GLU	M1124	E1006	L936	HIS	G775	G694	R597	R403	H217	K128	D31
Q1275	ASP	P1125	K1007	E939	S865	L776	V696	R597	R403	D218	A136	S39
D1276	ILE	L1126	V1011	G942	F870	T777	S697	L600	D442	I222	S138	L43
A1277	LVS	E1127	L1012	L943	D871	G778	F698	R601	T443	Q225	K139	V44
D1278	GLY	P1129	K1017	I944	A872	E779	G699	T602	R444	Q235	Q140	D45
W1281	SER	D1130	I945	R945	H873	D780	I700	V603	E445	P233	K143	I49
K1282	VAL	A1131	S946	S946	E874	I781	T704	L604	R448	M234	G50	G50
L1283	G1197	S1132	H1021	F948	L878	L790	L705	A617	L459	D235	I144	K51
E1284	L1198	L1134	I1024	T949	Y879	E796	M706	D629	R462	L236	A145	Q60
E1285	L1199	A1135	V1025	F950	N880	F797	F708	L631	D463	G238	P146	K63
E1286	L1203	N1136	R1026	L951	H884	D709	D709	R634	G464	I239	S147	N64
G1287	V1210	R1137	F1029	K955	K882	F804	A714	E635	S465	R240	F151	Q65
L1288	A1211	L1138	S1030	Q956	I883	Q807	D715	R639	F466	S245	L154	T66
Y1289	E1212	L1139	F1031	K956	S885	R808	D716	N640	N467	S252	S155	D67
Y1290	I1216	D1140	D1040	V959	S886	A718	I717	R641	L474	K291	R156	F68
D1297	D1219	L1142	L1043	N960	N887	L721	A718	Q645	L479	D164	D164	K69
V1298	N1220	E1143	K1044	A961	N890	A726	V646	V646	L484	M295	L165	A70
E1300	F1221	R1144	L1045	S982	S812	E727	V647	V647	L484	Q305	M168	I72
L1303	L1222	R1147	H1048	P963	S813	N728	L729	Y648	I494	I312	A74	I73
A1304	A1223	Y1148	W1057	N966	A814	L729	V732	A850	P513	Q318	D75	A74
R1305	Q1224	W1149	N1058	K968	L815	V732	V732	G651	R516	Q319	L172	D75
L1306	N1225	R1150	D1059	P969	D817	G652	G652	S653	T518	R320	L176	G77
R1307	N1226	F1060	F1060	V970	L818	L735	L735	W656	F517	S319	L176	D78
C1308	E1227	L1061	V1062	A971	E821	L736	L736	H657	D184	S185	D184	E79
E1309	F1228	T1155	L1062	D972	N908	M737	M737	I661	V341	F342	S185	K82
G1310	P1229	L1159	R1066	S973	L909	Q913	Q913	D741	V341	F342	S185	K82
R1311	E1230	C1162	W1070	N974	G311	T912	T912	D741	V341	F342	S185	K82
D1314	L1231	S1163	D975	S973	C311	Q913	Q913	D741	V341	F342	S185	K82
L1315	L1232	L1166	L976	S973	G311	Q913	Q913	D741	V341	F342	S185	K82
F1316	A1233	T1166	L976	S973	G311	Q913	Q913	D741	V341	F342	S185	K82
T1317	P1234	H1167	N978	S973	G311	Q913	Q913	D741	V341	F342	S185	K82
	L1236	L1167	N978	S973	G311	Q913	Q913	D741	V341	F342	S185	K82
	R1237	D1168	S981	S981	S914	S914	S914	S914	S914	S914	S914	S914

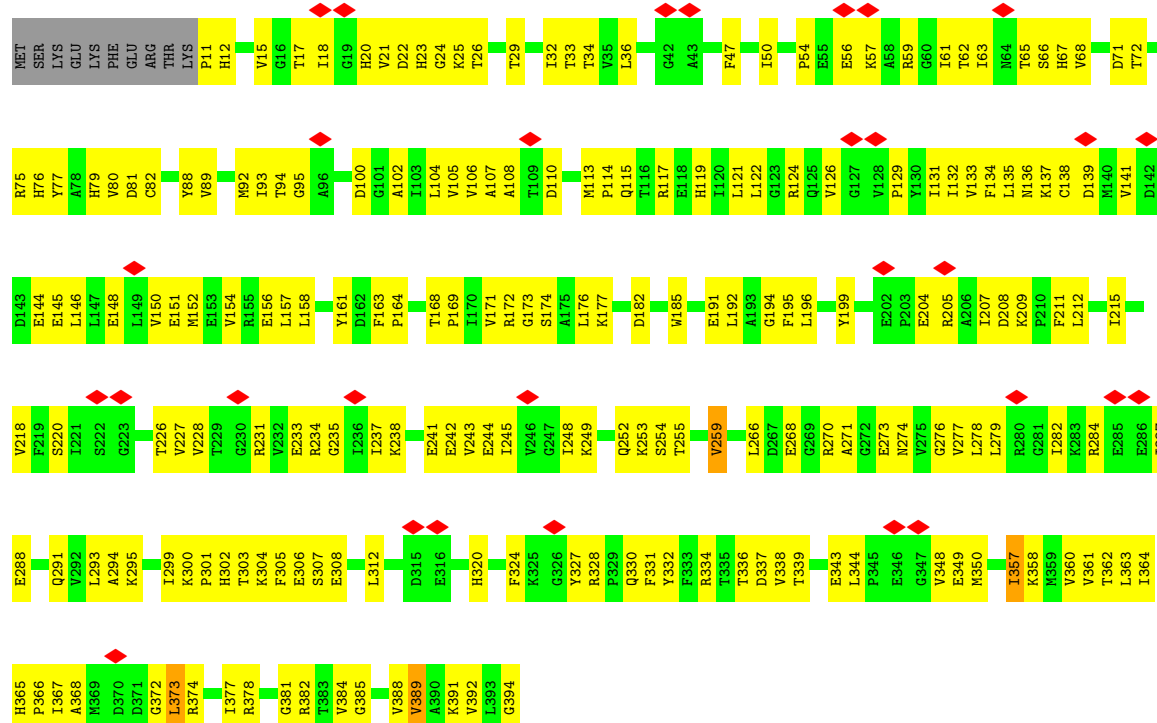
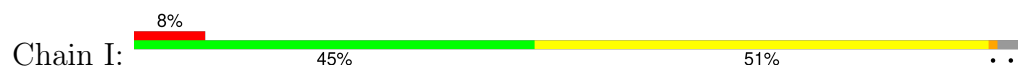


• Molecule 1: AAA family ATPase



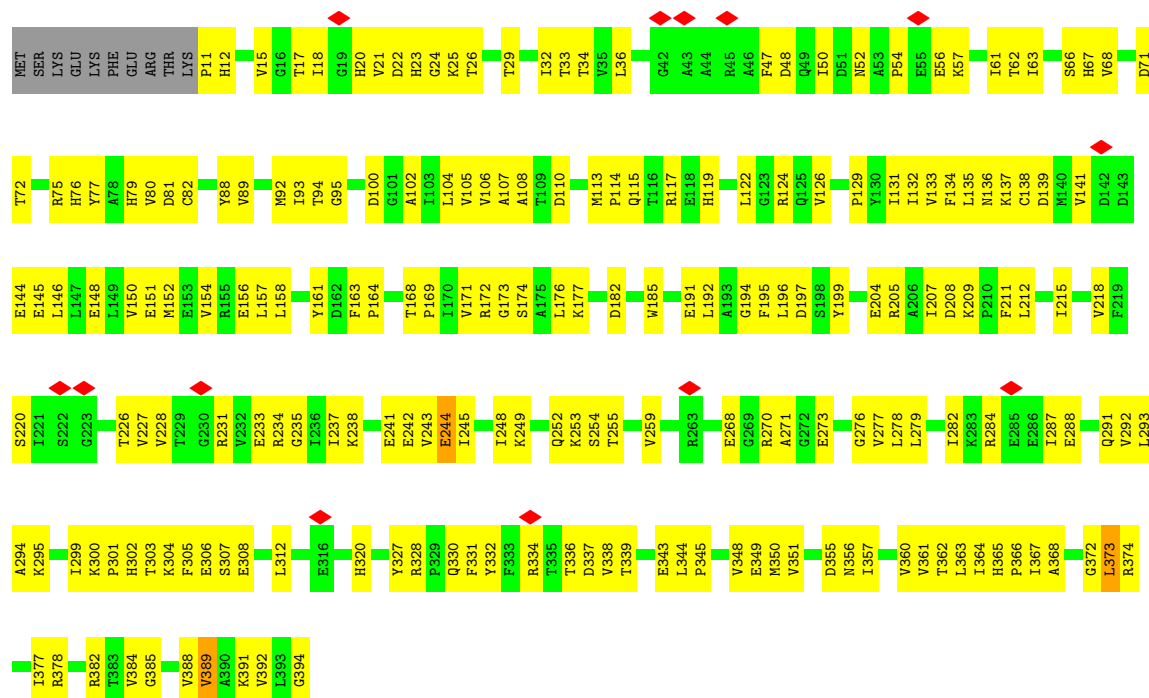


• Molecule 2: Elongation factor Tu 1

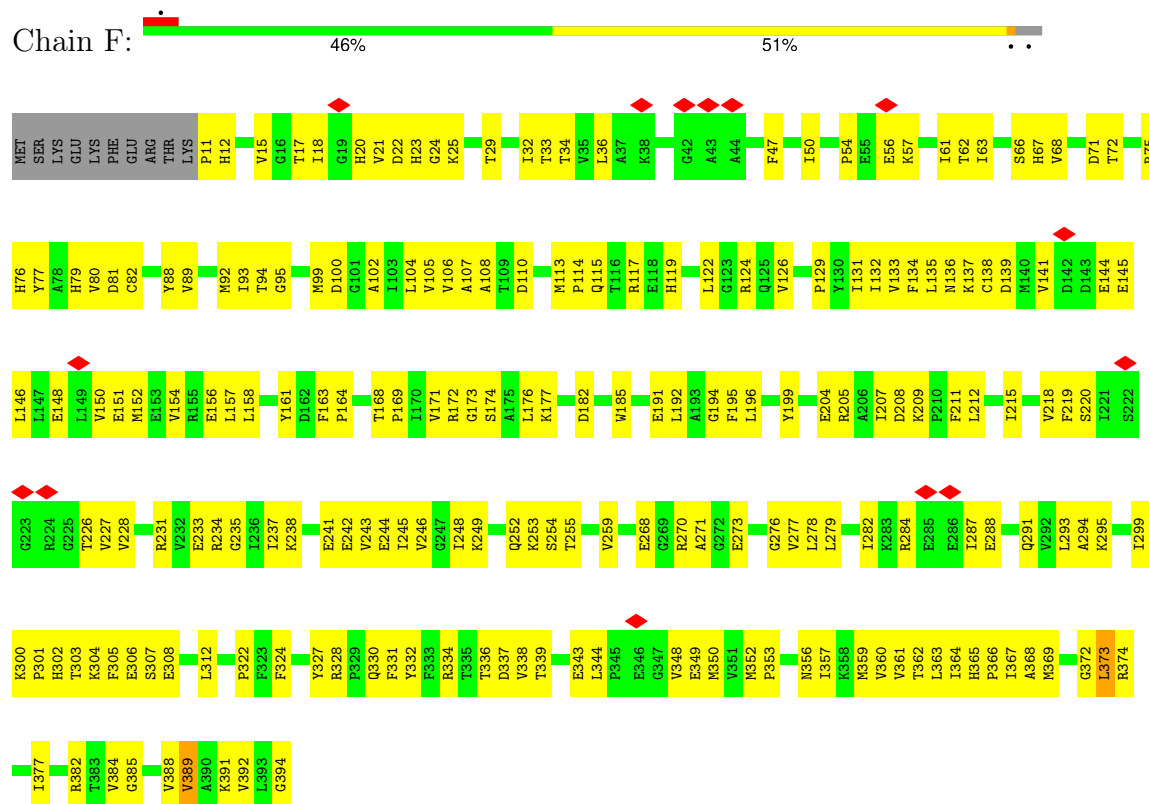


• Molecule 2: Elongation factor Tu 1



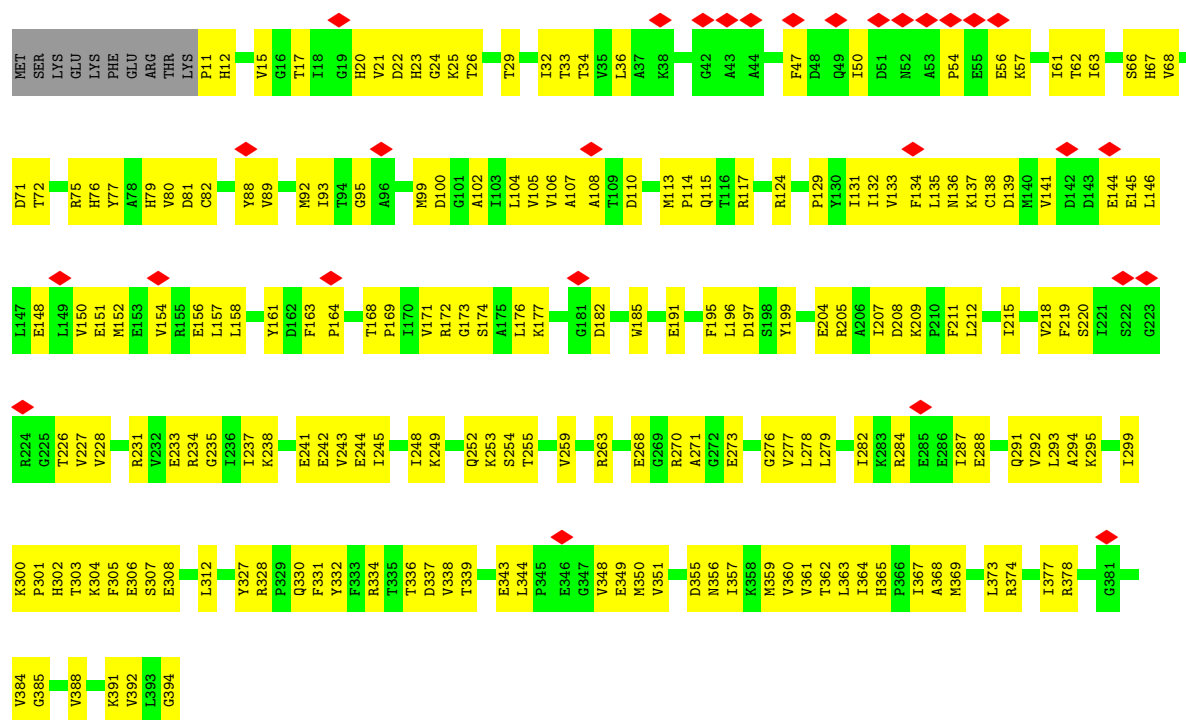


• Molecule 2: Elongation factor Tu 1

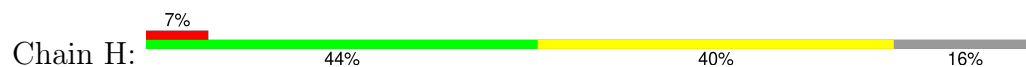


• Molecule 2: Elongation factor Tu 1





• Molecule 3: Major capsid protein



• Molecule 3: Major capsid protein





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	78090	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	86.305	Depositor
Minimum map value	-49.602	Depositor
Average map value	0.027	Depositor
Map value standard deviation	1.283	Depositor
Recommended contour level	7	Depositor
Map size ($\text{\AA}$)	456.0, 456.0, 456.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.95, 0.95, 0.95	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.32	0/12206	0.47	0/16537
1	D	0.29	0/12069	0.46	0/16353
1	G	0.27	0/12206	0.46	0/16537
1	J	0.28	0/12069	0.45	0/16353
2	C	0.32	0/3009	0.77	0/4074
2	F	0.33	0/3009	0.76	0/4074
2	I	0.32	0/3009	0.77	0/4074
2	L	0.32	0/3009	0.77	0/4074
3	B	0.45	0/2097	0.73	0/2860
3	E	0.45	0/2097	0.73	0/2860
3	H	0.45	0/2097	0.72	0/2860
3	K	0.45	0/2097	0.72	0/2860
All	All	0.32	0/68974	0.56	0/93516

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	11960	0	11843	334	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	11824	0	11703	350	0
1	G	11960	0	11844	441	0
1	J	11824	0	11703	329	0
2	C	2954	0	2963	242	0
2	F	2954	0	2963	219	0
2	I	2954	0	2963	217	0
2	L	2954	0	2963	215	0
3	B	2047	0	2015	99	0
3	E	2047	0	2015	109	0
3	H	2047	0	2015	122	0
3	K	2047	0	2015	108	0
4	A	31	0	12	0	0
4	D	31	0	12	1	0
4	G	31	0	12	0	0
4	J	31	0	12	4	0
5	A	1	0	0	0	0
5	D	1	0	0	0	0
5	G	1	0	0	0	0
5	J	1	0	0	0	0
6	C	32	0	12	4	0
6	F	32	0	12	4	0
6	I	32	0	12	4	0
6	L	32	0	12	4	0
All	All	67828	0	67101	2652	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 20.

All (2652) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:344:LEU:CD1	2:C:345:PRO:HD3	1.46	1.46
1:A:192:MET:HE1	1:G:187:PHE:CE1	1.70	1.25
2:F:344:LEU:CD2	2:F:359:MET:HG2	1.67	1.22
2:C:344:LEU:HG	2:C:345:PRO:CD	1.67	1.21
3:H:273:THR:HA	3:H:291:SER:OG	1.41	1.20
3:E:273:THR:HA	3:E:291:SER:OG	1.41	1.19
3:B:273:THR:HA	3:B:291:SER:OG	1.41	1.18
3:K:273:THR:HA	3:K:291:SER:OG	1.41	1.17
2:F:133:VAL:HG11	2:F:154:VAL:HG11	1.18	1.17
1:G:180:VAL:CG1	1:G:228:SER:HB3	1.73	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:133:VAL:HG11	2:L:154:VAL:CG1	1.76	1.16
2:C:133:VAL:HG11	2:C:154:VAL:CG1	1.76	1.15
1:G:270:ILE:HD11	1:G:283:LEU:HD11	1.23	1.15
2:C:344:LEU:HD11	2:C:357:ILE:HG21	1.18	1.15
2:I:133:VAL:HG11	2:I:154:VAL:CG1	1.76	1.14
2:F:133:VAL:HG11	2:F:154:VAL:CG1	1.76	1.14
2:C:133:VAL:HG11	2:C:154:VAL:HG11	1.18	1.13
1:G:893:GLU:OE1	1:G:921:LEU:HD13	1.46	1.12
2:L:133:VAL:HG11	2:L:154:VAL:HG11	1.18	1.11
1:G:1019:HIS:ND1	3:H:111:LEU:HD12	1.64	1.11
2:I:133:VAL:HG11	2:I:154:VAL:HG11	1.18	1.10
1:G:180:VAL:CG1	1:G:228:SER:CB	2.31	1.08
1:G:180:VAL:HG13	1:G:228:SER:CB	1.84	1.07
2:C:344:LEU:HD12	2:C:345:PRO:HD3	1.09	1.06
1:G:180:VAL:HG13	1:G:228:SER:HB3	1.06	1.05
1:D:22:TRP:HB3	1:D:49:ILE:HD11	1.34	1.04
2:C:244:GLU:HB2	2:C:294:ALA:O	1.58	1.02
2:C:344:LEU:CD1	2:C:345:PRO:CD	2.38	1.02
2:C:344:LEU:CD1	2:C:357:ILE:HG21	1.90	1.02
2:C:344:LEU:HD11	2:C:357:ILE:CG2	1.89	1.02
2:C:344:LEU:HG	2:C:345:PRO:HD2	1.38	1.01
1:G:980:LYS:HD3	3:H:282:ASP:OD2	1.59	1.01
1:G:270:ILE:CD1	1:G:283:LEU:HD11	1.90	1.00
1:G:893:GLU:CD	1:G:921:LEU:HD13	1.87	0.99
2:C:344:LEU:CG	2:C:345:PRO:HD3	1.91	0.99
2:F:356:ASN:O	2:F:357:ILE:HD13	1.64	0.97
1:A:192:MET:HE1	1:G:187:PHE:HE1	1.04	0.97
2:C:344:LEU:CG	2:C:345:PRO:CD	2.42	0.96
1:G:283:LEU:HD23	1:G:414:LEU:HB2	1.42	0.96
3:E:217:LEU:HD22	3:E:222:THR:O	1.65	0.95
3:K:217:LEU:HD22	3:K:222:THR:O	1.65	0.95
3:H:217:LEU:HD22	3:H:222:THR:O	1.66	0.95
1:G:283:LEU:CD2	1:G:414:LEU:HB2	1.97	0.94
3:B:217:LEU:HD22	3:B:222:THR:O	1.65	0.94
2:I:133:VAL:CG1	2:I:154:VAL:HG11	1.98	0.94
2:F:133:VAL:CG1	2:F:154:VAL:HG11	1.98	0.94
2:L:133:VAL:CG1	2:L:154:VAL:HG11	1.98	0.94
2:L:292:VAL:HG11	2:L:334:ARG:NH2	1.84	0.93
2:F:344:LEU:HD23	2:F:359:MET:HG2	1.52	0.92
1:G:1057:TRP:H	3:H:279:GLN:HE22	1.17	0.92
2:C:133:VAL:CG1	2:C:154:VAL:HG11	1.98	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:211:PHE:HA	2:I:235:GLY:HA3	1.53	0.91
2:C:292:VAL:HG11	2:C:334:ARG:NH2	1.86	0.90
2:C:211:PHE:HA	2:C:235:GLY:HA3	1.53	0.90
2:L:211:PHE:HA	2:L:235:GLY:HA3	1.53	0.89
2:F:211:PHE:HA	2:F:235:GLY:HA3	1.53	0.89
2:L:334:ARG:NH2	2:L:368:ALA:HB3	1.88	0.89
1:G:1139:LEU:HD12	1:G:1171:LYS:HE3	1.56	0.88
1:D:305:ARG:HD3	1:D:312:ILE:HD12	1.53	0.88
2:L:351:VAL:CG1	2:L:357:ILE:CD1	2.52	0.88
2:C:344:LEU:CD1	2:C:357:ILE:CG2	2.50	0.87
2:I:104:LEU:HB2	2:I:131:ILE:HD11	1.57	0.87
2:L:334:ARG:HH22	2:L:368:ALA:HB3	1.39	0.87
2:L:104:LEU:HB2	2:L:131:ILE:HD11	1.57	0.86
2:C:351:VAL:CG1	2:C:357:ILE:CD1	2.52	0.86
2:F:104:LEU:HB2	2:F:131:ILE:HD11	1.57	0.85
2:I:66:SER:HB2	2:I:81:ASP:OD1	1.76	0.85
2:C:104:LEU:HB2	2:C:131:ILE:HD11	1.57	0.85
3:K:217:LEU:HA	3:K:224:SER:HA	1.59	0.85
1:G:76:LEU:HB3	1:G:80:LEU:HG	1.57	0.85
2:I:349:GLU:HG2	2:I:350:MET:HG2	1.59	0.85
3:B:217:LEU:HA	3:B:224:SER:HA	1.58	0.84
2:F:89:VAL:CG1	2:F:93:ILE:HD12	2.07	0.84
2:I:89:VAL:CG1	2:I:93:ILE:HD12	2.07	0.84
3:H:217:LEU:HA	3:H:224:SER:HA	1.58	0.84
2:L:89:VAL:CG1	2:L:93:ILE:HD12	2.07	0.84
2:C:89:VAL:CG1	2:C:93:ILE:HD12	2.07	0.83
2:C:351:VAL:CG1	2:C:357:ILE:HD13	2.08	0.83
2:F:344:LEU:HD22	2:F:359:MET:HG2	1.57	0.83
3:E:217:LEU:HA	3:E:224:SER:HA	1.58	0.83
2:C:349:GLU:HG2	2:C:350:MET:HG2	1.59	0.83
2:L:349:GLU:HG2	2:L:350:MET:HG2	1.59	0.83
2:L:351:VAL:CG1	2:L:357:ILE:HD13	2.08	0.83
1:G:220:ARG:HG2	1:G:230:LEU:CD2	2.07	0.83
3:K:57:VAL:HG13	3:K:267:ILE:O	1.79	0.83
2:F:349:GLU:HG2	2:F:350:MET:HG2	1.59	0.82
2:L:20:HIS:HB3	2:L:23:HIS:HD2	1.44	0.82
2:F:356:ASN:O	2:F:357:ILE:CD1	2.27	0.82
3:H:57:VAL:HG13	3:H:267:ILE:O	1.79	0.82
1:D:1357:THR:HA	1:D:1362:MET:HE3	1.62	0.82
2:F:20:HIS:HB3	2:F:23:HIS:HD2	1.44	0.82
3:E:57:VAL:HG13	3:E:267:ILE:O	1.79	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:57:VAL:HG13	3:B:267:ILE:O	1.79	0.82
2:L:369:MET:HB2	2:L:373:LEU:HD12	1.62	0.82
2:I:20:HIS:HB3	2:I:23:HIS:HD2	1.44	0.82
2:C:20:HIS:HB3	2:C:23:HIS:HD2	1.44	0.82
1:G:1057:TRP:HB3	2:I:382:ARG:HH12	1.44	0.81
2:L:344:LEU:HD11	2:L:359:MET:HE3	1.62	0.81
2:L:244:GLU:HB2	2:L:294:ALA:O	1.80	0.81
2:I:244:GLU:HB2	2:I:294:ALA:O	1.80	0.81
2:C:24:GLY:HA2	6:C:401:GTP:H5''	1.63	0.81
2:I:24:GLY:HA2	6:I:401:GTP:H5''	1.63	0.80
2:C:288:GLU:H	2:C:291:GLN:HE22	1.30	0.80
2:L:288:GLU:H	2:L:291:GLN:HE22	1.29	0.80
1:G:571:LEU:HD13	1:G:577:VAL:HG21	1.63	0.80
1:G:180:VAL:HG12	1:G:181:SER:O	1.81	0.80
1:D:318:GLN:HE21	1:D:320:ARG:HB2	1.45	0.80
1:G:556:ARG:HG2	1:G:560:ASN:HD21	1.47	0.80
1:G:220:ARG:HG2	1:G:230:LEU:HD23	1.63	0.79
1:J:1172:ALA:HB3	1:J:1229:PRO:HG2	1.65	0.79
2:C:334:ARG:HH22	2:C:368:ALA:HB3	1.47	0.79
2:L:24:GLY:HA2	6:L:401:GTP:H5''	1.63	0.79
2:C:135:LEU:HD22	2:C:151:GLU:HG2	1.65	0.79
2:F:24:GLY:HA2	6:F:401:GTP:H5''	1.63	0.79
2:C:334:ARG:NH2	2:C:368:ALA:HB3	1.97	0.79
2:F:246:VAL:HG11	2:F:299:ILE:CG2	2.12	0.78
2:F:288:GLU:H	2:F:291:GLN:HE22	1.30	0.78
2:I:288:GLU:H	2:I:291:GLN:HE22	1.29	0.78
2:F:135:LEU:HD22	2:F:151:GLU:HG2	1.65	0.78
2:C:351:VAL:HG12	2:C:357:ILE:HD13	1.66	0.78
1:G:180:VAL:HG11	1:G:228:SER:CB	2.15	0.77
2:I:135:LEU:HD22	2:I:151:GLU:HG2	1.65	0.77
2:F:244:GLU:HB3	2:F:294:ALA:O	1.84	0.77
1:G:1013:ILE:HD13	2:I:378:ARG:HD2	1.65	0.77
1:G:1252:LEU:HD21	1:G:1284:ALA:HB2	1.64	0.77
2:C:292:VAL:HG12	2:C:334:ARG:HH12	1.49	0.77
1:A:952:PRO:HD2	1:A:955:LYS:HD2	1.68	0.76
2:C:344:LEU:HD12	2:C:345:PRO:CD	2.03	0.76
1:G:289:SER:OG	1:G:416:CYS:SG	2.41	0.76
2:I:89:VAL:HG13	2:I:93:ILE:HD12	1.68	0.76
2:L:89:VAL:HG13	2:L:93:ILE:HD12	1.67	0.76
1:G:105:ASP:HA	1:G:108:LYS:HD2	1.66	0.76
2:C:351:VAL:HG12	2:C:357:ILE:CD1	2.15	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:113:MET:HB2	2:F:114:PRO:HD2	1.67	0.76
2:I:113:MET:HB2	2:I:114:PRO:HD2	1.67	0.76
2:F:344:LEU:HD21	2:F:359:MET:HE3	1.66	0.76
2:C:113:MET:HB2	2:C:114:PRO:HD2	1.67	0.76
2:L:89:VAL:HG13	2:L:93:ILE:CD1	2.16	0.76
2:L:135:LEU:HD22	2:L:151:GLU:HG2	1.65	0.76
1:D:305:ARG:CD	1:D:312:ILE:HD12	2.15	0.76
2:C:89:VAL:HG13	2:C:93:ILE:CD1	2.16	0.76
2:F:17:THR:HG23	2:F:79:HIS:NE2	2.01	0.76
2:I:17:THR:HG23	2:I:79:HIS:NE2	2.01	0.75
2:C:292:VAL:HG11	2:C:334:ARG:HH22	1.48	0.75
2:L:17:THR:HG23	2:L:79:HIS:NE2	2.02	0.75
1:G:1492:GLY:HA2	1:G:1495:LEU:HD13	1.67	0.75
2:I:89:VAL:HG13	2:I:93:ILE:CD1	2.16	0.75
2:L:20:HIS:HB3	2:L:23:HIS:CD2	2.22	0.75
2:L:351:VAL:HG12	2:L:357:ILE:CD1	2.15	0.75
2:L:351:VAL:HG12	2:L:357:ILE:HD13	1.66	0.75
2:C:17:THR:HG23	2:C:79:HIS:NE2	2.02	0.75
2:L:113:MET:HB2	2:L:114:PRO:HD2	1.68	0.75
2:F:20:HIS:HB3	2:F:23:HIS:CD2	2.22	0.75
2:F:89:VAL:HG13	2:F:93:ILE:CD1	2.16	0.75
1:D:879:TYR:HA	1:D:882:LYS:HE2	1.68	0.74
1:J:700:ILE:HG13	1:J:735:LEU:HD12	1.69	0.74
2:L:259:VAL:HG22	2:L:277:VAL:HG22	1.69	0.74
2:L:356:ASN:O	2:L:357:ILE:HG13	1.87	0.74
1:A:967:TRP:HE3	1:A:970:VAL:HG21	1.52	0.74
2:L:292:VAL:HG11	2:L:334:ARG:HH22	1.51	0.74
2:C:20:HIS:HB3	2:C:23:HIS:CD2	2.22	0.74
1:G:1007:LYS:O	2:I:59:ARG:N	2.21	0.74
1:A:1437:ASN:OD1	1:A:1478:ARG:NH1	2.21	0.74
2:C:259:VAL:HG22	2:C:277:VAL:HG22	1.69	0.74
1:A:325:LEU:HD11	1:A:334:GLN:HE21	1.53	0.74
1:G:893:GLU:OE1	1:G:921:LEU:CD1	2.33	0.74
1:G:1488:GLU:HA	1:G:1491:ARG:HH22	1.53	0.74
1:J:1173:GLU:HA	1:J:1176:LEU:HD12	1.69	0.74
2:I:20:HIS:HB3	2:I:23:HIS:CD2	2.22	0.74
2:I:177:LYS:HB3	2:I:182:ASP:HB3	1.70	0.74
2:F:246:VAL:HG11	2:F:299:ILE:HG23	1.70	0.74
2:C:356:ASN:O	2:C:357:ILE:HG13	1.87	0.73
1:G:879:TYR:HD1	1:G:882:LYS:HZ3	1.35	0.73
1:A:684:ILE:HD12	1:A:695:VAL:HG23	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:980:LYS:CD	3:H:282:ASP:OD2	2.35	0.73
1:G:270:ILE:HD11	1:G:283:LEU:CD1	2.13	0.73
2:C:89:VAL:HG13	2:C:93:ILE:HD12	1.68	0.73
1:A:44:VAL:HG13	1:A:60:GLN:HG2	1.70	0.73
1:D:110:LYS:NZ	1:D:154:LEU:O	2.21	0.73
1:D:197:LEU:HD13	1:D:214:LEU:HD11	1.71	0.73
1:G:893:GLU:OE2	1:G:921:LEU:CD1	2.37	0.73
1:D:193:LYS:O	1:D:197:LEU:HG	1.89	0.73
2:F:259:VAL:HG22	2:F:277:VAL:HG22	1.69	0.73
1:D:986:ILE:HB	1:D:1002:LEU:HD21	1.72	0.72
3:B:276:LEU:HB2	3:B:288:PRO:HG2	1.71	0.72
1:G:893:GLU:OE2	1:G:921:LEU:HD13	1.89	0.72
1:J:809:MET:HA	1:J:809:MET:HE3	1.70	0.72
2:F:89:VAL:HG13	2:F:93:ILE:HD12	1.68	0.72
2:L:177:LYS:HB3	2:L:182:ASP:HB3	1.70	0.72
2:I:372:GLY:H	2:I:389:VAL:HG13	1.55	0.72
2:F:177:LYS:HB3	2:F:182:ASP:HB3	1.70	0.72
2:F:372:GLY:H	2:F:389:VAL:HG13	1.55	0.72
1:A:192:MET:CE	1:G:187:PHE:HE1	1.95	0.72
2:L:292:VAL:HG12	2:L:334:ARG:HH12	1.54	0.72
2:L:356:ASN:C	2:L:357:ILE:HG13	2.14	0.72
2:I:133:VAL:HG11	2:I:154:VAL:HG13	1.71	0.72
1:J:1437:ASN:OD1	1:J:1478:ARG:NH1	2.23	0.72
2:C:177:LYS:HB3	2:C:182:ASP:HB3	1.70	0.72
2:C:356:ASN:C	2:C:357:ILE:HG13	2.14	0.72
1:G:1253:ARG:O	3:H:92:VAL:HG11	1.89	0.71
1:D:718:ALA:HA	1:D:721:LEU:HD12	1.71	0.71
2:C:372:GLY:H	2:C:389:VAL:HG13	1.55	0.71
2:L:211:PHE:O	2:L:295:LYS:NZ	2.23	0.71
3:E:276:LEU:HB2	3:E:288:PRO:HG2	1.72	0.71
1:A:370:ARG:NH1	1:J:330:GLU:OE2	2.24	0.71
2:I:152:MET:O	2:I:156:GLU:HG2	1.91	0.71
2:L:71:ASP:OD1	2:L:76:HIS:ND1	2.24	0.71
2:I:211:PHE:O	2:I:295:LYS:NZ	2.23	0.71
1:D:479:LEU:HD21	1:D:552:LEU:CD1	2.20	0.71
2:F:211:PHE:O	2:F:295:LYS:NZ	2.23	0.71
1:D:651:GLY:O	1:D:683:ARG:NH2	2.24	0.71
2:C:211:PHE:O	2:C:295:LYS:NZ	2.23	0.71
2:L:152:MET:O	2:L:156:GLU:HG2	1.91	0.70
2:C:71:ASP:OD1	2:C:76:HIS:ND1	2.24	0.70
2:I:71:ASP:OD1	2:I:76:HIS:ND1	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:152:MET:O	2:F:156:GLU:HG2	1.91	0.70
3:K:276:LEU:HB2	3:K:288:PRO:HG2	1.71	0.70
1:J:905:TYR:HA	1:J:908:ILE:HD12	1.73	0.70
2:C:152:MET:O	2:C:156:GLU:HG2	1.91	0.70
1:G:1057:TRP:H	3:H:279:GLN:NE2	1.90	0.70
2:I:227:VAL:HA	2:I:277:VAL:O	1.92	0.70
3:H:276:LEU:HB2	3:H:288:PRO:HG2	1.72	0.70
2:F:71:ASP:OD1	2:F:76:HIS:ND1	2.24	0.70
3:E:265:MET:HE2	3:E:304:MET:HE3	1.74	0.70
1:G:1435:TRP:HE3	1:G:1436:LEU:HD22	1.57	0.70
1:D:1448:LEU:HD22	1:D:1494:MET:HE3	1.74	0.70
2:C:133:VAL:HG11	2:C:154:VAL:HG13	1.71	0.70
1:G:1057:TRP:HB2	2:I:320:HIS:NE2	2.07	0.70
2:L:227:VAL:HA	2:L:277:VAL:O	1.92	0.70
2:L:133:VAL:HG11	2:L:154:VAL:HG13	1.71	0.69
3:K:265:MET:HE2	3:K:304:MET:HE3	1.74	0.69
1:D:1173:GLU:HG2	1:D:1229:PRO:HB3	1.73	0.69
2:C:351:VAL:HG11	2:C:357:ILE:CD1	2.22	0.69
2:F:344:LEU:CD2	2:F:359:MET:CG	2.60	0.69
1:D:668:LEU:HD13	1:D:677:VAL:HG12	1.75	0.69
2:C:227:VAL:HA	2:C:277:VAL:O	1.92	0.69
2:F:227:VAL:HA	2:F:277:VAL:O	1.92	0.69
3:H:265:MET:HE2	3:H:304:MET:HE3	1.74	0.69
2:C:331:PHE:O	2:C:337:ASP:HA	1.92	0.69
2:L:331:PHE:O	2:L:337:ASP:HA	1.93	0.69
1:G:893:GLU:CD	1:G:921:LEU:CD1	2.66	0.69
2:I:331:PHE:O	2:I:337:ASP:HA	1.92	0.69
2:L:351:VAL:HG11	2:L:357:ILE:CD1	2.22	0.69
1:D:562:VAL:HG13	1:D:566:GLU:HB2	1.74	0.69
1:D:1307:ARG:NH1	1:D:1339:ASP:OD2	2.25	0.69
1:D:479:LEU:HD21	1:D:552:LEU:HD11	1.74	0.69
2:C:135:LEU:HD11	2:C:154:VAL:HG21	1.74	0.69
3:B:271:GLU:OE2	3:B:274:ASN:ND2	2.27	0.68
2:I:218:VAL:HG21	2:I:287:ILE:HG22	1.75	0.68
2:L:135:LEU:HD11	2:L:154:VAL:HG21	1.74	0.68
1:A:432:LEU:HB3	1:A:461:ARG:HH22	1.58	0.68
1:D:773:THR:HA	1:D:776:LEU:HD13	1.74	0.68
2:C:292:VAL:HB	2:C:334:ARG:NH1	2.08	0.68
1:A:809:MET:HG3	1:A:872:ALA:HB1	1.76	0.68
2:F:218:VAL:HG21	2:F:287:ILE:HG22	1.75	0.68
2:I:135:LEU:HD11	2:I:154:VAL:HG21	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:1160:GLU:HA	1:J:1213:ALA:HB2	1.73	0.68
3:B:265:MET:HE2	3:B:304:MET:HE3	1.74	0.68
2:F:331:PHE:O	2:F:337:ASP:HA	1.93	0.68
3:E:271:GLU:OE2	3:E:274:ASN:ND2	2.26	0.68
3:K:271:GLU:OE2	3:K:274:ASN:ND2	2.27	0.68
2:F:135:LEU:HD11	2:F:154:VAL:HG21	1.74	0.67
1:D:1017:LYS:HE2	1:D:1057:TRP:CZ2	2.29	0.67
2:I:139:ASP:HB3	2:I:185:TRP:HE1	1.60	0.67
3:H:271:GLU:OE2	3:H:274:ASN:ND2	2.26	0.67
2:F:139:ASP:HB3	2:F:185:TRP:HE1	1.60	0.67
2:L:218:VAL:HG21	2:L:287:ILE:HG22	1.75	0.67
1:D:597:ARG:NH2	1:D:629:ASP:OD1	2.26	0.67
2:I:249:LYS:HB3	2:I:252:GLN:HE22	1.60	0.67
1:G:364:SER:OG	1:G:525:ARG:NH2	2.26	0.67
1:G:781:ILE:HG22	1:G:830:GLN:HG3	1.76	0.67
3:B:76:VAL:O	3:B:76:VAL:HG12	1.95	0.67
1:G:143:LYS:HG3	1:G:144:ILE:HG12	1.77	0.67
1:J:688:SER:HA	1:J:695:VAL:HG21	1.76	0.67
2:C:218:VAL:HG21	2:C:287:ILE:HG22	1.75	0.67
1:A:1485:GLU:O	1:J:601:ARG:NH2	2.23	0.67
1:G:497:ILE:HD12	1:G:552:LEU:HD21	1.75	0.67
1:G:597:ARG:NH2	1:G:629:ASP:OD1	2.27	0.67
1:J:726:ALA:HA	1:J:729:LEU:HG	1.77	0.67
2:C:351:VAL:HG11	2:C:357:ILE:HD13	1.77	0.67
2:L:139:ASP:HB3	2:L:185:TRP:HE1	1.60	0.67
2:L:249:LYS:HB3	2:L:252:GLN:HE22	1.60	0.67
1:D:145:ALA:HB1	1:D:148:LEU:HD23	1.77	0.66
3:H:76:VAL:O	3:H:76:VAL:HG12	1.95	0.66
1:A:688:SER:HA	1:A:695:VAL:HG11	1.75	0.66
2:C:292:VAL:CG1	2:C:334:ARG:NH1	2.59	0.66
1:G:817:ASP:O	1:G:821:GLU:HG2	1.96	0.66
1:G:960:MET:HE2	1:G:995:SER:H	1.59	0.66
1:G:1135:ALA:HA	1:G:1138:ILE:HD12	1.77	0.66
2:F:108:ALA:HA	2:F:150:VAL:HG11	1.78	0.66
2:L:89:VAL:HG12	2:L:93:ILE:HD12	1.77	0.66
2:L:108:ALA:HA	2:L:150:VAL:HG11	1.78	0.66
3:K:76:VAL:O	3:K:76:VAL:HG12	1.95	0.66
1:J:1373:ILE:HD11	1:J:1391:MET:HG2	1.78	0.66
2:I:108:ALA:HA	2:I:150:VAL:HG11	1.78	0.66
2:C:89:VAL:HG12	2:C:93:ILE:HD12	1.77	0.66
2:F:211:PHE:N	2:F:295:LYS:HZ2	1.93	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:13:GLY:HA3	1:G:201:MET:HE1	1.78	0.66
1:A:916:GLU:HA	1:A:919:ILE:HD11	1.78	0.66
1:D:1282:LYS:HE3	1:D:1314:ASP:HA	1.77	0.66
2:C:108:ALA:HA	2:C:150:VAL:HG11	1.78	0.66
2:C:132:ILE:HD13	2:C:196:LEU:HD23	1.78	0.66
2:F:89:VAL:HG12	2:F:93:ILE:HD12	1.77	0.66
2:L:348:VAL:HG12	2:L:350:MET:H	1.61	0.66
1:G:780:ASP:HA	1:G:783:GLN:HE21	1.59	0.66
2:I:89:VAL:HG12	2:I:93:ILE:HD12	1.76	0.66
2:C:249:LYS:HB3	2:C:252:GLN:HE22	1.60	0.66
2:L:132:ILE:HD13	2:L:196:LEU:HD23	1.78	0.65
2:C:139:ASP:HB3	2:C:185:TRP:HE1	1.60	0.65
2:F:356:ASN:C	2:F:357:ILE:HG12	2.20	0.65
1:J:515:GLN:HG2	1:J:516:ARG:HE	1.62	0.65
1:A:127:GLY:O	1:A:131:ARG:N	2.27	0.65
1:A:630:TRP:HB2	1:A:663:ASN:HD22	1.60	0.65
1:A:1170:ARG:HH11	1:A:1171:LYS:HE3	1.62	0.65
1:J:358:ASP:OD1	1:J:359:SER:N	2.30	0.65
2:F:249:LYS:HB3	2:F:252:GLN:HE22	1.60	0.65
3:E:76:VAL:O	3:E:76:VAL:HG12	1.95	0.65
2:L:292:VAL:CG1	2:L:334:ARG:NH2	2.57	0.65
2:L:351:VAL:HG11	2:L:357:ILE:HD13	1.77	0.65
1:G:1498:VAL:HA	1:G:1501:ILE:HD12	1.79	0.65
2:I:132:ILE:HD13	2:I:196:LEU:HD23	1.78	0.65
1:G:986:ILE:HB	1:G:1002:LEU:HD11	1.77	0.65
1:J:960:MET:HE1	1:J:989:ILE:HG21	1.79	0.65
2:C:344:LEU:HD11	2:C:345:PRO:HD3	1.70	0.65
2:I:25:LYS:NZ	6:I:401:GTP:O2G	2.27	0.65
2:I:136:ASN:HB3	2:I:137:LYS:HG3	1.79	0.65
1:A:980:LYS:O	1:A:984:GLU:HG3	1.96	0.65
1:D:1017:LYS:NZ	3:E:111:LEU:HD11	2.11	0.65
2:I:348:VAL:HG12	2:I:350:MET:H	1.61	0.65
1:G:636:LEU:HD11	1:G:643:VAL:HB	1.78	0.65
1:D:305:ARG:HD3	1:D:312:ILE:CD1	2.27	0.65
2:F:348:VAL:HG12	2:F:350:MET:H	1.61	0.65
1:J:446:LEU:HD21	1:J:545:HIS:CD2	2.33	0.64
2:F:132:ILE:CD1	2:F:196:LEU:HD23	2.27	0.64
3:E:273:THR:HA	3:E:291:SER:HG	1.62	0.64
1:A:729:LEU:HD13	1:A:732:VAL:HG11	1.80	0.64
1:G:232:PRO:HB3	1:G:346:ARG:NH2	2.12	0.64
1:D:1139:LEU:HD21	1:D:1175:LEU:HD23	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:1393:ARG:HA	1:J:1396:HIS:HD2	1.63	0.64
2:C:136:ASN:HB3	2:C:137:LYS:HG3	1.79	0.64
2:L:136:ASN:HB3	2:L:137:LYS:HG3	1.79	0.64
1:G:1353:THR:O	1:G:1357:THR:HG23	1.98	0.64
1:D:714:ALA:HA	1:D:717:ILE:HD12	1.79	0.64
1:J:1288:LEU:HD12	1:J:1299:VAL:HG13	1.78	0.64
2:F:132:ILE:HD13	2:F:196:LEU:HD23	1.78	0.64
1:G:145:ALA:HB1	1:G:148:LEU:HD13	1.78	0.64
1:J:1462:LYS:HD3	3:K:231:ARG:NH2	2.12	0.64
1:G:1176:LEU:O	1:G:1180:ILE:HG12	1.97	0.64
1:D:752:GLU:OE1	1:D:801:ASN:ND2	2.30	0.64
1:J:1436:LEU:HD13	1:J:1439:ILE:HD11	1.79	0.64
2:F:21:VAL:HG23	2:F:22:ASP:OD2	1.98	0.64
2:L:212:LEU:HD12	2:L:294:ALA:HB2	1.80	0.64
2:L:215:ILE:HD12	2:L:291:GLN:HB2	1.80	0.64
1:G:295:MET:HE1	1:G:391:VAL:HG12	1.79	0.64
2:I:132:ILE:CD1	2:I:196:LEU:HD23	2.28	0.64
2:F:133:VAL:HG11	2:F:154:VAL:HG13	1.71	0.64
1:A:1173:GLU:HA	1:A:1176:LEU:HD12	1.80	0.64
1:G:503:GLU:OE1	1:G:516:ARG:NH2	2.31	0.64
1:G:1015:GLN:HG3	2:I:381:GLY:HA2	1.79	0.64
1:G:1019:HIS:CE1	3:H:111:LEU:HD12	2.33	0.64
1:D:922:ILE:HA	1:D:925:MET:HE2	1.80	0.64
1:D:986:ILE:HG23	1:D:989:ILE:HD12	1.79	0.64
2:C:292:VAL:CG1	2:C:334:ARG:NH2	2.61	0.64
1:G:755:ALA:HB1	1:G:801:ASN:HD22	1.62	0.63
1:J:953:SER:HB2	2:L:263:ARG:HD3	1.78	0.63
1:J:1042:VAL:HG23	1:J:1043:LEU:HD22	1.81	0.63
2:C:292:VAL:HB	2:C:334:ARG:CZ	2.28	0.63
2:F:136:ASN:HB3	2:F:137:LYS:HG3	1.79	0.63
2:L:15:VAL:HG13	2:L:79:HIS:HD2	1.63	0.63
1:A:1169:PRO:HA	1:A:1221:PHE:HZ	1.63	0.63
1:G:700:ILE:HG12	1:G:735:LEU:HD13	1.80	0.63
1:D:385:ILE:HB	1:D:388:ILE:HD12	1.80	0.63
2:C:15:VAL:HG13	2:C:79:HIS:HD2	1.63	0.63
2:F:212:LEU:HD12	2:F:294:ALA:HB2	1.80	0.63
1:D:445:GLU:HA	1:D:448:ARG:HD3	1.79	0.63
2:C:348:VAL:HG12	2:C:350:MET:H	1.61	0.63
1:J:908:ILE:O	1:J:912:THR:HG23	1.97	0.63
2:I:212:LEU:HD12	2:I:294:ALA:HB2	1.80	0.63
2:C:21:VAL:HG23	2:C:22:ASP:OD2	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:132:ILE:CD1	2:L:196:LEU:HD23	2.28	0.63
2:C:132:ILE:CD1	2:C:196:LEU:HD23	2.28	0.63
2:C:215:ILE:HD12	2:C:291:GLN:HB2	1.80	0.63
1:D:683:ARG:NH1	1:D:686:GLN:OE1	2.32	0.63
2:C:134:PHE:CD1	2:C:192:LEU:HD21	2.34	0.63
2:F:15:VAL:HG13	2:F:79:HIS:HD2	1.63	0.63
1:A:1159:LEU:HD12	1:A:1210:VAL:HG12	1.81	0.63
2:I:21:VAL:HG23	2:I:22:ASP:OD2	1.98	0.63
2:C:243:VAL:CG1	2:C:293:LEU:HG	2.29	0.63
1:A:1134:LEU:O	1:A:1138:ILE:HG12	1.99	0.63
1:D:601:ARG:HG2	1:D:601:ARG:HH11	1.64	0.63
1:D:952:PRO:HD2	1:D:955:LYS:HD2	1.80	0.63
1:D:1288:LEU:HD12	1:D:1299:VAL:HG13	1.79	0.63
1:J:916:GLU:HA	1:J:919:ILE:HD11	1.81	0.63
2:L:292:VAL:HB	2:L:334:ARG:CZ	2.29	0.63
1:A:167:ARG:NH2	1:J:25:THR:OG1	2.31	0.62
1:G:986:ILE:HG23	1:G:989:ILE:HD12	1.80	0.62
1:G:1393:ARG:NH1	3:H:196:GLN:O	2.32	0.62
1:G:1489:SER:HB3	1:D:601:ARG:HH12	1.64	0.62
2:C:292:VAL:HG12	2:C:334:ARG:NH1	2.13	0.62
2:F:134:PHE:CD1	2:F:192:LEU:HD21	2.34	0.62
2:L:374:ARG:HG3	2:L:388:VAL:HG22	1.81	0.62
1:D:9:ASN:O	1:D:13:GLY:N	2.28	0.62
1:J:1252:LEU:HD13	1:J:1273:VAL:HG11	1.80	0.62
2:I:134:PHE:CD1	2:I:192:LEU:HD21	2.35	0.62
2:L:21:VAL:HG23	2:L:22:ASP:OD2	1.98	0.62
2:L:292:VAL:HG12	2:L:334:ARG:NH1	2.14	0.62
3:K:273:THR:HA	3:K:291:SER:HG	1.62	0.62
1:J:291:LYS:NZ	4:J:1601:ATP:O1B	2.23	0.62
2:F:25:LYS:NZ	6:F:401:GTP:O2G	2.27	0.62
2:F:215:ILE:HD12	2:F:291:GLN:HB2	1.80	0.62
1:A:346:ARG:NH1	1:A:346:ARG:O	2.31	0.62
1:G:873:VAL:O	1:G:877:ILE:HG12	2.00	0.62
1:D:1362:MET:HA	1:D:1369:CYS:SG	2.39	0.62
1:J:236:LEU:HD23	1:J:239:ILE:HD12	1.81	0.62
2:I:15:VAL:HG13	2:I:79:HIS:HD2	1.63	0.62
2:I:374:ARG:HG3	2:I:388:VAL:HG22	1.81	0.62
3:H:114:THR:HB	3:H:285:PHE:HE2	1.65	0.62
1:G:1110:LEU:HD21	1:G:1164:HIS:HB2	1.81	0.62
1:J:992:HIS:CE1	1:J:993:LEU:HG	2.35	0.62
2:C:212:LEU:HD12	2:C:294:ALA:HB2	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:114:THR:HB	3:E:285:PHE:HE2	1.65	0.62
1:A:223:ILE:HB	1:A:230:LEU:HD22	1.82	0.62
1:A:801:ASN:HB3	1:A:804:PHE:HB2	1.81	0.62
1:D:1281:TRP:CE2	1:D:1306:LEU:HD13	2.34	0.62
2:C:374:ARG:HG3	2:C:388:VAL:HG22	1.81	0.62
3:B:84:ASP:OD1	3:B:85:TYR:N	2.28	0.62
1:J:716:GLN:O	1:J:719:MET:HB2	2.00	0.62
1:D:22:TRP:HB3	1:D:49:ILE:CD1	2.20	0.62
1:D:22:TRP:CB	1:D:49:ILE:HD11	2.21	0.62
2:I:215:ILE:HD12	2:I:291:GLN:HB2	1.80	0.62
1:D:26:VAL:O	1:D:216:LYS:NZ	2.33	0.62
2:F:243:VAL:CG1	2:F:293:LEU:HG	2.29	0.62
1:A:1310:GLY:O	1:A:1311:ARG:NH1	2.32	0.61
1:D:65:GLN:HE22	1:D:71:TRP:HA	1.64	0.61
2:I:145:GLU:OE1	2:I:145:GLU:N	2.33	0.61
1:D:1310:GLY:O	1:D:1311:ARG:NH1	2.33	0.61
1:J:697:SER:HA	1:J:700:ILE:HD12	1.82	0.61
2:I:307:SER:OG	2:I:308:GLU:N	2.33	0.61
2:F:145:GLU:N	2:F:145:GLU:OE1	2.33	0.61
2:F:374:ARG:HG3	2:F:388:VAL:HG22	1.81	0.61
2:L:145:GLU:OE1	2:L:145:GLU:N	2.33	0.61
3:K:114:THR:HB	3:K:285:PHE:HE2	1.65	0.61
2:C:25:LYS:NZ	6:C:401:GTP:O2G	2.27	0.61
1:G:980:LYS:O	1:G:984:GLU:HG2	2.01	0.61
1:D:193:LYS:O	1:D:196:GLN:HG3	2.00	0.61
2:C:145:GLU:N	2:C:145:GLU:OE1	2.33	0.61
2:C:307:SER:OG	2:C:308:GLU:N	2.33	0.61
2:L:292:VAL:CG1	2:L:334:ARG:NH1	2.64	0.61
1:G:597:ARG:HG3	1:G:632:LEU:HD22	1.83	0.61
1:J:136:ALA:HA	1:J:139:LYS:HD3	1.82	0.61
1:J:1134:LEU:O	1:J:1138:ILE:HG12	1.99	0.61
2:F:330:GLN:HB3	2:F:337:ASP:OD1	2.00	0.61
2:L:243:VAL:CG1	2:L:293:LEU:HG	2.29	0.61
2:L:307:SER:OG	2:L:308:GLU:N	2.33	0.61
1:A:1059:ASP:HB2	1:A:1062:VAL:HG22	1.82	0.61
2:I:243:VAL:CG1	2:I:293:LEU:HG	2.29	0.61
2:L:61:ILE:CD1	2:L:312:LEU:HD21	2.31	0.61
1:A:254:ARG:HB3	1:D:403:ARG:HH22	1.65	0.61
1:A:600:LEU:HD13	1:A:620:PHE:HD1	1.66	0.61
1:G:645:GLN:O	1:G:649:VAL:HG12	2.01	0.61
1:G:1406:ILE:H	1:G:1406:ILE:HD12	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:185:SER:HA	1:D:188:ASN:HD21	1.66	0.61
1:J:1170:ARG:HG3	1:J:1171:LYS:HG2	1.81	0.61
1:G:668:LEU:HD11	1:G:676:GLY:HA3	1.83	0.61
2:L:338:VAL:HG21	2:L:367:ILE:HD11	1.83	0.61
1:D:90:ASN:OD1	1:D:92:LYS:NZ	2.31	0.60
3:B:273:THR:HA	3:B:291:SER:HG	1.62	0.60
1:D:870:PHE:HA	1:D:873:VAL:HG12	1.84	0.60
1:J:1462:LYS:HD3	3:K:231:ARG:HH21	1.66	0.60
2:I:330:GLN:HB3	2:I:337:ASP:OD1	2.00	0.60
1:A:1180:ILE:O	1:A:1183:VAL:HG22	2.02	0.60
3:H:225:TYR:O	3:H:228:LEU:N	2.35	0.60
1:G:332:GLN:OE1	1:G:338:GLN:N	2.35	0.60
1:G:1515:ASP:O	1:G:1518:LYS:HG3	2.02	0.60
2:L:292:VAL:HB	2:L:334:ARG:NH1	2.15	0.60
1:D:239:ILE:HG23	1:D:343:LYS:HB3	1.84	0.60
2:L:330:GLN:HB3	2:L:337:ASP:OD1	2.00	0.60
1:A:353:VAL:HB	1:A:388:ILE:HD13	1.83	0.60
1:A:1307:ARG:NH1	1:A:1339:ASP:OD1	2.34	0.60
1:J:126:LEU:O	1:J:131:ARG:NH1	2.34	0.60
1:J:987:VAL:HG13	1:J:1002:LEU:HD11	1.84	0.60
2:C:238:LYS:N	2:C:241:GLU:OE1	2.35	0.60
2:C:330:GLN:HB3	2:C:337:ASP:OD1	2.00	0.60
2:F:238:LYS:HA	2:F:268:GLU:HA	1.84	0.60
1:A:1485:GLU:HG2	1:J:601:ARG:HE	1.66	0.60
1:A:1417:GLU:OE1	1:A:1457:TYR:HA	2.02	0.60
1:D:1180:ILE:O	1:D:1183:VAL:HG22	2.02	0.60
1:D:1260:SER:OG	1:D:1261:LYS:NZ	2.31	0.60
2:I:238:LYS:HA	2:I:268:GLU:HA	1.84	0.60
3:B:114:THR:HB	3:B:285:PHE:HE2	1.65	0.60
2:F:205:ARG:NH1	2:F:208:ASP:OD2	2.35	0.60
1:A:1282:LYS:HE3	1:A:1314:ASP:HA	1.83	0.60
1:G:595:GLU:OE2	1:G:599:GLN:NE2	2.35	0.60
3:B:225:TYR:O	3:B:228:LEU:N	2.35	0.60
1:A:763:ILE:HB	1:A:767:LEU:HD13	1.84	0.60
1:G:65:GLN:HE22	1:G:71:TRP:HA	1.67	0.60
1:D:814:ALA:O	1:D:818:LEU:HG	2.02	0.60
2:I:66:SER:CB	2:I:81:ASP:OD1	2.49	0.60
2:C:338:VAL:HG21	2:C:367:ILE:HD11	1.83	0.60
1:G:991:CYS:O	2:I:274:ASN:ND2	2.34	0.59
1:J:664:LEU:O	1:J:668:LEU:HG	2.02	0.59
2:F:307:SER:OG	2:F:308:GLU:N	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:21:ASP:OD1	1:G:175:ARG:NH2	2.33	0.59
1:G:357:ILE:HB	1:G:392:THR:HG22	1.84	0.59
1:D:908:ILE:O	1:D:912:THR:HG23	2.02	0.59
2:I:338:VAL:HG21	2:I:367:ILE:HD11	1.83	0.59
2:C:205:ARG:NH1	2:C:208:ASP:OD2	2.35	0.59
2:L:238:LYS:N	2:L:241:GLU:OE1	2.35	0.59
3:K:225:TYR:O	3:K:228:LEU:N	2.35	0.59
1:D:916:GLU:HA	1:D:919:ILE:HD11	1.84	0.59
1:D:1159:LEU:HD12	1:D:1210:VAL:HG12	1.82	0.59
3:B:78:ILE:HA	3:B:81:ILE:HB	1.84	0.59
2:F:338:VAL:HG21	2:F:367:ILE:HD11	1.83	0.59
2:L:238:LYS:HA	2:L:268:GLU:HA	1.84	0.59
3:K:77:GLY:O	3:K:80:GLN:HG3	2.02	0.59
1:G:1160:GLU:HA	1:G:1213:ALA:HB2	1.84	0.59
1:J:628:GLU:CD	1:J:628:GLU:H	2.10	0.59
3:E:78:ILE:HA	3:E:81:ILE:HB	1.84	0.59
2:L:292:VAL:CG1	2:L:334:ARG:CZ	2.80	0.59
1:A:995:SER:OG	1:A:997:GLU:OE1	2.20	0.59
1:A:1462:LYS:HD3	3:B:231:ARG:NH2	2.18	0.59
1:G:1010:GLY:N	2:I:59:ARG:HA	2.18	0.59
1:G:312:ILE:HD13	1:G:352:HIS:HB3	1.85	0.59
1:G:878:LEU:HD12	1:G:882:LYS:HZ2	1.67	0.59
1:G:1500:ALA:O	1:G:1504:THR:HG23	2.02	0.59
1:D:119:GLU:HG3	1:D:151:PHE:HB3	1.84	0.59
1:D:1058:ASN:CG	2:F:382:ARG:HD3	2.27	0.59
2:L:351:VAL:CG1	2:L:357:ILE:HD12	2.32	0.59
3:K:78:ILE:HA	3:K:81:ILE:HB	1.84	0.59
1:G:163:ASP:OD2	1:G:164:ASP:N	2.29	0.59
1:G:1176:LEU:HD13	1:G:1231:LEU:HB3	1.85	0.59
3:H:77:GLY:O	3:H:80:GLN:HG3	2.02	0.59
2:C:351:VAL:CG1	2:C:357:ILE:HD12	2.33	0.59
1:A:76:LEU:HB3	1:A:80:LEU:HD23	1.83	0.59
1:A:1428:ARG:HH21	1:A:1430:PHE:HE2	1.50	0.59
1:G:944:ILE:HG23	1:G:948:PHE:HD2	1.67	0.59
1:G:1059:ASP:HB2	2:I:320:HIS:HD2	1.64	0.59
1:G:1447:ALA:O	1:G:1451:THR:HG23	2.02	0.59
3:B:77:GLY:O	3:B:80:GLN:HG3	2.02	0.59
3:E:225:TYR:O	3:E:228:LEU:N	2.35	0.59
1:G:1008:LYS:HB3	2:I:57:LYS:HG3	1.85	0.59
1:D:1103:MET:HE1	1:D:1155:THR:HA	1.85	0.59
3:H:84:ASP:OD1	3:H:85:TYR:N	2.28	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:25:LYS:NZ	6:L:401:GTP:O2G	2.27	0.59
2:L:205:ARG:NH1	2:L:208:ASP:OD2	2.35	0.59
1:G:220:ARG:HG2	1:G:230:LEU:HD21	1.82	0.59
1:G:929:ARG:NH2	1:G:969:ASP:OD2	2.36	0.59
1:D:998:ALA:O	1:D:1002:LEU:HG	2.02	0.59
1:J:1497:ARG:O	1:J:1501:ILE:HG12	2.03	0.59
2:C:238:LYS:HA	2:C:268:GLU:HA	1.84	0.59
2:F:238:LYS:N	2:F:241:GLU:OE1	2.35	0.59
3:E:77:GLY:O	3:E:80:GLN:HG3	2.02	0.59
1:A:445:GLU:OE2	1:A:448:ARG:NH1	2.36	0.58
1:G:820:VAL:HA	1:G:823:ILE:HD12	1.83	0.58
2:I:211:PHE:N	2:I:295:LYS:HZ2	2.01	0.58
1:G:849:THR:OG1	1:G:850:SER:N	2.35	0.58
1:G:1082:ARG:O	1:G:1086:LEU:HG	2.03	0.58
1:J:395:ARG:NH2	4:J:1601:ATP:O1G	2.24	0.58
1:J:1281:TRP:CE2	1:J:1306:LEU:HD13	2.38	0.58
3:H:78:ILE:HA	3:H:81:ILE:HB	1.84	0.58
2:C:292:VAL:CG1	2:C:334:ARG:CZ	2.81	0.58
1:A:1281:TRP:CE2	1:A:1306:LEU:HD13	2.39	0.58
1:G:519:ALA:HB1	1:G:523:ILE:HD12	1.84	0.58
1:G:783:GLN:HG3	1:G:785:ARG:HB2	1.85	0.58
1:J:380:ASP:CG	1:J:408:ARG:HH22	2.11	0.58
2:L:349:GLU:OE1	2:L:349:GLU:N	2.28	0.58
3:K:84:ASP:OD1	3:K:85:TYR:N	2.28	0.58
1:A:143:LYS:HB2	1:A:144:ILE:HD12	1.84	0.58
1:G:980:LYS:HD3	3:H:282:ASP:CG	2.28	0.58
1:J:716:GLN:HA	1:J:719:MET:HB2	1.84	0.58
1:D:688:SER:HA	1:D:695:VAL:HG21	1.85	0.58
1:D:966:MET:HG3	1:D:967:TRP:HD1	1.68	0.58
2:I:205:ARG:NH1	2:I:208:ASP:OD2	2.35	0.58
1:A:601:ARG:NH2	1:D:1485:GLU:O	2.35	0.58
1:A:781:ILE:HG22	1:A:830:GLN:HG3	1.85	0.58
1:A:1370:PHE:HD1	1:A:1373:ILE:HD11	1.69	0.58
1:G:983:ALA:O	1:G:987:VAL:HG23	2.03	0.58
3:E:84:ASP:OD1	3:E:85:TYR:N	2.28	0.58
1:G:757:CYS:SG	1:G:763:ILE:HG12	2.43	0.58
1:J:1180:ILE:O	1:J:1183:VAL:HG22	2.04	0.58
1:G:445:GLU:HA	1:G:448:ARG:HG3	1.85	0.58
1:D:1382:ARG:HH12	1:D:1385:LEU:HD23	1.69	0.58
1:A:983:ALA:O	1:A:987:VAL:HG23	2.04	0.58
1:G:230:LEU:HG	1:G:231:ALA:N	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:16:THR:HG23	1:D:194:LEU:HD22	1.85	0.58
1:D:983:ALA:O	1:D:987:VAL:HG23	2.04	0.58
1:D:1505:LEU:HD13	1:D:1513:ILE:HG13	1.86	0.58
1:J:628:GLU:OE1	1:J:628:GLU:N	2.33	0.58
2:F:113:MET:CB	2:F:114:PRO:HD2	2.34	0.58
1:D:194:LEU:HA	1:D:197:LEU:HD12	1.86	0.58
1:D:645:GLN:O	1:D:649:VAL:HG12	2.04	0.58
1:A:807:GLN:O	1:A:811:GLN:NE2	2.37	0.57
1:A:933:GLU:OE2	1:A:967:TRP:N	2.36	0.57
1:A:1212:GLU:OE2	1:A:1254:ARG:NH2	2.37	0.57
2:C:343:GLU:HB2	2:C:360:VAL:HG13	1.86	0.57
1:A:1166:ILE:HG13	1:A:1175:LEU:HD11	1.86	0.57
2:F:305:PHE:HE1	2:F:363:LEU:HD21	1.69	0.57
2:L:305:PHE:HE1	2:L:363:LEU:HD21	1.69	0.57
2:L:308:GLU:OE1	2:L:357:ILE:N	2.37	0.57
1:G:1251:ILE:HG21	1:G:1269:LEU:HD11	1.85	0.57
1:J:809:MET:HG2	1:J:872:ALA:O	2.04	0.57
1:J:929:ARG:NH2	1:J:969:ASP:OD2	2.35	0.57
2:I:95:GLY:HA3	2:I:374:ARG:HH21	1.69	0.57
3:H:273:THR:HA	3:H:291:SER:HG	1.61	0.57
2:F:308:GLU:OE1	2:F:357:ILE:N	2.37	0.57
2:L:331:PHE:HE2	2:L:361:VAL:HG11	1.69	0.57
1:A:1017:LYS:NZ	1:A:1018:ILE:O	2.37	0.57
1:G:915:PRO:HB2	1:G:947:ILE:HD13	1.86	0.57
1:G:1489:SER:HB3	1:D:601:ARG:NH1	2.19	0.57
1:D:44:VAL:HG22	1:D:86:LEU:HD13	1.84	0.57
1:J:1031:PHE:N	1:J:1071:GLN:OE1	2.38	0.57
2:I:18:ILE:HB	2:I:119:HIS:HD2	1.69	0.57
2:C:95:GLY:HA3	2:C:374:ARG:HH21	1.69	0.57
2:C:305:PHE:HE1	2:C:363:LEU:HD21	1.69	0.57
1:A:51:LYS:HD3	1:A:55:ASN:HB2	1.86	0.57
1:G:81:ASP:O	1:G:85:LEU:HG	2.04	0.57
3:E:114:THR:HG22	3:E:283:LEU:HD12	1.86	0.57
1:D:987:VAL:HG21	1:D:1012:LEU:HD11	1.87	0.57
1:J:452:GLU:OE2	1:J:452:GLU:N	2.30	0.57
2:I:343:GLU:HB2	2:I:360:VAL:HG13	1.86	0.57
2:C:344:LEU:HD23	2:C:348:VAL:HB	1.87	0.57
2:F:95:GLY:HA3	2:F:374:ARG:HH21	1.69	0.57
2:L:332:TYR:HA	2:L:336:THR:O	2.05	0.57
1:J:365:ILE:O	1:J:367:ARG:NH1	2.32	0.57
2:I:332:TYR:HA	2:I:336:THR:O	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:308:GLU:OE1	2:C:357:ILE:N	2.37	0.57
2:F:106:VAL:O	2:F:136:ASN:N	2.35	0.57
2:I:308:GLU:OE1	2:I:357:ILE:N	2.37	0.57
2:C:332:TYR:HA	2:C:336:THR:O	2.05	0.57
2:L:95:GLY:HA3	2:L:374:ARG:HH21	1.69	0.57
1:A:137:LEU:HA	1:A:140:GLN:NE2	2.20	0.57
1:A:893:GLU:OE1	1:A:893:GLU:N	2.38	0.57
1:G:108:LYS:O	1:G:111:GLU:HG2	2.05	0.57
1:G:814:ALA:O	1:G:818:LEU:HG	2.04	0.57
1:J:1215:MET:SD	1:J:1251:ILE:HG13	2.45	0.57
2:C:331:PHE:HE2	2:C:361:VAL:HG11	1.69	0.57
1:J:318:GLN:OE1	1:J:320:ARG:NH1	2.38	0.57
1:J:952:PRO:HD2	1:J:955:LYS:HD2	1.87	0.57
2:I:305:PHE:HE1	2:I:363:LEU:HD21	1.69	0.57
2:L:343:GLU:HB2	2:L:360:VAL:HG13	1.86	0.57
3:B:217:LEU:HD23	3:B:224:SER:HB2	1.87	0.56
2:L:205:ARG:NH2	2:L:208:ASP:OD1	2.38	0.56
1:A:465:SER:OG	1:A:467:ASN:OD1	2.22	0.56
1:G:140:GLN:HA	1:G:143:LYS:HZ1	1.69	0.56
1:G:786:PHE:HB3	1:G:790:LEU:HD11	1.86	0.56
1:J:126:LEU:HD21	1:J:131:ARG:HA	1.87	0.56
1:J:588:LEU:HB3	1:J:596:TYR:HD2	1.70	0.56
1:J:801:ASN:HB3	1:J:804:PHE:HB2	1.87	0.56
1:J:849:THR:OG1	1:J:850:SER:N	2.36	0.56
2:C:211:PHE:N	2:C:295:LYS:HZ2	2.03	0.56
2:F:57:LYS:HA	2:F:62:THR:HA	1.88	0.56
2:L:331:PHE:HE1	2:L:377:ILE:HG23	1.71	0.56
1:A:829:THR:O	1:A:832:SER:OG	2.23	0.56
1:A:1374:LYS:O	1:A:1378:ASN:ND2	2.38	0.56
1:G:1310:GLY:O	1:G:1311:ARG:NH1	2.32	0.56
1:D:1212:GLU:OE2	1:D:1254:ARG:NH2	2.38	0.56
2:I:238:LYS:N	2:I:241:GLU:OE1	2.34	0.56
2:F:331:PHE:HE2	2:F:361:VAL:HG11	1.70	0.56
1:A:67:ASP:C	1:J:108:LYS:HZ1	2.14	0.56
1:G:1338:ASN:HA	1:G:1341:ASN:HD21	1.70	0.56
1:D:234:MET:HA	1:D:237:VAL:HG12	1.88	0.56
1:D:736:LEU:HB3	1:D:737:MET:HE2	1.87	0.56
3:K:217:LEU:HD23	3:K:224:SER:HB2	1.87	0.56
1:G:718:ALA:HB2	1:G:739:LEU:HD11	1.88	0.56
1:G:1274:MET:HE1	1:G:1280:LEU:HB2	1.87	0.56
3:H:299:TYR:O	3:H:301:PRO:HD3	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:205:ARG:NH2	2:C:208:ASP:OD1	2.38	0.56
3:B:299:TYR:O	3:B:301:PRO:HD3	2.06	0.56
2:F:331:PHE:HE1	2:F:377:ILE:HG23	1.71	0.56
3:E:217:LEU:HD23	3:E:224:SER:HB2	1.88	0.56
1:G:563:THR:OG1	1:G:564:LEU:N	2.39	0.56
1:D:64:ASN:ND2	1:D:65:GLN:O	2.36	0.56
1:D:1024:ILE:HG13	3:E:106:PHE:CE1	2.40	0.56
2:I:57:LYS:HA	2:I:62:THR:HA	1.88	0.56
2:C:292:VAL:CB	2:C:334:ARG:NH1	2.69	0.56
3:E:187:MET:SD	3:E:257:ALA:HB2	2.46	0.56
3:E:299:TYR:O	3:E:301:PRO:HD3	2.06	0.56
3:K:299:TYR:O	3:K:301:PRO:HD3	2.06	0.56
1:A:166:ASP:HB2	1:G:205:ARG:HH22	1.71	0.56
1:G:67:ASP:HA	1:D:108:LYS:HZ3	1.70	0.56
1:D:692:THR:OG1	1:D:728:ASN:ND2	2.39	0.56
1:D:1066:ARG:HG3	1:D:1070:TRP:CH2	2.40	0.56
2:C:57:LYS:HA	2:C:62:THR:HA	1.88	0.56
2:F:205:ARG:NH2	2:F:208:ASP:OD1	2.38	0.56
1:G:908:ILE:O	1:G:912:THR:HG23	2.05	0.56
1:G:1354:THR:CG2	3:H:82:ILE:CD1	2.84	0.56
1:J:700:ILE:O	1:J:704:THR:HG23	2.06	0.56
2:I:331:PHE:HE1	2:I:377:ILE:HG23	1.71	0.56
2:F:244:GLU:CB	2:F:294:ALA:O	2.53	0.56
2:F:343:GLU:HB2	2:F:360:VAL:HG13	1.86	0.56
2:F:356:ASN:C	2:F:357:ILE:CG1	2.79	0.56
3:K:173:ASP:HA	3:K:312:PHE:HA	1.88	0.56
1:A:1417:GLU:OE2	1:A:1460:HIS:ND1	2.39	0.56
1:G:255:ARG:HH12	1:G:300:GLU:CD	2.13	0.56
1:D:1423:GLU:HG2	1:D:1425:LYS:HG3	1.87	0.56
3:B:173:ASP:O	3:B:179:ASN:ND2	2.39	0.56
3:B:187:MET:SD	3:B:257:ALA:HB2	2.46	0.56
1:G:316:PHE:CE2	1:G:318:GLN:HG2	2.40	0.56
1:G:980:LYS:HG2	3:H:282:ASP:OD2	2.05	0.56
2:I:61:ILE:HD12	2:I:94:THR:CG2	2.36	0.56
1:G:99:SER:OG	1:G:100:ARG:N	2.39	0.55
1:D:700:ILE:O	1:D:704:THR:HG23	2.05	0.55
1:D:781:ILE:HG22	1:D:830:GLN:HG3	1.88	0.55
1:J:1117:LEU:HD21	3:K:100:GLN:HG3	1.86	0.55
2:I:113:MET:CB	2:I:114:PRO:HD2	2.34	0.55
2:F:61:ILE:HD12	2:F:94:THR:CG2	2.36	0.55
1:A:1066:ARG:HG3	1:A:1070:TRP:CH2	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:578:ARG:HD3	1:G:1521:GLU:HG2	1.89	0.55
1:G:922:ILE:HD12	1:G:943:LEU:HD21	1.89	0.55
1:G:1159:LEU:HD21	1:G:1210:VAL:HG12	1.87	0.55
1:G:1354:THR:HG22	3:H:82:ILE:HD12	1.86	0.55
1:J:825:TYR:O	1:J:829:THR:HG23	2.06	0.55
2:I:205:ARG:NH2	2:I:208:ASP:OD1	2.38	0.55
1:A:110:LYS:NZ	1:A:154:LEU:O	2.34	0.55
1:G:1354:THR:HG22	3:H:82:ILE:CD1	2.36	0.55
1:G:1383:HIS:O	1:G:1387:VAL:HG23	2.07	0.55
1:D:442:ASP:OD2	1:D:443:THR:N	2.40	0.55
1:D:1413:PHE:O	1:D:1417:GLU:HG2	2.06	0.55
1:J:12:ASP:O	1:J:16:THR:OG1	2.20	0.55
1:J:819:ALA:O	1:J:823:ILE:HG13	2.06	0.55
1:J:1163:SER:OG	1:J:1216:ILE:HB	2.07	0.55
2:C:113:MET:CB	2:C:114:PRO:HD2	2.34	0.55
2:C:331:PHE:HE1	2:C:377:ILE:HG23	1.71	0.55
3:E:253:LYS:HB2	3:E:310:ILE:HB	1.89	0.55
2:L:47:PHE:HA	2:L:50:ILE:HD11	1.89	0.55
2:L:72:THR:HG21	2:L:77:TYR:HE2	1.71	0.55
3:K:187:MET:SD	3:K:257:ALA:HB2	2.46	0.55
1:A:26:VAL:HG22	1:A:32:PHE:HB3	1.87	0.55
1:A:1139:LEU:HD21	1:A:1175:LEU:HD23	1.89	0.55
1:A:1228:PHE:CG	1:A:1232:LEU:HD23	2.41	0.55
1:A:1448:LEU:HD13	1:A:1479:LEU:HD22	1.87	0.55
1:D:641:ARG:HH21	1:D:679:MET:HE1	1.72	0.55
1:D:1424:LYS:HD3	1:D:1426:HIS:HE1	1.71	0.55
1:D:1459:ASP:OD1	1:D:1460:HIS:N	2.40	0.55
3:H:187:MET:SD	3:H:257:ALA:HB2	2.46	0.55
2:C:12:HIS:CD2	2:C:76:HIS:HD2	2.25	0.55
1:A:1031:PHE:N	1:A:1071:GLN:OE1	2.40	0.55
1:A:1169:PRO:HA	1:A:1221:PHE:CZ	2.41	0.55
2:I:72:THR:HG21	2:I:77:TYR:HE2	1.71	0.55
3:H:173:ASP:HA	3:H:312:PHE:HA	1.88	0.55
3:H:253:LYS:HB2	3:H:310:ILE:HB	1.89	0.55
1:G:668:LEU:HG	1:G:677:VAL:HG12	1.87	0.55
1:D:1467:ASP:CG	1:D:1472:LEU:HB2	2.31	0.55
1:J:990:PRO:HG2	1:J:993:LEU:HD12	1.88	0.55
3:H:217:LEU:HD23	3:H:224:SER:HB2	1.87	0.55
2:C:47:PHE:HA	2:C:50:ILE:HD11	1.89	0.55
2:F:12:HIS:CD2	2:F:76:HIS:HD2	2.25	0.55
2:L:106:VAL:O	2:L:136:ASN:N	2.35	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:253:LYS:HB2	3:K:310:ILE:HB	1.89	0.55
1:A:668:LEU:HD13	1:A:673:ASP:HB3	1.87	0.55
1:A:1070:TRP:CD2	3:B:66:LYS:HG2	2.41	0.55
1:A:1211:ALA:HB1	1:A:1251:ILE:HD11	1.89	0.55
1:G:771:TYR:HA	1:G:774:ASP:OD1	2.07	0.55
1:D:1173:GLU:HA	1:D:1176:LEU:HD12	1.88	0.55
1:J:1252:LEU:HD21	1:J:1284:ALA:HB2	1.89	0.55
1:J:1406:ILE:H	1:J:1406:ILE:HD12	1.72	0.55
2:I:12:HIS:CD2	2:I:76:HIS:HD2	2.25	0.55
2:F:244:GLU:HG2	2:F:245:ILE:N	2.21	0.55
3:E:173:ASP:HA	3:E:312:PHE:HA	1.88	0.55
1:A:201:MET:SD	1:G:165:LEU:HD23	2.47	0.55
1:G:1136:ASN:HD22	1:G:1171:LYS:HE2	1.72	0.55
1:G:1166:ILE:HG21	1:G:1175:LEU:HD11	1.87	0.55
1:D:465:SER:OG	1:D:467:ASN:OD1	2.25	0.55
1:J:341:VAL:HG21	1:J:378:GLN:OE1	2.07	0.55
1:J:645:GLN:O	1:J:649:VAL:HG12	2.07	0.55
3:B:253:LYS:HB2	3:B:310:ILE:HB	1.89	0.55
2:F:72:THR:HG21	2:F:77:TYR:HE2	1.71	0.55
1:D:236:LEU:HD22	1:D:347:LEU:HD23	1.88	0.55
2:C:89:VAL:HG13	2:C:93:ILE:HD11	1.89	0.55
2:L:57:LYS:HA	2:L:62:THR:HA	1.88	0.55
1:A:216:LYS:O	1:A:220:ARG:HD2	2.07	0.54
1:G:676:GLY:HA2	1:G:679:MET:HE2	1.88	0.54
1:G:971:ALA:HB3	1:G:978:VAL:HG11	1.89	0.54
1:D:184:ASP:OD1	1:D:184:ASP:N	2.39	0.54
1:D:951:LEU:HD23	1:D:955:LYS:HG3	1.88	0.54
2:I:331:PHE:HE2	2:I:361:VAL:HG11	1.70	0.54
2:C:72:THR:HG21	2:C:77:TYR:HE2	1.71	0.54
1:A:515:GLN:OE1	1:A:515:GLN:N	2.38	0.54
1:G:1269:LEU:O	1:G:1273:VAL:HG23	2.07	0.54
1:J:600:LEU:HD13	1:J:620:PHE:HD1	1.72	0.54
2:C:332:TYR:HB2	2:C:378:ARG:HD3	1.89	0.54
2:F:349:GLU:OE1	2:F:349:GLU:N	2.28	0.54
1:A:825:TYR:O	1:A:829:THR:HG23	2.08	0.54
1:D:821:GLU:OE2	1:D:894:ARG:NH2	2.41	0.54
1:D:1183:VAL:HG21	1:D:1238:ARG:HH11	1.72	0.54
1:J:877:ILE:HA	1:J:880:ASN:HD21	1.72	0.54
3:B:173:ASP:HA	3:B:312:PHE:HA	1.88	0.54
3:B:264:ASN:OD1	3:B:303:THR:HG21	2.08	0.54
2:F:344:LEU:HD21	2:F:359:MET:HG2	1.81	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:985:VAL:O	1:A:988:SER:OG	2.24	0.54
1:G:134:ASP:O	1:G:138:SER:OG	2.24	0.54
1:G:572:PRO:HG2	1:G:574:VAL:HG22	1.88	0.54
3:K:264:ASN:OD1	3:K:303:THR:HG21	2.08	0.54
1:D:700:ILE:HG13	1:D:735:LEU:HD22	1.90	0.54
1:J:1403:PHE:HZ	1:J:1442:GLN:HG3	1.72	0.54
2:I:332:TYR:HB2	2:I:378:ARG:HD3	1.89	0.54
1:A:1338:ASN:HA	1:A:1341:ASN:HD21	1.72	0.54
1:D:1172:ALA:HA	1:D:1175:LEU:HD12	1.88	0.54
1:J:1142:LEU:HD23	1:J:1178:LEU:HD13	1.89	0.54
1:J:1207:LYS:HA	1:J:1210:VAL:HG22	1.90	0.54
2:I:11:PRO:HB2	2:I:75:ARG:HG2	1.90	0.54
3:H:264:ASN:OD1	3:H:303:THR:HG21	2.08	0.54
2:F:47:PHE:HA	2:F:50:ILE:HD11	1.89	0.54
1:A:670:ALA:O	1:A:672:ARG:NH2	2.41	0.54
1:G:86:LEU:HD11	1:G:93:VAL:HG21	1.90	0.54
1:G:283:LEU:HD21	1:G:414:LEU:HD12	1.89	0.54
1:G:1505:LEU:HD12	1:G:1513:ILE:HG12	1.89	0.54
1:D:76:LEU:O	1:D:79:GLU:HG2	2.08	0.54
1:D:364:SER:HA	1:D:372:LEU:HD22	1.90	0.54
1:D:670:ALA:O	1:D:672:ARG:NH2	2.40	0.54
2:C:61:ILE:HD12	2:C:94:THR:CG2	2.36	0.54
3:E:264:ASN:OD1	3:E:303:THR:HG21	2.07	0.54
2:L:11:PRO:HB2	2:L:75:ARG:HG2	1.90	0.54
1:A:166:ASP:HB2	1:G:205:ARG:NH2	2.23	0.54
1:G:1168:ASP:OD2	1:G:1170:ARG:NH1	2.41	0.54
1:D:1059:ASP:HB3	1:D:1062:VAL:HG22	1.90	0.54
1:J:1236:LEU:HB3	1:J:1269:LEU:HD11	1.89	0.54
2:C:344:LEU:CD1	2:C:357:ILE:HG22	2.37	0.54
2:L:12:HIS:CD2	2:L:76:HIS:HD2	2.25	0.54
3:K:272:VAL:O	3:K:273:THR:HG23	2.08	0.54
1:G:677:VAL:O	1:G:681:VAL:HG23	2.08	0.54
1:G:739:LEU:O	1:G:742:THR:OG1	2.26	0.54
1:G:1215:MET:SD	1:G:1251:ILE:HG23	2.48	0.54
1:D:1134:LEU:O	1:D:1138:ILE:HG12	2.08	0.54
1:D:1343:LEU:HB3	1:D:1345:THR:HG22	1.89	0.54
2:I:33:THR:HG23	2:I:34:THR:HG23	1.90	0.54
3:E:114:THR:HB	3:E:285:PHE:CE2	2.43	0.54
2:L:113:MET:CB	2:L:114:PRO:HD2	2.34	0.54
2:L:244:GLU:CB	2:L:294:ALA:O	2.53	0.54
1:D:1177:PHE:HA	1:D:1180:ILE:HD12	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1483:ALA:HB2	1:D:1498:VAL:HG21	1.90	0.54
1:J:444:ARG:O	1:J:448:ARG:HG3	2.08	0.54
2:I:89:VAL:HG13	2:I:93:ILE:HD11	1.89	0.54
2:C:113:MET:SD	2:C:115:GLN:HG3	2.48	0.54
3:E:173:ASP:O	3:E:179:ASN:ND2	2.39	0.54
3:K:59:ASN:N	3:K:60:GLU:OE2	2.41	0.54
1:A:592:GLU:CD	1:A:594:ARG:H	2.16	0.53
1:A:1383:HIS:O	1:A:1387:VAL:HG23	2.08	0.53
1:G:332:GLN:OE1	1:G:338:GLN:HG2	2.08	0.53
1:D:1269:LEU:O	1:D:1273:VAL:HG23	2.08	0.53
1:J:1095:PRO:HG2	1:J:1098:PHE:CD2	2.43	0.53
1:J:1270:PHE:O	1:J:1273:VAL:HG12	2.08	0.53
3:H:168:VAL:HB	3:H:307:ILE:HG12	1.90	0.53
3:B:89:LEU:HD12	3:B:90:PRO:HD2	1.91	0.53
2:F:33:THR:HG23	2:F:34:THR:HG23	1.90	0.53
2:L:33:THR:HG23	2:L:34:THR:HG23	1.90	0.53
1:G:1134:LEU:HD23	1:G:1138:ILE:HD11	1.90	0.53
1:D:825:TYR:O	1:D:829:THR:HG23	2.08	0.53
1:D:1327:MET:HE1	1:D:1361:ASN:HB3	1.89	0.53
3:H:59:ASN:N	3:H:60:GLU:OE2	2.41	0.53
3:H:89:LEU:HD12	3:H:90:PRO:HD2	1.91	0.53
3:B:272:VAL:O	3:B:273:THR:HG23	2.08	0.53
2:F:11:PRO:HB2	2:F:75:ARG:HG2	1.90	0.53
2:F:356:ASN:O	2:F:357:ILE:CG1	2.56	0.53
3:E:272:VAL:O	3:E:273:THR:HG23	2.08	0.53
2:L:113:MET:SD	2:L:115:GLN:HG3	2.48	0.53
2:L:332:TYR:HB2	2:L:378:ARG:HD3	1.89	0.53
1:A:63:LYS:CG	1:A:100:ARG:HH12	2.20	0.53
1:G:630:TRP:HH2	1:G:664:LEU:HD13	1.74	0.53
1:J:983:ALA:HB1	1:J:1002:LEU:HD12	1.90	0.53
1:J:1297:ASP:OD2	1:J:1297:ASP:N	2.41	0.53
2:I:226:THR:HG21	2:I:282:ILE:HG22	1.90	0.53
3:H:213:VAL:HG12	3:H:214:MET:HE2	1.91	0.53
2:C:33:THR:HG23	2:C:34:THR:HG23	1.90	0.53
2:F:113:MET:SD	2:F:115:GLN:HG3	2.48	0.53
3:E:168:VAL:HB	3:E:307:ILE:HG12	1.90	0.53
2:L:211:PHE:N	2:L:295:LYS:HZ2	2.06	0.53
1:G:425:ILE:O	1:G:429:LEU:HG	2.08	0.53
2:I:47:PHE:HA	2:I:50:ILE:HD11	1.89	0.53
3:H:272:VAL:O	3:H:273:THR:HG23	2.08	0.53
2:F:226:THR:HG21	2:F:282:ILE:HG22	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:63:LYS:O	1:A:100:ARG:NH1	2.41	0.53
1:G:703:LEU:HD21	1:G:738:ARG:HB3	1.91	0.53
1:D:459:LEU:HD12	1:D:462:ARG:HG3	1.90	0.53
1:D:1024:ILE:H	1:D:1024:ILE:HD12	1.74	0.53
1:D:1488:GLU:N	1:D:1488:GLU:OE1	2.36	0.53
1:J:500:ILE:HD11	1:J:517:PHE:CD1	2.44	0.53
2:C:349:GLU:OE1	2:C:349:GLU:N	2.28	0.53
3:E:59:ASN:N	3:E:60:GLU:OE2	2.42	0.53
3:E:246:ASN:OD1	3:E:251:GLY:N	2.42	0.53
2:L:89:VAL:HG13	2:L:93:ILE:HD11	1.90	0.53
3:K:111:LEU:O	3:K:131:LYS:NZ	2.30	0.53
1:A:1163:SER:OG	1:A:1216:ILE:HB	2.07	0.53
3:K:213:VAL:HG12	3:K:214:MET:HE2	1.91	0.53
1:A:6:ILE:HD11	1:G:200:ARG:CZ	2.38	0.53
1:G:1393:ARG:HA	1:G:1396:HIS:CD2	2.42	0.53
1:D:65:GLN:NE2	1:D:71:TRP:HA	2.23	0.53
1:D:717:ILE:O	1:D:721:LEU:HG	2.08	0.53
1:D:1017:LYS:HE2	1:D:1057:TRP:HZ2	1.74	0.53
1:J:1107:SER:OG	1:J:1158:ALA:HA	2.09	0.53
2:C:11:PRO:HB2	2:C:75:ARG:HG2	1.90	0.53
2:L:226:THR:HG21	2:L:282:ILE:HG22	1.90	0.53
1:A:127:GLY:O	1:A:131:ARG:HG2	2.09	0.53
1:A:1252:LEU:HD21	1:A:1284:ALA:HB2	1.91	0.53
1:D:139:LYS:O	1:D:143:LYS:HG3	2.09	0.53
1:D:1488:GLU:CD	1:D:1488:GLU:H	2.16	0.53
1:J:180:VAL:HG12	1:J:230:LEU:HD23	1.91	0.53
1:J:891:ASN:HD22	1:J:894:ARG:NH1	2.07	0.53
1:J:1393:ARG:HA	1:J:1396:HIS:CD2	2.43	0.53
2:I:113:MET:SD	2:I:115:GLN:HG3	2.48	0.53
3:B:114:THR:HB	3:B:285:PHE:CE2	2.43	0.53
3:B:213:VAL:HG12	3:B:214:MET:HE2	1.91	0.53
3:K:74:ASP:O	3:K:76:VAL:N	2.42	0.53
3:K:246:ASN:OD1	3:K:251:GLY:N	2.42	0.53
1:A:809:MET:HE1	1:A:816:LEU:HG	1.91	0.53
1:G:864:ASP:OD1	1:G:865:SER:N	2.40	0.53
3:H:246:ASN:OD1	3:H:251:GLY:N	2.42	0.53
3:K:168:VAL:HB	3:K:307:ILE:HG12	1.90	0.53
1:A:486:ASP:OD1	1:A:488:ASP:N	2.33	0.53
1:D:116:GLN:HG2	1:D:122:TYR:HA	1.91	0.53
1:J:809:MET:HE1	1:J:816:LEU:N	2.24	0.53
2:I:117:ARG:O	2:I:121:LEU:HG	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:168:VAL:HB	3:B:307:ILE:HG12	1.90	0.53
1:A:162:SER:OG	1:A:163:ASP:N	2.41	0.52
1:G:1281:TRP:CE2	1:G:1306:LEU:HD13	2.44	0.52
1:G:1411:ARG:O	1:G:1415:VAL:HG13	2.08	0.52
1:D:1017:LYS:NZ	1:D:1018:ILE:O	2.34	0.52
1:J:1149:TRP:O	1:J:1155:THR:HG21	2.08	0.52
1:J:1281:TRP:HZ3	1:J:1302:LEU:HD21	1.74	0.52
1:J:1321:ILE:HG13	1:J:1322:SER:N	2.23	0.52
1:J:1428:ARG:NH2	1:J:1463:GLN:HB3	2.24	0.52
3:H:114:THR:HB	3:H:285:PHE:CE2	2.43	0.52
2:C:226:THR:HG21	2:C:282:ILE:HG22	1.90	0.52
1:J:1413:PHE:HB3	1:J:1457:TYR:HB2	1.91	0.52
1:G:396:ASP:OD1	1:G:397:PHE:N	2.41	0.52
1:J:1482:GLU:HB3	1:J:1494:MET:HE1	1.92	0.52
3:H:52:VAL:HG13	3:H:57:VAL:HG21	1.92	0.52
2:F:303:THR:H	2:F:394:GLY:C	2.18	0.52
2:L:220:SER:HB2	2:L:284:ARG:NH2	2.25	0.52
1:A:966:MET:HG3	1:A:967:TRP:HD1	1.75	0.52
1:D:951:LEU:HB3	1:D:955:LYS:HG3	1.91	0.52
1:D:1462:LYS:HB2	1:D:1464:ARG:HH22	1.73	0.52
1:J:893:GLU:OE1	1:J:893:GLU:N	2.41	0.52
3:K:89:LEU:HD12	3:K:90:PRO:HD2	1.91	0.52
1:A:57:ILE:HD13	1:A:94:ASN:HB2	1.92	0.52
1:D:653:SER:HG	1:D:656:TRP:HD1	1.58	0.52
1:D:991:CYS:SG	1:D:994:ARG:NH1	2.82	0.52
1:D:1081:SER:OG	1:D:1137:ARG:NH1	2.39	0.52
2:F:220:SER:HB2	2:F:284:ARG:NH2	2.25	0.52
3:E:213:VAL:HG12	3:E:214:MET:HE2	1.91	0.52
1:A:103:PHE:CD2	1:A:159:PHE:HB3	2.45	0.52
1:G:638:GLU:HG3	1:G:639:LYS:HG3	1.91	0.52
1:G:736:LEU:HB3	1:G:737:MET:HE2	1.90	0.52
1:G:1003:ASP:O	1:G:1007:LYS:HG2	2.09	0.52
1:D:563:THR:N	1:D:566:GLU:OE1	2.27	0.52
1:J:295:MET:HE2	1:J:393:ALA:HB2	1.92	0.52
1:J:1214:LEU:HG	1:J:1236:LEU:HG	1.91	0.52
3:B:76:VAL:O	3:B:76:VAL:CG1	2.57	0.52
3:B:91:LEU:HB3	3:B:94:ALA:HB2	1.92	0.52
3:B:246:ASN:OD1	3:B:251:GLY:N	2.42	0.52
1:A:422:ASN:OD1	1:A:423:ASN:N	2.43	0.52
1:A:1439:ILE:HG21	1:A:1446:TYR:HD2	1.75	0.52
1:G:721:LEU:HD13	1:G:724:ILE:HD12	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1057:TRP:N	3:H:279:GLN:HE22	1.97	0.52
1:G:1435:TRP:CE3	1:G:1436:LEU:HD22	2.42	0.52
1:D:817:ASP:O	1:D:821:GLU:HG2	2.09	0.52
1:J:877:ILE:HA	1:J:880:ASN:ND2	2.25	0.52
2:F:68:VAL:HG22	2:F:79:HIS:HB3	1.92	0.52
3:E:76:VAL:O	3:E:76:VAL:CG1	2.57	0.52
2:L:292:VAL:CG1	2:L:334:ARG:HH22	2.21	0.52
2:L:351:VAL:HG11	2:L:357:ILE:HD12	1.92	0.52
1:G:682:HIS:CD2	3:H:217:LEU:HD11	2.45	0.52
1:G:952:PRO:O	1:G:956:GLN:HG2	2.10	0.52
1:G:980:LYS:CG	3:H:282:ASP:OD2	2.57	0.52
1:D:305:ARG:CD	1:D:312:ILE:CD1	2.86	0.52
3:H:76:VAL:O	3:H:76:VAL:CG1	2.57	0.52
3:B:111:LEU:O	3:B:131:LYS:NZ	2.30	0.52
3:E:265:MET:CE	3:E:304:MET:HE3	2.40	0.52
1:A:145:ALA:HB1	1:A:148:LEU:HG	1.92	0.52
1:A:177:ARG:HA	1:A:183:THR:CG2	2.40	0.52
1:A:537:GLN:O	1:J:462:ARG:NH2	2.43	0.52
1:A:1160:GLU:HA	1:A:1213:ALA:HB2	1.92	0.52
1:D:1024:ILE:HG13	3:E:106:PHE:HE1	1.75	0.52
1:J:126:LEU:HD23	1:J:131:ARG:CZ	2.40	0.52
1:J:1467:ASP:OD1	1:J:1472:LEU:HB3	2.10	0.52
2:I:220:SER:HB2	2:I:284:ARG:NH2	2.25	0.52
3:E:52:VAL:HG13	3:E:57:VAL:HG21	1.91	0.52
3:K:52:VAL:HG13	3:K:57:VAL:HG21	1.92	0.52
3:K:91:LEU:HB3	3:K:94:ALA:HB2	1.92	0.52
3:K:114:THR:HB	3:K:285:PHE:CE2	2.43	0.52
1:A:891:ASN:OD1	1:A:894:ARG:NH1	2.43	0.52
1:A:960:MET:HA	1:A:963:ILE:HD12	1.91	0.52
1:A:1124:ASN:OD1	1:A:1124:ASN:N	2.43	0.52
1:D:1180:ILE:HD11	1:D:1231:LEU:HD13	1.91	0.52
1:D:1297:ASP:OD2	1:D:1297:ASP:N	2.42	0.52
1:J:11:GLY:HA2	1:J:63:LYS:HD3	1.91	0.52
2:I:68:VAL:HG22	2:I:79:HIS:HB3	1.92	0.52
3:E:89:LEU:HD12	3:E:90:PRO:HD2	1.91	0.52
1:G:43:LEU:HB3	1:G:82:LYS:HG2	1.91	0.51
1:G:251:ARG:NH2	1:G:303:GLU:OE1	2.41	0.51
1:G:424:GLU:O	1:G:428:LEU:HD23	2.10	0.51
1:G:1282:LYS:NZ	1:G:1314:ASP:OD1	2.37	0.51
1:D:136:ALA:O	1:D:139:LYS:HG3	2.09	0.51
1:D:1070:TRP:CD2	3:E:66:LYS:HG2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:675:GLU:CD	1:J:675:GLU:H	2.18	0.51
1:J:1353:THR:O	1:J:1357:THR:HG23	2.10	0.51
3:H:91:LEU:HB3	3:H:94:ALA:HB2	1.92	0.51
2:C:18:ILE:HD12	2:C:119:HIS:HB3	1.92	0.51
2:C:138:CYS:SG	2:C:172:ARG:HB3	2.50	0.51
3:K:76:VAL:O	3:K:76:VAL:CG1	2.57	0.51
1:A:1120:ASP:OD2	1:A:1122:THR:OG1	2.25	0.51
1:A:1155:THR:O	1:A:1159:LEU:HG	2.11	0.51
1:G:597:ARG:HD3	1:G:631:LEU:HD11	1.92	0.51
1:G:1483:ALA:HA	1:G:1494:MET:HE2	1.92	0.51
1:D:1183:VAL:HG11	1:D:1238:ARG:HD2	1.92	0.51
1:J:720:HIS:O	1:J:723:VAL:HG12	2.10	0.51
1:J:807:GLN:O	1:J:811:GLN:NE2	2.43	0.51
2:I:138:CYS:SG	2:I:172:ARG:HB3	2.50	0.51
3:H:265:MET:CE	3:H:304:MET:HE3	2.40	0.51
3:B:52:VAL:HG13	3:B:57:VAL:HG21	1.92	0.51
3:B:59:ASN:N	3:B:60:GLU:OE2	2.42	0.51
3:E:91:LEU:HB3	3:E:94:ALA:HB2	1.92	0.51
1:D:1437:ASN:OD1	1:D:1478:ARG:NH1	2.43	0.51
3:H:111:LEU:O	3:H:131:LYS:NZ	2.30	0.51
2:F:138:CYS:SG	2:F:172:ARG:HB3	2.51	0.51
1:A:15:GLN:NE2	1:A:46:ASP:O	2.43	0.51
1:A:1214:LEU:HD21	1:A:1236:LEU:HA	1.91	0.51
1:A:1433:ILE:HA	1:A:1436:LEU:HD12	1.93	0.51
1:G:952:PRO:HD2	1:G:955:LYS:HD2	1.90	0.51
1:G:1159:LEU:HD11	1:G:1210:VAL:HA	1.91	0.51
1:G:1286:ARG:HG3	1:G:1290:TYR:HE2	1.74	0.51
1:G:1437:ASN:OD1	1:G:1478:ARG:NH1	2.44	0.51
1:D:73:ILE:HG21	1:D:137:LEU:HD21	1.91	0.51
1:D:797:PHE:HB2	1:D:801:ASN:O	2.11	0.51
1:D:986:ILE:HG21	1:D:998:ALA:HB1	1.93	0.51
1:D:1377:LEU:HD11	1:D:1391:MET:HE1	1.92	0.51
2:I:303:THR:H	2:I:394:GLY:C	2.18	0.51
1:G:1248:ARG:HB3	1:G:1273:VAL:HG13	1.93	0.51
1:D:218:ASP:O	1:D:222:ILE:HG12	2.10	0.51
2:C:220:SER:HB2	2:C:284:ARG:NH2	2.25	0.51
2:C:303:THR:H	2:C:394:GLY:C	2.18	0.51
2:F:302:HIS:N	2:F:367:ILE:O	2.35	0.51
2:L:303:THR:H	2:L:394:GLY:C	2.18	0.51
1:A:60:GLN:HB3	1:A:62:LYS:HZ3	1.75	0.51
1:G:367:ARG:HA	1:G:367:ARG:CZ	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1057:TRP:HB3	2:I:382:ARG:NH1	2.19	0.51
1:J:43:LEU:C	1:J:82:LYS:HZ1	2.18	0.51
3:H:173:ASP:O	3:H:179:ASN:ND2	2.39	0.51
2:C:68:VAL:HG22	2:C:79:HIS:HB3	1.92	0.51
2:C:233:GLU:OE1	2:C:234:ARG:HG2	2.11	0.51
2:C:377:ILE:O	2:C:384:VAL:HG22	2.11	0.51
2:F:233:GLU:OE1	2:F:234:ARG:HG2	2.11	0.51
2:L:138:CYS:SG	2:L:172:ARG:HB3	2.50	0.51
1:G:489:LEU:HD21	1:G:526:LYS:HB3	1.93	0.51
1:G:634:ARG:HG3	1:G:635:GLU:N	2.26	0.51
1:G:1026:ARG:HH21	1:G:1061:LEU:HB3	1.76	0.51
1:D:1393:ARG:HA	1:D:1396:HIS:CD2	2.46	0.51
2:I:61:ILE:HD12	2:I:94:THR:HG21	1.93	0.51
2:F:332:TYR:HA	2:F:336:THR:O	2.09	0.51
2:F:377:ILE:O	2:F:384:VAL:HG22	2.11	0.51
2:L:20:HIS:ND1	2:L:113:MET:SD	2.84	0.51
2:L:82:CYS:HB2	2:L:88:TYR:CE1	2.46	0.51
2:L:233:GLU:OE1	2:L:234:ARG:HG2	2.11	0.51
1:A:63:LYS:HG2	1:A:100:ARG:HH12	1.76	0.51
1:G:1439:ILE:HG23	1:G:1447:ALA:HB2	1.93	0.51
1:D:975:ASP:HB2	1:D:978:VAL:HG12	1.93	0.51
1:J:64:ASN:ND2	1:J:65:GLN:O	2.44	0.51
1:J:1375:ALA:HA	1:J:1378:ASN:HD21	1.75	0.51
2:C:20:HIS:ND1	2:C:113:MET:SD	2.84	0.51
2:C:61:ILE:HD12	2:C:94:THR:HG21	1.93	0.51
2:C:191:GLU:HG2	2:C:195:PHE:CE2	2.46	0.51
2:F:82:CYS:HB2	2:F:88:TYR:CE1	2.46	0.51
1:G:1413:PHE:O	1:G:1417:GLU:HG2	2.10	0.51
1:J:312:ILE:HD13	1:J:352:HIS:HB3	1.92	0.51
2:F:89:VAL:HG13	2:F:93:ILE:HD11	1.90	0.51
3:E:108:ASN:HB3	3:E:289:VAL:HG22	1.93	0.51
1:G:1025:VAL:HG21	3:H:105:ARG:HD2	1.93	0.51
2:I:191:GLU:HG2	2:I:195:PHE:CE2	2.46	0.51
2:C:82:CYS:HB2	2:C:88:TYR:CE1	2.46	0.51
2:F:20:HIS:ND1	2:F:113:MET:SD	2.84	0.51
2:F:391:LYS:HG3	2:F:392:VAL:H	1.76	0.51
2:L:391:LYS:HG3	2:L:392:VAL:H	1.76	0.51
1:G:736:LEU:O	1:G:740:LEU:HG	2.11	0.50
1:D:893:GLU:OE2	1:D:893:GLU:N	2.44	0.50
1:D:1414:SER:O	1:D:1418:ASN:ND2	2.44	0.50
2:I:20:HIS:ND1	2:I:113:MET:SD	2.84	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:100:ASP:O	2:I:129:PRO:HG2	2.12	0.50
2:I:141:VAL:HG11	2:I:146:LEU:HD22	1.94	0.50
2:I:391:LYS:HG3	2:I:392:VAL:H	1.76	0.50
2:C:304:LYS:HE2	2:C:362:THR:HG23	1.93	0.50
2:C:305:PHE:HD2	2:C:306:GLU:O	1.94	0.50
2:F:144:GLU:CD	2:F:172:ARG:HH12	2.19	0.50
1:A:1315:LEU:HD13	1:A:1345:THR:HG21	1.93	0.50
1:G:86:LEU:HD21	1:G:93:VAL:HG11	1.91	0.50
1:D:790:LEU:HB2	1:D:865:SER:HB2	1.94	0.50
1:J:828:TYR:HA	1:J:842:ARG:HH12	1.76	0.50
1:J:1393:ARG:NH1	3:K:196:GLN:O	2.44	0.50
3:H:192:GLU:OE1	3:H:200:HIS:ND1	2.40	0.50
2:C:391:LYS:HG3	2:C:392:VAL:H	1.76	0.50
3:B:74:ASP:O	3:B:76:VAL:N	2.42	0.50
2:F:336:THR:HG22	2:F:337:ASP:H	1.76	0.50
2:L:68:VAL:HG22	2:L:79:HIS:HB3	1.92	0.50
2:L:191:GLU:HG2	2:L:195:PHE:CE2	2.46	0.50
3:K:173:ASP:O	3:K:179:ASN:ND2	2.39	0.50
1:G:1139:LEU:O	1:G:1143:GLU:HG2	2.12	0.50
1:G:1320:ARG:HD3	3:H:81:ILE:HG22	1.92	0.50
1:D:1163:SER:OG	1:D:1216:ILE:HB	2.11	0.50
1:J:18:VAL:HG22	1:J:168:MET:HE1	1.93	0.50
1:J:715:ASP:OD1	1:J:715:ASP:N	2.44	0.50
1:J:736:LEU:O	1:J:740:LEU:HD12	2.12	0.50
1:J:1338:ASN:HA	1:J:1341:ASN:HD21	1.76	0.50
2:I:349:GLU:OE1	2:I:349:GLU:N	2.28	0.50
2:C:106:VAL:O	2:C:136:ASN:N	2.35	0.50
2:C:351:VAL:HG11	2:C:357:ILE:HD12	1.93	0.50
1:G:763:ILE:HG21	1:G:767:LEU:HD22	1.92	0.50
1:D:1415:VAL:HA	1:D:1418:ASN:HD21	1.77	0.50
2:I:82:CYS:HB2	2:I:88:TYR:CE1	2.46	0.50
3:E:78:ILE:HA	3:E:81:ILE:HD12	1.94	0.50
1:A:981:SER:HA	1:A:984:GLU:CD	2.36	0.50
1:G:733:VAL:O	1:G:737:MET:HG2	2.11	0.50
1:G:841:TYR:CE2	1:G:931:MET:HG3	2.47	0.50
1:G:1433:ILE:HD12	1:G:1433:ILE:H	1.75	0.50
1:D:359:SER:O	1:D:359:SER:OG	2.19	0.50
1:J:574:VAL:HG22	1:J:577:VAL:HG23	1.93	0.50
2:I:336:THR:HG22	2:I:337:ASP:H	1.77	0.50
2:I:343:GLU:O	2:I:360:VAL:HG12	2.12	0.50
2:F:305:PHE:HD2	2:F:306:GLU:O	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:25:LYS:N	6:L:401:GTP:O2B	2.39	0.50
2:L:377:ILE:O	2:L:384:VAL:HG22	2.11	0.50
3:K:165:ILE:HA	3:K:301:PRO:O	2.12	0.50
1:A:1282:LYS:NZ	1:A:1313:LYS:O	2.37	0.50
1:G:522:ASP:OD1	1:G:523:ILE:N	2.44	0.50
1:D:736:LEU:O	1:D:740:LEU:HG	2.12	0.50
1:J:1414:SER:O	1:J:1418:ASN:ND2	2.44	0.50
3:B:148:TRP:HB3	3:B:243:PHE:CZ	2.47	0.50
2:F:100:ASP:O	2:F:129:PRO:HG2	2.12	0.50
2:F:191:GLU:HG2	2:F:195:PHE:CE2	2.46	0.50
2:F:343:GLU:O	2:F:360:VAL:HG12	2.12	0.50
2:L:305:PHE:HD2	2:L:306:GLU:O	1.94	0.50
1:A:249:ILE:HD11	1:D:381:ARG:HD2	1.94	0.50
1:G:945:ARG:HE	1:G:988:SER:HA	1.77	0.50
1:G:1024:ILE:HG21	3:H:104:PHE:HD1	1.76	0.50
1:D:807:GLN:O	1:D:811:GLN:NE2	2.44	0.50
2:I:144:GLU:CD	2:I:172:ARG:HH12	2.19	0.50
2:I:244:GLU:CB	2:I:294:ALA:O	2.53	0.50
3:B:201:VAL:HG11	3:B:257:ALA:HB1	1.93	0.50
1:G:116:GLN:HG3	1:G:122:TYR:HA	1.94	0.50
1:G:1004:THR:O	1:G:1008:LYS:NZ	2.44	0.50
1:G:1488:GLU:CD	1:G:1488:GLU:H	2.19	0.50
2:I:304:LYS:HE2	2:I:362:THR:HG23	1.93	0.50
3:H:78:ILE:HA	3:H:81:ILE:HD12	1.94	0.50
3:H:201:VAL:HG11	3:H:257:ALA:HB1	1.94	0.50
2:C:82:CYS:HB2	2:C:88:TYR:CD1	2.47	0.50
2:C:144:GLU:CD	2:C:172:ARG:HH12	2.19	0.50
3:E:71:PRO:HB3	3:E:96:MET:HE3	1.94	0.50
2:L:144:GLU:CD	2:L:172:ARG:HH12	2.19	0.50
3:K:148:TRP:HB3	3:K:243:PHE:CZ	2.47	0.50
1:G:1241:ARG:HG3	1:G:1275:GLN:HE22	1.75	0.50
1:J:729:LEU:O	1:J:732:VAL:HG12	2.11	0.50
1:J:733:VAL:HG12	1:J:737:MET:HE1	1.94	0.50
2:I:82:CYS:HB2	2:I:88:TYR:CD1	2.47	0.50
2:C:343:GLU:O	2:C:360:VAL:HG12	2.12	0.50
3:B:71:PRO:HB3	3:B:96:MET:HE3	1.94	0.50
3:B:165:ILE:HA	3:B:301:PRO:O	2.12	0.50
2:L:100:ASP:O	2:L:129:PRO:HG2	2.12	0.50
1:A:634:ARG:HG3	1:A:635:GLU:N	2.27	0.49
1:A:1043:LEU:HD22	1:A:1093:ASP:HB3	1.93	0.49
1:A:1269:LEU:O	1:A:1273:VAL:HG23	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:233:GLU:OE1	2:I:234:ARG:HG2	2.11	0.49
3:H:148:TRP:HB3	3:H:243:PHE:CZ	2.47	0.49
2:C:25:LYS:N	6:C:401:GTP:O2B	2.39	0.49
2:F:331:PHE:CE1	2:F:377:ILE:HG23	2.47	0.49
3:E:192:GLU:OE1	3:E:200:HIS:ND1	2.40	0.49
2:L:292:VAL:CB	2:L:334:ARG:NH1	2.75	0.49
1:G:680:HIS:O	1:G:684:ILE:HG13	2.12	0.49
1:D:164:ASP:OD1	1:D:165:LEU:N	2.39	0.49
1:D:748:SER:OG	1:D:750:LEU:HG	2.11	0.49
1:D:1203:LEU:HD12	3:E:71:PRO:HD3	1.93	0.49
2:I:211:PHE:CD1	2:I:212:LEU:N	2.81	0.49
3:H:165:ILE:HA	3:H:301:PRO:O	2.12	0.49
3:E:261:ASP:OD1	3:E:262:PRO:HD2	2.12	0.49
2:L:141:VAL:HG11	2:L:146:LEU:HD22	1.94	0.49
2:L:331:PHE:CE1	2:L:377:ILE:HG23	2.47	0.49
2:L:343:GLU:O	2:L:360:VAL:HG12	2.12	0.49
1:A:1370:PHE:CD1	1:A:1373:ILE:HD11	2.46	0.49
1:G:180:VAL:CG1	1:G:228:SER:OG	2.60	0.49
1:G:318:GLN:HE21	1:G:320:ARG:HG2	1.77	0.49
2:I:331:PHE:CE1	2:I:377:ILE:HG23	2.47	0.49
2:I:377:ILE:O	2:I:384:VAL:HG22	2.11	0.49
2:C:100:ASP:O	2:C:129:PRO:HG2	2.12	0.49
3:B:149:SER:O	3:B:158:SER:HB3	2.13	0.49
3:B:261:ASP:OD1	3:B:262:PRO:HD2	2.12	0.49
2:F:304:LYS:HE2	2:F:362:THR:HG23	1.93	0.49
3:E:148:TRP:HB3	3:E:243:PHE:CZ	2.47	0.49
2:L:82:CYS:HB2	2:L:88:TYR:CD1	2.47	0.49
2:L:304:LYS:HE2	2:L:362:THR:HG23	1.93	0.49
3:K:71:PRO:HB3	3:K:96:MET:HE3	1.94	0.49
1:A:1375:ALA:HA	1:A:1378:ASN:HD21	1.77	0.49
1:G:668:LEU:HD21	1:G:676:GLY:C	2.37	0.49
1:G:779:GLU:HG3	1:G:783:GLN:NE2	2.27	0.49
1:G:1057:TRP:HD1	2:I:320:HIS:CE1	2.31	0.49
1:G:1136:ASN:HA	1:G:1171:LYS:HE2	1.93	0.49
1:G:1377:LEU:HD11	1:G:1415:VAL:HG11	1.94	0.49
1:G:1468:HIS:CE1	3:H:182:ASN:HD22	2.29	0.49
1:D:1338:ASN:HA	1:D:1341:ASN:HD21	1.76	0.49
1:J:966:MET:HG3	1:J:967:TRP:HD1	1.77	0.49
2:I:26:THR:O	2:I:29:THR:OG1	2.28	0.49
2:I:242:GLU:OE1	2:I:253:LYS:NZ	2.43	0.49
2:C:141:VAL:HG11	2:C:146:LEU:HD22	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:82:CYS:HB2	2:F:88:TYR:CD1	2.47	0.49
2:F:211:PHE:CD1	2:F:212:LEU:N	2.81	0.49
2:L:61:ILE:HD13	2:L:312:LEU:HD21	1.93	0.49
3:K:261:ASP:OD1	3:K:262:PRO:HD2	2.12	0.49
3:K:265:MET:CE	3:K:304:MET:HE3	2.40	0.49
1:A:139:LYS:O	1:A:143:LYS:HG3	2.13	0.49
1:A:754:ILE:O	1:A:758:VAL:HG23	2.13	0.49
1:J:1415:VAL:HA	1:J:1418:ASN:HD21	1.76	0.49
2:I:367:ILE:HG22	2:I:368:ALA:N	2.28	0.49
3:H:71:PRO:HB3	3:H:96:MET:HE3	1.94	0.49
3:H:261:ASP:OD1	3:H:262:PRO:HD2	2.12	0.49
2:C:336:THR:HG22	2:C:337:ASP:H	1.77	0.49
3:K:204:ILE:O	3:K:205:LEU:HD23	2.13	0.49
1:A:677:VAL:O	1:A:681:VAL:HG23	2.13	0.49
1:D:948:PHE:HA	1:D:951:LEU:HD13	1.93	0.49
1:D:1017:LYS:HZ1	3:E:111:LEU:HD11	1.77	0.49
1:J:692:THR:O	1:J:696:VAL:HG12	2.12	0.49
2:I:245:ILE:HD13	2:I:287:ILE:HD11	1.95	0.49
2:I:305:PHE:HD2	2:I:306:GLU:O	1.94	0.49
2:C:331:PHE:CE2	2:C:361:VAL:HG11	2.47	0.49
2:L:331:PHE:CE2	2:L:361:VAL:HG11	2.47	0.49
3:K:149:SER:O	3:K:158:SER:HB3	2.12	0.49
1:A:270:ILE:HD11	1:A:283:LEU:HD12	1.95	0.49
1:D:234:MET:SD	1:D:237:VAL:HG11	2.52	0.49
1:D:693:ALA:O	1:D:697:SER:OG	2.27	0.49
1:D:849:THR:OG1	1:D:850:SER:N	2.44	0.49
1:D:987:VAL:HG21	1:D:1012:LEU:HD21	1.95	0.49
1:D:1411:ARG:HA	1:D:1414:SER:OG	2.12	0.49
2:C:292:VAL:CG1	2:C:334:ARG:HH22	2.23	0.49
2:F:242:GLU:OE1	2:F:253:LYS:NZ	2.43	0.49
2:L:367:ILE:HG22	2:L:368:ALA:N	2.28	0.49
3:K:178:GLN:O	3:K:182:ASN:HB2	2.13	0.49
1:A:733:VAL:O	1:A:737:MET:HG2	2.13	0.49
1:A:1058:ASN:OD1	2:C:382:ARG:NH1	2.45	0.49
1:J:820:VAL:HA	1:J:823:ILE:HD12	1.95	0.49
1:J:1103:MET:SD	1:J:1158:ALA:HB2	2.52	0.49
2:I:124:ARG:HD2	2:I:161:TYR:HB3	1.95	0.49
3:H:204:ILE:O	3:H:205:LEU:HD23	2.13	0.49
2:C:243:VAL:HG11	2:C:293:LEU:HG	1.95	0.49
3:B:178:GLN:O	3:B:182:ASN:HB2	2.13	0.49
2:F:61:ILE:HD12	2:F:94:THR:HG21	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:336:THR:HG22	2:L:337:ASP:H	1.77	0.49
1:A:697:SER:HA	1:A:700:ILE:HD12	1.94	0.49
1:G:1024:ILE:HG23	3:H:104:PHE:HB3	1.95	0.49
1:G:1510:VAL:O	1:G:1513:ILE:HG22	2.13	0.49
1:D:1048:HIS:CD2	2:F:322:PRO:HD3	2.47	0.49
1:D:1356:TRP:CD1	1:D:1369:CYS:HA	2.48	0.49
1:J:507:MET:HG3	1:J:509:SER:HB3	1.95	0.49
1:J:1112:HIS:CE1	1:J:1117:LEU:HD22	2.48	0.49
1:J:1435:TRP:HE3	1:J:1436:LEU:HD22	1.77	0.49
1:J:1487:GLU:OE1	1:J:1492:GLY:HA2	2.12	0.49
2:I:235:GLY:H	2:I:271:ALA:HB2	1.78	0.49
2:I:243:VAL:HG11	2:I:293:LEU:CD2	2.43	0.49
3:B:204:ILE:O	3:B:205:LEU:HD23	2.13	0.49
2:F:141:VAL:HG11	2:F:146:LEU:HD22	1.94	0.49
2:F:268:GLU:CD	2:F:270:ARG:HH12	2.21	0.49
3:E:201:VAL:HG11	3:E:257:ALA:HB1	1.93	0.49
1:A:205:ARG:HH11	1:A:211:GLN:HG3	1.78	0.49
1:A:1362:MET:HA	1:A:1369:CYS:SG	2.53	0.49
1:G:1115:GLY:HA2	1:G:1164:HIS:CE1	2.48	0.49
1:G:1159:LEU:HD11	1:G:1210:VAL:HG12	1.95	0.49
2:I:268:GLU:CD	2:I:270:ARG:HH12	2.21	0.49
2:I:331:PHE:CE2	2:I:361:VAL:HG11	2.47	0.49
3:H:74:ASP:O	3:H:76:VAL:N	2.42	0.49
3:H:149:SER:O	3:H:158:SER:HB3	2.12	0.49
3:H:178:GLN:O	3:H:182:ASN:HB2	2.13	0.49
3:H:269:ILE:HG13	3:H:269:ILE:O	2.13	0.49
3:H:278:ALA:HB2	3:H:287:TYR:CZ	2.48	0.49
2:C:245:ILE:HD13	2:C:287:ILE:HD11	1.95	0.49
2:C:268:GLU:CD	2:C:270:ARG:HH12	2.21	0.49
3:E:149:SER:O	3:E:158:SER:HB3	2.12	0.49
3:E:178:GLN:O	3:E:182:ASN:HB2	2.13	0.49
2:L:211:PHE:CD1	2:L:212:LEU:N	2.81	0.49
1:A:714:ALA:HB1	1:A:739:LEU:HD11	1.95	0.48
1:A:1393:ARG:HA	1:A:1396:HIS:CD2	2.48	0.48
1:G:454:ALA:O	1:G:458:GLU:HG2	2.13	0.48
1:G:1214:LEU:HD22	1:G:1236:LEU:HD13	1.95	0.48
1:G:1242:ASP:OD1	1:G:1247:VAL:HG21	2.12	0.48
1:D:1176:LEU:HD21	1:D:1232:LEU:HA	1.95	0.48
1:J:513:PRO:HB2	1:J:515:GLN:HE22	1.78	0.48
1:J:1117:LEU:HA	3:K:98:GLU:HB2	1.94	0.48
3:H:163:PRO:O	3:H:164:ASN:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:211:PHE:CD1	2:C:212:LEU:N	2.81	0.48
2:C:243:VAL:HG11	2:C:293:LEU:CD2	2.43	0.48
3:B:269:ILE:O	3:B:269:ILE:HG13	2.13	0.48
3:E:114:THR:CG2	3:E:283:LEU:HD12	2.42	0.48
3:E:165:ILE:HA	3:E:301:PRO:O	2.12	0.48
2:L:268:GLU:CD	2:L:270:ARG:HH12	2.21	0.48
1:D:733:VAL:O	1:D:737:MET:HG2	2.12	0.48
1:D:1155:THR:O	1:D:1159:LEU:HG	2.13	0.48
1:J:1310:GLY:O	1:J:1311:ARG:NH1	2.40	0.48
2:C:254:SER:OG	2:C:255:THR:N	2.46	0.48
3:B:78:ILE:HA	3:B:81:ILE:HD12	1.94	0.48
2:F:331:PHE:CE2	2:F:361:VAL:HG11	2.47	0.48
3:K:201:VAL:HG11	3:K:257:ALA:HB1	1.94	0.48
1:A:767:LEU:H	1:A:767:LEU:HD12	1.78	0.48
1:G:1136:ASN:ND2	1:G:1171:LYS:HE2	2.28	0.48
1:D:1172:ALA:HB3	1:D:1229:PRO:HG2	1.95	0.48
1:J:262:ILE:O	4:J:1601:ATP:N6	2.47	0.48
2:C:331:PHE:CE1	2:C:377:ILE:HG23	2.47	0.48
3:B:278:ALA:HB2	3:B:287:TYR:CZ	2.48	0.48
3:E:74:ASP:O	3:E:76:VAL:N	2.42	0.48
3:E:204:ILE:O	3:E:205:LEU:HD23	2.13	0.48
2:L:254:SER:OG	2:L:255:THR:N	2.46	0.48
3:K:78:ILE:HA	3:K:81:ILE:HD12	1.94	0.48
1:A:105:ASP:HA	1:A:108:LYS:HG2	1.96	0.48
1:A:922:ILE:HA	1:A:925:MET:HG2	1.94	0.48
1:D:1448:LEU:HD13	1:D:1479:LEU:HD22	1.95	0.48
2:C:299:ILE:C	2:C:300:LYS:HD3	2.39	0.48
2:C:367:ILE:HG22	2:C:368:ALA:N	2.28	0.48
2:F:367:ILE:HG22	2:F:368:ALA:N	2.28	0.48
2:L:299:ILE:C	2:L:300:LYS:HD3	2.39	0.48
3:K:269:ILE:HG13	3:K:269:ILE:O	2.13	0.48
1:A:201:MET:HE1	1:G:165:LEU:HB3	1.96	0.48
1:G:85:LEU:HD23	1:G:144:ILE:HG21	1.95	0.48
1:G:1501:ILE:O	1:G:1505:LEU:HG	2.13	0.48
1:D:929:ARG:NH2	1:D:969:ASP:OD1	2.47	0.48
1:J:126:LEU:HG	1:J:131:ARG:HG2	1.94	0.48
2:I:20:HIS:CD2	2:I:22:ASP:H	2.32	0.48
2:L:169:PRO:HG3	2:L:199:TYR:CE2	2.49	0.48
2:L:218:VAL:HG21	2:L:287:ILE:CG2	2.44	0.48
1:A:870:PHE:HA	1:A:873:VAL:HG12	1.96	0.48
1:A:1056:ASP:HB3	1:A:1059:ASP:OD2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1058:ASN:ND2	2:C:382:ARG:HD3	2.28	0.48
1:G:922:ILE:HG21	1:G:947:ILE:HG21	1.94	0.48
1:D:808:ARG:O	1:D:812:SER:OG	2.31	0.48
1:D:1462:LYS:HD3	3:E:231:ARG:NH2	2.28	0.48
2:C:235:GLY:H	2:C:271:ALA:HB2	1.78	0.48
3:B:265:MET:CE	3:B:304:MET:HE3	2.40	0.48
2:F:174:SER:HB3	2:F:185:TRP:NE1	2.29	0.48
2:L:302:HIS:N	2:L:367:ILE:O	2.35	0.48
1:G:536:THR:HG22	1:G:540:LYS:H	1.78	0.48
1:G:692:THR:OG1	1:G:728:ASN:ND2	2.47	0.48
1:G:757:CYS:SG	1:G:762:VAL:HB	2.53	0.48
1:G:956:GLN:O	1:G:960:MET:HG2	2.14	0.48
1:G:1299:VAL:HG13	1:G:1303:LEU:HD13	1.96	0.48
1:D:1333:PHE:O	1:D:1337:LEU:HG	2.14	0.48
1:J:267:VAL:O	1:J:271:LEU:HG	2.14	0.48
1:J:614:ARG:HG2	1:J:618:GLU:OE2	2.13	0.48
2:I:174:SER:HB3	2:I:185:TRP:NE1	2.29	0.48
2:F:169:PRO:HG3	2:F:199:TYR:CE2	2.49	0.48
3:K:192:GLU:OE1	3:K:200:HIS:ND1	2.40	0.48
3:K:278:ALA:HB2	3:K:287:TYR:CZ	2.48	0.48
1:A:497:ILE:O	1:A:500:ILE:HG22	2.14	0.48
1:A:1172:ALA:HA	1:A:1175:LEU:HD12	1.96	0.48
1:G:1448:LEU:HD12	1:G:1479:LEU:HD11	1.96	0.48
1:D:1424:LYS:HD3	1:D:1426:HIS:CE1	2.49	0.48
1:J:103:PHE:CD1	1:J:159:PHE:HD1	2.32	0.48
2:I:299:ILE:C	2:I:300:LYS:HD3	2.39	0.48
2:F:245:ILE:HD13	2:F:287:ILE:HD11	1.95	0.48
2:L:124:ARG:HD2	2:L:161:TYR:HB3	1.95	0.48
2:L:235:GLY:H	2:L:271:ALA:HB2	1.78	0.48
2:L:243:VAL:HG11	2:L:293:LEU:CD2	2.43	0.48
1:G:439:ILE:HB	1:G:444:ARG:HH21	1.79	0.48
1:G:668:LEU:HD12	1:G:673:ASP:HB3	1.95	0.48
1:G:992:HIS:HD2	2:I:274:ASN:O	1.97	0.48
1:G:1005:TYR:HE2	1:G:1012:LEU:HD22	1.79	0.48
1:G:1488:GLU:OE1	1:G:1488:GLU:N	2.44	0.48
1:D:140:GLN:HA	1:D:143:LYS:HE2	1.96	0.48
1:J:1203:LEU:CD1	3:K:71:PRO:HD3	2.44	0.48
1:J:1285:GLU:CD	1:J:1317:THR:HG22	2.39	0.48
1:J:1400:GLU:OE1	1:J:1401:VAL:N	2.47	0.48
2:C:124:ARG:HD2	2:C:161:TYR:HB3	1.95	0.48
2:C:174:SER:HB3	2:C:185:TRP:NE1	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:163:PRO:O	3:B:164:ASN:HB2	2.13	0.48
2:F:243:VAL:HG11	2:F:293:LEU:HG	1.95	0.48
1:A:78:ASP:OD1	1:A:78:ASP:N	2.45	0.48
1:A:126:LEU:HD13	1:A:134:ASP:OD2	2.14	0.48
1:A:920:ASP:OD2	1:A:920:ASP:N	2.47	0.48
1:A:1300:GLU:O	1:A:1303:LEU:HG	2.14	0.48
1:D:1103:MET:HG2	1:D:1149:TRP:CH2	2.49	0.48
1:J:185:SER:OG	1:J:226:SER:OG	2.32	0.48
1:J:1100:ASP:OD2	1:J:1152:ARG:NH1	2.46	0.48
1:J:1154:SER:HA	1:J:1157:LYS:HE2	1.96	0.48
1:J:1350:HIS:O	1:J:1354:THR:HG23	2.13	0.48
3:H:185:THR:HA	3:H:188:ILE:HG12	1.96	0.48
2:C:138:CYS:SG	2:C:173:GLY:N	2.75	0.48
2:C:169:PRO:HG3	2:C:199:TYR:CE2	2.49	0.48
2:L:238:LYS:HB2	2:L:241:GLU:CD	2.39	0.48
2:L:245:ILE:HD13	2:L:287:ILE:HD11	1.95	0.48
1:A:1123:TRP:CH2	1:A:1125:PRO:HG3	2.49	0.47
1:D:1166:ILE:HG13	1:D:1175:LEU:HD11	1.95	0.47
1:J:36:GLU:HG2	1:J:213:ARG:HA	1.96	0.47
1:J:76:LEU:O	1:J:80:LEU:HG	2.13	0.47
2:I:391:LYS:HG3	2:I:392:VAL:N	2.29	0.47
2:F:243:VAL:HG11	2:F:293:LEU:CD2	2.43	0.47
2:L:20:HIS:CD2	2:L:22:ASP:H	2.32	0.47
1:A:201:MET:HE3	1:A:201:MET:HB3	1.62	0.47
1:A:1175:LEU:HD13	1:A:1217:LEU:HD21	1.95	0.47
1:G:733:VAL:HG13	1:G:737:MET:HE3	1.94	0.47
1:D:756:ASN:O	1:D:759:ALA:HB3	2.13	0.47
1:D:757:CYS:SG	1:D:762:VAL:HB	2.54	0.47
1:D:874:GLU:HB2	1:D:906:PHE:CE1	2.49	0.47
1:J:586:ALA:O	1:J:589:ALA:HB3	2.15	0.47
1:J:1203:LEU:HD12	3:K:71:PRO:HD3	1.96	0.47
1:J:1208:GLY:N	1:J:1247:VAL:HG12	2.28	0.47
3:B:185:THR:HA	3:B:188:ILE:HG12	1.96	0.47
2:F:218:VAL:HG21	2:F:287:ILE:CG2	2.44	0.47
3:E:105:ARG:HG3	3:E:105:ARG:HH11	1.79	0.47
3:E:163:PRO:O	3:E:164:ASN:HB2	2.14	0.47
3:E:278:ALA:HB2	3:E:287:TYR:CZ	2.48	0.47
3:K:105:ARG:HH11	3:K:105:ARG:HG3	1.79	0.47
1:A:1406:ILE:H	1:A:1406:ILE:HD12	1.79	0.47
1:G:207:SER:OG	1:G:209:ALA:O	2.30	0.47
1:G:327:THR:O	1:G:331:ARG:NH1	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1007:LYS:C	2:I:59:ARG:H	2.17	0.47
1:D:1362:MET:HE1	1:D:1394:ILE:HG12	1.95	0.47
1:J:1000:ALA:O	1:J:1004:THR:HG23	2.14	0.47
3:B:105:ARG:HH11	3:B:105:ARG:HG3	1.79	0.47
2:F:151:GLU:O	2:F:152:MET:HE2	2.15	0.47
2:F:235:GLY:H	2:F:271:ALA:HB2	1.78	0.47
2:F:299:ILE:C	2:F:300:LYS:HD3	2.39	0.47
2:F:391:LYS:HG3	2:F:392:VAL:N	2.30	0.47
2:L:243:VAL:HG11	2:L:293:LEU:HG	1.95	0.47
3:K:185:THR:HA	3:K:188:ILE:HG12	1.97	0.47
1:A:198:GLY:O	1:G:9:ASN:ND2	2.47	0.47
1:A:771:TYR:HA	1:A:774:ASP:OD2	2.14	0.47
1:A:1323:ALA:HB3	1:A:1355:VAL:HG11	1.97	0.47
1:A:1499:VAL:HG22	1:A:1502:GLN:HE22	1.79	0.47
1:D:990:PRO:HB3	2:F:219:PHE:CE2	2.48	0.47
1:D:1021:HIS:O	3:E:108:ASN:HA	2.14	0.47
1:J:1019:HIS:ND1	1:J:1020:SER:HB3	2.29	0.47
1:J:1494:MET:O	1:J:1498:VAL:HG13	2.13	0.47
2:I:228:VAL:O	2:I:276:GLY:HA2	2.14	0.47
2:C:26:THR:O	2:C:29:THR:OG1	2.28	0.47
2:C:88:TYR:O	2:C:92:MET:HG2	2.15	0.47
2:C:158:LEU:HD12	2:C:168:THR:HG21	1.97	0.47
2:L:174:SER:HB3	2:L:185:TRP:NE1	2.29	0.47
2:L:356:ASN:O	2:L:357:ILE:CG1	2.60	0.47
1:A:54:GLY:C	1:A:92:LYS:HE3	2.40	0.47
1:A:1459:ASP:OD1	1:A:1508:LEU:HD21	2.14	0.47
1:D:1004:THR:HA	1:D:1007:LYS:HD2	1.96	0.47
1:J:422:ASN:OD1	1:J:423:ASN:N	2.46	0.47
1:J:563:THR:HG1	1:J:564:LEU:H	1.60	0.47
2:I:357:ILE:HG13	2:I:358:LYS:N	2.28	0.47
2:C:238:LYS:HB2	2:C:241:GLU:CD	2.39	0.47
2:C:391:LYS:HG3	2:C:392:VAL:N	2.30	0.47
2:F:88:TYR:O	2:F:92:MET:HG2	2.15	0.47
2:L:339:THR:O	2:L:364:ILE:HG12	2.15	0.47
2:L:391:LYS:HG3	2:L:392:VAL:N	2.30	0.47
1:A:588:LEU:HB3	1:A:596:TYR:HD2	1.80	0.47
1:A:1215:MET:SD	1:A:1251:ILE:HG23	2.55	0.47
1:G:517:PHE:HE2	1:G:519:ALA:HB3	1.79	0.47
1:G:728:ASN:O	1:G:731:VAL:HG12	2.14	0.47
1:G:1417:GLU:OE1	1:G:1457:TYR:HA	2.15	0.47
1:D:193:LYS:HD3	1:D:196:GLN:HE21	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:136:ALA:O	1:J:139:LYS:HG2	2.14	0.47
1:J:1472:LEU:HD21	1:J:1505:LEU:HD11	1.95	0.47
2:I:305:PHE:CE1	2:I:363:LEU:HD21	2.50	0.47
2:C:15:VAL:HG13	2:C:79:HIS:CD2	2.48	0.47
2:F:124:ARG:HD2	2:F:161:TYR:HB3	1.95	0.47
2:F:176:LEU:HB2	6:F:401:GTP:C5	2.50	0.47
1:A:2:SER:OG	1:A:3:ILE:N	2.48	0.47
1:A:123:GLN:HA	1:A:126:LEU:HD12	1.96	0.47
1:A:557:ALA:O	1:A:562:VAL:HG12	2.15	0.47
1:G:598:LYS:HD3	1:G:599:GLN:HE22	1.79	0.47
1:G:1236:LEU:HD23	1:G:1265:PHE:CZ	2.49	0.47
1:D:878:LEU:O	1:D:882:LYS:HG3	2.14	0.47
1:J:888:TRP:HZ3	1:J:895:LEU:HD23	1.78	0.47
2:I:25:LYS:N	6:I:401:GTP:O2B	2.39	0.47
2:I:66:SER:HB2	2:I:81:ASP:O	2.15	0.47
2:I:106:VAL:O	2:I:136:ASN:N	2.35	0.47
2:I:243:VAL:HG11	2:I:293:LEU:HG	1.95	0.47
2:I:339:THR:O	2:I:364:ILE:HG12	2.15	0.47
3:H:105:ARG:HG3	3:H:105:ARG:HH11	1.79	0.47
2:C:20:HIS:CD2	2:C:22:ASP:H	2.32	0.47
2:C:344:LEU:CD2	2:C:348:VAL:HB	2.44	0.47
3:E:269:ILE:O	3:E:269:ILE:HG13	2.13	0.47
2:L:228:VAL:O	2:L:276:GLY:HA2	2.14	0.47
3:K:218:VAL:HB	3:K:221:THR:OG1	2.15	0.47
1:A:24:LEU:HD23	1:A:24:LEU:HA	1.75	0.47
1:A:651:GLY:O	1:A:683:ARG:NH2	2.48	0.47
1:D:1124:ASN:OD1	1:D:1124:ASN:N	2.48	0.47
1:D:1374:LYS:O	1:D:1378:ASN:ND2	2.47	0.47
1:J:1374:LYS:O	1:J:1378:ASN:ND2	2.47	0.47
2:F:20:HIS:CD2	2:F:22:ASP:H	2.32	0.47
2:F:25:LYS:N	6:F:401:GTP:O2B	2.39	0.47
2:F:339:THR:O	2:F:364:ILE:HG12	2.15	0.47
2:L:151:GLU:O	2:L:152:MET:HE2	2.15	0.47
1:A:966:MET:HG3	1:A:967:TRP:CD1	2.50	0.47
1:A:1423:GLU:HG2	1:A:1425:LYS:HG3	1.97	0.47
1:G:499:ALA:HA	1:G:556:ARG:NH1	2.29	0.47
1:G:1199:LEU:O	1:G:1203:LEU:HG	2.15	0.47
1:D:374:TYR:O	1:D:378:GLN:HG2	2.14	0.47
1:D:750:LEU:O	1:D:753:VAL:HB	2.15	0.47
1:D:1104:SER:O	1:D:1108:THR:HG23	2.15	0.47
1:D:1286:ARG:HH21	3:E:80:GLN:HE21	1.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1333:PHE:CZ	1:D:1337:LEU:HD21	2.50	0.47
1:J:1476:MET:O	1:J:1479:LEU:HG	2.15	0.47
2:I:176:LEU:HB2	6:I:401:GTP:C5	2.50	0.47
2:I:238:LYS:HB2	2:I:241:GLU:CD	2.39	0.47
2:C:117:ARG:HH21	2:C:157:LEU:HD23	1.80	0.47
2:C:176:LEU:HB2	6:C:401:GTP:C5	2.50	0.47
2:F:117:ARG:HH21	2:F:157:LEU:HD23	1.80	0.47
1:A:1338:ASN:HA	1:A:1341:ASN:ND2	2.30	0.47
1:G:816:LEU:HD21	1:G:877:ILE:HD13	1.96	0.47
1:D:1048:HIS:HD2	2:F:322:PRO:HD3	1.80	0.47
1:D:1431:GLY:O	1:D:1434:GLU:HG2	2.14	0.47
1:D:1502:GLN:NE2	1:D:1517:LEU:HD13	2.30	0.47
1:J:326:ALA:HB2	1:J:368:GLU:HG3	1.95	0.47
1:J:328:SER:OG	1:J:338:GLN:HG2	2.15	0.47
1:J:948:PHE:HA	1:J:951:LEU:HD13	1.96	0.47
1:J:1143:GLU:OE2	1:J:1174:GLN:NE2	2.48	0.47
2:I:138:CYS:SG	2:I:173:GLY:N	2.75	0.47
2:I:169:PRO:HG3	2:I:199:TYR:CE2	2.49	0.47
2:C:228:VAL:O	2:C:276:GLY:HA2	2.14	0.47
3:B:192:GLU:OE1	3:B:200:HIS:ND1	2.40	0.47
2:F:67:HIS:HD1	2:F:80:VAL:HA	1.79	0.47
3:E:139:HIS:NE2	3:E:291:SER:HB2	2.30	0.47
2:L:176:LEU:HB2	6:L:401:GTP:C5	2.50	0.47
3:K:163:PRO:O	3:K:164:ASN:HB2	2.13	0.47
1:A:191:TRP:CD1	1:G:192:MET:HG2	2.51	0.46
1:A:1103:MET:HE1	1:A:1155:THR:HA	1.97	0.46
1:A:1264:ASP:OD2	1:A:1264:ASP:N	2.46	0.46
1:G:904:LEU:O	1:G:908:ILE:HG13	2.15	0.46
1:G:1133:LEU:HA	1:G:1136:ASN:OD1	2.15	0.46
1:J:266:ILE:O	1:J:270:ILE:HG13	2.16	0.46
1:J:1277:ALA:HA	1:J:1280:LEU:HD21	1.96	0.46
2:C:242:GLU:OE1	2:C:253:LYS:NZ	2.43	0.46
2:F:228:VAL:O	2:F:276:GLY:HA2	2.14	0.46
3:E:225:TYR:O	3:E:226:GLY:C	2.59	0.46
2:L:67:HIS:HD1	2:L:80:VAL:HA	1.79	0.46
1:A:179:LEU:HD23	1:A:179:LEU:HA	1.68	0.46
1:A:500:ILE:HD12	1:A:500:ILE:HA	1.81	0.46
1:G:586:ALA:O	1:G:589:ALA:HB3	2.14	0.46
1:D:571:LEU:HD13	1:D:577:VAL:HB	1.97	0.46
1:D:657:HIS:HB2	1:D:687:TRP:CD2	2.50	0.46
1:D:1117:LEU:HA	3:E:98:GLU:HB2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:600:LEU:HA	1:J:600:LEU:HD23	1.55	0.46
1:J:1510:VAL:O	1:J:1513:ILE:HG22	2.14	0.46
3:H:139:HIS:NE2	3:H:291:SER:HB2	2.30	0.46
2:F:66:SER:HB3	2:F:81:ASP:O	2.15	0.46
2:F:238:LYS:HB2	2:F:241:GLU:CD	2.39	0.46
2:F:344:LEU:HD21	2:F:359:MET:CE	2.40	0.46
2:L:15:VAL:HG13	2:L:79:HIS:CD2	2.48	0.46
2:L:344:LEU:CD1	2:L:359:MET:HE3	2.41	0.46
3:K:139:HIS:NE2	3:K:291:SER:HB2	2.30	0.46
1:A:1484:GLU:O	1:A:1487:GLU:HG2	2.16	0.46
1:G:326:ALA:O	1:G:331:ARG:NH1	2.37	0.46
1:G:554:ILE:HD12	1:G:584:PHE:HA	1.97	0.46
1:G:1118:LYS:HE2	3:H:99:LYS:HE3	1.96	0.46
2:I:102:ALA:O	2:I:131:ILE:HA	2.16	0.46
2:I:117:ARG:HH21	2:I:157:LEU:HD23	1.80	0.46
2:I:151:GLU:O	2:I:152:MET:HE2	2.15	0.46
3:H:136:PHE:O	3:H:137:GLU:C	2.58	0.46
3:E:278:ALA:HB1	3:E:285:PHE:HB3	1.98	0.46
2:L:88:TYR:O	2:L:92:MET:HG2	2.15	0.46
1:A:152:GLU:OE2	1:A:156:ARG:HD3	2.16	0.46
1:A:1128:GLU:N	1:A:1128:GLU:OE1	2.48	0.46
1:G:600:LEU:HG	1:G:604:LEU:HG	1.97	0.46
1:G:1339:ASP:O	1:G:1343:LEU:HG	2.15	0.46
1:D:968:LYS:HD3	1:D:968:LYS:HA	1.63	0.46
1:D:980:LYS:O	1:D:984:GLU:HG2	2.15	0.46
3:H:97:THR:HG22	3:H:98:GLU:H	1.81	0.46
3:H:218:VAL:HB	3:H:221:THR:OG1	2.15	0.46
3:H:278:ALA:HB1	3:H:285:PHE:HB3	1.98	0.46
2:C:66:SER:HB2	2:C:81:ASP:O	2.15	0.46
2:F:158:LEU:HD12	2:F:168:THR:HG21	1.97	0.46
2:L:305:PHE:CE1	2:L:363:LEU:HD21	2.50	0.46
1:A:631:LEU:H	1:A:631:LEU:HD12	1.80	0.46
1:A:779:GLU:O	1:A:782:LEU:HG	2.16	0.46
1:A:808:ARG:HD2	1:A:808:ARG:HA	1.63	0.46
1:G:571:LEU:HB2	1:G:577:VAL:HG11	1.97	0.46
1:G:687:TRP:CD1	1:G:690:ILE:HD11	2.51	0.46
1:G:1042:VAL:HG23	1:G:1043:LEU:HD22	1.98	0.46
1:D:617:ALA:HB1	1:D:647:VAL:HG13	1.97	0.46
1:D:1228:PHE:CG	1:D:1232:LEU:HD22	2.50	0.46
2:I:71:ASP:CG	2:I:76:HIS:HD1	2.23	0.46
2:I:88:TYR:O	2:I:92:MET:HG2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:241:MET:HE2	3:H:241:MET:HA	1.98	0.46
3:B:218:VAL:HB	3:B:221:THR:OG1	2.15	0.46
3:B:278:ALA:HB1	3:B:285:PHE:HB3	1.98	0.46
1:G:421:TRP:CD1	1:G:444:ARG:HD2	2.50	0.46
1:G:1214:LEU:HD11	1:G:1235:THR:HB	1.97	0.46
2:I:67:HIS:HD1	2:I:80:VAL:HA	1.79	0.46
2:I:158:LEU:HD12	2:I:168:THR:HG21	1.97	0.46
2:C:151:GLU:O	2:C:152:MET:HE2	2.15	0.46
2:F:305:PHE:CE1	2:F:363:LEU:HD21	2.50	0.46
2:L:71:ASP:CG	2:L:76:HIS:HD1	2.24	0.46
1:A:73:ILE:HD12	1:A:140:GLN:OE1	2.16	0.46
1:G:68:PHE:HD2	1:G:101:ASN:HD21	1.64	0.46
1:G:127:GLY:O	1:G:131:ARG:N	2.37	0.46
1:G:641:ARG:HA	1:G:644:PHE:HB3	1.97	0.46
1:D:1285:GLU:OE2	1:D:1320:ARG:NH1	2.45	0.46
1:J:109:LEU:HA	1:J:109:LEU:HD13	1.76	0.46
1:J:828:TYR:HA	1:J:842:ARG:NH1	2.31	0.46
2:F:102:ALA:O	2:F:131:ILE:HA	2.16	0.46
2:L:66:SER:HB2	2:L:81:ASP:O	2.15	0.46
2:L:158:LEU:HD12	2:L:168:THR:HG21	1.97	0.46
1:A:131:ARG:HA	1:A:134:ASP:OD2	2.16	0.46
1:A:1426:HIS:HB3	1:A:1457:TYR:OH	2.16	0.46
1:G:790:LEU:HB2	1:G:865:SER:HB2	1.96	0.46
1:G:1506:LEU:HD21	1:G:1514:ALA:HB2	1.98	0.46
1:D:79:GLU:O	1:D:82:LYS:HG2	2.16	0.46
1:D:236:LEU:O	1:D:240:ARG:HG3	2.16	0.46
1:D:796:GLU:O	3:E:212:ARG:NH2	2.49	0.46
1:J:440:ASP:OD1	1:J:441:ALA:N	2.49	0.46
1:J:494:ILE:HD13	1:J:497:ILE:HD11	1.98	0.46
1:J:752:GLU:HG3	3:K:212:ARG:NH1	2.31	0.46
2:I:209:LYS:HE2	2:I:234:ARG:HB3	1.98	0.46
2:C:132:ILE:CD1	2:C:196:LEU:CD2	2.94	0.46
2:C:339:THR:O	2:C:364:ILE:HG12	2.15	0.46
2:F:278:LEU:C	2:F:279:LEU:HD12	2.41	0.46
2:L:231:ARG:HA	2:L:273:GLU:O	2.16	0.46
3:K:225:TYR:O	3:K:226:GLY:C	2.59	0.46
1:A:1487:GLU:O	1:A:1492:GLY:N	2.49	0.46
1:G:136:ALA:O	1:G:140:GLN:HG2	2.15	0.46
1:G:205:ARG:N	1:G:205:ARG:HD2	2.30	0.46
1:D:715:ASP:OD1	1:D:715:ASP:N	2.42	0.46
1:D:1017:LYS:HD2	1:D:1018:ILE:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:1136:ASN:HD21	1:J:1170:ARG:HH21	1.64	0.46
1:J:1495:LEU:HA	1:J:1498:VAL:HG22	1.97	0.46
2:I:278:LEU:C	2:I:279:LEU:HD12	2.41	0.46
3:B:97:THR:HG22	3:B:98:GLU:H	1.81	0.46
3:E:276:LEU:CB	3:E:288:PRO:HG2	2.45	0.46
2:L:102:ALA:O	2:L:131:ILE:HA	2.16	0.46
1:A:24:LEU:HD22	1:A:179:LEU:HD12	1.96	0.46
1:G:779:GLU:HG3	1:G:783:GLN:HE22	1.81	0.46
1:G:1464:ARG:HH21	1:G:1509:GLY:HA3	1.79	0.46
1:G:1495:LEU:HA	1:G:1498:VAL:HG22	1.96	0.46
1:J:367:ARG:HA	1:J:367:ARG:CZ	2.46	0.46
1:J:1487:GLU:OE2	1:J:1495:LEU:HB3	2.16	0.46
3:H:138:ALA:O	3:H:142:LEU:HG	2.16	0.46
3:H:225:TYR:O	3:H:226:GLY:C	2.59	0.46
2:C:102:ALA:O	2:C:131:ILE:HA	2.16	0.46
2:C:249:LYS:HB3	2:C:252:GLN:NE2	2.31	0.46
2:C:278:LEU:C	2:C:279:LEU:HD12	2.41	0.46
2:F:138:CYS:H	2:F:174:SER:HB2	1.81	0.46
2:F:235:GLY:N	2:F:271:ALA:HB2	2.31	0.46
3:E:185:THR:HA	3:E:188:ILE:HG12	1.96	0.46
1:A:119:GLU:HB2	1:A:151:PHE:CG	2.50	0.45
1:D:729:LEU:O	1:D:732:VAL:HG12	2.16	0.45
1:D:1286:ARG:HG3	1:D:1290:TYR:HE2	1.81	0.45
1:J:39:SER:N	1:J:45:ASP:HB2	2.31	0.45
2:I:235:GLY:N	2:I:271:ALA:HB2	2.31	0.45
2:I:259:VAL:HG13	2:I:266:LEU:O	2.16	0.45
2:C:302:HIS:N	2:C:367:ILE:O	2.35	0.45
3:B:136:PHE:O	3:B:137:GLU:C	2.58	0.45
3:B:276:LEU:CB	3:B:288:PRO:HG2	2.45	0.45
2:L:209:LYS:HE2	2:L:234:ARG:HB3	1.98	0.45
2:L:278:LEU:C	2:L:279:LEU:HD12	2.41	0.45
3:K:281:LYS:HB3	3:K:281:LYS:HE3	1.32	0.45
1:A:26:VAL:O	1:A:26:VAL:HG12	2.16	0.45
1:A:672:ARG:HG3	1:A:707:TRP:CZ3	2.51	0.45
1:G:785:ARG:HD3	1:G:789:LYS:HE3	1.98	0.45
1:D:665:VAL:O	1:D:669:LYS:HE3	2.17	0.45
1:J:1031:PHE:HB2	1:J:1075:ALA:HB2	1.97	0.45
1:J:1417:GLU:HG2	1:J:1460:HIS:CE1	2.51	0.45
3:H:113:SER:O	3:H:117:ILE:HG13	2.17	0.45
2:C:209:LYS:HE2	2:C:234:ARG:HB3	1.98	0.45
3:B:139:HIS:NE2	3:B:291:SER:HB2	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:209:LYS:HE2	2:F:234:ARG:HB3	1.98	0.45
3:E:97:THR:HG22	3:E:98:GLU:H	1.81	0.45
2:L:132:ILE:CD1	2:L:196:LEU:CD2	2.94	0.45
2:L:235:GLY:N	2:L:271:ALA:HB2	2.31	0.45
3:K:278:ALA:HB1	3:K:285:PHE:HB3	1.98	0.45
1:A:91:PRO:HA	1:A:156:ARG:NH1	2.32	0.45
1:A:367:ARG:NH1	1:A:367:ARG:HA	2.32	0.45
1:G:390:VAL:HG12	1:G:392:THR:HG23	1.99	0.45
1:G:879:TYR:CE2	1:G:883:ILE:HD13	2.51	0.45
1:G:1033:LEU:HD11	2:I:349:GLU:HB2	1.98	0.45
1:G:1257:TYR:HA	3:H:89:LEU:HD23	1.98	0.45
1:D:1149:TRP:O	1:D:1155:THR:HG21	2.15	0.45
1:J:115:SER:OG	1:J:116:GLN:NE2	2.49	0.45
1:J:154:LEU:HA	1:J:154:LEU:HD23	1.78	0.45
1:J:509:SER:OG	1:J:511:VAL:O	2.31	0.45
1:J:1124:ASN:OD1	1:J:1124:ASN:N	2.48	0.45
1:J:1136:ASN:HD21	1:J:1170:ARG:NH2	2.13	0.45
2:I:218:VAL:HG21	2:I:287:ILE:CG2	2.44	0.45
3:B:241:MET:HE2	3:B:241:MET:HA	1.98	0.45
3:E:113:SER:O	3:E:117:ILE:HG13	2.17	0.45
3:E:138:ALA:O	3:E:142:LEU:HG	2.16	0.45
1:A:980:LYS:HG2	1:A:1005:TYR:CZ	2.50	0.45
1:G:1152:ARG:O	1:G:1155:THR:OG1	2.33	0.45
1:G:1168:ASP:HB2	1:G:1170:ARG:HG3	1.98	0.45
1:D:1411:ARG:O	1:D:1415:VAL:HG13	2.16	0.45
1:J:634:ARG:HG3	1:J:635:GLU:N	2.32	0.45
1:J:1377:LEU:HD13	1:J:1411:ARG:HB3	1.99	0.45
2:I:237:ILE:HG13	2:I:238:LYS:N	2.32	0.45
2:C:67:HIS:HD1	2:C:80:VAL:HA	1.79	0.45
3:B:225:TYR:O	3:B:226:GLY:C	2.59	0.45
2:L:29:THR:HG21	2:L:81:ASP:OD2	2.17	0.45
2:L:138:CYS:H	2:L:174:SER:HB2	1.81	0.45
1:A:36:GLU:HB2	1:A:48:VAL:HG22	1.97	0.45
1:G:700:ILE:O	1:G:704:THR:HG23	2.16	0.45
1:G:966:MET:SD	1:G:982:GLN:HA	2.57	0.45
1:D:1253:ARG:O	3:E:92:VAL:HG11	2.17	0.45
1:D:1408:LEU:HD12	1:D:1408:LEU:H	1.81	0.45
1:J:353:VAL:HB	1:J:388:ILE:HD13	1.98	0.45
1:J:797:PHE:HB2	1:J:801:ASN:O	2.16	0.45
1:J:985:VAL:O	1:J:988:SER:OG	2.31	0.45
1:J:1328:THR:O	1:J:1328:THR:HG22	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:231:ARG:HA	2:I:273:GLU:O	2.16	0.45
2:C:29:THR:HG21	2:C:81:ASP:OD2	2.16	0.45
2:C:231:ARG:HA	2:C:273:GLU:O	2.16	0.45
3:E:218:VAL:HB	3:E:221:THR:OG1	2.15	0.45
2:L:117:ARG:HH21	2:L:157:LEU:HD23	1.80	0.45
1:A:166:ASP:N	1:A:166:ASP:OD1	2.48	0.45
1:A:1333:PHE:CE1	1:A:1337:LEU:HD21	2.51	0.45
1:G:100:ARG:HH21	1:G:165:LEU:HD13	1.81	0.45
1:G:726:ALA:O	1:G:729:LEU:HG	2.16	0.45
1:D:726:ALA:HA	1:D:729:LEU:HG	1.97	0.45
1:J:980:LYS:HG2	1:J:984:GLU:OE1	2.17	0.45
2:I:81:ASP:OD1	2:I:81:ASP:O	2.34	0.45
3:H:113:SER:OG	3:H:116:GLU:N	2.39	0.45
2:F:71:ASP:CG	2:F:76:HIS:HD1	2.23	0.45
3:E:174:TRP:HB2	3:E:312:PHE:CE2	2.52	0.45
3:K:174:TRP:HB2	3:K:312:PHE:CE2	2.52	0.45
1:A:128:LYS:C	1:A:128:LYS:HD2	2.42	0.45
1:A:703:LEU:HD23	1:A:703:LEU:HA	1.76	0.45
1:A:883:ILE:HD12	1:A:883:ILE:HA	1.86	0.45
1:A:1370:PHE:O	1:A:1374:LYS:HG2	2.17	0.45
1:G:141:LEU:HD21	1:G:150:THR:HG22	1.99	0.45
1:G:808:ARG:HD2	1:G:808:ARG:HA	1.78	0.45
1:G:1338:ASN:HA	1:G:1341:ASN:ND2	2.31	0.45
1:D:1416:PHE:HE2	1:D:1429:PHE:HZ	1.65	0.45
1:J:1437:ASN:O	1:J:1440:SER:OG	2.34	0.45
2:C:32:ILE:O	2:C:36:LEU:HD13	2.17	0.45
2:C:138:CYS:H	2:C:174:SER:HB2	1.82	0.45
1:A:81:ASP:O	1:A:85:LEU:HG	2.17	0.45
1:A:600:LEU:HD13	1:A:620:PHE:CD1	2.51	0.45
1:A:1297:ASP:OD2	1:A:1297:ASP:N	2.48	0.45
1:A:1332:GLU:OE1	1:A:1334:ASN:N	2.49	0.45
1:G:105:ASP:OD1	1:G:108:LYS:NZ	2.39	0.45
1:G:700:ILE:HG13	1:G:735:LEU:HD22	1.99	0.45
1:G:1006:GLU:O	2:I:59:ARG:HG2	2.16	0.45
1:G:1166:ILE:HG21	1:G:1175:LEU:CD1	2.47	0.45
1:G:1175:LEU:O	1:G:1178:LEU:HG	2.17	0.45
1:D:10:ARG:HG3	1:D:11:GLY:N	2.32	0.45
1:D:184:ASP:O	1:D:188:ASN:ND2	2.49	0.45
1:D:1026:ARG:NH2	1:D:1061:LEU:HD11	2.31	0.45
1:J:78:ASP:OD2	1:J:78:ASP:N	2.49	0.45
2:I:303:THR:O	2:I:363:LEU:HD23	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:355:ASP:OD2	2:C:357:ILE:HD11	2.17	0.45
2:F:18:ILE:HD12	2:F:119:HIS:HB3	1.98	0.45
2:F:254:SER:OG	2:F:255:THR:N	2.46	0.45
2:F:334:ARG:HH11	2:F:369:MET:HA	1.82	0.45
3:E:58:THR:HB	3:E:60:GLU:OE2	2.17	0.45
2:L:32:ILE:O	2:L:36:LEU:HD13	2.17	0.45
3:K:97:THR:HG22	3:K:98:GLU:H	1.80	0.45
3:K:138:ALA:O	3:K:142:LEU:HG	2.16	0.45
1:A:60:GLN:HB3	1:A:62:LYS:NZ	2.32	0.45
1:A:287:PRO:HG2	1:A:531:ASN:HB2	1.99	0.45
1:A:943:LEU:O	1:A:946:SER:OG	2.33	0.45
1:G:563:THR:HG23	1:G:566:GLU:HG2	1.99	0.45
1:G:841:TYR:CZ	1:G:931:MET:HG3	2.51	0.45
1:G:1029:PHE:O	1:G:1071:GLN:HG3	2.17	0.45
1:D:168:MET:O	1:D:172:LEU:HG	2.17	0.45
1:D:234:MET:HA	1:D:237:VAL:CG1	2.47	0.45
1:D:295:MET:HE1	1:D:391:VAL:HG12	1.99	0.45
1:D:1045:LEU:HD21	2:F:324:PHE:CE1	2.52	0.45
1:D:1375:ALA:HA	1:D:1378:ASN:HD21	1.81	0.45
1:J:1299:VAL:HG12	1:J:1303:LEU:HD23	1.99	0.45
2:I:254:SER:OG	2:I:255:THR:N	2.46	0.45
3:H:58:THR:HB	3:H:60:GLU:OE2	2.17	0.45
2:C:71:ASP:CG	2:C:76:HIS:HD1	2.24	0.45
2:C:102:ALA:O	2:C:131:ILE:HD12	2.17	0.45
3:B:58:THR:HB	3:B:60:GLU:OE2	2.17	0.45
3:E:241:MET:HE2	3:E:241:MET:HA	1.98	0.45
2:L:292:VAL:CB	2:L:334:ARG:CZ	2.94	0.45
3:K:241:MET:HE2	3:K:241:MET:HA	1.98	0.45
1:D:653:SER:OG	1:D:656:TRP:HD1	2.00	0.45
1:D:700:ILE:HG12	1:D:735:LEU:HD13	1.99	0.45
1:D:922:ILE:HG12	1:D:925:MET:HE2	1.98	0.45
1:J:1037:ILE:HD13	2:L:349:GLU:HG3	1.99	0.45
3:H:261:ASP:HB3	3:H:264:ASN:ND2	2.32	0.45
2:C:303:THR:O	2:C:363:LEU:HD23	2.17	0.45
2:C:356:ASN:O	2:C:357:ILE:CG1	2.60	0.45
3:B:113:SER:O	3:B:117:ILE:HG13	2.17	0.45
2:L:54:PRO:HG2	2:L:56:GLU:OE1	2.18	0.45
2:L:185:TRP:HA	2:L:185:TRP:CE3	2.52	0.45
2:L:237:ILE:HG13	2:L:238:LYS:N	2.32	0.45
3:K:113:SER:O	3:K:117:ILE:HG13	2.17	0.45
1:A:1024:ILE:HG21	3:B:104:PHE:HD1	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1118:LYS:CE	3:H:99:LYS:HE3	2.46	0.44
1:D:215:THR:HG22	1:D:218:ASP:CG	2.42	0.44
1:D:952:PRO:HB2	1:D:955:LYS:HZ3	1.82	0.44
1:D:1252:LEU:HD21	1:D:1284:ALA:HB2	1.99	0.44
1:J:58:ALA:O	1:J:95:VAL:HA	2.16	0.44
1:J:981:SER:HA	1:J:984:GLU:CD	2.42	0.44
2:I:15:VAL:HG13	2:I:79:HIS:CD2	2.48	0.44
2:I:185:TRP:HA	2:I:185:TRP:CE3	2.52	0.44
3:H:164:ASN:O	3:H:301:PRO:HB2	2.17	0.44
2:C:185:TRP:HA	2:C:185:TRP:CE3	2.52	0.44
2:F:29:THR:HG21	2:F:81:ASP:OD2	2.17	0.44
2:F:54:PRO:HG2	2:F:56:GLU:OE1	2.18	0.44
3:E:136:PHE:O	3:E:137:GLU:C	2.58	0.44
3:E:281:LYS:CD	3:E:286:ARG:HH12	2.30	0.44
2:L:303:THR:O	2:L:363:LEU:HD23	2.17	0.44
1:A:1495:LEU:HD12	1:A:1495:LEU:HA	1.79	0.44
1:A:1512:GLU:OE1	1:A:1512:GLU:N	2.37	0.44
1:G:255:ARG:NH2	1:G:300:GLU:OE2	2.44	0.44
1:G:1139:LEU:HB3	1:G:1174:GLN:HE22	1.81	0.44
1:G:1286:ARG:HG3	1:G:1290:TYR:CE2	2.51	0.44
1:D:797:PHE:O	1:D:801:ASN:HB2	2.17	0.44
1:D:1138:ILE:O	1:D:1142:LEU:HG	2.17	0.44
1:D:1360:GLU:CD	1:D:1360:GLU:H	2.26	0.44
1:D:1421:ASP:OD2	1:D:1421:ASP:N	2.49	0.44
1:J:47:VAL:HG12	1:J:49:ILE:CD1	2.47	0.44
1:J:790:LEU:HB2	1:J:865:SER:HB2	1.99	0.44
3:B:138:ALA:O	3:B:142:LEU:HG	2.17	0.44
3:E:261:ASP:HB3	3:E:264:ASN:ND2	2.32	0.44
1:A:588:LEU:HA	1:A:588:LEU:HD23	1.65	0.44
1:A:1356:TRP:CD1	1:A:1369:CYS:HA	2.53	0.44
1:G:65:GLN:NE2	1:G:71:TRP:HA	2.32	0.44
1:G:1059:ASP:HB2	2:I:320:HIS:CD2	2.50	0.44
1:D:120:GLY:O	1:D:123:GLN:HG3	2.18	0.44
1:D:912:THR:OG1	1:D:913:GLN:NE2	2.51	0.44
1:J:291:LYS:NZ	4:J:1601:ATP:O3G	2.51	0.44
1:J:299:GLN:OE1	1:J:316:PHE:HB2	2.17	0.44
1:J:869:LEU:O	1:J:873:VAL:HG13	2.17	0.44
1:J:1115:GLY:HA2	1:J:1164:HIS:CE1	2.53	0.44
1:J:1292:TYR:OH	3:K:85:TYR:HB2	2.17	0.44
1:J:1461:SER:O	1:J:1461:SER:OG	2.35	0.44
2:C:292:VAL:CB	2:C:334:ARG:CZ	2.94	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:305:PHE:CE1	2:C:363:LEU:HD21	2.50	0.44
2:F:102:ALA:O	2:F:131:ILE:HD12	2.17	0.44
2:F:132:ILE:CD1	2:F:196:LEU:CD2	2.94	0.44
3:E:218:VAL:HG21	3:E:228:LEU:HD22	2.00	0.44
1:A:600:LEU:HD23	1:A:600:LEU:HA	1.81	0.44
1:A:1238:ARG:O	1:A:1238:ARG:NH1	2.39	0.44
1:A:1282:LYS:NZ	1:A:1317:THR:H	2.16	0.44
1:A:1359:ALA:O	1:A:1362:MET:HG2	2.18	0.44
1:A:1472:LEU:HD12	1:A:1472:LEU:HA	1.78	0.44
1:G:330:GLU:O	1:G:333:VAL:HG12	2.18	0.44
1:G:713:ILE:HA	1:G:716:GLN:CD	2.42	0.44
1:D:236:LEU:O	1:D:239:ILE:HB	2.17	0.44
1:J:719:MET:HE2	3:K:216:ARG:HG2	1.99	0.44
1:J:1282:LYS:HD2	1:J:1317:THR:HG23	1.98	0.44
2:I:138:CYS:H	2:I:174:SER:HB2	1.81	0.44
3:H:213:VAL:HG12	3:H:214:MET:CE	2.47	0.44
2:C:235:GLY:N	2:C:271:ALA:HB2	2.31	0.44
3:B:174:TRP:HB2	3:B:312:PHE:CE2	2.52	0.44
2:F:134:PHE:HD1	2:F:171:VAL:HB	1.82	0.44
3:K:58:THR:HB	3:K:60:GLU:OE2	2.17	0.44
3:K:160:PHE:HZ	3:K:244:LEU:HD21	1.83	0.44
3:K:276:LEU:CB	3:K:288:PRO:HG2	2.45	0.44
1:A:562:VAL:CG2	1:A:566:GLU:HB2	2.48	0.44
1:A:1059:ASP:OD1	2:C:320:HIS:HD2	2.00	0.44
1:A:1487:GLU:HG3	1:A:1488:GLU:N	2.32	0.44
1:G:353:VAL:HB	1:G:388:ILE:HD12	1.98	0.44
1:G:939:GLU:CD	1:G:939:GLU:H	2.25	0.44
1:D:801:ASN:HB3	1:D:804:PHE:HB2	2.00	0.44
2:I:102:ALA:O	2:I:131:ILE:HD12	2.17	0.44
3:H:160:PHE:HZ	3:H:244:LEU:HD21	1.83	0.44
3:B:160:PHE:HZ	3:B:244:LEU:HD21	1.83	0.44
3:K:218:VAL:HG21	3:K:228:LEU:HD22	2.00	0.44
1:A:1499:VAL:HG22	1:A:1502:GLN:NE2	2.32	0.44
1:D:39:SER:N	1:D:45:ASP:HB2	2.33	0.44
1:D:592:GLU:HG3	1:D:594:ARG:HB3	1.99	0.44
1:D:665:VAL:HB	1:D:666:PRO:HD3	1.99	0.44
1:D:666:PRO:HA	1:D:669:LYS:HG2	1.99	0.44
1:J:47:VAL:HG12	1:J:49:ILE:HD11	1.99	0.44
1:J:255:ARG:NH1	1:J:300:GLU:OE2	2.50	0.44
1:J:665:VAL:HB	1:J:666:PRO:HD3	1.98	0.44
3:H:184:VAL:HG11	3:H:229:PHE:CE1	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:237:ILE:HG13	2:C:238:LYS:N	2.32	0.44
2:F:303:THR:O	2:F:363:LEU:HD23	2.17	0.44
3:E:281:LYS:HB3	3:E:281:LYS:HE3	1.28	0.44
1:A:895:LEU:HD12	1:A:903:LEU:HB3	1.99	0.44
1:A:1468:HIS:CE1	3:B:182:ASN:HD22	2.36	0.44
1:G:282:LEU:HD11	1:G:394:CYS:SG	2.58	0.44
1:G:556:ARG:HG2	1:G:560:ASN:ND2	2.25	0.44
1:G:984:GLU:CD	1:G:1012:LEU:HD21	2.43	0.44
1:G:1316:GLU:HB2	1:G:1347:GLU:OE1	2.18	0.44
1:D:673:ASP:O	1:D:677:VAL:HG22	2.17	0.44
1:D:966:MET:HG3	1:D:967:TRP:CD1	2.52	0.44
1:D:1436:LEU:HD13	1:D:1436:LEU:HA	1.72	0.44
1:J:574:VAL:HG23	1:J:576:PHE:H	1.81	0.44
1:J:1374:LYS:HE3	1:J:1374:LYS:HB3	1.82	0.44
2:I:134:PHE:HD1	2:I:171:VAL:HB	1.83	0.44
2:C:211:PHE:CE2	2:C:237:ILE:HD13	2.53	0.44
3:B:261:ASP:HB3	3:B:264:ASN:ND2	2.33	0.44
2:F:32:ILE:O	2:F:36:LEU:HD13	2.17	0.44
2:F:237:ILE:HG13	2:F:238:LYS:N	2.32	0.44
2:L:148:GLU:O	2:L:152:MET:HG2	2.18	0.44
2:L:242:GLU:OE1	2:L:253:LYS:NZ	2.43	0.44
2:L:248:ILE:CD1	2:L:365:HIS:HB3	2.47	0.44
2:L:355:ASP:OD2	2:L:357:ILE:HD11	2.18	0.44
1:G:128:LYS:HD2	1:G:129:ALA:N	2.32	0.44
1:D:10:ARG:HH22	1:D:100:ARG:CZ	2.30	0.44
1:D:84:SER:O	1:D:88:ALA:N	2.48	0.44
1:D:361:ASP:O	1:D:365:ILE:HG13	2.17	0.44
1:D:1081:SER:HG	1:D:1137:ARG:HH12	1.63	0.44
1:J:255:ARG:HH12	1:J:300:GLU:CD	2.26	0.44
1:J:1421:ASP:OD2	1:J:1421:ASP:N	2.51	0.44
2:I:54:PRO:HG2	2:I:56:GLU:OE1	2.18	0.44
2:I:295:LYS:HE2	2:I:295:LYS:HB2	1.69	0.44
2:C:248:ILE:CD1	2:C:365:HIS:HB3	2.47	0.44
3:B:184:VAL:HG11	3:B:229:PHE:CE1	2.53	0.44
3:K:261:ASP:HB3	3:K:264:ASN:ND2	2.32	0.44
1:A:901:GLY:HA2	1:A:904:LEU:HB3	2.00	0.44
1:A:1103:MET:HG2	1:A:1149:TRP:CH2	2.53	0.44
1:G:180:VAL:HG12	1:G:181:SER:N	2.32	0.44
1:G:1006:GLU:OE1	1:G:1011:VAL:HA	2.18	0.44
1:G:1138:ILE:O	1:G:1142:LEU:HD23	2.18	0.44
1:G:1286:ARG:HH21	3:H:80:GLN:HE21	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1486:ARG:HD2	1:G:1494:MET:SD	2.58	0.44
1:D:1029:PHE:O	1:D:1071:GLN:HG3	2.17	0.44
1:D:1117:LEU:HD21	3:E:100:GLN:HG3	2.00	0.44
1:J:94:ASN:OD1	1:J:95:VAL:N	2.51	0.44
1:J:479:LEU:HA	1:J:479:LEU:HD23	1.71	0.44
2:I:32:ILE:O	2:I:36:LEU:HD13	2.17	0.44
3:H:174:TRP:HB2	3:H:312:PHE:CE2	2.52	0.44
3:H:254:ALA:HA	3:H:307:ILE:O	2.18	0.44
2:C:243:VAL:HG11	2:C:293:LEU:HD23	2.00	0.44
3:B:213:VAL:HG12	3:B:214:MET:CE	2.47	0.44
2:F:133:VAL:HG12	2:F:135:LEU:HD12	2.00	0.44
2:F:148:GLU:O	2:F:152:MET:HG2	2.18	0.44
2:F:185:TRP:HA	2:F:185:TRP:CE3	2.52	0.44
2:F:249:LYS:HB3	2:F:252:GLN:NE2	2.31	0.44
1:A:96:ARG:NE	1:A:158:ASN:HD22	2.16	0.43
1:A:1123:TRP:CZ2	1:A:1125:PRO:HG3	2.53	0.43
1:G:126:LEU:HB2	1:G:131:ARG:NH2	2.32	0.43
1:G:140:GLN:O	1:G:143:LYS:HG2	2.18	0.43
1:G:221:ASN:HA	1:G:224:GLN:CD	2.43	0.43
1:G:545:HIS:CE1	1:G:547:THR:HG23	2.53	0.43
1:G:956:GLN:HA	1:G:959:VAL:HG22	1.99	0.43
1:G:1237:ARG:O	1:G:1272:LEU:HD21	2.18	0.43
1:J:1435:TRP:O	1:J:1439:ILE:HG12	2.17	0.43
2:I:211:PHE:CE2	2:I:237:ILE:HD13	2.53	0.43
2:C:133:VAL:HG12	2:C:135:LEU:HD12	2.00	0.43
3:B:274:ASN:O	3:B:289:VAL:HA	2.18	0.43
2:F:215:ILE:HG23	2:F:228:VAL:HG23	2.00	0.43
2:F:248:ILE:CD1	2:F:365:HIS:HB3	2.47	0.43
3:E:184:VAL:HG11	3:E:229:PHE:CE1	2.53	0.43
2:L:205:ARG:HG2	2:L:207:ILE:HD12	2.00	0.43
1:A:963:ILE:HD13	1:A:989:ILE:HD11	2.00	0.43
1:G:136:ALA:O	1:G:139:LYS:HG2	2.18	0.43
1:G:1174:GLN:HA	1:G:1177:PHE:CD1	2.54	0.43
1:G:1436:LEU:HA	1:G:1439:ILE:HG22	2.00	0.43
1:G:1449:ALA:HA	1:G:1497:ARG:NH2	2.32	0.43
1:D:192:MET:O	1:D:192:MET:HE3	2.18	0.43
1:D:1040:ASP:O	1:D:1043:LEU:HG	2.18	0.43
1:J:404:ARG:H	1:J:404:ARG:HG3	1.64	0.43
1:J:1037:ILE:HD11	2:L:349:GLU:OE2	2.18	0.43
1:J:1274:MET:HE3	1:J:1274:MET:HB2	1.86	0.43
1:J:1435:TRP:CE3	1:J:1436:LEU:HD22	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:373:LEU:H	2:I:389:VAL:CG1	2.32	0.43
3:H:218:VAL:HG21	3:H:228:LEU:HD22	2.00	0.43
2:F:211:PHE:CE2	2:F:237:ILE:HD13	2.53	0.43
2:F:231:ARG:HA	2:F:273:GLU:O	2.16	0.43
2:L:211:PHE:CE2	2:L:237:ILE:HD13	2.53	0.43
1:A:1057:TRP:HB2	3:B:279:GLN:NE2	2.33	0.43
1:G:1230:GLU:H	1:G:1230:GLU:CD	2.26	0.43
1:J:664:LEU:HG	1:J:668:LEU:HD21	1.99	0.43
2:I:215:ILE:HG23	2:I:228:VAL:HG23	2.00	0.43
2:I:248:ILE:CD1	2:I:365:HIS:HB3	2.47	0.43
2:C:54:PRO:HG2	2:C:56:GLU:OE1	2.18	0.43
3:B:164:ASN:O	3:B:301:PRO:HB2	2.17	0.43
3:E:114:THR:HA	3:E:117:ILE:HB	2.00	0.43
2:L:134:PHE:HD1	2:L:171:VAL:HB	1.83	0.43
3:K:136:PHE:O	3:K:137:GLU:C	2.58	0.43
1:A:1098:PHE:O	1:A:1102:VAL:HG23	2.19	0.43
1:G:613:ARG:HA	1:G:616:VAL:HG22	1.99	0.43
1:G:1292:TYR:HA	1:G:1299:VAL:HG21	2.01	0.43
1:D:367:ARG:NE	1:D:367:ARG:HA	2.33	0.43
1:D:604:LEU:HD23	1:D:604:LEU:HA	1.82	0.43
1:D:809:MET:HG2	1:D:872:ALA:O	2.18	0.43
1:D:1104:SER:O	1:D:1107:SER:HB2	2.18	0.43
1:D:1434:GLU:O	1:D:1438:VAL:HG23	2.18	0.43
1:J:140:GLN:HA	1:J:143:LYS:NZ	2.33	0.43
1:J:1274:MET:HE2	1:J:1280:LEU:HD13	2.00	0.43
2:I:133:VAL:HG12	2:I:135:LEU:HD12	2.00	0.43
2:I:243:VAL:HG11	2:I:293:LEU:HD23	2.00	0.43
3:H:258:PHE:HB3	3:H:304:MET:HG2	2.01	0.43
2:C:107:ALA:HB3	2:C:110:ASP:OD2	2.19	0.43
2:C:334:ARG:NH2	2:C:368:ALA:O	2.51	0.43
3:B:243:PHE:C	3:B:245:ASP:H	2.27	0.43
2:F:205:ARG:HG2	2:F:207:ILE:HD12	2.00	0.43
3:E:160:PHE:HZ	3:E:244:LEU:HD21	1.83	0.43
3:E:164:ASN:O	3:E:301:PRO:HB2	2.18	0.43
2:L:243:VAL:HG11	2:L:293:LEU:HD23	2.00	0.43
3:K:184:VAL:HG11	3:K:229:PHE:CE1	2.53	0.43
3:K:213:VAL:HG12	3:K:214:MET:CE	2.47	0.43
3:K:274:ASN:O	3:K:289:VAL:HA	2.18	0.43
1:A:374:TYR:O	1:A:378:GLN:HG2	2.19	0.43
1:A:691:ASP:O	1:A:695:VAL:HG12	2.17	0.43
1:A:757:CYS:SG	1:A:763:ILE:HG12	2.58	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1203:LEU:CD1	3:H:71:PRO:HD3	2.48	0.43
1:J:119:GLU:CD	1:J:119:GLU:H	2.26	0.43
1:J:1411:ARG:HA	1:J:1414:SER:OG	2.18	0.43
2:I:18:ILE:HB	2:I:119:HIS:CD2	2.50	0.43
2:I:205:ARG:HG2	2:I:207:ILE:HD12	2.00	0.43
3:E:213:VAL:HG12	3:E:214:MET:CE	2.48	0.43
3:E:254:ALA:HA	3:E:307:ILE:O	2.18	0.43
2:L:72:THR:HG21	2:L:77:TYR:CE2	2.53	0.43
2:L:102:ALA:O	2:L:131:ILE:HD12	2.17	0.43
2:L:133:VAL:HG12	2:L:135:LEU:HD12	2.00	0.43
3:K:114:THR:HA	3:K:117:ILE:HB	2.01	0.43
3:K:243:PHE:C	3:K:245:ASP:H	2.27	0.43
1:A:1142:LEU:HD23	1:A:1178:LEU:HD13	2.00	0.43
1:G:966:MET:HG3	1:G:967:TRP:HD1	1.84	0.43
1:G:1315:LEU:O	1:G:1318:TRP:HB3	2.18	0.43
1:D:527:LEU:HD23	1:D:527:LEU:HA	1.90	0.43
1:D:1140:ASP:OD1	1:D:1141:GLU:N	2.52	0.43
1:D:1281:TRP:CE3	1:D:1306:LEU:HD22	2.54	0.43
1:D:1405:PRO:HD2	1:D:1408:LEU:HD13	2.01	0.43
1:D:1463:GLN:O	1:D:1464:ARG:NH1	2.51	0.43
1:J:185:SER:OG	1:J:226:SER:O	2.32	0.43
1:J:725:LYS:HA	1:J:725:LYS:HD2	1.79	0.43
1:J:735:LEU:HD23	1:J:739:LEU:HD11	2.01	0.43
1:J:934:PHE:HD2	1:J:936:LEU:HD23	1.83	0.43
1:J:1065:GLU:HG2	1:J:1098:PHE:CZ	2.54	0.43
1:J:1110:LEU:HB2	1:J:1161:ALA:HB1	1.99	0.43
1:J:1243:LYS:HD3	1:J:1243:LYS:C	2.44	0.43
2:I:72:THR:HG21	2:I:77:TYR:CE2	2.53	0.43
3:H:300:ARG:O	3:H:303:THR:HG22	2.18	0.43
2:C:373:LEU:H	2:C:389:VAL:CG1	2.31	0.43
3:B:176:ALA:HB3	3:B:179:ASN:ND2	2.34	0.43
2:F:138:CYS:SG	2:F:173:GLY:N	2.75	0.43
2:F:138:CYS:HB2	2:F:185:TRP:CH2	2.54	0.43
2:L:215:ILE:HG23	2:L:228:VAL:HG23	2.00	0.43
1:A:443:THR:O	1:A:447:ILE:HG23	2.18	0.43
1:A:966:MET:SD	1:A:982:GLN:HA	2.58	0.43
1:A:1333:PHE:O	1:A:1337:LEU:HG	2.19	0.43
1:A:1508:LEU:HD23	1:A:1508:LEU:HA	1.89	0.43
1:G:180:VAL:HG11	1:G:228:SER:OG	2.17	0.43
1:G:190:LEU:HD13	1:G:190:LEU:HA	1.90	0.43
1:G:216:LYS:HB3	1:G:220:ARG:NH1	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1354:THR:CG2	3:H:82:ILE:HG13	2.49	0.43
1:D:699:TRP:HB3	1:D:735:LEU:HD21	2.01	0.43
1:J:1307:ARG:HB2	1:J:1318:TRP:HE1	1.84	0.43
2:I:212:LEU:HD21	2:I:334:ARG:HH22	1.84	0.43
3:H:73:PHE:O	3:H:74:ASP:OD2	2.37	0.43
2:C:134:PHE:HD1	2:C:171:VAL:HB	1.82	0.43
2:C:148:GLU:O	2:C:152:MET:HG2	2.18	0.43
2:F:373:LEU:H	2:F:389:VAL:CG1	2.32	0.43
3:E:258:PHE:HB3	3:E:304:MET:HG2	2.01	0.43
2:L:23:HIS:NE2	2:L:110:ASP:OD1	2.52	0.43
3:K:164:ASN:O	3:K:301:PRO:HB2	2.18	0.43
3:K:176:ALA:HB3	3:K:179:ASN:ND2	2.34	0.43
1:A:37:ILE:HD11	1:A:194:LEU:HD22	2.01	0.43
1:A:348:ALA:HB2	1:A:388:ILE:HD11	2.00	0.43
1:A:660:TRP:CE3	1:A:664:LEU:HD22	2.54	0.43
1:A:1299:VAL:HG12	1:A:1303:LEU:HD23	2.00	0.43
1:G:253:TRP:O	1:G:255:ARG:HG3	2.18	0.43
1:D:1031:PHE:N	1:D:1071:GLN:OE1	2.51	0.43
1:D:1169:PRO:HA	1:D:1221:PHE:CZ	2.54	0.43
1:J:121:SER:O	1:J:125:SER:OG	2.30	0.43
1:J:923:GLY:HA2	1:J:951:LEU:HD21	2.01	0.43
1:J:1068:VAL:HG13	1:J:1098:PHE:HE1	1.83	0.43
1:J:1343:LEU:HB3	1:J:1345:THR:HG22	2.00	0.43
3:H:97:THR:HG22	3:H:98:GLU:N	2.34	0.43
2:F:23:HIS:NE2	2:F:110:ASP:OD1	2.52	0.43
3:E:73:PHE:O	3:E:74:ASP:OD2	2.37	0.43
3:E:176:ALA:HB3	3:E:179:ASN:ND2	2.34	0.43
1:A:1333:PHE:CZ	1:A:1337:LEU:HD21	2.53	0.43
1:D:20:PHE:CD2	1:D:172:LEU:HD13	2.53	0.43
1:D:926:LEU:HD21	1:D:944:ILE:HG12	2.00	0.43
1:D:948:PHE:HE2	1:D:959:VAL:HG11	1.83	0.43
1:D:1011:VAL:HG11	2:F:332:TYR:CE2	2.54	0.43
1:J:383:LEU:HD23	1:J:383:LEU:HA	1.83	0.43
1:J:527:LEU:HD23	1:J:527:LEU:HA	1.79	0.43
2:I:23:HIS:NE2	2:I:110:ASP:OD1	2.52	0.43
3:H:274:ASN:O	3:H:289:VAL:HA	2.18	0.43
3:B:258:PHE:HB3	3:B:304:MET:HG2	2.01	0.43
2:F:56:GLU:N	2:F:63:ILE:O	2.52	0.43
2:F:107:ALA:HB3	2:F:110:ASP:OD2	2.19	0.43
3:E:51:VAL:HG21	3:E:147:VAL:HG11	2.01	0.43
3:E:97:THR:HG22	3:E:98:GLU:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:300:ARG:O	3:E:303:THR:HG22	2.18	0.43
2:L:26:THR:O	2:L:29:THR:OG1	2.28	0.43
2:L:327:TYR:CD2	2:L:328:ARG:N	2.83	0.43
3:K:51:VAL:HG21	3:K:147:VAL:HG11	2.01	0.43
3:K:97:THR:HG22	3:K:98:GLU:N	2.34	0.43
1:A:576:PHE:CE2	1:A:1522:ARG:HG2	2.54	0.43
1:A:682:HIS:NE2	1:A:716:GLN:HG3	2.34	0.43
1:G:1313:LYS:HA	1:G:1347:GLU:CD	2.44	0.43
1:D:176:LEU:HA	1:D:176:LEU:HD23	1.69	0.43
1:D:935:GLU:OE1	1:D:935:GLU:N	2.52	0.43
1:D:1199:LEU:HD12	3:E:96:MET:HE1	2.00	0.43
1:J:696:VAL:HG23	1:J:735:LEU:HD13	2.01	0.43
1:J:1264:ASP:OD1	1:J:1265:PHE:N	2.51	0.43
1:J:1415:VAL:HA	1:J:1418:ASN:ND2	2.34	0.43
2:I:148:GLU:O	2:I:152:MET:HG2	2.18	0.43
3:H:176:ALA:HB3	3:H:179:ASN:ND2	2.34	0.43
2:C:331:PHE:HE2	2:C:361:VAL:CG1	2.32	0.43
3:B:97:THR:HG22	3:B:98:GLU:N	2.34	0.43
3:B:218:VAL:HG21	3:B:228:LEU:HD22	2.00	0.43
2:L:331:PHE:HE2	2:L:361:VAL:CG1	2.32	0.43
1:A:395:ARG:NH1	1:A:529:SER:OG	2.47	0.42
1:G:220:ARG:CG	1:G:230:LEU:HD23	2.43	0.42
1:G:358:ASP:OD1	1:G:359:SER:N	2.52	0.42
1:G:364:SER:HA	1:G:372:LEU:HD22	2.01	0.42
1:G:425:ILE:HG22	1:G:429:LEU:HD11	2.00	0.42
1:G:726:ALA:HA	1:G:729:LEU:HG	2.00	0.42
1:G:783:GLN:HG3	1:G:785:ARG:CB	2.49	0.42
1:G:948:PHE:CE2	1:G:989:ILE:HG12	2.54	0.42
1:G:1173:GLU:OE1	1:G:1229:PRO:HB3	2.19	0.42
1:D:1103:MET:SD	1:D:1154:SER:HB2	2.59	0.42
1:J:1307:ARG:HH12	1:J:1308:CYS:HB3	1.84	0.42
1:J:1333:PHE:O	1:J:1337:LEU:HG	2.19	0.42
2:I:107:ALA:HB3	2:I:110:ASP:OD2	2.19	0.42
2:C:23:HIS:NE2	2:C:110:ASP:OD1	2.52	0.42
2:C:215:ILE:HG23	2:C:228:VAL:HG23	2.00	0.42
3:B:300:ARG:O	3:B:303:THR:HG22	2.18	0.42
2:F:301:PRO:HA	2:F:367:ILE:O	2.19	0.42
2:L:226:THR:HG22	2:L:284:ARG:NH2	2.34	0.42
3:K:254:ALA:HA	3:K:307:ILE:O	2.18	0.42
1:A:123:GLN:O	1:A:131:ARG:NH1	2.52	0.42
1:A:223:ILE:HG21	1:A:230:LEU:HD13	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:522:ASP:N	1:A:522:ASP:OD2	2.52	0.42
1:A:816:LEU:HD22	1:A:887:TRP:CZ2	2.55	0.42
1:A:1001:VAL:O	1:A:1004:THR:OG1	2.33	0.42
1:G:287:PRO:HG2	1:G:531:ASN:HB2	2.01	0.42
1:G:1176:LEU:HD11	1:G:1232:LEU:HD23	2.00	0.42
1:D:90:ASN:O	1:D:93:VAL:HG12	2.19	0.42
1:D:233:PRO:C	1:D:235:ASP:H	2.27	0.42
1:D:1078:ARG:HG2	1:D:1125:PRO:HA	2.01	0.42
1:J:282:LEU:HD21	1:J:399:LYS:HD2	2.00	0.42
1:J:392:THR:OG1	1:J:393:ALA:N	2.51	0.42
1:J:929:ARG:CZ	1:J:968:LYS:HG2	2.48	0.42
1:J:1345:THR:OG1	1:J:1347:GLU:OE2	2.37	0.42
3:H:51:VAL:HG21	3:H:147:VAL:HG11	2.01	0.42
3:H:68:PHE:O	3:H:100:GLN:HA	2.20	0.42
3:H:213:VAL:C	3:H:214:MET:HE2	2.44	0.42
3:H:243:PHE:C	3:H:245:ASP:H	2.26	0.42
2:C:301:PRO:HA	2:C:367:ILE:O	2.20	0.42
3:B:254:ALA:HA	3:B:307:ILE:O	2.18	0.42
2:F:244:GLU:HG2	2:F:245:ILE:H	1.84	0.42
3:E:91:LEU:HG	3:E:93:ASP:H	1.84	0.42
3:E:274:ASN:O	3:E:289:VAL:HA	2.18	0.42
3:K:73:PHE:O	3:K:74:ASP:OD2	2.37	0.42
1:A:33:GLN:HE22	1:A:52:ILE:HB	1.85	0.42
1:A:176:LEU:O	1:A:179:LEU:N	2.51	0.42
1:A:604:LEU:HA	1:A:604:LEU:HD23	1.73	0.42
1:A:1000:ALA:O	1:A:1004:THR:HG23	2.20	0.42
1:A:1170:ARG:NH1	1:A:1171:LYS:HE3	2.31	0.42
1:A:1255:LEU:HD21	1:A:1259:GLN:NE2	2.33	0.42
1:G:191:TRP:CD1	1:G:191:TRP:C	2.97	0.42
1:G:432:LEU:HD22	1:G:461:ARG:NH2	2.33	0.42
1:G:868:ILE:H	1:G:868:ILE:HG13	1.70	0.42
1:G:1257:TYR:HA	3:H:89:LEU:CD2	2.49	0.42
1:D:479:LEU:HD11	1:D:548:LEU:CD1	2.50	0.42
1:D:545:HIS:O	1:D:548:LEU:HB2	2.18	0.42
1:D:951:LEU:O	1:D:956:GLN:NE2	2.52	0.42
1:J:552:LEU:HA	1:J:552:LEU:HD23	1.80	0.42
1:J:738:ARG:O	1:J:742:THR:HG23	2.19	0.42
1:J:986:ILE:HD13	1:J:998:ALA:HB1	2.02	0.42
1:J:1424:LYS:HE2	1:J:1424:LYS:HB2	1.87	0.42
2:I:226:THR:HG22	2:I:284:ARG:NH2	2.34	0.42
2:I:357:ILE:HG13	2:I:358:LYS:H	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:114:THR:HA	3:H:117:ILE:HB	2.01	0.42
2:C:72:THR:HG21	2:C:77:TYR:CE2	2.53	0.42
2:C:205:ARG:NH1	2:C:205:ARG:HB3	2.34	0.42
3:B:51:VAL:HG21	3:B:147:VAL:HG11	2.01	0.42
3:B:73:PHE:O	3:B:74:ASP:OD2	2.37	0.42
2:F:205:ARG:NH1	2:F:205:ARG:HB3	2.34	0.42
2:F:312:LEU:HD13	2:F:385:GLY:HA2	2.02	0.42
2:L:138:CYS:HB2	2:L:185:TRP:CH2	2.54	0.42
2:L:249:LYS:HB3	2:L:252:GLN:NE2	2.31	0.42
1:A:177:ARG:HA	1:A:183:THR:HG22	2.00	0.42
1:A:809:MET:SD	1:A:815:LEU:HG	2.59	0.42
1:A:1405:PRO:HD2	1:A:1408:LEU:HD12	2.01	0.42
1:G:420:ASP:O	1:G:425:ILE:HD12	2.19	0.42
1:G:675:GLU:OE1	1:G:675:GLU:N	2.51	0.42
1:G:986:ILE:HA	1:G:989:ILE:HD12	2.01	0.42
1:G:1411:ARG:HA	1:G:1414:SER:OG	2.20	0.42
1:D:164:ASP:O	1:D:168:MET:HG3	2.20	0.42
1:D:463:ASP:CG	1:D:467:ASN:HD21	2.27	0.42
1:D:966:MET:SD	1:D:982:GLN:HA	2.59	0.42
1:D:992:HIS:CE1	1:D:993:LEU:HG	2.54	0.42
1:D:1048:HIS:CG	2:F:352:MET:SD	3.13	0.42
1:D:1415:VAL:HA	1:D:1418:ASN:ND2	2.34	0.42
1:J:39:SER:H	1:J:45:ASP:HB2	1.84	0.42
1:J:47:VAL:CG1	1:J:49:ILE:HD11	2.49	0.42
1:J:513:PRO:HB2	1:J:515:GLN:NE2	2.34	0.42
1:J:517:PHE:CE2	1:J:524:GLN:HB2	2.54	0.42
1:J:1066:ARG:HG3	1:J:1070:TRP:CH2	2.54	0.42
2:I:25:LYS:HA	2:I:105:VAL:HG11	2.02	0.42
3:B:114:THR:HA	3:B:117:ILE:HB	2.01	0.42
1:A:15:GLN:HE22	1:A:37:ILE:HG23	1.84	0.42
1:A:934:PHE:HD2	1:A:936:LEU:HD23	1.83	0.42
1:A:1008:LYS:HZ3	1:A:1008:LYS:HG2	1.56	0.42
1:A:1518:LYS:HA	1:A:1518:LYS:HD3	1.77	0.42
1:G:166:ASP:N	1:G:166:ASP:OD1	2.52	0.42
1:G:289:SER:OG	1:G:289:SER:O	2.36	0.42
1:G:444:ARG:O	1:G:447:ILE:HG22	2.19	0.42
1:G:1005:TYR:CE2	1:G:1012:LEU:HD22	2.54	0.42
1:G:1410:SER:HB2	1:G:1411:ARG:HH21	1.84	0.42
1:G:1420:GLY:O	1:G:1424:LYS:HG2	2.20	0.42
1:D:43:LEU:HB2	1:D:86:LEU:HD12	2.02	0.42
1:D:252:SER:O	1:D:252:SER:OG	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1024:ILE:HG23	3:E:104:PHE:HB3	2.02	0.42
1:J:604:LEU:HD23	1:J:604:LEU:HA	1.85	0.42
2:I:138:CYS:HB2	2:I:185:TRP:CH2	2.54	0.42
2:C:92:MET:SD	2:C:122:LEU:HB3	2.60	0.42
2:F:212:LEU:HD21	2:F:334:ARG:HH22	1.84	0.42
2:F:244:GLU:CG	2:F:245:ILE:N	2.82	0.42
3:E:177:PRO:HG3	3:E:213:VAL:HG13	2.01	0.42
3:E:213:VAL:C	3:E:214:MET:HE2	2.44	0.42
2:L:301:PRO:HA	2:L:367:ILE:O	2.19	0.42
2:L:312:LEU:HD13	2:L:385:GLY:HA2	2.02	0.42
3:K:213:VAL:C	3:K:214:MET:HE2	2.44	0.42
3:K:300:ARG:O	3:K:303:THR:HG22	2.18	0.42
1:A:334:GLN:O	1:A:334:GLN:HG3	2.20	0.42
1:A:1296:PHE:CE2	1:A:1330:HIS:HB3	2.55	0.42
1:A:1413:PHE:O	1:A:1417:GLU:HG2	2.19	0.42
1:G:874:GLU:HB2	1:G:906:PHE:CE1	2.55	0.42
1:G:925:MET:HE1	1:G:940:LEU:HD21	2.01	0.42
1:G:1315:LEU:HD13	1:G:1345:THR:HG21	2.01	0.42
1:D:31:ASP:OD2	1:D:51:LYS:HB3	2.20	0.42
1:D:634:ARG:HG3	1:D:635:GLU:N	2.33	0.42
1:D:960:MET:HA	1:D:963:ILE:HG22	2.01	0.42
1:D:1243:LYS:HD3	1:D:1243:LYS:C	2.44	0.42
1:D:1300:GLU:O	1:D:1303:LEU:HG	2.20	0.42
1:D:1315:LEU:HD13	1:D:1345:THR:HG21	2.01	0.42
1:J:99:SER:O	1:J:161:THR:HA	2.20	0.42
2:I:25:LYS:HG2	2:I:105:VAL:HB	2.02	0.42
2:I:67:HIS:ND1	2:I:80:VAL:HA	2.35	0.42
2:I:205:ARG:NH1	2:I:205:ARG:HB3	2.34	0.42
2:C:25:LYS:HA	2:C:105:VAL:HG11	2.02	0.42
2:C:56:GLU:N	2:C:63:ILE:O	2.52	0.42
2:C:138:CYS:HB2	2:C:185:TRP:CH2	2.54	0.42
2:C:218:VAL:HG21	2:C:287:ILE:CG2	2.44	0.42
3:B:177:PRO:HG3	3:B:213:VAL:HG13	2.01	0.42
3:B:213:VAL:C	3:B:214:MET:HE2	2.44	0.42
2:F:92:MET:SD	2:F:122:LEU:HB3	2.60	0.42
2:F:243:VAL:HG11	2:F:293:LEU:HD23	2.00	0.42
2:L:205:ARG:NH1	2:L:205:ARG:HB3	2.34	0.42
1:A:24:LEU:HD11	1:A:176:LEU:HD13	2.02	0.42
1:A:672:ARG:HA	1:A:707:TRP:CH2	2.54	0.42
1:A:1511:LYS:HB3	1:A:1511:LYS:HE3	1.74	0.42
1:G:692:THR:O	1:G:696:VAL:HG12	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:866:MET:N	1:G:866:MET:SD	2.93	0.42
1:G:1029:PHE:HD1	2:I:324:PHE:CZ	2.38	0.42
1:G:1243:LYS:HD3	1:G:1243:LYS:C	2.44	0.42
1:G:1296:PHE:CE2	1:G:1330:HIS:HB3	2.55	0.42
1:G:1409:LEU:HD12	1:G:1409:LEU:H	1.85	0.42
1:G:1477:THR:HG22	1:G:1516:TRP:HE1	1.84	0.42
1:D:934:PHE:CD2	1:D:936:LEU:HD13	2.55	0.42
1:D:1222:LEU:HD23	1:D:1222:LEU:HA	1.87	0.42
1:J:82:LYS:HB3	1:J:82:LYS:HE3	1.78	0.42
1:J:115:SER:HG	1:J:116:GLN:NE2	2.17	0.42
1:J:1061:LEU:HD23	1:J:1061:LEU:HA	1.84	0.42
1:J:1259:GLN:NE2	1:J:1287:CYS:SG	2.86	0.42
2:I:132:ILE:CD1	2:I:196:LEU:CD2	2.94	0.42
2:I:139:ASP:OD1	2:I:174:SER:OG	2.38	0.42
2:C:139:ASP:OD1	2:C:174:SER:OG	2.38	0.42
2:C:205:ARG:HG2	2:C:207:ILE:HD12	2.00	0.42
2:C:282:ILE:HG21	2:C:287:ILE:HD12	2.02	0.42
3:B:113:SER:O	3:B:117:ILE:N	2.46	0.42
2:F:356:ASN:O	2:F:357:ILE:HG12	2.19	0.42
3:E:68:PHE:O	3:E:100:GLN:HA	2.19	0.42
3:E:78:ILE:O	3:E:82:ILE:HG12	2.20	0.42
2:L:107:ALA:HB3	2:L:110:ASP:OD2	2.19	0.42
1:A:295:MET:HE1	1:A:391:VAL:HG12	2.02	0.42
1:A:383:LEU:HD23	1:A:383:LEU:HA	1.82	0.42
1:A:1107:SER:OG	1:A:1158:ALA:HA	2.19	0.42
1:A:1417:GLU:OE1	1:A:1460:HIS:HB3	2.20	0.42
1:G:633:ILE:O	1:G:637:ARG:N	2.49	0.42
1:D:997:GLU:O	1:D:1001:VAL:HG23	2.20	0.42
1:D:1338:ASN:HA	1:D:1341:ASN:ND2	2.34	0.42
1:J:971:ALA:HB3	1:J:978:VAL:HG11	2.00	0.42
1:J:1426:HIS:HB3	1:J:1457:TYR:OH	2.19	0.42
2:I:92:MET:SD	2:I:122:LEU:HB3	2.60	0.42
3:H:82:ILE:HD13	3:H:82:ILE:HA	1.89	0.42
3:H:91:LEU:HG	3:H:93:ASP:H	1.85	0.42
2:F:331:PHE:HE2	2:F:361:VAL:CG1	2.32	0.42
3:E:118:LYS:HA	3:E:118:LYS:HD2	1.80	0.42
3:E:243:PHE:C	3:E:245:ASP:H	2.27	0.42
2:L:56:GLU:N	2:L:63:ILE:O	2.52	0.42
3:K:113:SER:OG	3:K:116:GLU:N	2.39	0.42
3:K:271:GLU:HB3	3:K:292:LYS:H	1.85	0.42
1:A:470:THR:HG23	1:A:473:ALA:H	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:554:ILE:HD11	1:A:583:SER:HB3	2.02	0.42
1:A:786:PHE:HD2	1:A:790:LEU:HD11	1.83	0.42
1:G:421:TRP:O	1:G:426:VAL:HG23	2.19	0.42
1:G:967:TRP:NE1	1:G:981:SER:OG	2.52	0.42
1:G:1376:GLY:HA3	1:G:1387:VAL:HG11	2.01	0.42
1:D:1026:ARG:NH1	1:D:1062:VAL:HG12	2.35	0.42
2:I:113:MET:HE2	2:I:114:PRO:HD2	2.02	0.42
2:I:134:PHE:CD1	2:I:192:LEU:HD11	2.54	0.42
3:H:78:ILE:O	3:H:82:ILE:HG12	2.20	0.42
3:H:177:PRO:HG3	3:H:213:VAL:HG13	2.01	0.42
2:C:226:THR:HG22	2:C:284:ARG:NH2	2.34	0.42
2:F:226:THR:HG22	2:F:284:ARG:NH2	2.34	0.42
2:L:67:HIS:ND1	2:L:80:VAL:HA	2.35	0.42
1:A:624:LYS:N	1:A:624:LYS:HD2	2.35	0.42
1:D:1282:LYS:NZ	1:D:1317:THR:H	2.18	0.42
1:D:1346:THR:HG22	1:D:1383:HIS:HD2	1.84	0.42
1:J:120:GLY:O	1:J:123:GLN:HG2	2.20	0.42
1:J:929:ARG:HE	1:J:966:MET:HA	1.85	0.42
2:I:249:LYS:HB3	2:I:252:GLN:NE2	2.31	0.42
2:I:302:HIS:N	2:I:367:ILE:O	2.35	0.42
3:H:271:GLU:HB3	3:H:292:LYS:H	1.85	0.42
3:B:271:GLU:HB3	3:B:292:LYS:H	1.85	0.42
2:F:15:VAL:HG13	2:F:79:HIS:CD2	2.48	0.42
2:F:29:THR:HG22	2:F:79:HIS:HE1	1.85	0.42
2:F:134:PHE:CD1	2:F:192:LEU:HD11	2.55	0.42
2:L:29:THR:HG22	2:L:79:HIS:HE1	1.85	0.42
1:A:63:LYS:HG3	1:A:100:ARG:HH12	1.85	0.41
1:A:87:LEU:HD21	1:A:152:GLU:OE2	2.20	0.41
1:A:116:GLN:HG2	1:A:122:TYR:HA	2.02	0.41
1:G:516:ARG:HA	1:G:516:ARG:HD2	1.85	0.41
1:G:676:GLY:O	1:G:679:MET:HG2	2.20	0.41
1:G:922:ILE:HD13	1:G:922:ILE:HA	1.83	0.41
1:G:1166:ILE:HD12	1:G:1217:LEU:HD13	2.00	0.41
1:D:639:LYS:HB3	1:D:639:LYS:HE3	1.91	0.41
1:J:22:TRP:O	1:J:26:VAL:HG23	2.20	0.41
1:J:103:PHE:CD1	1:J:159:PHE:CD1	3.08	0.41
1:J:474:LEU:HD12	1:J:474:LEU:HA	1.85	0.41
1:J:874:GLU:HB2	1:J:906:PHE:CE1	2.55	0.41
1:J:1162:CYS:O	1:J:1166:ILE:HG12	2.19	0.41
2:I:301:PRO:HA	2:I:367:ILE:O	2.19	0.41
2:F:25:LYS:HG2	2:F:105:VAL:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:25:LYS:HG2	2:L:105:VAL:HB	2.02	0.41
3:K:68:PHE:O	3:K:100:GLN:HA	2.20	0.41
3:K:82:ILE:HD13	3:K:82:ILE:HA	1.89	0.41
3:K:181:ILE:HG23	3:K:229:PHE:HD1	1.85	0.41
1:A:1121:GLU:H	1:A:1121:GLU:HG3	1.70	0.41
1:G:68:PHE:C	1:G:69:LYS:HD3	2.45	0.41
1:G:421:TRP:NE1	1:G:444:ARG:HD2	2.35	0.41
1:G:632:LEU:O	1:G:635:GLU:HB2	2.19	0.41
1:G:1388:ALA:HA	1:G:1391:MET:HG2	2.01	0.41
1:G:1388:ALA:O	1:G:1391:MET:HG2	2.20	0.41
1:D:173:ARG:HH12	1:D:184:ASP:HA	1.84	0.41
1:D:479:LEU:HD11	1:D:548:LEU:HD11	2.02	0.41
1:D:1299:VAL:HG12	1:D:1303:LEU:HD23	2.01	0.41
1:J:36:GLU:OE2	1:J:213:ARG:NE	2.51	0.41
1:J:69:LYS:HD2	1:J:69:LYS:HA	1.65	0.41
1:J:752:GLU:HG3	3:K:212:ARG:HH12	1.84	0.41
1:J:918:ASN:HB2	1:J:921:LEU:HB3	2.02	0.41
1:J:1003:ASP:CG	2:L:231:ARG:HH12	2.28	0.41
1:J:1332:GLU:OE1	1:J:1334:ASN:N	2.53	0.41
1:J:1333:PHE:CZ	1:J:1337:LEU:HD21	2.55	0.41
1:J:1377:LEU:HD21	1:J:1388:ALA:HB2	2.01	0.41
1:J:1448:LEU:HD13	1:J:1494:MET:HE3	2.02	0.41
2:I:331:PHE:HE2	2:I:361:VAL:CG1	2.32	0.41
2:C:61:ILE:HD12	2:C:94:THR:HG22	2.02	0.41
2:C:134:PHE:CG	2:C:192:LEU:HD11	2.56	0.41
2:F:67:HIS:ND1	2:F:80:VAL:HA	2.35	0.41
2:L:139:ASP:OD1	2:L:174:SER:OG	2.38	0.41
2:L:295:LYS:N	2:L:295:LYS:HD3	2.35	0.41
3:K:91:LEU:HG	3:K:93:ASP:H	1.84	0.41
1:A:446:LEU:HD12	1:A:446:LEU:HA	1.91	0.41
1:A:1070:TRP:CZ2	3:B:66:LYS:HB2	2.55	0.41
1:A:1112:HIS:CE1	1:A:1119:ALA:HB2	2.56	0.41
1:G:699:TRP:HB3	1:G:735:LEU:HD21	2.03	0.41
1:G:739:LEU:HD22	1:G:750:LEU:HD21	2.02	0.41
1:D:69:LYS:HA	1:D:69:LYS:HD2	1.82	0.41
1:J:773:THR:HA	1:J:776:LEU:HD23	2.01	0.41
1:J:1053:SER:OG	1:J:1054:GLY:N	2.52	0.41
1:J:1256:PRO:HA	1:J:1259:GLN:OE1	2.20	0.41
2:I:56:GLU:N	2:I:63:ILE:O	2.52	0.41
2:C:67:HIS:HE1	2:C:80:VAL:HG13	1.86	0.41
2:C:134:PHE:CD1	2:C:192:LEU:HD11	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:68:PHE:O	3:B:100:GLN:HA	2.19	0.41
2:F:282:ILE:HG21	2:F:287:ILE:HD12	2.02	0.41
2:F:363:LEU:HD13	2:F:363:LEU:HA	1.86	0.41
3:K:258:PHE:HB3	3:K:304:MET:HG2	2.01	0.41
1:A:33:GLN:NE2	1:A:52:ILE:HB	2.36	0.41
1:A:578:ARG:NE	1:A:1521:GLU:OE2	2.45	0.41
1:A:672:ARG:HG3	1:A:707:TRP:CE3	2.55	0.41
1:A:1182:PHE:CD1	1:A:1210:VAL:HG11	2.56	0.41
1:A:1485:GLU:OE2	1:J:601:ARG:HD3	2.20	0.41
1:G:367:ARG:HA	1:G:367:ARG:NH1	2.35	0.41
1:G:447:ILE:HG13	1:G:453:LEU:HA	2.02	0.41
1:G:459:LEU:HA	1:G:459:LEU:HD23	1.86	0.41
1:G:1022:GLY:HA2	3:H:107:GLY:O	2.20	0.41
1:G:1156:ALA:O	1:G:1159:LEU:HG	2.21	0.41
1:G:1351:GLY:O	1:G:1355:VAL:HG23	2.20	0.41
1:D:63:LYS:HG3	1:D:64:ASN:OD1	2.21	0.41
1:D:513:PRO:HD2	1:D:516:ARG:HG3	2.02	0.41
1:J:673:ASP:OD2	1:J:676:GLY:HA3	2.20	0.41
1:J:1098:PHE:O	1:J:1102:VAL:HG23	2.20	0.41
1:J:1388:ALA:HA	1:J:1391:MET:HG3	2.01	0.41
1:J:1411:ARG:O	1:J:1415:VAL:HG22	2.20	0.41
2:I:61:ILE:HD12	2:I:94:THR:HG22	2.02	0.41
2:I:67:HIS:HE1	2:I:80:VAL:HG13	1.86	0.41
2:I:163:PHE:HB3	2:I:164:PRO:HD2	2.03	0.41
3:H:281:LYS:HB3	3:H:281:LYS:HE3	1.31	0.41
2:C:113:MET:SD	2:C:114:PRO:HD2	2.61	0.41
2:C:122:LEU:O	2:C:126:VAL:HG12	2.20	0.41
2:C:312:LEU:HD13	2:C:385:GLY:HA2	2.02	0.41
2:F:25:LYS:HA	2:F:105:VAL:HG11	2.02	0.41
2:F:61:ILE:HD12	2:F:94:THR:HG22	2.02	0.41
2:F:295:LYS:HE2	2:F:295:LYS:HB2	1.69	0.41
3:E:271:GLU:HB3	3:E:292:LYS:H	1.85	0.41
3:E:283:LEU:O	3:E:283:LEU:HG	2.19	0.41
2:L:113:MET:SD	2:L:114:PRO:HD2	2.61	0.41
2:L:151:GLU:C	2:L:152:MET:HE2	2.45	0.41
1:A:108:LYS:O	1:A:111:GLU:HG2	2.21	0.41
1:A:381:ARG:HD2	1:J:249:ILE:HD11	2.02	0.41
1:A:720:HIS:O	1:A:723:VAL:HG12	2.20	0.41
1:A:963:ILE:HG21	1:A:986:ILE:HG12	2.02	0.41
1:A:1214:LEU:HG	1:A:1236:LEU:HG	2.02	0.41
1:G:78:ASP:HA	1:G:81:ASP:OD1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:627:ASN:HA	1:G:659:PHE:HE1	1.86	0.41
1:G:805:LEU:HD12	1:G:805:LEU:HA	1.69	0.41
1:G:864:ASP:O	1:G:868:ILE:HG13	2.20	0.41
1:G:1121:GLU:H	1:G:1121:GLU:CD	2.29	0.41
1:G:1173:GLU:OE2	1:G:1229:PRO:HG3	2.20	0.41
1:D:1136:ASN:CG	1:D:1171:LYS:HD2	2.45	0.41
1:D:1162:CYS:O	1:D:1166:ILE:HG12	2.21	0.41
1:D:1462:LYS:HB2	1:D:1464:ARG:NH2	2.35	0.41
1:J:721:LEU:O	1:J:724:ILE:HG22	2.21	0.41
2:I:282:ILE:HG21	2:I:287:ILE:HD12	2.02	0.41
2:I:327:TYR:CD2	2:I:328:ARG:N	2.83	0.41
2:C:67:HIS:ND1	2:C:80:VAL:HA	2.35	0.41
2:C:295:LYS:HD3	2:C:295:LYS:N	2.35	0.41
3:B:85:TYR:CE2	3:B:87:ASP:HA	2.55	0.41
3:B:188:ILE:HD12	3:B:236:MET:HE1	2.03	0.41
2:L:67:HIS:HE1	2:L:80:VAL:HG13	1.86	0.41
1:A:216:LYS:HB2	1:A:216:LYS:HE3	1.84	0.41
1:A:634:ARG:NH2	1:D:1441:LEU:O	2.53	0.41
1:G:6:ILE:HG13	1:G:7:ARG:N	2.36	0.41
1:G:65:GLN:HA	1:G:71:TRP:CH2	2.55	0.41
1:G:905:TYR:CZ	1:G:909:LEU:HD11	2.55	0.41
1:G:1407:GLY:O	1:G:1411:ARG:HG2	2.21	0.41
1:D:65:GLN:NE2	1:D:75:ASP:OD2	2.54	0.41
1:D:1017:LYS:CE	3:E:111:LEU:HD11	2.50	0.41
1:D:1374:LYS:HD2	1:D:1378:ASN:ND2	2.36	0.41
1:J:558:ILE:HD13	1:J:558:ILE:HA	1.89	0.41
1:J:908:ILE:HD11	1:J:936:LEU:HD22	2.03	0.41
3:H:108:ASN:OD1	3:H:109:ALA:N	2.54	0.41
2:C:32:ILE:O	2:C:32:ILE:HG22	2.21	0.41
2:C:363:LEU:HD13	2:C:363:LEU:HA	1.86	0.41
3:B:78:ILE:O	3:B:82:ILE:HG12	2.20	0.41
2:F:113:MET:SD	2:F:114:PRO:HD2	2.61	0.41
3:K:78:ILE:O	3:K:82:ILE:HG12	2.20	0.41
1:A:112:HIS:O	1:A:115:SER:OG	2.28	0.41
1:A:232:PRO:HB2	1:A:234:MET:HG2	2.03	0.41
1:A:592:GLU:OE1	1:A:594:ARG:HB3	2.20	0.41
1:A:692:THR:O	1:A:696:VAL:HG13	2.20	0.41
1:A:740:LEU:HD23	1:A:770:ARG:HH22	1.85	0.41
1:A:1136:ASN:CG	1:A:1171:LYS:HD2	2.46	0.41
1:A:1248:ARG:HB3	1:A:1273:VAL:HG13	2.02	0.41
1:G:395:ARG:HH11	1:G:529:SER:HB2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1052:HIS:NE2	2:I:320:HIS:O	2.54	0.41
1:G:1318:TRP:CZ3	1:G:1343:LEU:HD11	2.55	0.41
1:D:91:PRO:HA	1:D:156:ARG:NH1	2.36	0.41
1:D:222:ILE:O	1:D:225:GLN:HG2	2.20	0.41
1:D:1024:ILE:HG21	3:E:104:PHE:HD1	1.86	0.41
1:J:1118:LYS:NZ	3:K:97:THR:HG21	2.36	0.41
2:I:122:LEU:O	2:I:126:VAL:HG12	2.20	0.41
2:I:312:LEU:HD13	2:I:385:GLY:HA2	2.02	0.41
3:H:85:TYR:CE2	3:H:87:ASP:HA	2.55	0.41
2:C:113:MET:O	2:C:114:PRO:C	2.64	0.41
2:C:327:TYR:CD2	2:C:328:ARG:N	2.83	0.41
3:B:175:SER:O	3:B:177:PRO:HD3	2.21	0.41
3:B:181:ILE:HG23	3:B:229:PHE:HD1	1.85	0.41
2:F:67:HIS:HE1	2:F:80:VAL:HG13	1.86	0.41
2:F:113:MET:HE2	2:F:114:PRO:HD2	2.02	0.41
2:F:122:LEU:O	2:F:126:VAL:HG12	2.20	0.41
3:E:108:ASN:OD1	3:E:109:ALA:N	2.54	0.41
3:K:188:ILE:HD12	3:K:236:MET:HE1	2.03	0.41
1:A:35:ILE:HD11	1:A:47:VAL:HG13	2.02	0.41
1:A:739:LEU:HD12	1:A:739:LEU:HA	1.85	0.41
1:A:926:LEU:HD21	1:A:943:LEU:HD22	2.02	0.41
1:A:955:LYS:HE2	1:A:955:LYS:HB3	1.93	0.41
1:A:1434:GLU:O	1:A:1438:VAL:HG23	2.21	0.41
1:G:595:GLU:O	1:G:599:GLN:HG2	2.21	0.41
1:G:1061:LEU:HD23	1:G:1061:LEU:HA	1.76	0.41
1:G:1488:GLU:C	1:G:1491:ARG:HH12	2.27	0.41
1:D:527:LEU:HD22	1:D:532:VAL:HG11	2.03	0.41
1:J:141:LEU:HD12	1:J:142:ALA:N	2.36	0.41
1:J:236:LEU:HD23	1:J:236:LEU:HA	1.83	0.41
1:J:367:ARG:HA	1:J:367:ARG:NE	2.36	0.41
1:J:699:TRP:O	1:J:703:LEU:HD23	2.20	0.41
1:J:748:SER:OG	1:J:750:LEU:HG	2.21	0.41
1:J:1468:HIS:CE1	3:K:182:ASN:HD22	2.39	0.41
1:J:1518:LYS:HA	1:J:1518:LYS:HD3	1.73	0.41
2:I:32:ILE:O	2:I:32:ILE:HG22	2.21	0.41
2:I:215:ILE:HD11	2:I:293:LEU:CD1	2.51	0.41
2:C:25:LYS:HG2	2:C:105:VAL:HB	2.02	0.41
2:C:113:MET:HE2	2:C:114:PRO:HD2	2.02	0.41
2:F:25:LYS:HE2	2:F:25:LYS:HB2	1.84	0.41
2:F:192:LEU:C	2:F:194:GLY:N	2.79	0.41
2:L:138:CYS:HG	2:L:173:GLY:H	1.65	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:85:TYR:CE2	3:K:87:ASP:HA	2.55	0.41
1:A:71:TRP:HB3	1:A:76:LEU:CD2	2.50	0.41
1:A:612:ILE:O	1:A:616:VAL:HG23	2.21	0.41
1:A:1038:ASN:ND2	1:A:1040:ASP:OD2	2.53	0.41
1:A:1118:LYS:HE2	3:B:97:THR:HG21	2.03	0.41
1:A:1180:ILE:HD11	1:A:1231:LEU:HD13	2.02	0.41
1:A:1231:LEU:O	1:A:1235:THR:HG23	2.21	0.41
1:A:1411:ARG:HA	1:A:1414:SER:OG	2.21	0.41
1:G:68:PHE:HD1	1:D:108:LYS:HZ2	1.69	0.41
1:G:238:GLY:C	1:G:240:ARG:N	2.78	0.41
1:G:755:ALA:HB1	1:G:801:ASN:ND2	2.32	0.41
1:G:842:ARG:HE	1:G:842:ARG:HB3	1.72	0.41
1:G:890:LYS:NZ	1:G:891:ASN:HD21	2.18	0.41
1:G:1010:GLY:HA2	2:I:59:ARG:HB3	2.03	0.41
1:G:1112:HIS:ND1	1:G:1119:ALA:HB2	2.36	0.41
1:G:1118:LYS:HB3	1:G:1118:LYS:HE3	1.84	0.41
1:G:1166:ILE:HD13	1:G:1175:LEU:HD13	2.02	0.41
1:G:1297:ASP:N	1:G:1297:ASP:OD1	2.53	0.41
1:G:1421:ASP:OD1	1:G:1421:ASP:N	2.53	0.41
1:G:1488:GLU:HA	1:G:1491:ARG:NH2	2.28	0.41
1:G:1491:ARG:HA	1:G:1491:ARG:CZ	2.51	0.41
1:G:1514:ALA:HA	1:G:1517:LEU:HB3	2.03	0.41
1:D:60:GLN:HE22	1:D:82:LYS:NZ	2.19	0.41
1:D:291:LYS:N	4:D:1601:ATP:O1B	2.36	0.41
1:D:631:LEU:HD13	1:D:634:ARG:NH1	2.36	0.41
1:D:963:ILE:HD12	1:D:963:ILE:HA	1.83	0.41
1:D:1346:THR:HG22	1:D:1383:HIS:CD2	2.56	0.41
1:J:429:LEU:HA	1:J:429:LEU:HD23	1.80	0.41
1:J:705:LEU:HD23	1:J:705:LEU:HA	1.92	0.41
1:J:740:LEU:HD22	1:J:770:ARG:HH22	1.86	0.41
1:J:925:MET:SD	1:J:926:LEU:HG	2.61	0.41
1:J:1448:LEU:O	1:J:1451:THR:OG1	2.39	0.41
1:J:1468:HIS:CE1	3:K:182:ASN:ND2	2.89	0.41
2:I:25:LYS:HE2	2:I:25:LYS:HB2	1.84	0.41
2:I:56:GLU:OE2	2:I:65:THR:OG1	2.39	0.41
2:I:204:GLU:OE2	2:I:209:LYS:HG2	2.21	0.41
2:I:295:LYS:HD3	2:I:295:LYS:N	2.35	0.41
2:I:336:THR:HG22	2:I:337:ASP:N	2.36	0.41
3:H:175:SER:O	3:H:177:PRO:HD3	2.21	0.41
3:H:181:ILE:HG23	3:H:229:PHE:HD1	1.85	0.41
2:C:25:LYS:HE2	2:C:25:LYS:HB2	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:29:THR:HG22	2:C:79:HIS:HE1	1.85	0.41
2:C:151:GLU:C	2:C:152:MET:HE2	2.45	0.41
2:C:295:LYS:HB2	2:C:295:LYS:HE2	1.69	0.41
3:B:108:ASN:OD1	3:B:109:ALA:N	2.54	0.41
2:F:32:ILE:O	2:F:32:ILE:HG22	2.21	0.41
2:F:139:ASP:OD1	2:F:174:SER:OG	2.38	0.41
2:F:163:PHE:HB3	2:F:164:PRO:HD2	2.03	0.41
2:F:204:GLU:OE2	2:F:209:LYS:HG2	2.21	0.41
2:F:215:ILE:HD11	2:F:293:LEU:CD1	2.51	0.41
2:F:246:VAL:HG11	2:F:299:ILE:HG21	1.99	0.41
2:F:295:LYS:HD3	2:F:295:LYS:N	2.35	0.41
3:E:181:ILE:HG23	3:E:229:PHE:HD1	1.85	0.41
2:L:25:LYS:HA	2:L:105:VAL:HG11	2.02	0.41
2:L:113:MET:HE2	2:L:114:PRO:HD2	2.02	0.41
2:L:163:PHE:HB3	2:L:164:PRO:HD2	2.03	0.41
3:K:158:SER:C	3:K:160:PHE:N	2.79	0.41
1:A:367:ARG:HA	1:A:367:ARG:CZ	2.51	0.41
1:A:421:TRP:CH2	1:A:444:ARG:HG2	2.56	0.41
1:A:660:TRP:HE3	1:A:664:LEU:HB2	1.86	0.41
1:A:757:CYS:SG	1:A:762:VAL:HB	2.60	0.41
1:G:381:ARG:HD2	1:D:245:SER:OG	2.20	0.41
1:G:636:LEU:HD12	1:G:640:ASN:HB2	2.02	0.41
1:G:1296:PHE:HA	1:G:1299:VAL:HB	2.03	0.41
1:G:1404:VAL:HG21	1:G:1408:LEU:HD22	2.03	0.41
1:D:341:VAL:HG21	1:D:378:GLN:OE1	2.21	0.41
1:D:1393:ARG:HA	1:D:1396:HIS:HD2	1.83	0.41
1:J:17:LEU:HA	1:J:17:LEU:HD23	1.85	0.41
1:J:235:ASP:O	1:J:236:LEU:HB2	2.20	0.41
1:J:1346:THR:HG22	1:J:1383:HIS:HD2	1.85	0.41
2:I:113:MET:O	2:I:114:PRO:C	2.64	0.41
2:F:113:MET:O	2:F:114:PRO:C	2.64	0.41
2:F:151:GLU:C	2:F:152:MET:HE2	2.46	0.41
2:L:204:GLU:OE2	2:L:209:LYS:HG2	2.21	0.41
2:L:282:ILE:HG21	2:L:287:ILE:HD12	2.02	0.41
2:L:336:THR:HG22	2:L:337:ASP:N	2.36	0.41
2:L:344:LEU:HG	2:L:359:MET:HG2	2.03	0.41
3:K:108:ASN:OD1	3:K:109:ALA:N	2.54	0.41
3:K:177:PRO:HG3	3:K:213:VAL:HG13	2.01	0.41
1:A:462:ARG:HH21	1:D:537:GLN:HG2	1.86	0.40
1:A:714:ALA:HA	1:A:717:ILE:HD12	2.03	0.40
1:A:736:LEU:HD23	1:A:740:LEU:HD13	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1168:ASP:CG	1:A:1170:ARG:HG2	2.46	0.40
1:A:1231:LEU:C	1:A:1234:PRO:HD2	2.47	0.40
1:A:1350:HIS:O	1:A:1354:THR:HG23	2.21	0.40
1:G:119:GLU:H	1:G:119:GLU:CD	2.28	0.40
1:G:790:LEU:HD12	1:G:790:LEU:H	1.86	0.40
1:G:1495:LEU:H	1:G:1495:LEU:HD12	1.85	0.40
1:D:1374:LYS:HB3	1:D:1374:LYS:HE3	1.87	0.40
1:J:567:PHE:O	1:J:571:LEU:HG	2.21	0.40
1:J:590:LEU:HA	1:J:590:LEU:HD13	1.86	0.40
1:J:615:LEU:HA	1:J:618:GLU:OE1	2.20	0.40
1:J:1025:VAL:HG23	3:K:105:ARG:O	2.21	0.40
2:I:134:PHE:CG	2:I:192:LEU:HD11	2.55	0.40
2:I:302:HIS:O	2:I:366:PRO:HA	2.22	0.40
3:H:188:ILE:HD12	3:H:236:MET:HE1	2.03	0.40
2:C:163:PHE:HB3	2:C:164:PRO:HD2	2.03	0.40
2:C:204:GLU:OE2	2:C:209:LYS:HG2	2.21	0.40
2:C:302:HIS:O	2:C:366:PRO:HA	2.22	0.40
3:B:113:SER:OG	3:B:116:GLU:N	2.39	0.40
2:F:336:THR:HG22	2:F:337:ASP:N	2.35	0.40
2:L:195:PHE:C	2:L:197:ASP:H	2.30	0.40
3:K:175:SER:O	3:K:177:PRO:HD3	2.21	0.40
1:A:582:ARG:HH12	1:A:1518:LYS:NZ	2.18	0.40
1:A:908:ILE:O	1:A:912:THR:HG23	2.21	0.40
1:G:665:VAL:HG12	1:G:669:LYS:HE3	2.02	0.40
1:G:1207:LYS:HA	1:G:1210:VAL:HG22	2.03	0.40
1:G:1221:PHE:HD1	1:G:1226:ASN:HB2	1.85	0.40
1:G:1326:ALA:HA	1:G:1331:VAL:O	2.21	0.40
1:D:474:LEU:HD12	1:D:474:LEU:HA	1.86	0.40
1:D:600:LEU:HD23	1:D:600:LEU:HA	1.82	0.40
1:D:661:ILE:HD13	1:D:661:ILE:HA	1.92	0.40
1:J:164:ASP:OD1	1:J:165:LEU:N	2.50	0.40
1:J:500:ILE:HD11	1:J:517:PHE:CE1	2.56	0.40
1:J:766:THR:HG23	1:J:767:LEU:HD12	2.03	0.40
1:J:1120:ASP:N	1:J:1120:ASP:OD2	2.53	0.40
2:C:192:LEU:C	2:C:194:GLY:N	2.79	0.40
2:F:110:ASP:OD2	2:F:110:ASP:N	2.54	0.40
2:F:302:HIS:O	2:F:366:PRO:HA	2.21	0.40
3:E:85:TYR:CE2	3:E:87:ASP:HA	2.55	0.40
2:L:32:ILE:O	2:L:32:ILE:HG22	2.21	0.40
2:L:215:ILE:HD11	2:L:293:LEU:CD1	2.51	0.40
2:L:295:LYS:HB2	2:L:295:LYS:HE2	1.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:GLN:HA	1:A:143:LYS:HG3	2.03	0.40
1:A:630:TRP:HE1	1:A:634:ARG:HH21	1.69	0.40
1:A:1285:GLU:OE2	1:A:1320:ARG:NH1	2.50	0.40
1:A:1327:MET:N	1:A:1327:MET:SD	2.95	0.40
1:G:283:LEU:HA	1:G:414:LEU:O	2.21	0.40
1:G:477:ARG:O	1:G:481:THR:HG22	2.21	0.40
1:G:1149:TRP:O	1:G:1155:THR:HG21	2.22	0.40
1:D:10:ARG:HH12	1:D:100:ARG:NH1	2.20	0.40
1:D:60:GLN:HB2	1:D:97:PHE:HD2	1.86	0.40
1:D:547:THR:O	1:D:548:LEU:C	2.64	0.40
1:D:566:GLU:HG2	1:D:569:ARG:NH1	2.36	0.40
1:D:672:ARG:HG3	1:D:707:TRP:CZ3	2.56	0.40
1:D:714:ALA:O	1:D:717:ILE:HB	2.22	0.40
1:D:1080:PRO:HB2	1:D:1106:VAL:HG13	2.03	0.40
1:D:1130:ASP:OD2	1:D:1130:ASP:N	2.54	0.40
1:J:922:ILE:HG21	1:J:947:ILE:HG21	2.04	0.40
2:I:151:GLU:C	2:I:152:MET:HE2	2.46	0.40
2:I:344:LEU:H	2:I:344:LEU:HG	1.61	0.40
2:C:48:ASP:O	2:C:52:ASN:ND2	2.55	0.40
2:C:135:LEU:CD2	2:C:151:GLU:HG2	2.45	0.40
2:C:195:PHE:C	2:C:197:ASP:H	2.30	0.40
2:C:215:ILE:HD11	2:C:293:LEU:CD1	2.51	0.40
2:C:336:THR:HG22	2:C:337:ASP:N	2.36	0.40
1:G:640:ASN:O	1:G:643:VAL:N	2.54	0.40
1:G:944:ILE:HG23	1:G:948:PHE:CD2	2.52	0.40
1:G:991:CYS:SG	1:G:994:ARG:NH1	2.93	0.40
1:D:1003:ASP:C	1:D:1007:LYS:HZ2	2.29	0.40
1:D:1202:GLY:HA3	1:D:1250:MET:HE3	2.03	0.40
1:J:398:ASP:OD2	1:J:525:ARG:NH1	2.48	0.40
1:J:455:LEU:HD12	1:J:455:LEU:HA	1.73	0.40
1:J:916:GLU:H	1:J:916:GLU:CD	2.28	0.40
1:J:990:PRO:HG3	2:L:219:PHE:CE2	2.56	0.40
1:J:1070:TRP:CE3	3:K:66:LYS:HE3	2.56	0.40
1:J:1166:ILE:HD13	1:J:1166:ILE:HA	1.92	0.40
1:J:1170:ARG:NE	1:J:1171:LYS:HE3	2.36	0.40
2:I:192:LEU:C	2:I:194:GLY:N	2.79	0.40
3:H:70:TYR:CE1	3:H:99:LYS:HB2	2.57	0.40
2:C:207:ILE:HG22	2:C:207:ILE:O	2.22	0.40
3:B:170:ALA:HB2	3:B:307:ILE:CG2	2.52	0.40
2:F:134:PHE:CG	2:F:192:LEU:HD11	2.56	0.40
2:F:327:TYR:CD2	2:F:328:ARG:N	2.83	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:207:ILE:O	2:L:207:ILE:HG22	2.22	0.40
1:A:6:ILE:HD11	1:G:200:ARG:NH2	2.36	0.40
1:A:284:THR:HG22	1:A:285:GLY:H	1.85	0.40
1:A:440:ASP:O	1:A:444:ARG:HG3	2.21	0.40
1:A:668:LEU:CD1	1:A:673:ASP:HB3	2.52	0.40
1:A:1181:ASP:OD1	1:A:1181:ASP:N	2.53	0.40
1:A:1393:ARG:HA	1:A:1396:HIS:HD2	1.86	0.40
1:D:484:LEU:HD13	1:D:494:ILE:HG13	2.04	0.40
1:D:960:MET:O	1:D:963:ILE:HG22	2.21	0.40
1:D:1506:LEU:HA	1:D:1506:LEU:HD23	1.87	0.40
1:J:76:LEU:HD22	1:J:79:GLU:OE2	2.21	0.40
1:J:991:CYS:HA	1:J:994:ARG:NE	2.37	0.40
3:H:170:ALA:HB2	3:H:307:ILE:CG2	2.52	0.40
3:H:276:LEU:CB	3:H:288:PRO:HG2	2.45	0.40
2:C:338:VAL:HG12	2:C:339:THR:N	2.37	0.40
3:B:70:TYR:CE1	3:B:99:LYS:HB2	2.57	0.40
3:B:91:LEU:HG	3:B:93:ASP:H	1.84	0.40
2:F:322:PRO:HB3	2:F:353:PRO:HD3	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	1490/1523 (98%)	1447 (97%)	43 (3%)	0	100	100
1	D	1469/1523 (96%)	1426 (97%)	43 (3%)	0	100	100
1	G	1490/1523 (98%)	1438 (96%)	52 (4%)	0	100	100
1	J	1469/1523 (96%)	1432 (98%)	37 (2%)	0	100	100
2	C	382/394 (97%)	303 (79%)	79 (21%)	0	100	100
2	F	382/394 (97%)	302 (79%)	80 (21%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	I	382/394 (97%)	304 (80%)	78 (20%)	0	100	100
2	L	382/394 (97%)	305 (80%)	77 (20%)	0	100	100
3	B	263/314 (84%)	218 (83%)	45 (17%)	0	100	100
3	E	263/314 (84%)	218 (83%)	45 (17%)	0	100	100
3	H	263/314 (84%)	218 (83%)	45 (17%)	0	100	100
3	K	263/314 (84%)	218 (83%)	45 (17%)	0	100	100
All	All	8498/8924 (95%)	7829 (92%)	669 (8%)	0	100	100

There are no Ramachandran outliers to report.

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	1279/1301 (98%)	1261 (99%)	18 (1%)	59	71
1	D	1264/1301 (97%)	1247 (99%)	17 (1%)	61	72
1	G	1279/1301 (98%)	1260 (98%)	19 (2%)	57	71
1	J	1264/1301 (97%)	1246 (99%)	18 (1%)	59	71
2	C	316/326 (97%)	313 (99%)	3 (1%)	70	76
2	F	316/326 (97%)	313 (99%)	3 (1%)	70	76
2	I	316/326 (97%)	312 (99%)	4 (1%)	61	72
2	L	316/326 (97%)	315 (100%)	1 (0%)	86	84
3	B	221/257 (86%)	218 (99%)	3 (1%)	59	71
3	E	221/257 (86%)	217 (98%)	4 (2%)	51	68
3	H	221/257 (86%)	219 (99%)	2 (1%)	70	76
3	K	221/257 (86%)	218 (99%)	3 (1%)	59	71
All	All	7234/7536 (96%)	7139 (99%)	95 (1%)	59	72

All (95) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	236	LEU
1	A	271	LEU
1	A	371	VAL
1	A	384	LEU
1	A	389	THR
1	A	552	LEU
1	A	565	ASN
1	A	577	VAL
1	A	602	THR
1	A	619	SER
1	A	733	VAL
1	A	742	THR
1	A	766	THR
1	A	953	SER
1	A	1126	LEU
1	A	1142	LEU
1	A	1217	LEU
1	A	1274	MET
1	G	237	VAL
1	G	247	SER
1	G	405	ILE
1	G	494	ILE
1	G	563	THR
1	G	649	VAL
1	G	722	SER
1	G	842	ARG
1	G	1024	ILE
1	G	1043	LEU
1	G	1053	SER
1	G	1056	ASP
1	G	1061	LEU
1	G	1183	VAL
1	G	1236	LEU
1	G	1255	LEU
1	G	1404	VAL
1	G	1448	LEU
1	G	1462	LYS
1	D	235	ASP
1	D	236	LEU
1	D	518	THR
1	D	603	VAL
1	D	646	VAL
1	D	649	VAL

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Mol	Chain	Res	Type
1	D	671	THR
1	D	742	THR
1	D	766	THR
1	D	934	PHE
1	D	943	LEU
1	D	978	VAL
1	D	1120	ASP
1	D	1391	MET
1	D	1436	LEU
1	D	1513	ILE
1	D	1518	LYS
1	J	392	THR
1	J	482	ILE
1	J	520	SER
1	J	562	VAL
1	J	574	VAL
1	J	580	SER
1	J	731	VAL
1	J	766	THR
1	J	849	THR
1	J	987	VAL
1	J	992	HIS
1	J	996	LEU
1	J	1120	ASP
1	J	1122	THR
1	J	1343	LEU
1	J	1401	VAL
1	J	1436	LEU
1	J	1505	LEU
2	I	259	VAL
2	I	357	ILE
2	I	373	LEU
2	I	389	VAL
3	H	260	LYS
3	H	281	LYS
2	C	244	GLU
2	C	373	LEU
2	C	389	VAL
3	B	260	LYS
3	B	281	LYS
3	B	286	ARG
2	F	99	MET

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Mol	Chain	Res	Type
2	F	373	LEU
2	F	389	VAL
3	E	260	LYS
3	E	281	LYS
3	E	289	VAL
3	E	311	THR
2	L	99	MET
3	K	260	LYS
3	K	281	LYS
3	K	286	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (132) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	ASN
1	A	94	ASN
1	A	158	ASN
1	A	211	GLN
1	A	334	GLN
1	A	387	ASN
1	A	476	GLN
1	A	611	HIS
1	A	640	ASN
1	A	756	ASN
1	A	795	HIS
1	A	806	GLN
1	A	913	GLN
1	A	1052	HIS
1	A	1112	HIS
1	A	1116	ASN
1	A	1330	HIS
1	A	1350	HIS
1	A	1378	ASN
1	A	1396	HIS
1	A	1468	HIS
1	A	1471	ASN
1	A	1502	GLN
1	G	55	ASN
1	G	65	GLN
1	G	140	GLN
1	G	158	ASN
1	G	217	HIS

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Mol	Chain	Res	Type
1	G	221	ASN
1	G	318	GLN
1	G	338	GLN
1	G	378	GLN
1	G	472	GLN
1	G	560	ASN
1	G	599	GLN
1	G	706	ASN
1	G	728	ASN
1	G	756	ASN
1	G	783	GLN
1	G	801	ASN
1	G	853	ASN
1	G	965	ASN
1	G	992	HIS
1	G	1079	HIS
1	G	1116	ASN
1	G	1164	HIS
1	G	1167	HIS
1	G	1271	HIS
1	G	1275	GLN
1	G	1341	ASN
1	G	1396	HIS
1	D	60	GLN
1	D	65	GLN
1	D	112	HIS
1	D	178	ASN
1	D	188	ASN
1	D	196	GLN
1	D	221	ASN
1	D	225	GLN
1	D	241	HIS
1	D	318	GLN
1	D	449	ASN
1	D	657	HIS
1	D	728	ASN
1	D	886	ASN
1	D	891	ASN
1	D	913	GLN
1	D	965	ASN
1	D	974	ASN
1	D	1021	HIS

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Mol	Chain	Res	Type
1	D	1048	HIS
1	D	1058	ASN
1	D	1164	HIS
1	D	1341	ASN
1	D	1350	HIS
1	D	1378	ASN
1	D	1383	HIS
1	D	1396	HIS
1	D	1418	ASN
1	D	1426	HIS
1	D	1468	HIS
1	J	60	GLN
1	J	116	GLN
1	J	158	ASN
1	J	423	ASN
1	J	623	GLN
1	J	657	HIS
1	J	756	ASN
1	J	891	ASN
1	J	965	ASN
1	J	1021	HIS
1	J	1090	HIS
1	J	1136	ASN
1	J	1145	HIS
1	J	1341	ASN
1	J	1378	ASN
1	J	1383	HIS
1	J	1396	HIS
1	J	1418	ASN
1	J	1469	ASN
2	I	252	GLN
2	I	291	GLN
2	I	320	HIS
2	I	365	HIS
3	H	80	GLN
3	H	166	ASN
3	H	182	ASN
3	H	279	GLN
3	H	284	HIS
2	C	12	HIS
2	C	252	GLN
2	C	291	GLN

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Mol	Chain	Res	Type
2	C	365	HIS
3	B	166	ASN
3	B	182	ASN
3	B	284	HIS
2	F	252	GLN
2	F	291	GLN
2	F	320	HIS
2	F	365	HIS
3	E	80	GLN
3	E	166	ASN
3	E	182	ASN
3	E	284	HIS
2	L	12	HIS
2	L	252	GLN
2	L	291	GLN
2	L	320	HIS
2	L	365	HIS
3	K	166	ASN
3	K	182	ASN
3	K	284	HIS

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 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 for Mogul analysis.

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	ATP	A	1601	5	32,33,33	1.31	5 (15%)	48,52,52	1.80	10 (20%)
4	ATP	D	1601	5	32,33,33	1.33	5 (15%)	48,52,52	1.74	9 (18%)
6	GTP	L	401	-	33,34,34	0.95	1 (3%)	50,54,54	1.58	8 (16%)
4	ATP	G	1601	5	32,33,33	1.28	5 (15%)	48,52,52	1.79	9 (18%)
4	ATP	J	1601	5	32,33,33	1.31	5 (15%)	48,52,52	1.87	11 (22%)
6	GTP	C	401	-	33,34,34	0.96	1 (3%)	50,54,54	1.58	8 (16%)
6	GTP	F	401	-	33,34,34	0.95	1 (3%)	50,54,54	1.58	8 (16%)
6	GTP	I	401	-	33,34,34	0.95	1 (3%)	50,54,54	1.58	8 (16%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ATP	A	1601	5	-	1/22/38/38	0/3/3/3
4	ATP	D	1601	5	-	0/22/38/38	0/3/3/3
6	GTP	L	401	-	-	6/22/38/38	0/3/3/3
4	ATP	G	1601	5	-	7/22/38/38	0/3/3/3
4	ATP	J	1601	5	-	6/22/38/38	0/3/3/3
6	GTP	C	401	-	-	6/22/38/38	0/3/3/3
6	GTP	F	401	-	-	6/22/38/38	0/3/3/3
6	GTP	I	401	-	-	6/22/38/38	0/3/3/3

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	J	1601	ATP	C5-C4	4.17	1.46	1.39
4	G	1601	ATP	C5-C4	4.15	1.46	1.39
4	A	1601	ATP	C5-C4	3.98	1.46	1.39
4	D	1601	ATP	C5-C4	3.84	1.45	1.39
4	J	1601	ATP	C5-N7	-2.96	1.33	1.39
4	D	1601	ATP	C5-N7	-2.87	1.33	1.39
4	A	1601	ATP	C5-N7	-2.83	1.33	1.39
4	D	1601	ATP	C4-N9	-2.64	1.32	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1601	ATP	C4-N9	-2.62	1.32	1.37
4	G	1601	ATP	C5-C6	2.57	1.48	1.41
4	G	1601	ATP	C5-N7	-2.37	1.34	1.39
4	D	1601	ATP	C8-N9	-2.34	1.33	1.37
4	A	1601	ATP	C8-N9	-2.26	1.33	1.37
4	J	1601	ATP	C5-C6	2.22	1.47	1.41
4	G	1601	ATP	C4-N9	-2.20	1.33	1.37
4	D	1601	ATP	C5-C6	2.16	1.47	1.41
4	G	1601	ATP	C8-N7	2.15	1.35	1.31
4	J	1601	ATP	C4-N9	-2.13	1.33	1.37
6	F	401	GTP	C2-N3	2.13	1.38	1.33
4	A	1601	ATP	C5-C6	2.13	1.46	1.41
6	I	401	GTP	C2-N3	2.13	1.38	1.33
6	C	401	GTP	C2-N3	2.12	1.38	1.33
6	L	401	GTP	C2-N3	2.11	1.38	1.33
4	J	1601	ATP	C8-N7	2.04	1.35	1.31

All (71) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	J	1601	ATP	C5-C4-N3	-6.09	118.33	126.72
4	G	1601	ATP	C5-C4-N3	-5.78	118.76	126.72
4	A	1601	ATP	C5-C4-N3	-5.62	118.98	126.72
4	D	1601	ATP	C5-C4-N3	-5.45	119.22	126.72
6	L	401	GTP	C5-C4-N3	-5.05	120.34	128.39
6	I	401	GTP	C5-C4-N3	-5.04	120.36	128.39
6	F	401	GTP	C5-C4-N3	-5.03	120.38	128.39
6	C	401	GTP	C5-C4-N3	-5.03	120.39	128.39
4	J	1601	ATP	N3-C4-N9	4.72	135.20	127.17
4	A	1601	ATP	N3-C4-N9	4.66	135.09	127.17
6	C	401	GTP	C2-N3-C4	4.60	120.22	112.30
6	I	401	GTP	C2-N3-C4	4.59	120.21	112.30
4	G	1601	ATP	N3-C4-N9	4.59	134.97	127.17
6	L	401	GTP	C2-N3-C4	4.59	120.20	112.30
6	F	401	GTP	C2-N3-C4	4.58	120.18	112.30
4	D	1601	ATP	N3-C4-N9	4.51	134.83	127.17
4	G	1601	ATP	C2-N3-C4	3.73	120.94	111.83
4	J	1601	ATP	C2-N3-C4	3.71	120.89	111.83
4	D	1601	ATP	C2-N3-C4	3.53	120.46	111.83
4	G	1601	ATP	C4-C5-N7	-3.53	106.55	110.58
4	A	1601	ATP	C2-N3-C4	3.50	120.37	111.83
4	D	1601	ATP	C4-N9-C8	3.25	109.15	105.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L	401	GTP	N9-C4-N3	3.23	132.42	125.95
4	A	1601	ATP	C4-N9-C8	3.23	109.13	105.74
4	G	1601	ATP	N3-C2-N1	-3.23	123.70	128.58
6	I	401	GTP	N9-C4-N3	3.22	132.39	125.95
6	C	401	GTP	N9-C4-N3	3.21	132.38	125.95
4	J	1601	ATP	C4-C5-N7	-3.21	106.91	110.58
6	F	401	GTP	N9-C4-N3	3.20	132.36	125.95
4	D	1601	ATP	N3-C2-N1	-3.19	123.75	128.58
4	A	1601	ATP	C4-C5-N7	-3.16	106.97	110.58
4	D	1601	ATP	C4-C5-N7	-3.15	106.98	110.58
4	A	1601	ATP	C2'-C1'-N9	-3.08	105.64	113.30
4	A	1601	ATP	N3-C2-N1	-3.08	123.93	128.58
4	J	1601	ATP	N3-C2-N1	-3.08	123.93	128.58
4	G	1601	ATP	C4-N9-C8	3.06	108.96	105.74
6	L	401	GTP	C2-N1-C6	-3.04	119.59	125.11
6	I	401	GTP	C2-N1-C6	-3.04	119.59	125.11
6	F	401	GTP	C2-N1-C6	-3.03	119.62	125.11
6	C	401	GTP	C2-N1-C6	-3.02	119.64	125.11
4	J	1601	ATP	C3'-C2'-C1'	2.87	106.88	101.46
6	I	401	GTP	C5-C6-N1	2.58	119.82	113.25
6	F	401	GTP	C5-C6-N1	2.58	119.81	113.25
6	L	401	GTP	C5-C6-N1	2.57	119.80	113.25
4	G	1601	ATP	C5-N7-C8	2.56	107.47	103.45
6	C	401	GTP	C5-C6-N1	2.56	119.76	113.25
4	A	1601	ATP	C3'-C2'-C1'	2.52	106.23	101.46
4	J	1601	ATP	C5'-C4'-C3'	-2.52	106.15	115.21
6	I	401	GTP	N9-C8-N7	-2.52	108.73	113.40
6	F	401	GTP	N9-C8-N7	-2.51	108.75	113.40
6	C	401	GTP	N9-C8-N7	-2.50	108.76	113.40
6	L	401	GTP	N9-C8-N7	-2.48	108.79	113.40
6	F	401	GTP	C8-N7-C5	2.39	108.51	104.26
6	I	401	GTP	C8-N7-C5	2.38	108.50	104.26
6	I	401	GTP	O6-C6-C5	-2.37	120.29	126.53
6	C	401	GTP	C8-N7-C5	2.36	108.47	104.26
6	F	401	GTP	O6-C6-C5	-2.36	120.31	126.53
6	C	401	GTP	O6-C6-C5	-2.35	120.32	126.53
6	L	401	GTP	C8-N7-C5	2.35	108.45	104.26
6	L	401	GTP	O6-C6-C5	-2.35	120.34	126.53
4	D	1601	ATP	C5-N7-C8	2.33	107.11	103.45
4	A	1601	ATP	C5-N7-C8	2.32	107.10	103.45
4	J	1601	ATP	C5-N7-C8	2.28	107.04	103.45
4	G	1601	ATP	N9-C8-N7	-2.24	110.76	113.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1601	ATP	N9-C8-N7	-2.20	110.81	113.94
4	G	1601	ATP	C6-C5-N7	2.19	136.31	132.09
4	A	1601	ATP	N9-C8-N7	-2.16	110.87	113.94
4	D	1601	ATP	C3'-C2'-C1'	2.16	105.54	101.46
4	J	1601	ATP	C4-N9-C8	2.11	107.95	105.74
4	J	1601	ATP	C2'-C1'-N9	-2.10	108.08	113.30
4	J	1601	ATP	C2'-C3'-C4'	2.08	106.63	102.61

There are no chirality outliers.

All (38) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1601	ATP	C5'-O5'-PA-O2A
4	G	1601	ATP	C5'-O5'-PA-O1A
4	G	1601	ATP	C5'-O5'-PA-O3A
4	J	1601	ATP	C5'-O5'-PA-O2A
4	J	1601	ATP	C5'-O5'-PA-O3A
6	I	401	GTP	C5'-O5'-PA-O2A
6	C	401	GTP	C5'-O5'-PA-O2A
6	F	401	GTP	C5'-O5'-PA-O2A
6	L	401	GTP	C5'-O5'-PA-O2A
4	J	1601	ATP	C3'-C4'-C5'-O5'
4	J	1601	ATP	O4'-C4'-C5'-O5'
4	G	1601	ATP	C2'-C1'-N9-C8
4	J	1601	ATP	PA-O3A-PB-O1B
4	G	1601	ATP	C5'-O5'-PA-O2A
6	I	401	GTP	C5'-O5'-PA-O3A
6	I	401	GTP	C5'-O5'-PA-O1A
6	C	401	GTP	C5'-O5'-PA-O3A
6	C	401	GTP	C5'-O5'-PA-O1A
6	F	401	GTP	C5'-O5'-PA-O3A
6	F	401	GTP	C5'-O5'-PA-O1A
6	L	401	GTP	C5'-O5'-PA-O3A
6	L	401	GTP	C5'-O5'-PA-O1A
6	I	401	GTP	O4'-C4'-C5'-O5'
6	C	401	GTP	O4'-C4'-C5'-O5'
6	F	401	GTP	O4'-C4'-C5'-O5'
6	L	401	GTP	O4'-C4'-C5'-O5'
4	G	1601	ATP	C2'-C1'-N9-C4
6	I	401	GTP	C3'-C4'-C5'-O5'
6	C	401	GTP	C3'-C4'-C5'-O5'
6	F	401	GTP	C3'-C4'-C5'-O5'

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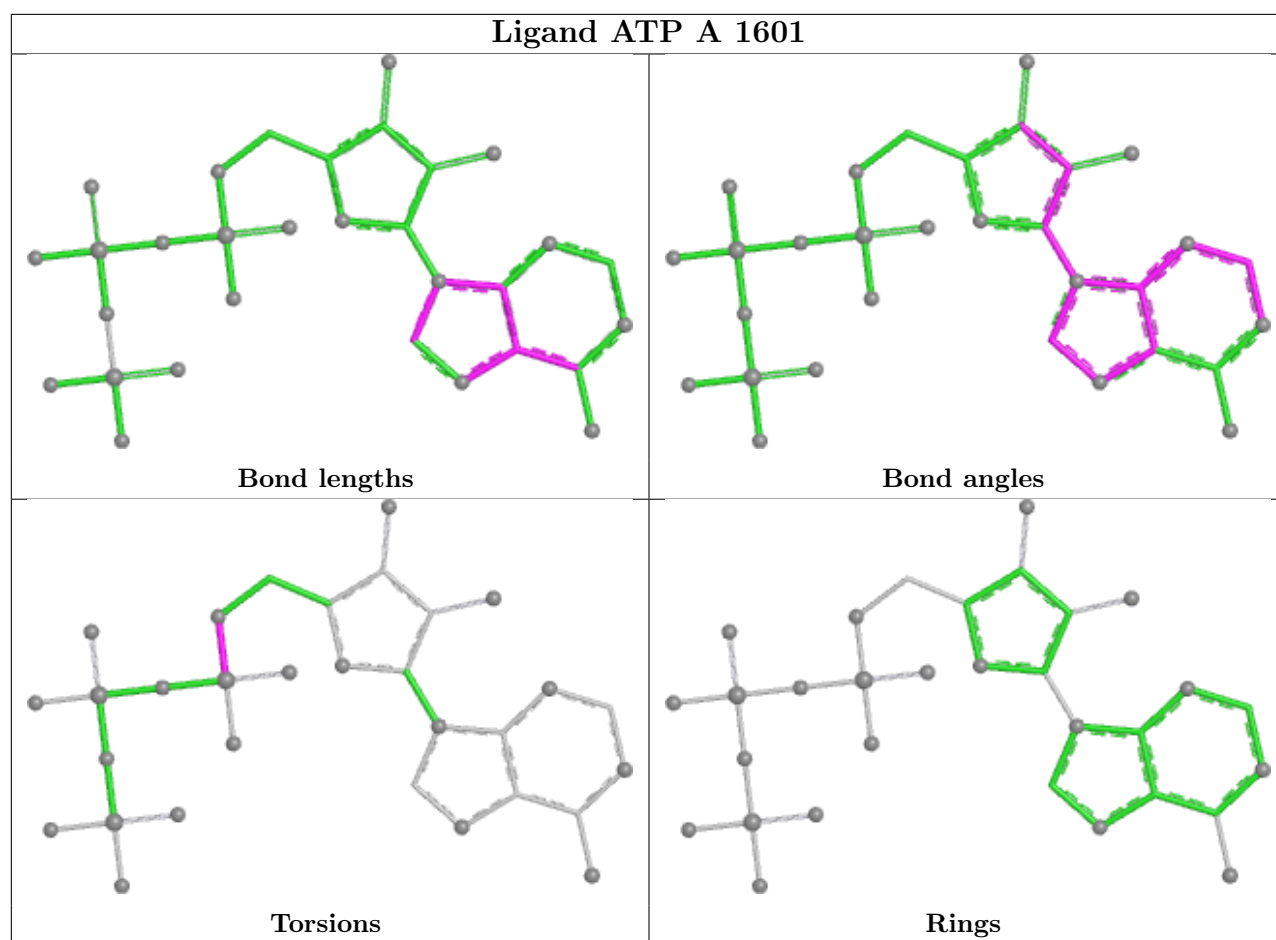
Mol	Chain	Res	Type	Atoms
6	L	401	GTP	C3'-C4'-C5'-O5'
4	G	1601	ATP	C4'-C5'-O5'-PA
4	J	1601	ATP	PA-O3A-PB-O2B
6	I	401	GTP	PB-O3A-PA-O2A
6	C	401	GTP	PB-O3A-PA-O2A
6	F	401	GTP	PB-O3A-PA-O2A
6	L	401	GTP	PB-O3A-PA-O2A
4	G	1601	ATP	O4'-C1'-N9-C8

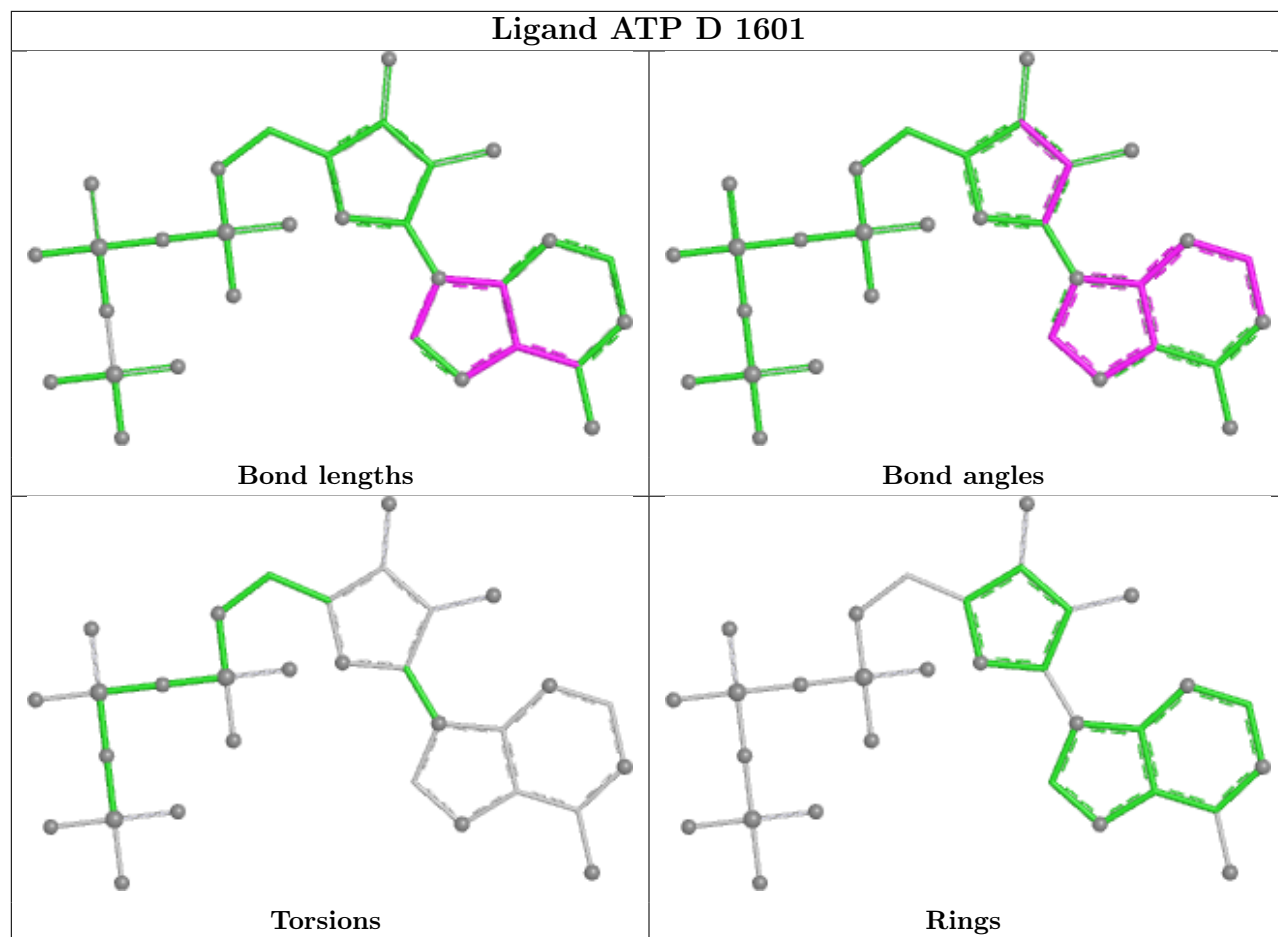
There are no ring outliers.

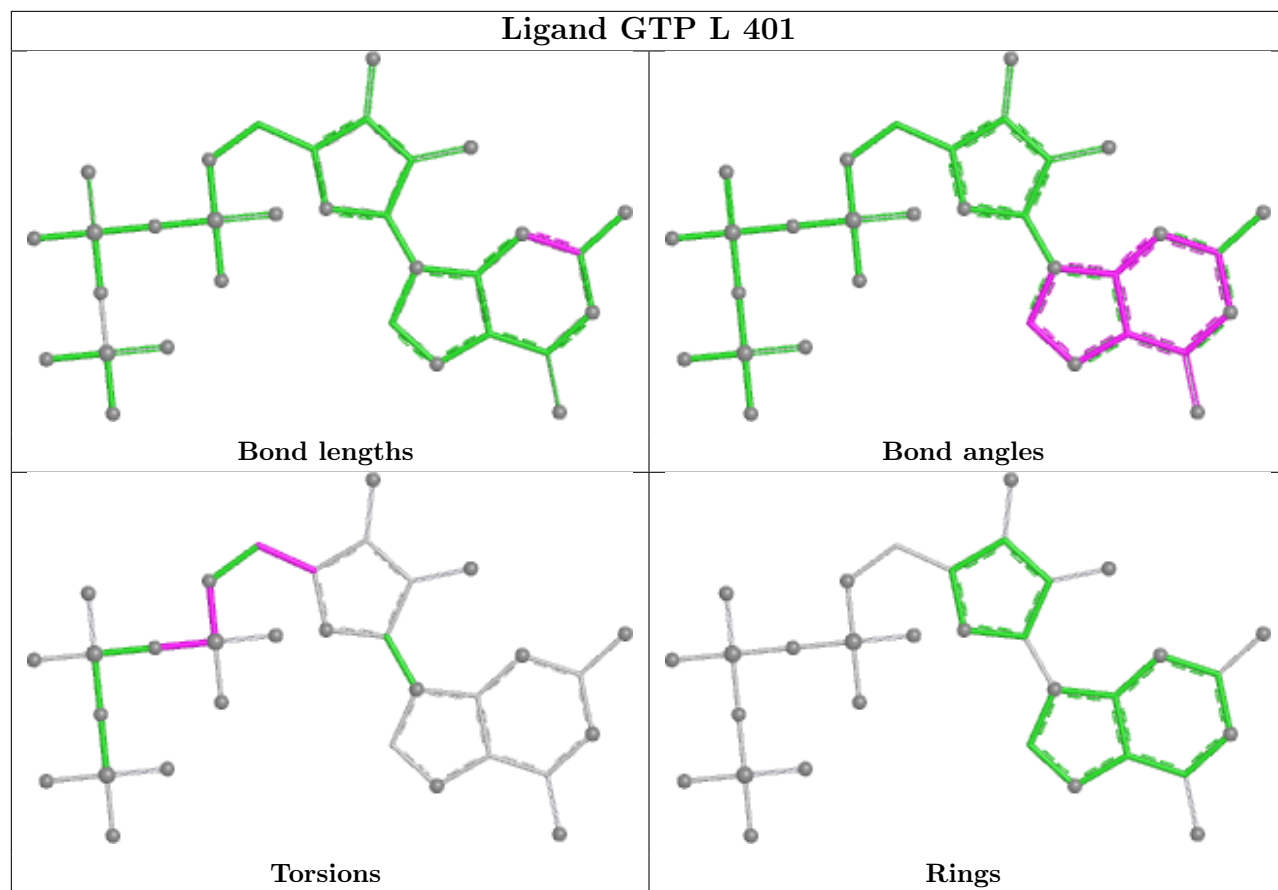
6 monomers are involved in 21 short contacts:

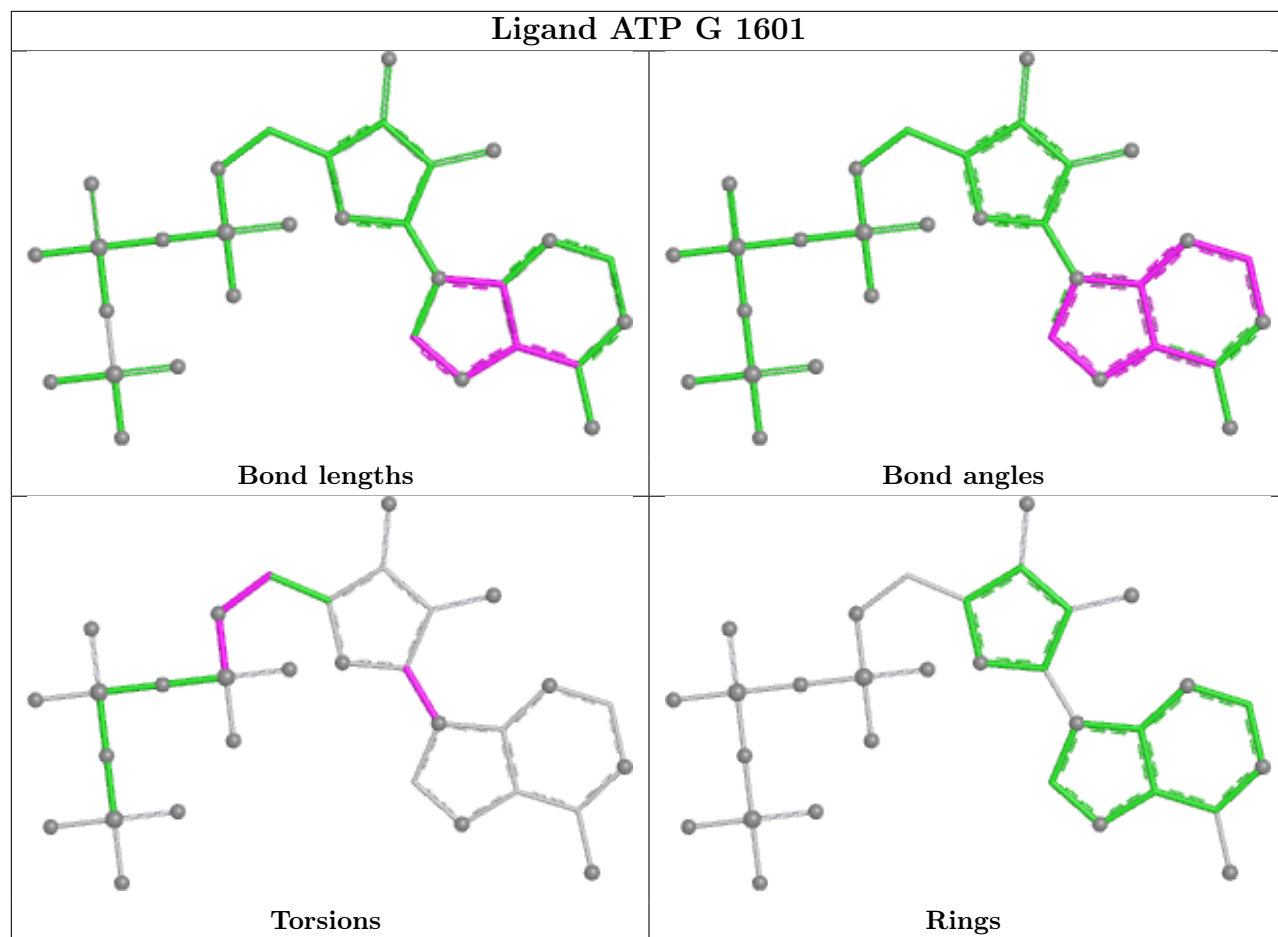
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	1601	ATP	1	0
6	L	401	GTP	4	0
4	J	1601	ATP	4	0
6	C	401	GTP	4	0
6	F	401	GTP	4	0
6	I	401	GTP	4	0

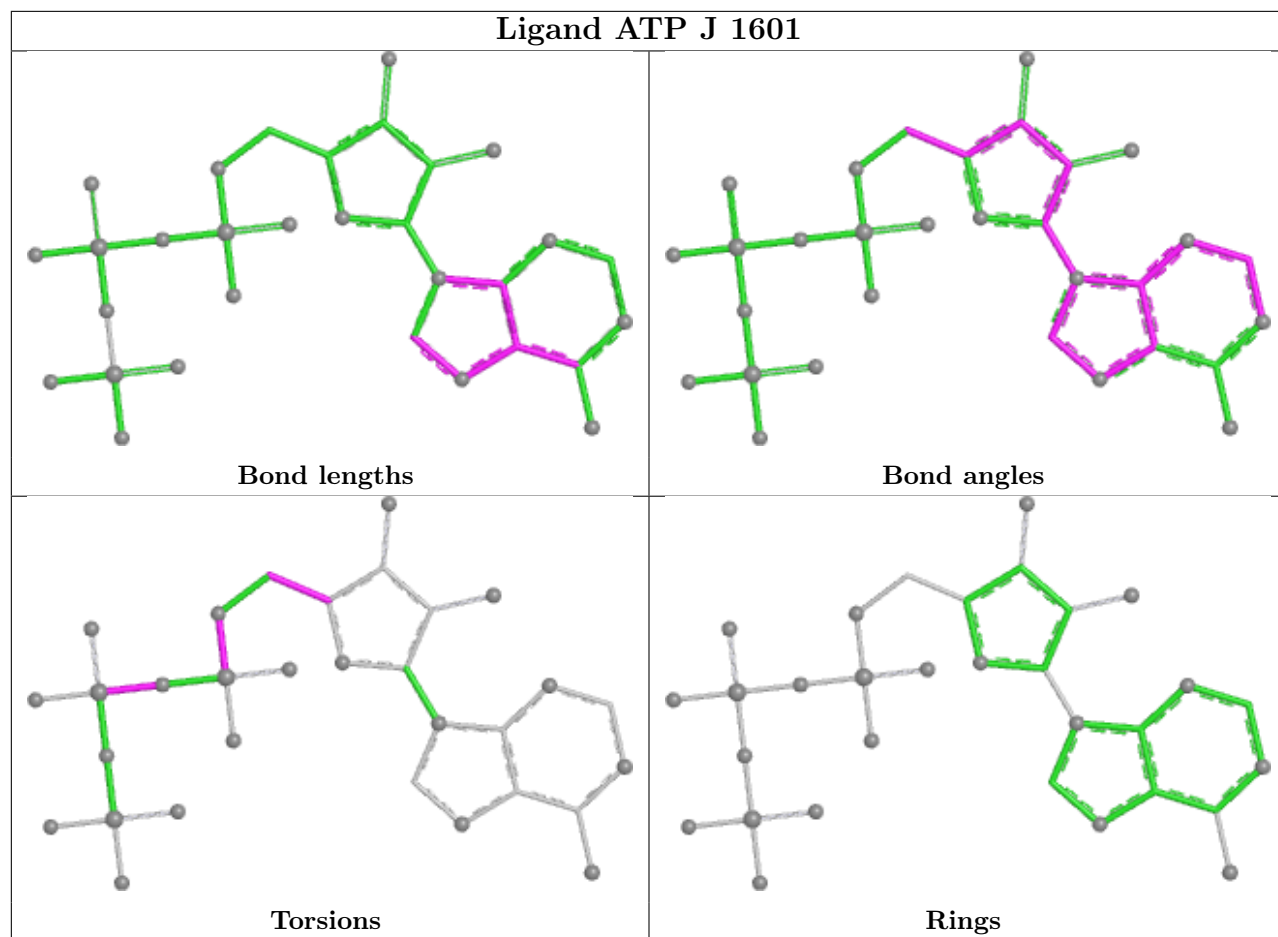
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



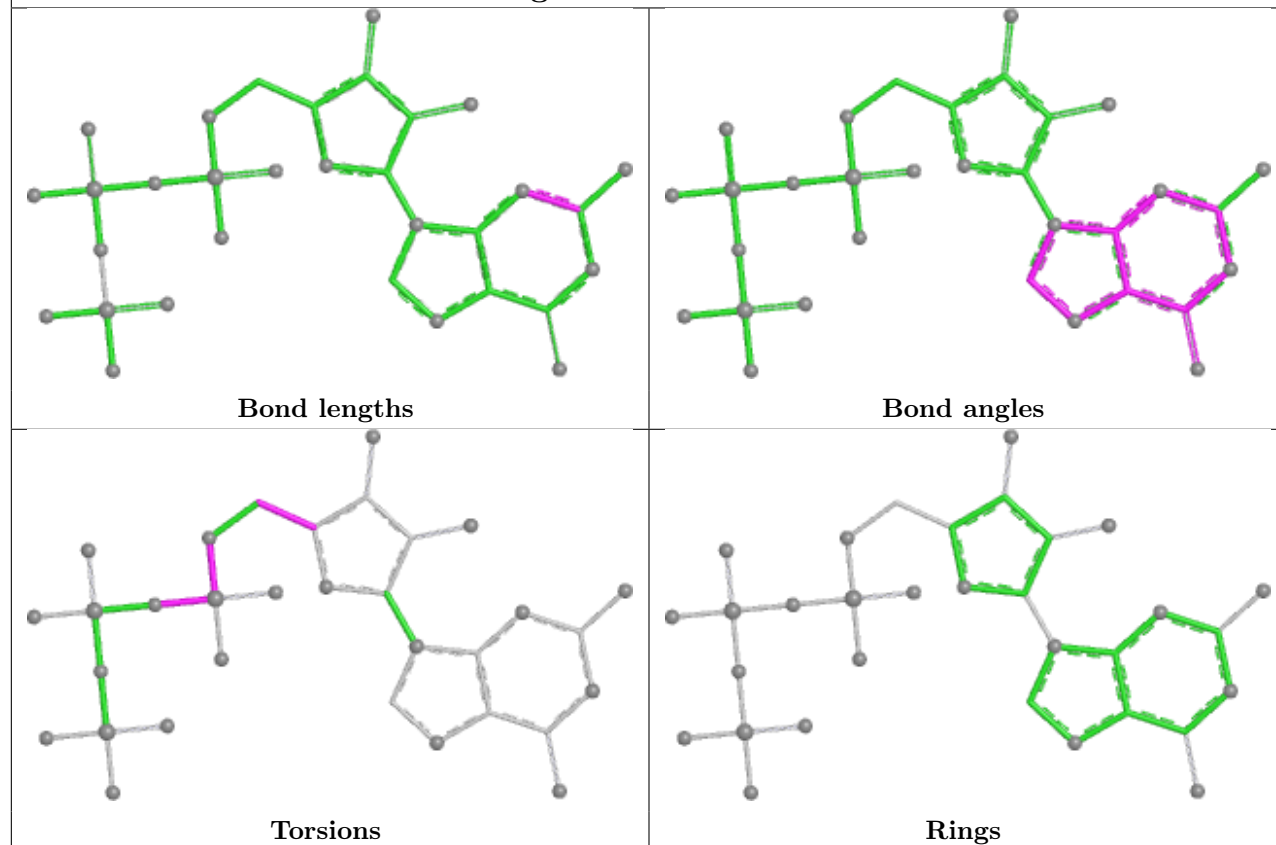




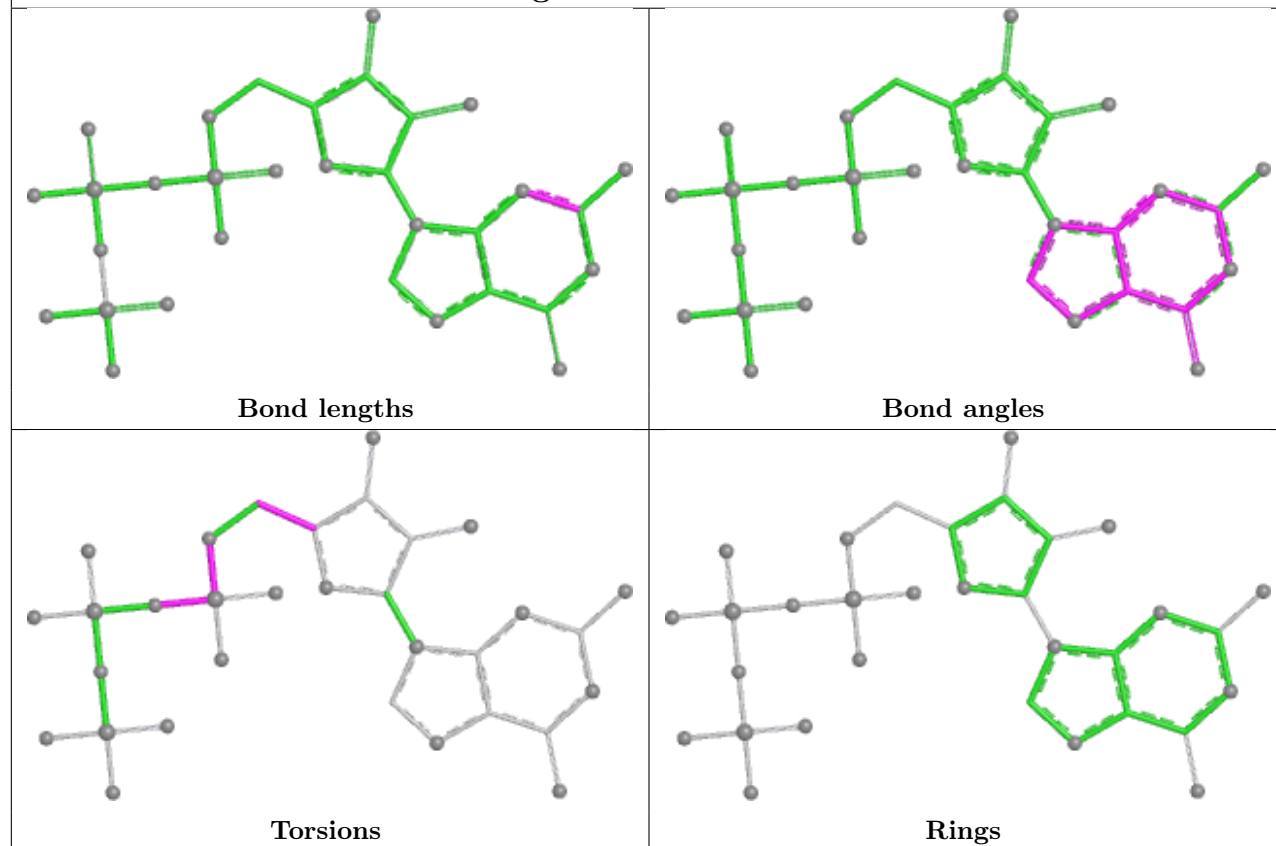


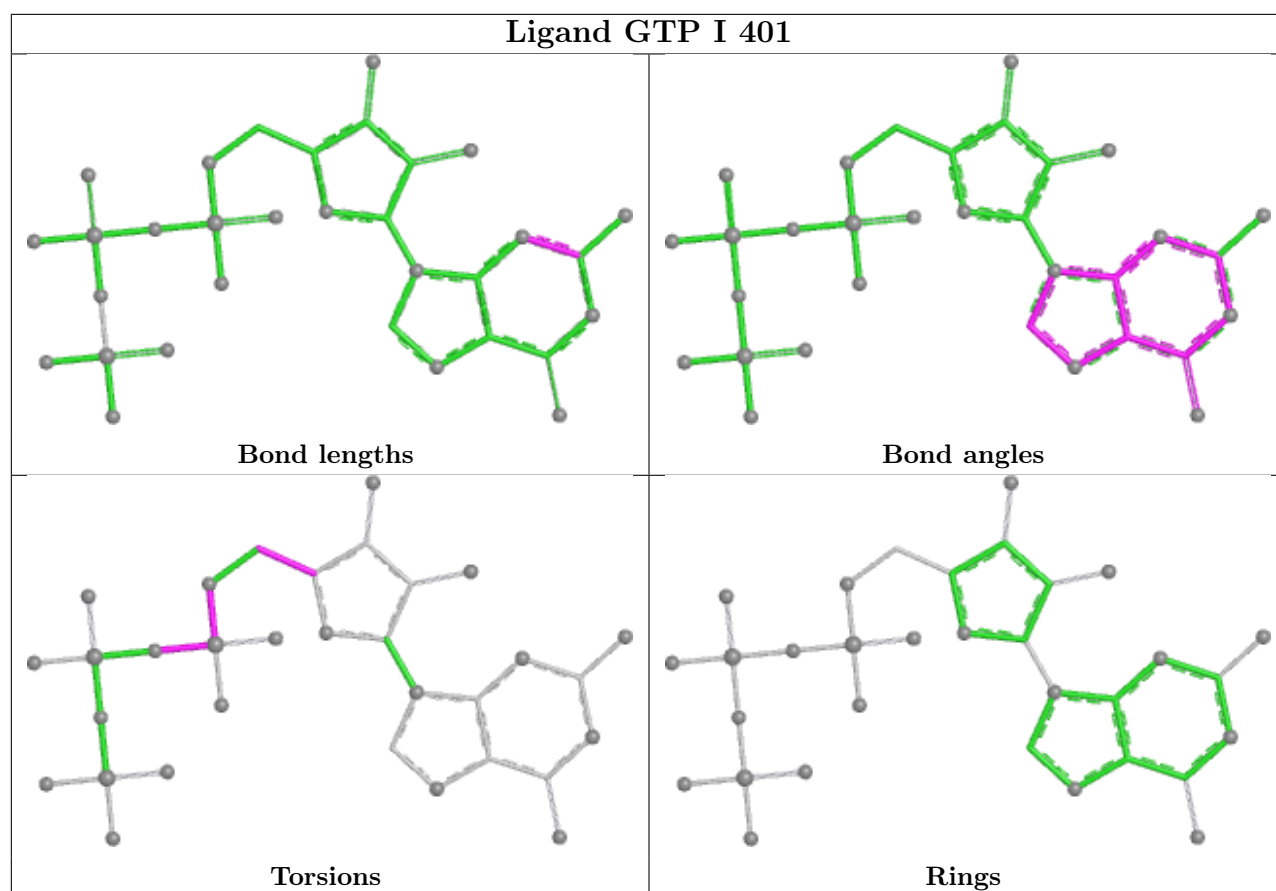


Ligand GTP C 401



Ligand GTP F 401





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.

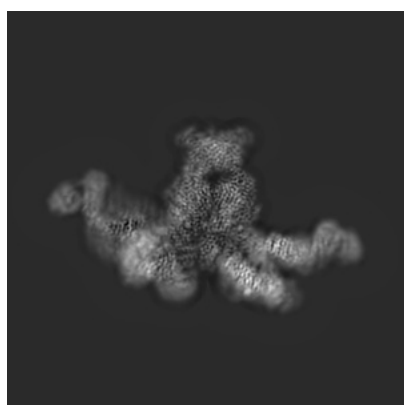
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73001. These allow visual inspection of the internal detail of the map and identification of artifacts.

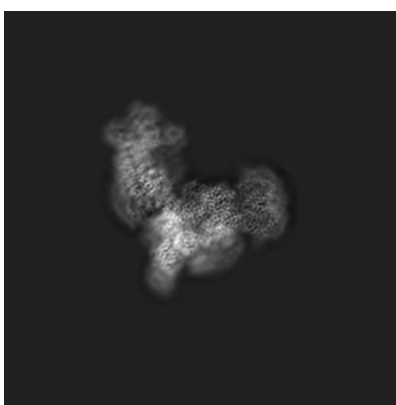
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

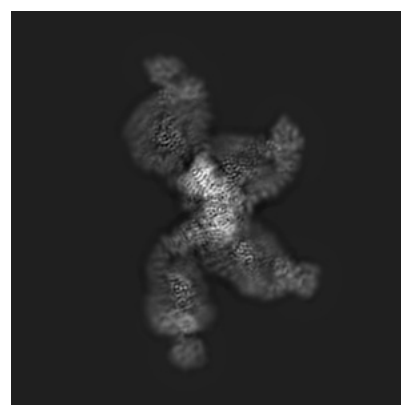
6.1.1 Primary map



X



Y

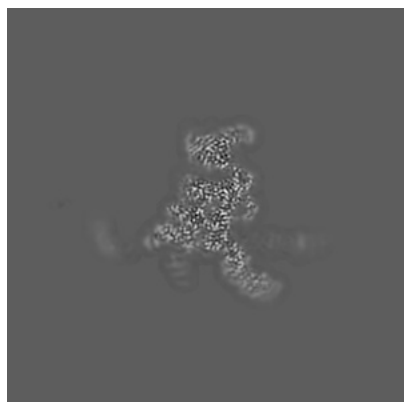


Z

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

6.2 Central slices [i](#)

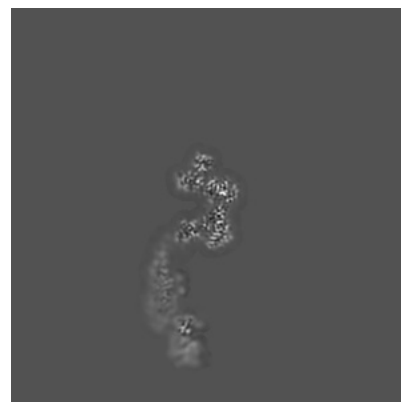
6.2.1 Primary map



X Index: 240



Y Index: 240

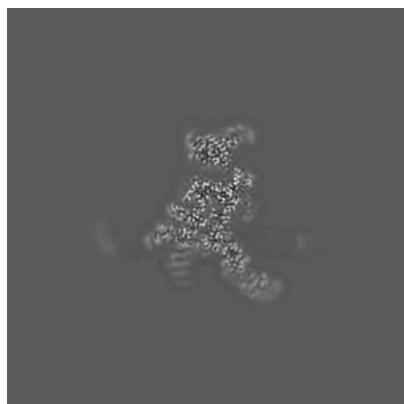


Z Index: 240

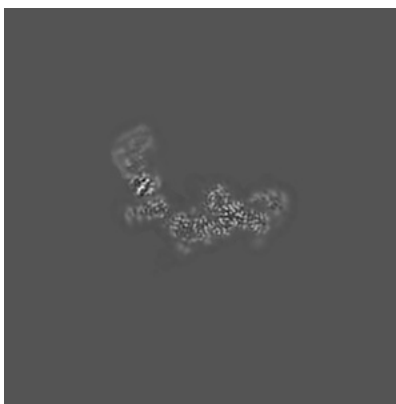
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 242



Y Index: 276

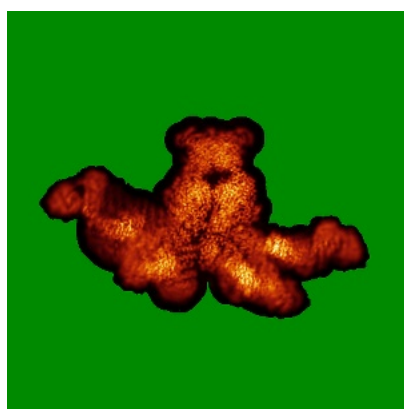


Z Index: 194

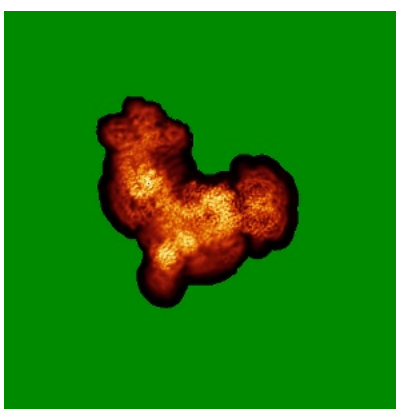
The images above show the largest variance slices of the map in three orthogonal directions.

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

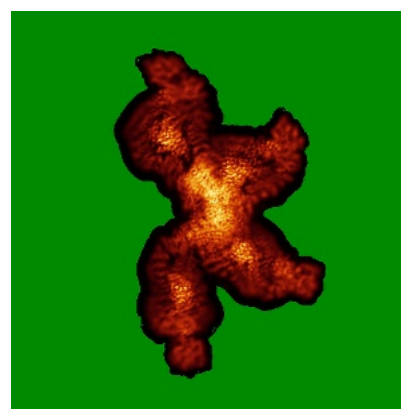
6.4.1 Primary map



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 7.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

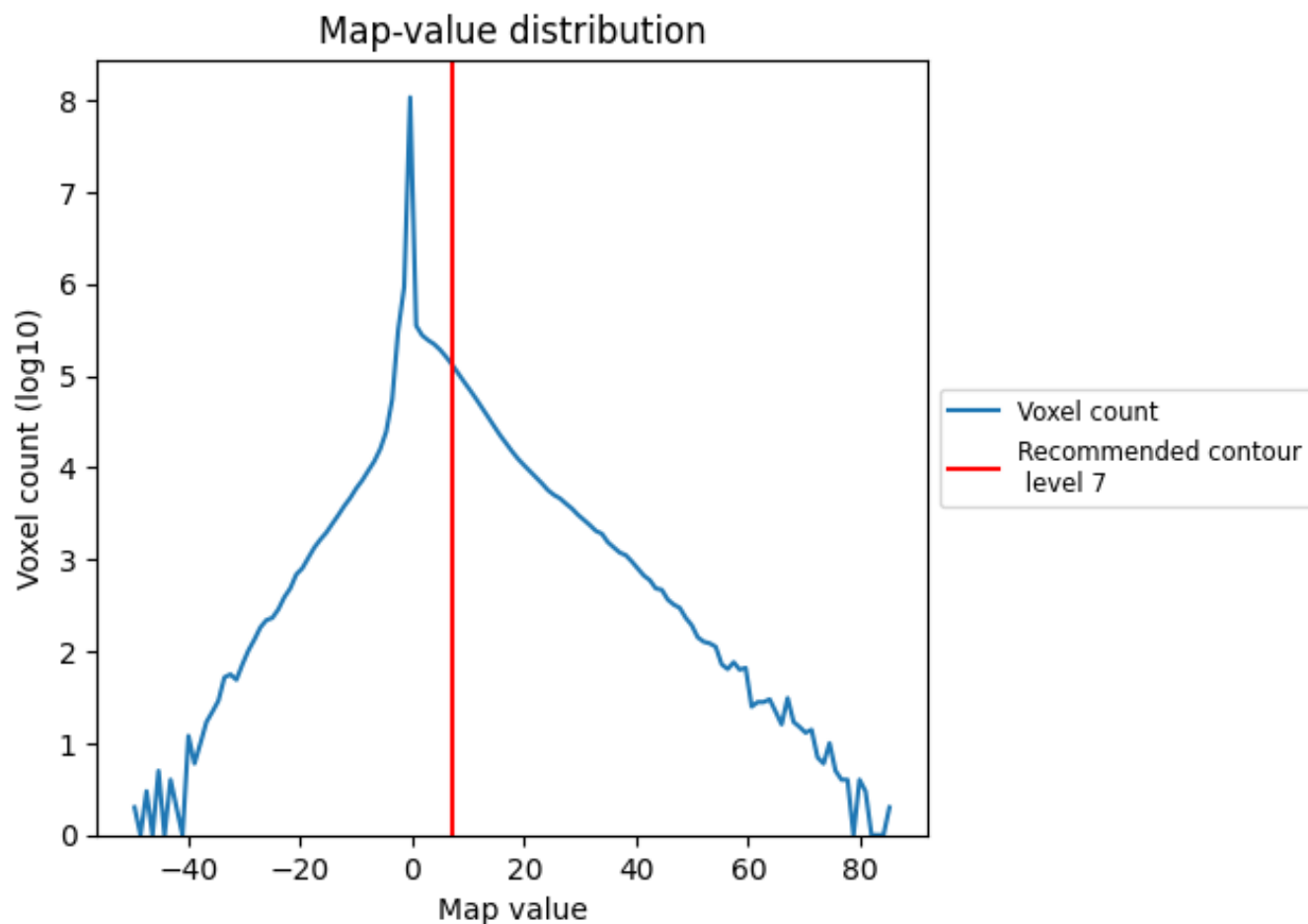
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

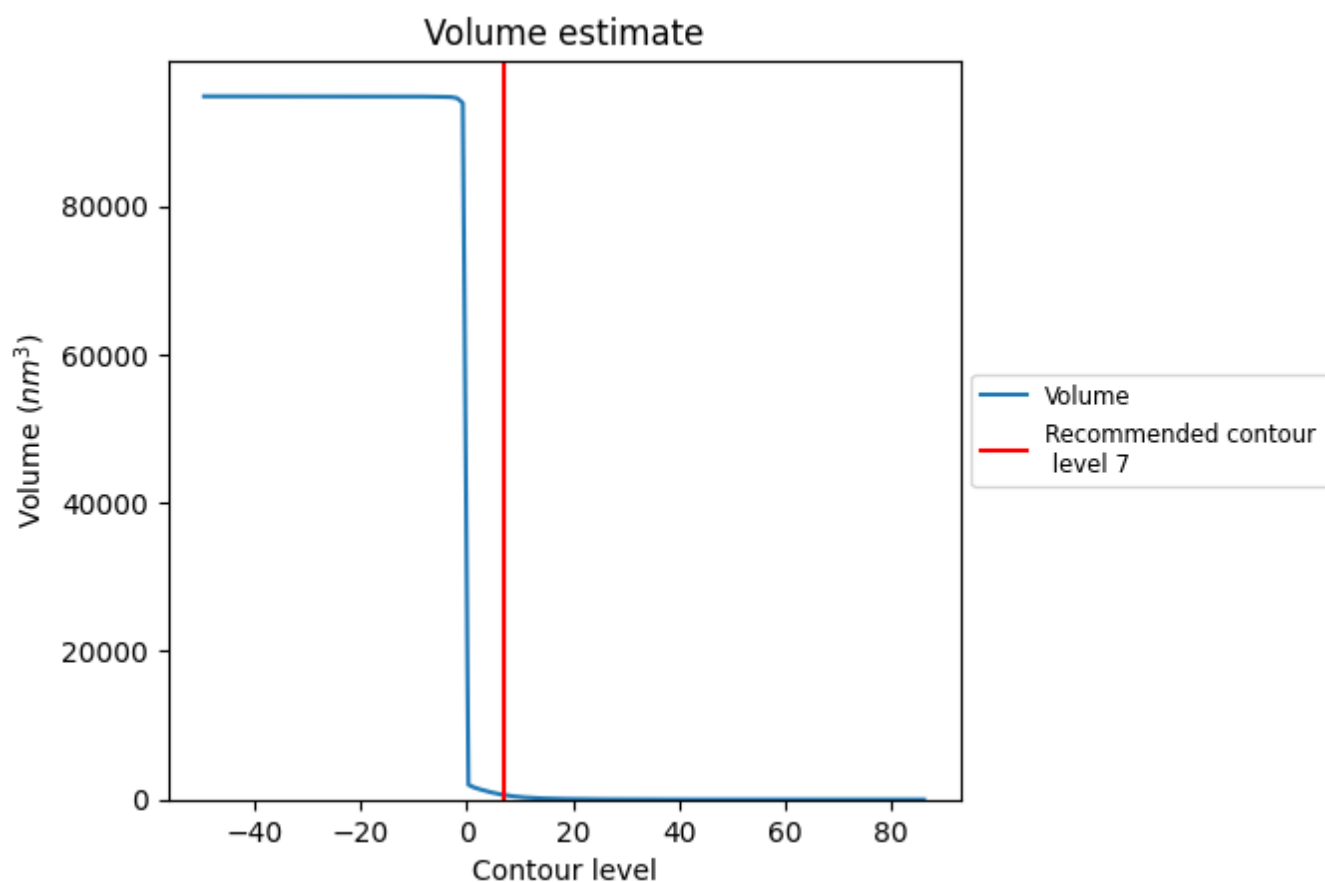
This section contains the results of statistical analysis of the map.

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.

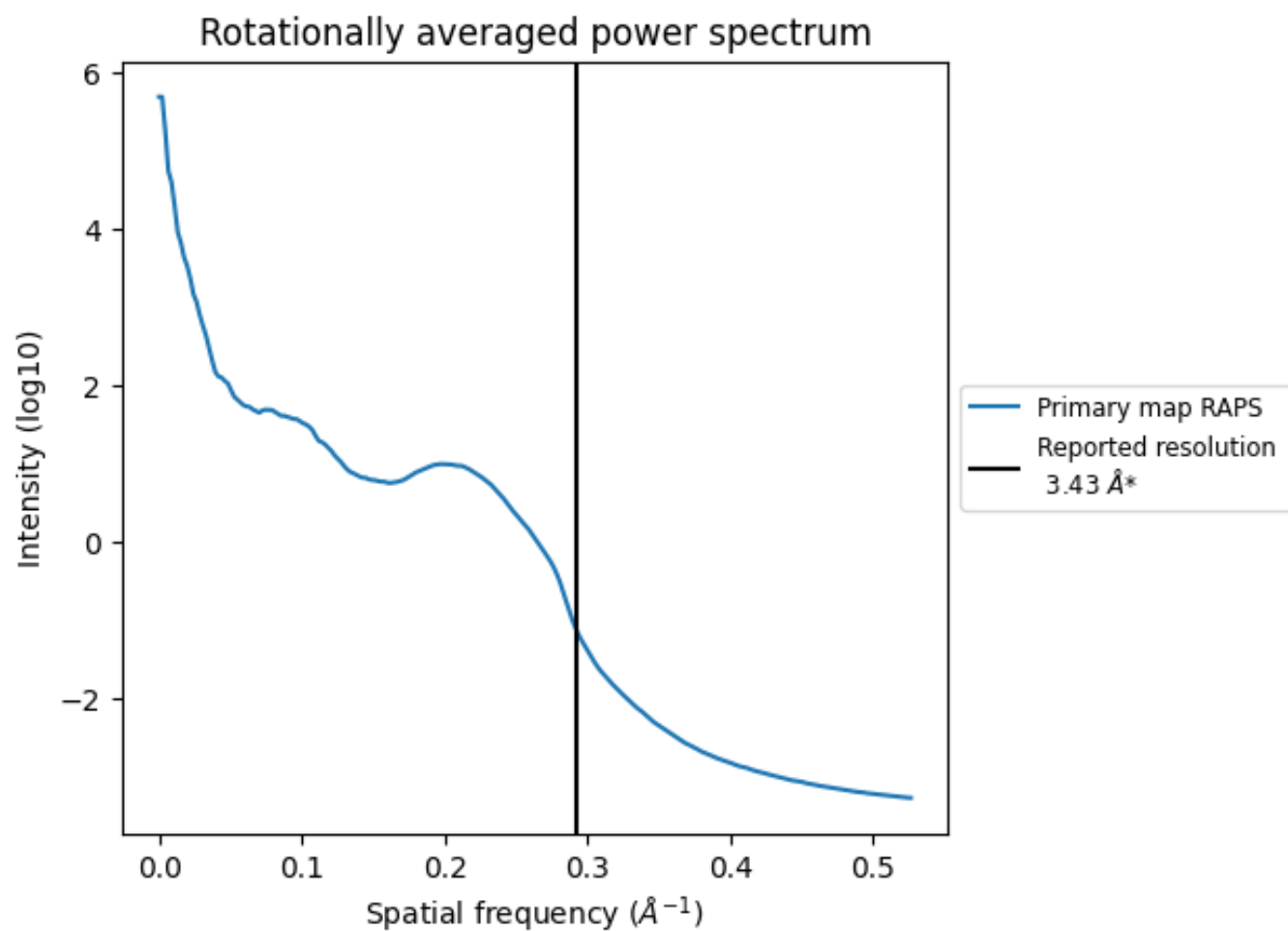
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 622 nm^3 ; this corresponds to an approximate mass of 562 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 0.292 Å⁻¹

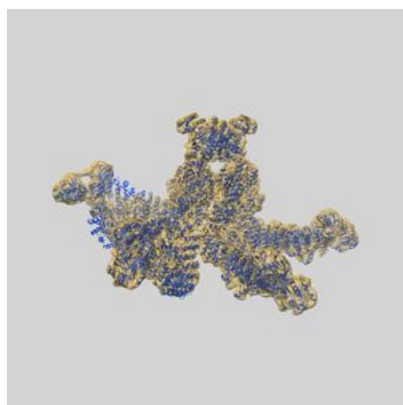
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

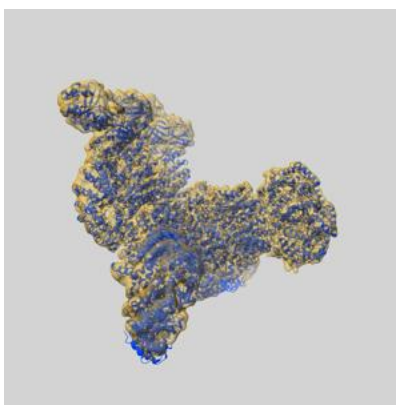
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-73001 and PDB model 9YIX. Per-residue inclusion information can be found in section [3](#) on page [7](#).

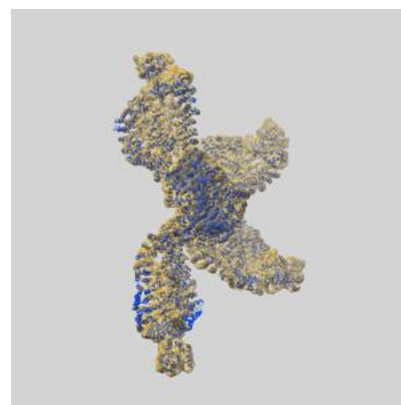
9.1 Map-model overlay [i](#)



X



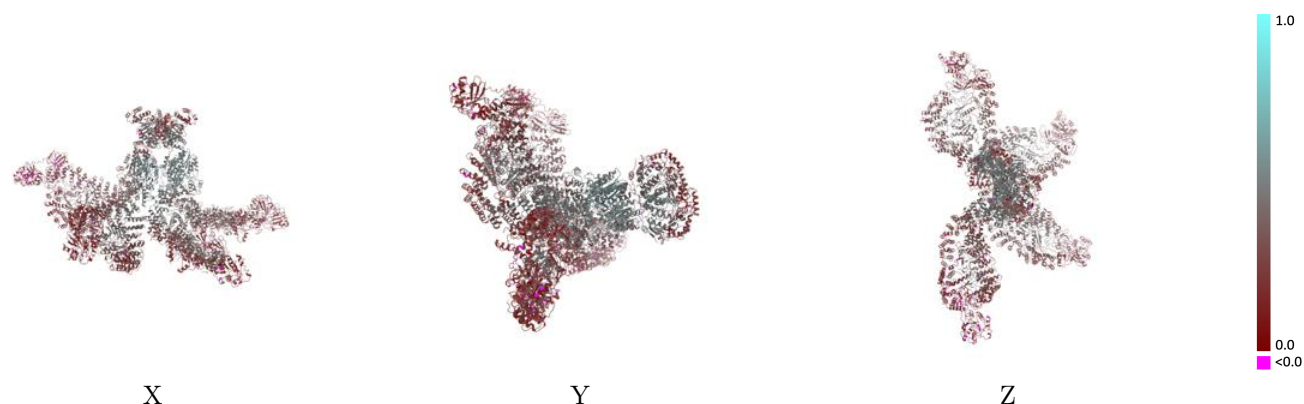
Y



Z

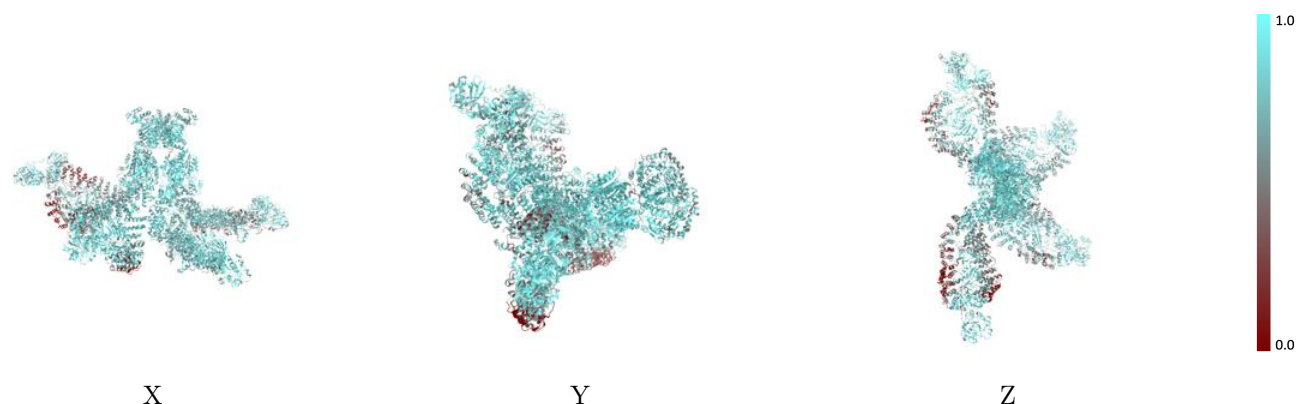
The images above show the 3D surface view of the map at the recommended contour level 7.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



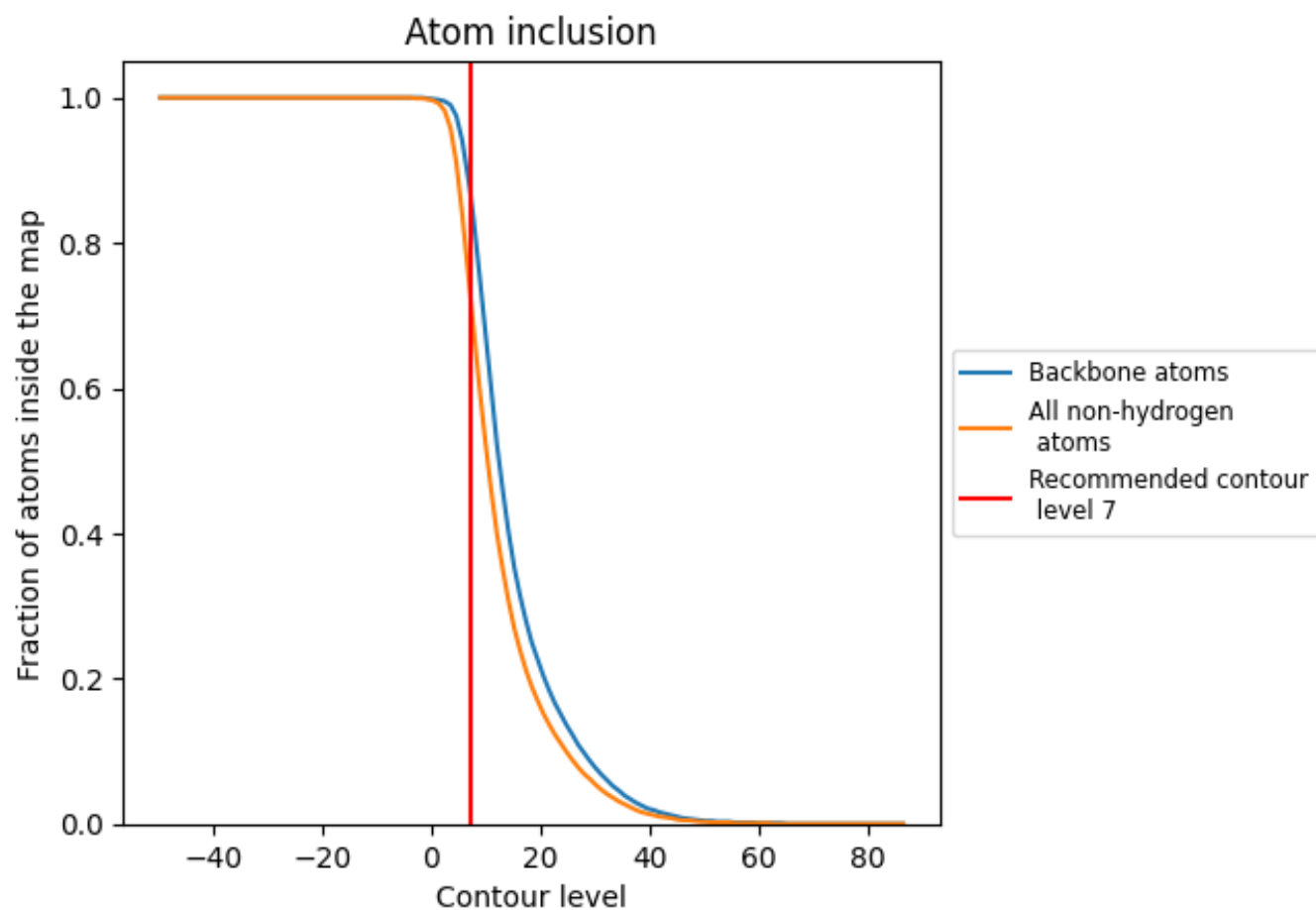
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 74% 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 (7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7360	0.3190
A	0.8080	0.3810
B	0.8760	0.3920
C	0.7940	0.2340
D	0.7500	0.3530
E	0.8670	0.3790
F	0.7940	0.2260
G	0.5470	0.2820
H	0.7820	0.3120
I	0.7730	0.1760
J	0.7140	0.3450
K	0.8550	0.3550
L	0.7870	0.1970

