



Full wwPDB EM Validation Report ⓘ

Aug 19, 2026 – 04:29 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

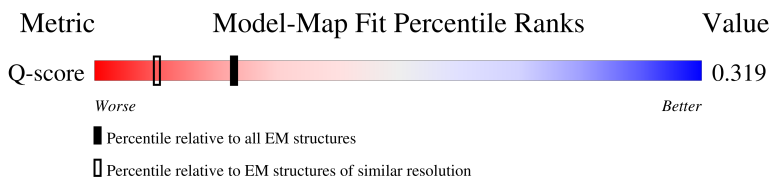
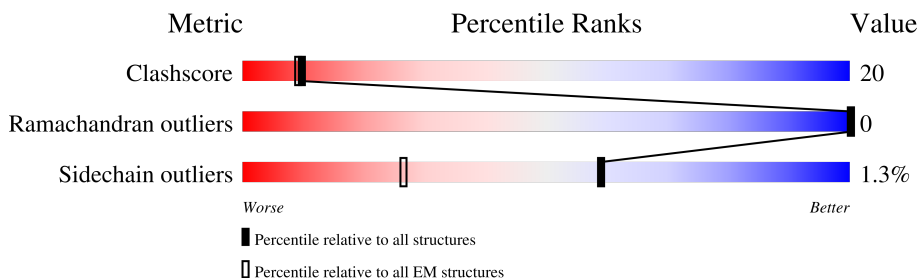
1 Overall quality at a glance

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.



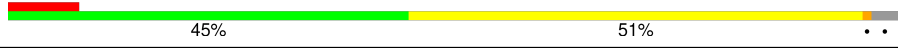
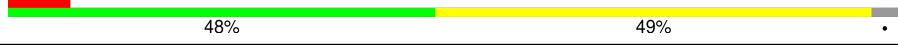
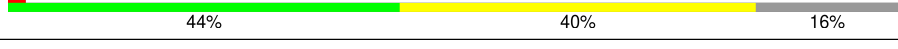
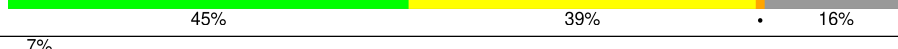
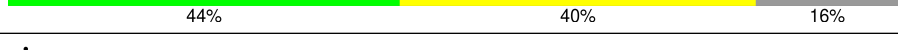
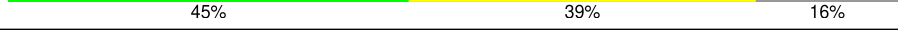
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13927 (2.93 - 3.93)

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	
1	D	1523	
1	G	1523	
1	J	1523	

Continued on next page...

Continued from previous page...

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.

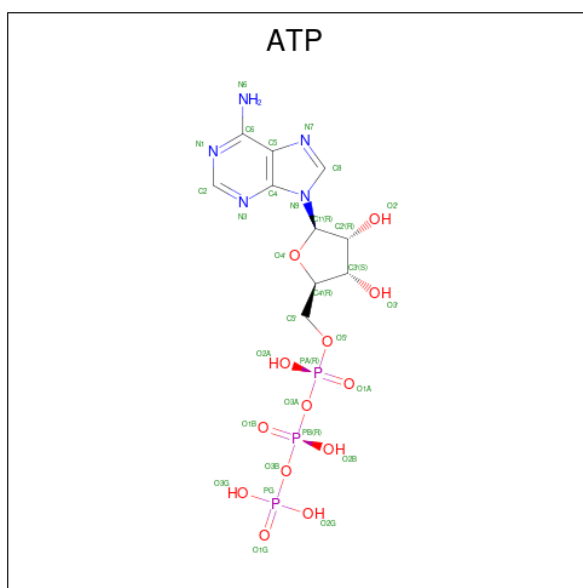
Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	384	Total	C	N	O	S	0	0
			2954	1867	508	566	13		
2	C	384	Total	C	N	O	S	0	0
			2954	1867	508	566	13		
2	F	384	Total	C	N	O	S	0	0
			2954	1867	508	566	13		
2	L	384	Total	C	N	O	S	0	0
			2954	1867	508	566	13		

- 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).

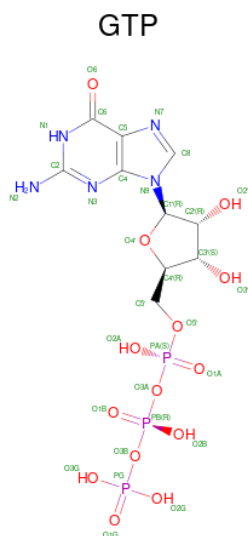


Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	G	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	D	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	J	1	Total	C	N	O	P	0
			31	10	5	13	3	

- 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).

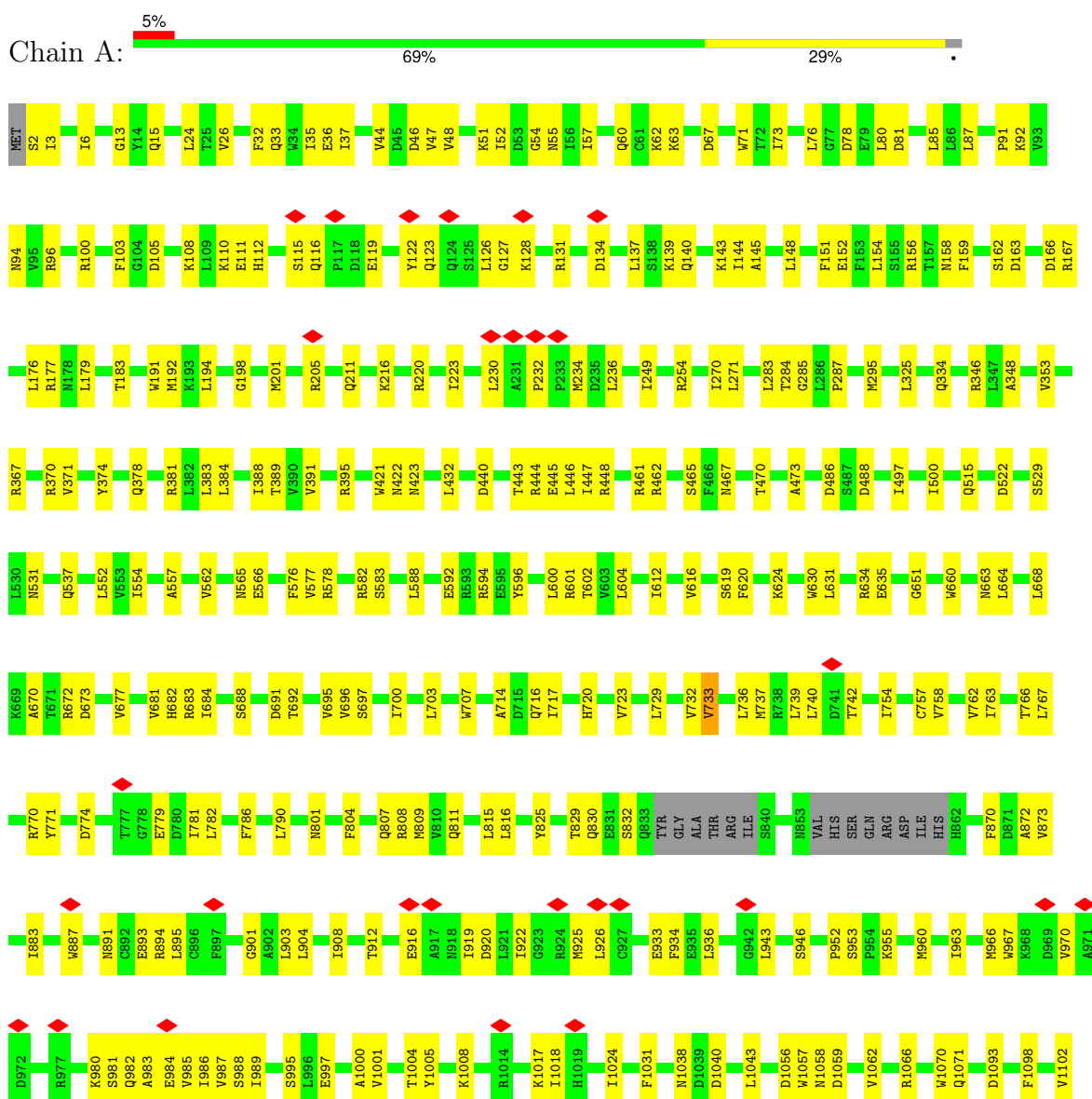


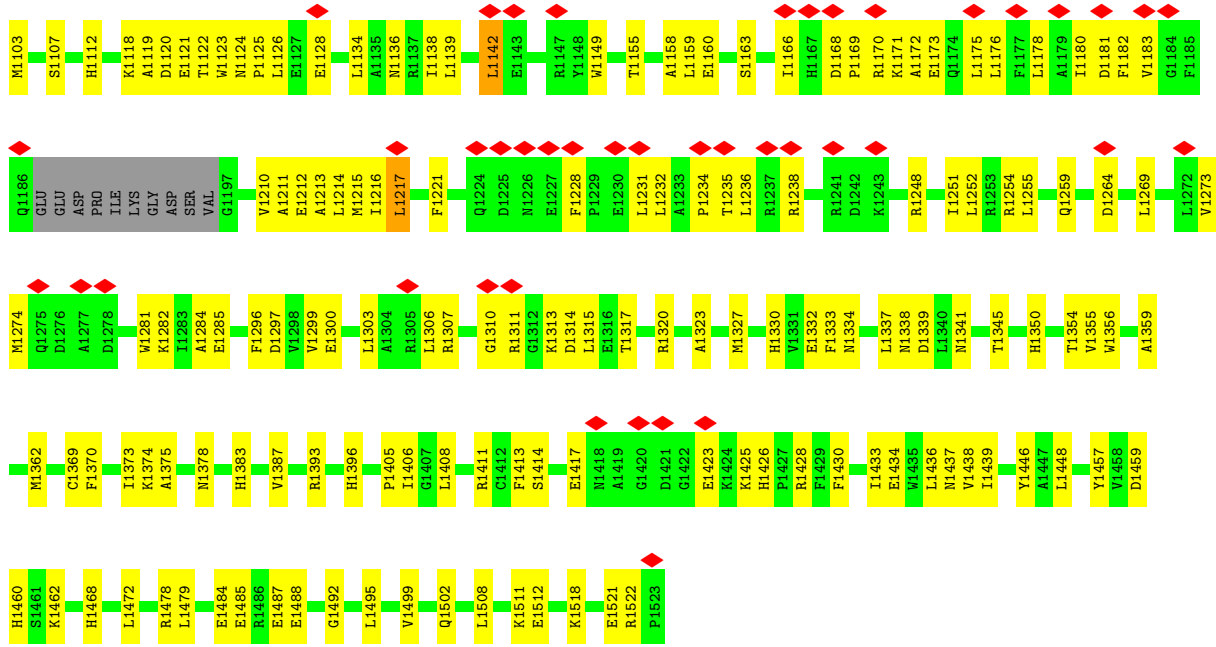
Mol	Chain	Residues	Atoms					AltConf
6	I	1	Total 32	C 10	N 5	O 14	P 3	0
6	C	1	Total 32	C 10	N 5	O 14	P 3	0
6	F	1	Total 32	C 10	N 5	O 14	P 3	0
6	L	1	Total 32	C 10	N 5	O 14	P 3	0

3 Residue-property plots

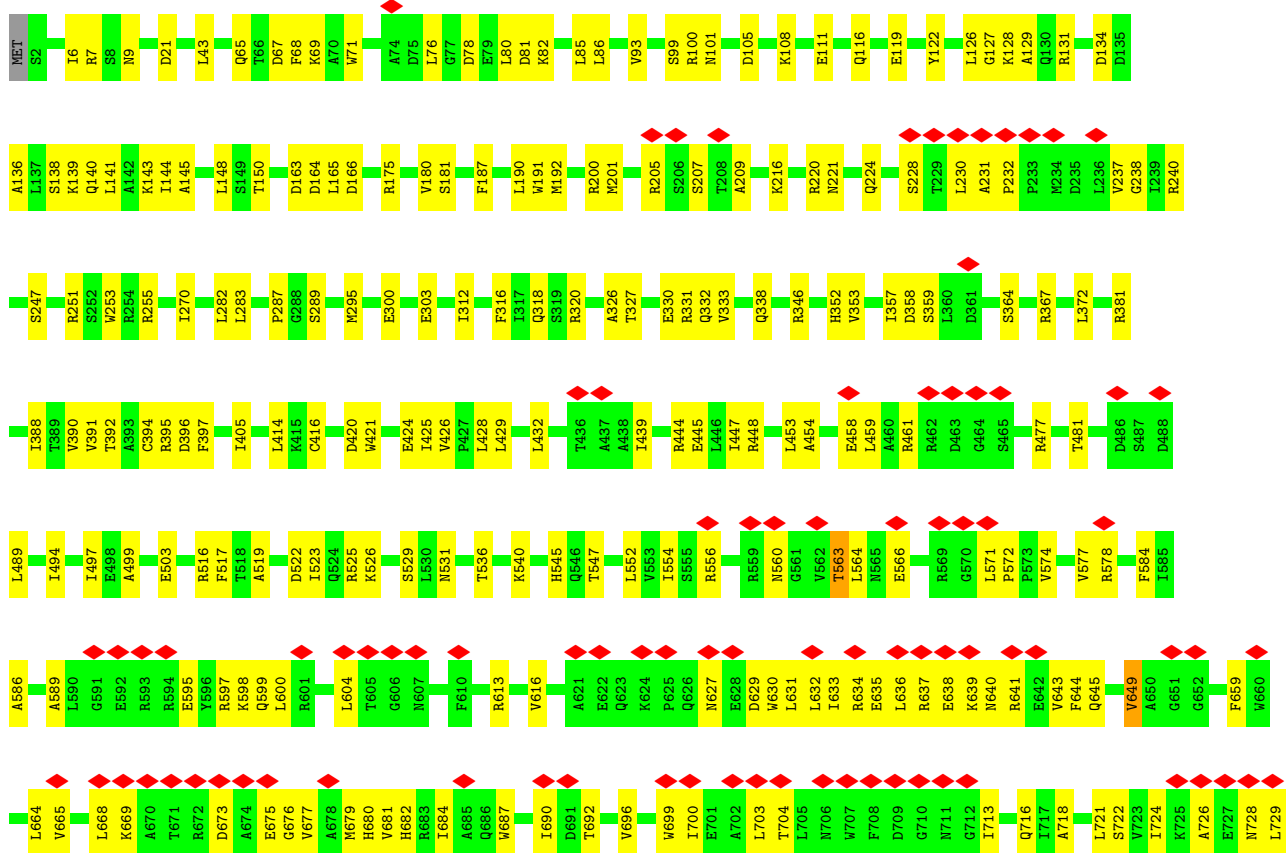
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

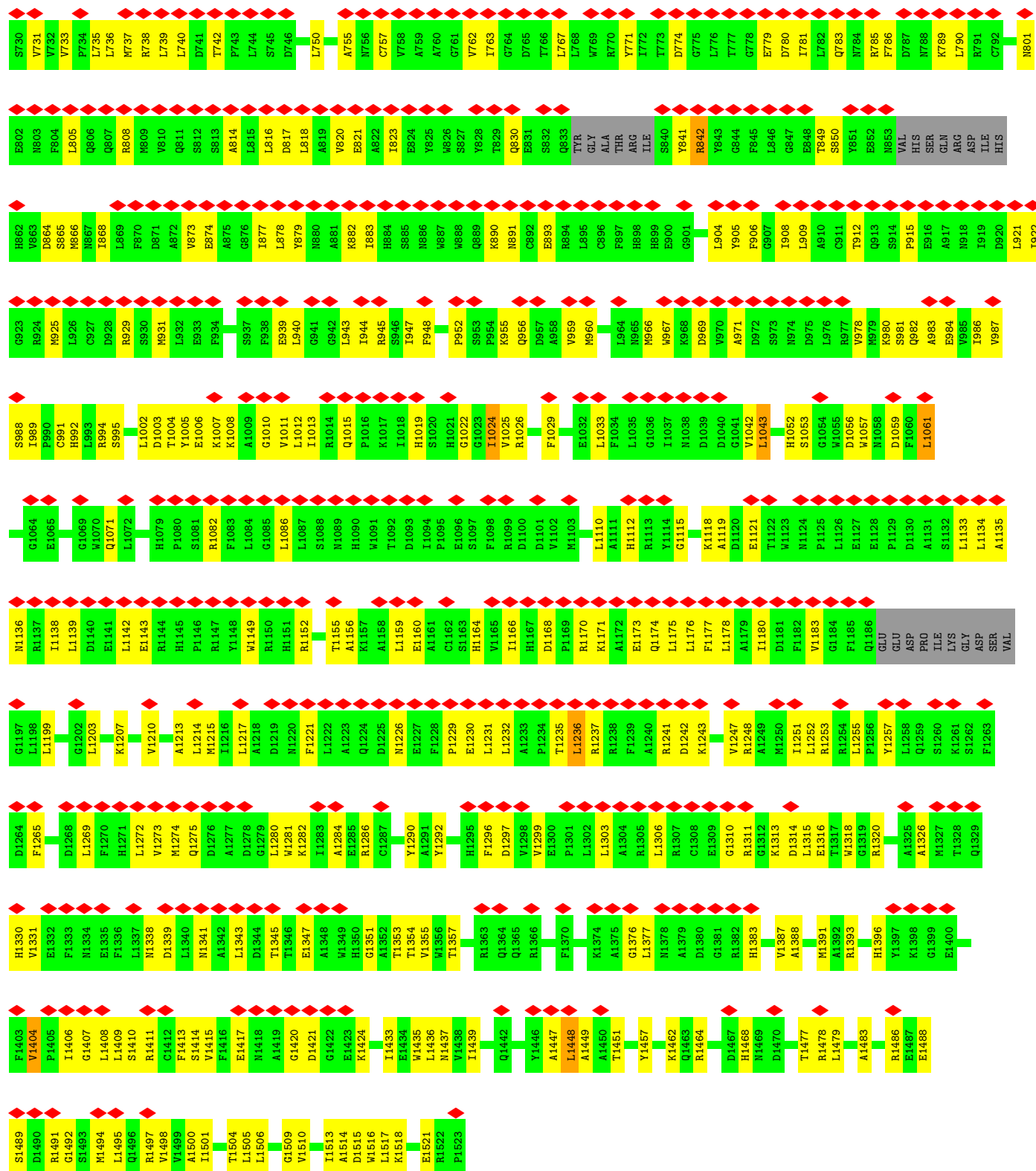
• Molecule 1: AAA family ATPase





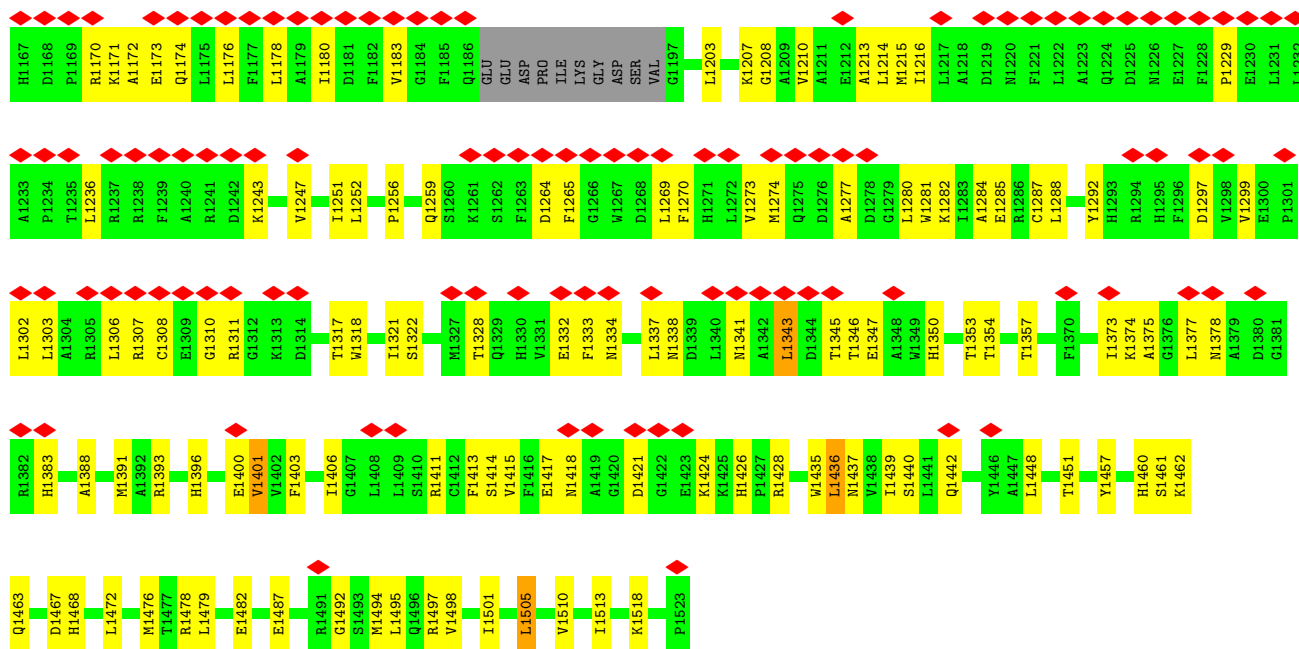
• Molecule 1: AAA family ATPase



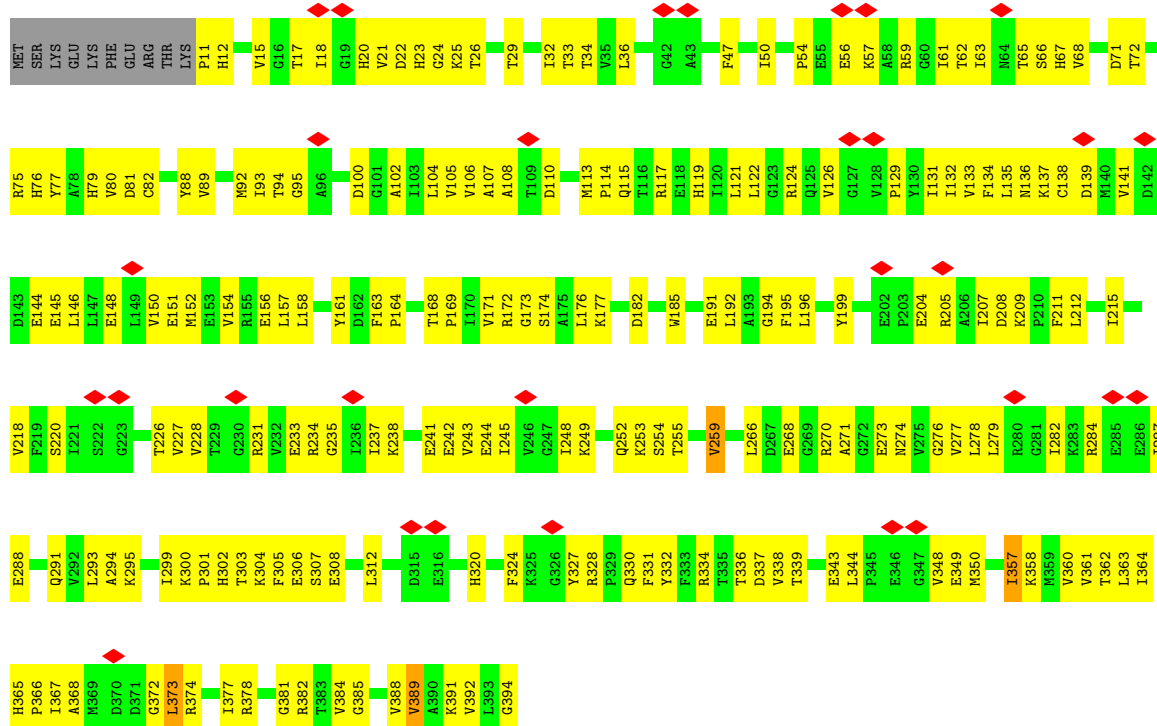
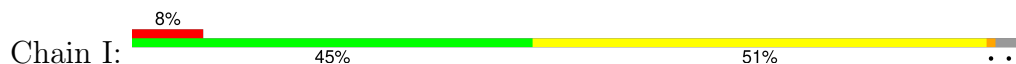


P1169	R1170	K1171	A1172	E1173	Q1174	L1175	L1176	F1177	L1178	L1252	R1253	R1254	I1180	D1181	F1182	V1183	G1184	F1185	Q1186	GLU	ASP	V1273	M1274	L1275	D1276	A1277	D1278	W1281	K1282	L1199	G1202	L1203	V1210	A1211	L1288	E1212	I1216	D1297	V1298	V1299	E1300	L1303	A1304	R1305	L1306	R1307	C1308	E1309	G1310	R1311	D1314	L1315	E1316	T1317
Q1071	R1078	P1080	F1079	S1081	R1082	F1083	L1084	M1103	S1104	G1105	V1106	S1107	T1108	L1117	D1120	E1121	M1124	ASP	P1125	L1126	E1127	P1129	D1130	A1131	S1132	L1133	L1134	A1135	N1136	R1137	L1138	L1139	D1140	E1141	L1142	E1143	R1144	R1147	Y1148	W1149	R1150	S1154	T1155	L1159	C1162	S1163	T1166	H1167	D1168					
Q982	A983	E984	V985	I986	V987	S988	R989	P990	C991	H992	L993	R994	E997	A998	V1001	L1002	D1003	T1004	Y1005	E1006	K1007	V1011	L1012	K1017	I1018	R1019	S1020	H1021	I1024	V1025	R1026	F1029	S1030	F1031	D1040	L1043	K1044	L1045	H1048	W1057	N1058	D1059	F1060	L1061	V1062	R1066	W1070							
P915	E916	A917	N918	I919	D920	G751	L921	I922	G923	R924	N925	L926	C927	D928	R929	E933	F934	E935	L936	E939	G942	L943	I944	R945	S946	H947	F948	T949	F950	L951	P952	K955	Q956	V959	N960	A961	S962	I963	M966	V967	K968	P969	V970	A971	D972	S973	N974	D975	L976	V978	K980			
Q833	TTR	GLY	ALA	THR	ARG	ILE	S840	G844	T849	S850	V853	VAL	HIS	SER	GLN	ARG	ASP	ILE	HIS	H862	S865	F870	D871	A872	H873	E874	L878	H879	N880	H881	K882	I883	H884	N886	W887	K890	E893	R894	F897	P906	G907	I908	L909	A910	C911	T912	Q913	S914						
T742	P743	S748	F749	L750	G751	T752	V753	N756	C757	V758	A759	V762	I763	G764	D765	T766	T773	D774	G775	L776	T777	G778	E779	D780	I781	L790	E796	F797	N801	F804	Q807	R808	N809	V810	Q811	S812	S813	A814	L815	L816	D817	L818	E821	Y825	T829	Q830								
V665	P666	L668	K669	A670	T671	R672	D673	V677	A678	M679	R683	Q686	G694	V695	S697	F698	G699	I700	T704	L705	M706	F708	D709	A714	D715	Q716	I717	A718	L721	A726	E727	N728	L729	V732	W733	G734	L735	L736	M737	L740	D741													
Q537	H545	T547	L548	L552	V562	T563	E566	R569	G570	L571	V577	E592	L593	R594	R597	L600	R601	T602	V603	L604	A617	D629	W630	L631	R634	E635	K639	N640	R641	Q645	V646	V647	Y648	A650	G651	G652	S653	W656	H657	I661														
L347	S359	D361	S364	L365	R367	L372	Q373	Y374	Q378	R381	T385	I388	V391	R403	D442	T443	R444	E445	R448	D459	R462	D463	G464	F466	N467	L474	L479	L484	I494	P513	R516	T518	L527	V532																				
A88	E89	N90	P91	K92	V93	F97	R100	K108	L109	K110	Q116	E119	G120	S121	Y122	Q123	K128	A136	S138	K139	Q140	K143	I144	A145	P146	S147	L148	F151	L154	S155	R156	D164	L165	M168	L172	R173	L176	D184	S185	M188	M192													
MET	SER	ILE	ALA	GLY	ILE	ARG	SER	N9	R10	G11	D12	G13	T16	F20	D21	W22	V26	D31	S39	L43	V44	D45	I49	G50	K51	Q60	K63	N64	Q65	T66	D67	F68	K69	A70	W71	I72	I73	A74	D75	L76	G77	D78	E79	K82	A83	S84	L85	L86	L87					



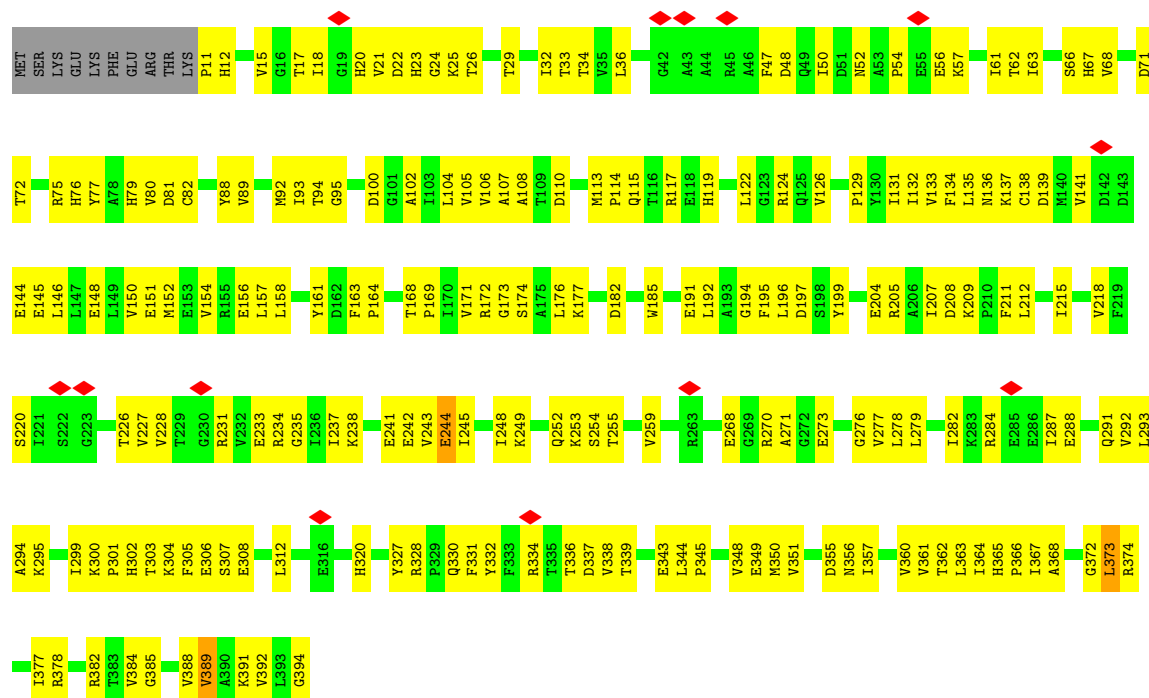


• Molecule 2: Elongation factor Tu 1

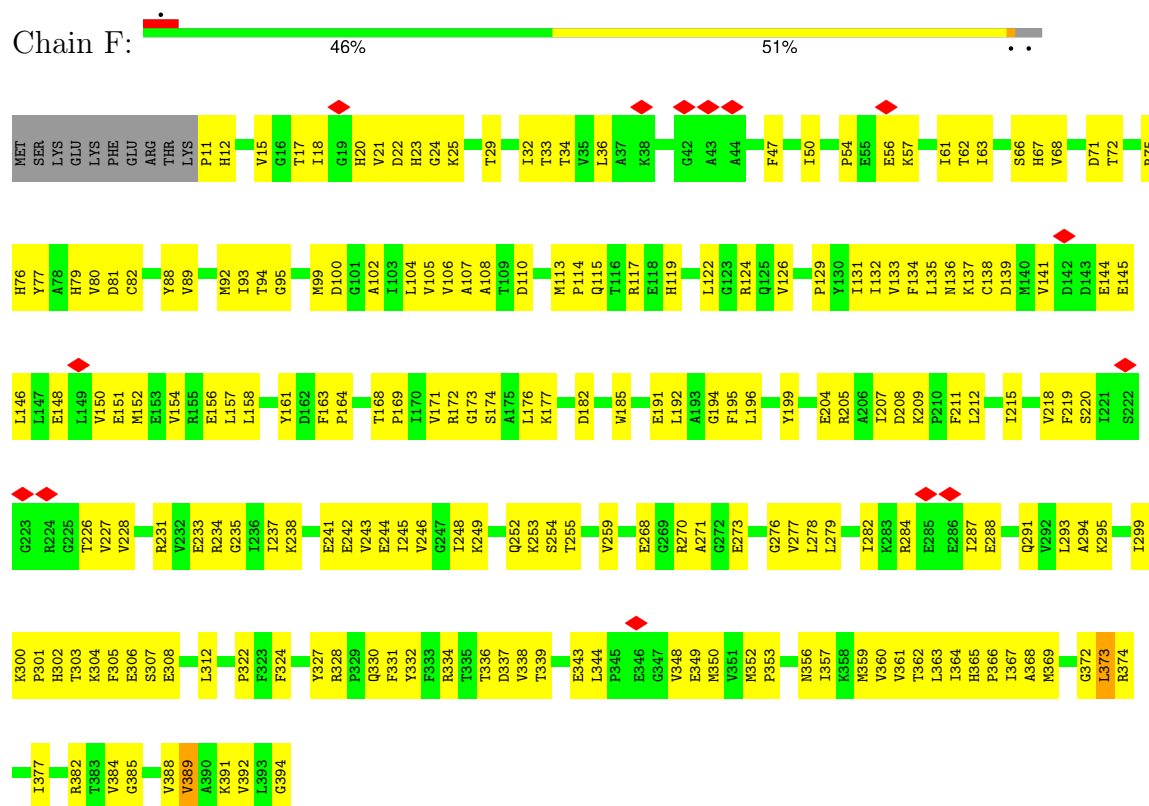


• Molecule 2: Elongation factor Tu 1



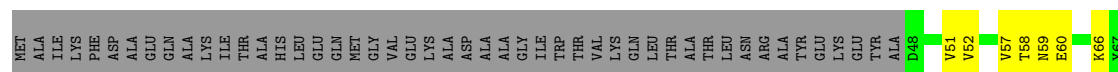
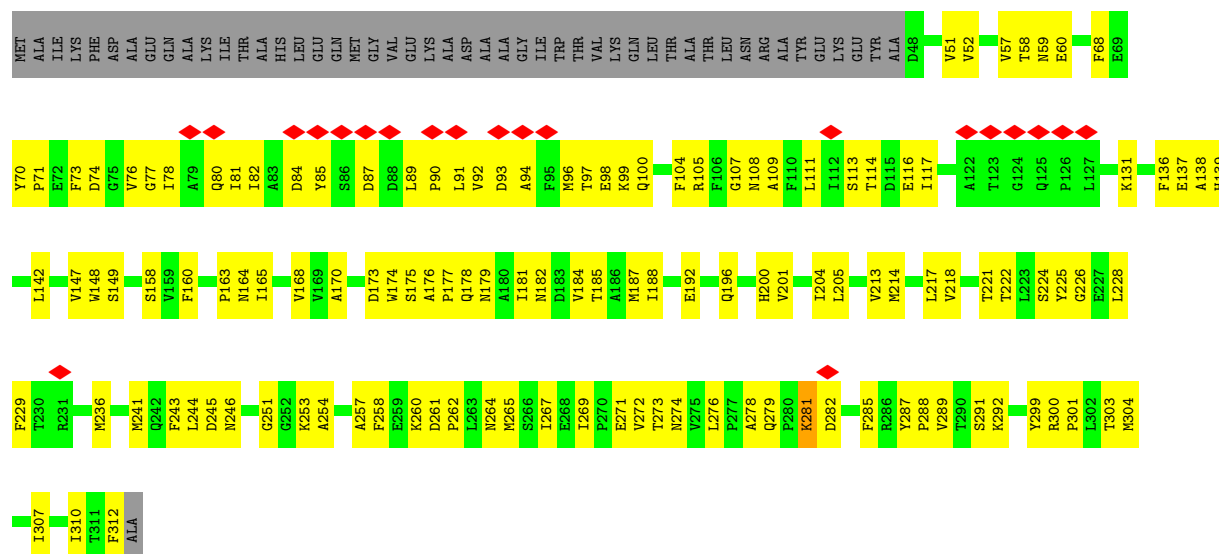
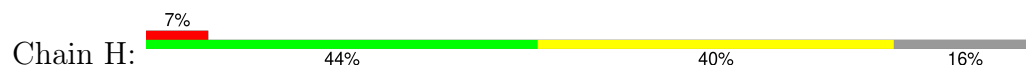
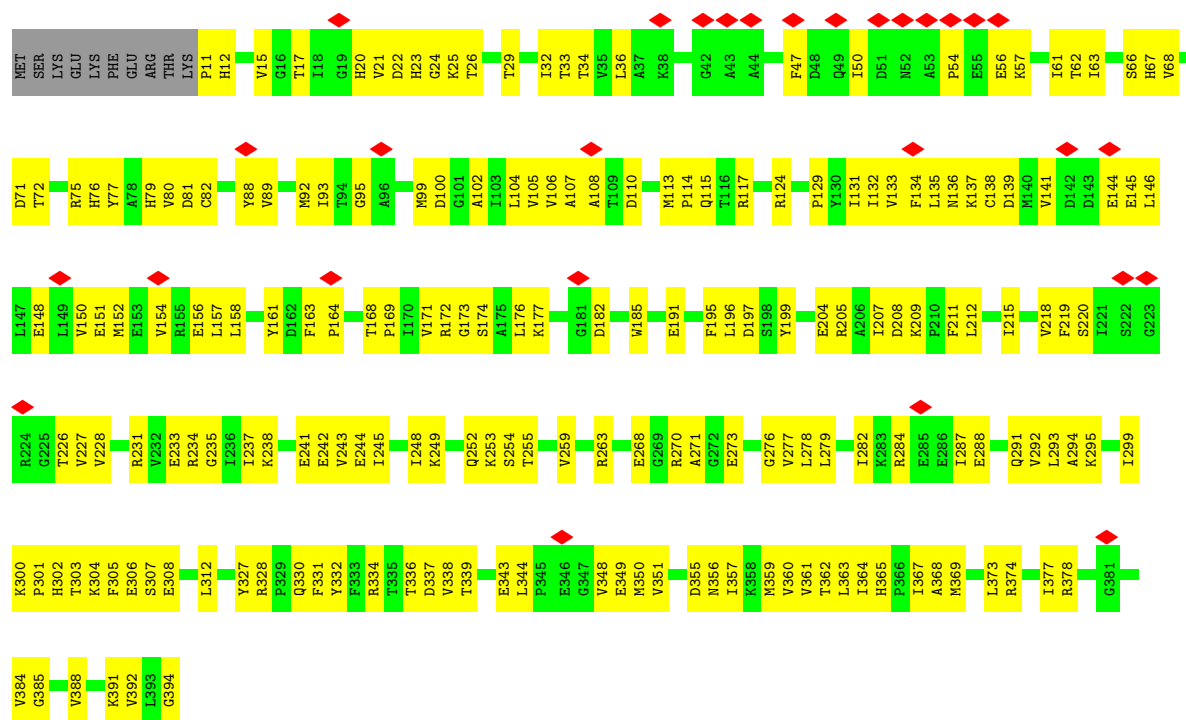


• Molecule 2: Elongation factor Tu 1



• Molecule 2: Elongation factor Tu 1







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: ATP, GTP, 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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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	J	1601	5	32,33,33	1.31	5 (15%)	48,52,52	1.87	11 (22%)
4	ATP	A	1601	5	32,33,33	1.31	5 (15%)	48,52,52	1.80	10 (20%)
6	GTP	C	401	-	33,34,34	0.96	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	D	1601	5	32,33,33	1.33	5 (15%)	48,52,52	1.74	9 (18%)
6	GTP	I	401	-	33,34,34	0.95	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	L	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	J	1601	5	-	6/22/38/38	0/3/3/3
4	ATP	A	1601	5	-	1/22/38/38	0/3/3/3
6	GTP	C	401	-	-	6/22/38/38	0/3/3/3
4	ATP	G	1601	5	-	7/22/38/38	0/3/3/3
4	ATP	D	1601	5	-	0/22/38/38	0/3/3/3
6	GTP	I	401	-	-	6/22/38/38	0/3/3/3
6	GTP	F	401	-	-	6/22/38/38	0/3/3/3
6	GTP	L	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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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'

Continued on next page...

Continued from previous page...

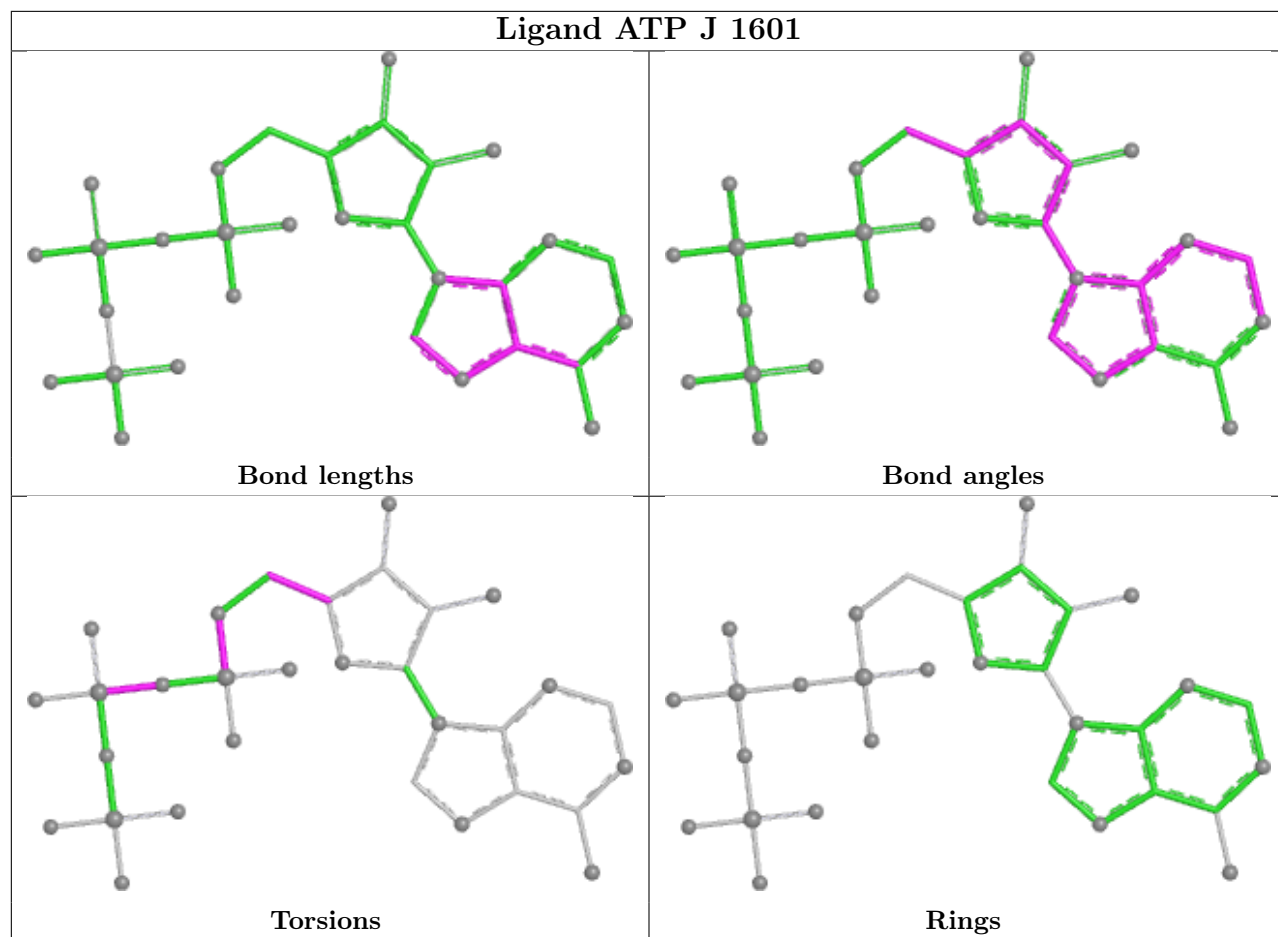
Mol	Chain	Res	Type	Atoms
6	L	401	GTP	C3'-C4'-C5'-O5'
4	G	1601	ATP	C4'-C5'-O5'-PA
4	J	1601	ATP	PA-O3A-PB-O2B
6	I	401	GTP	PB-O3A-PA-O2A
6	C	401	GTP	PB-O3A-PA-O2A
6	F	401	GTP	PB-O3A-PA-O2A
6	L	401	GTP	PB-O3A-PA-O2A
4	G	1601	ATP	O4'-C1'-N9-C8

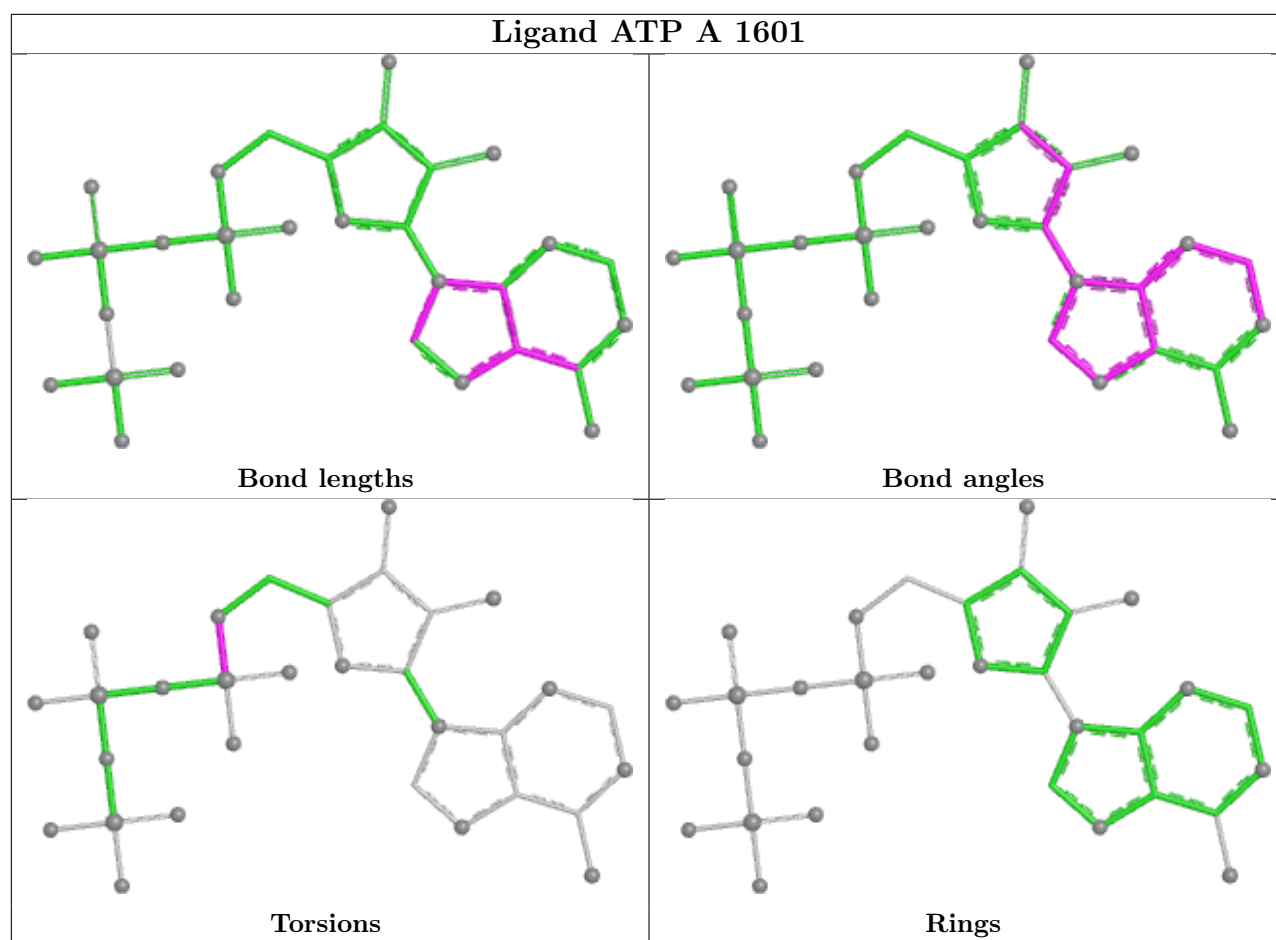
There are no ring outliers.

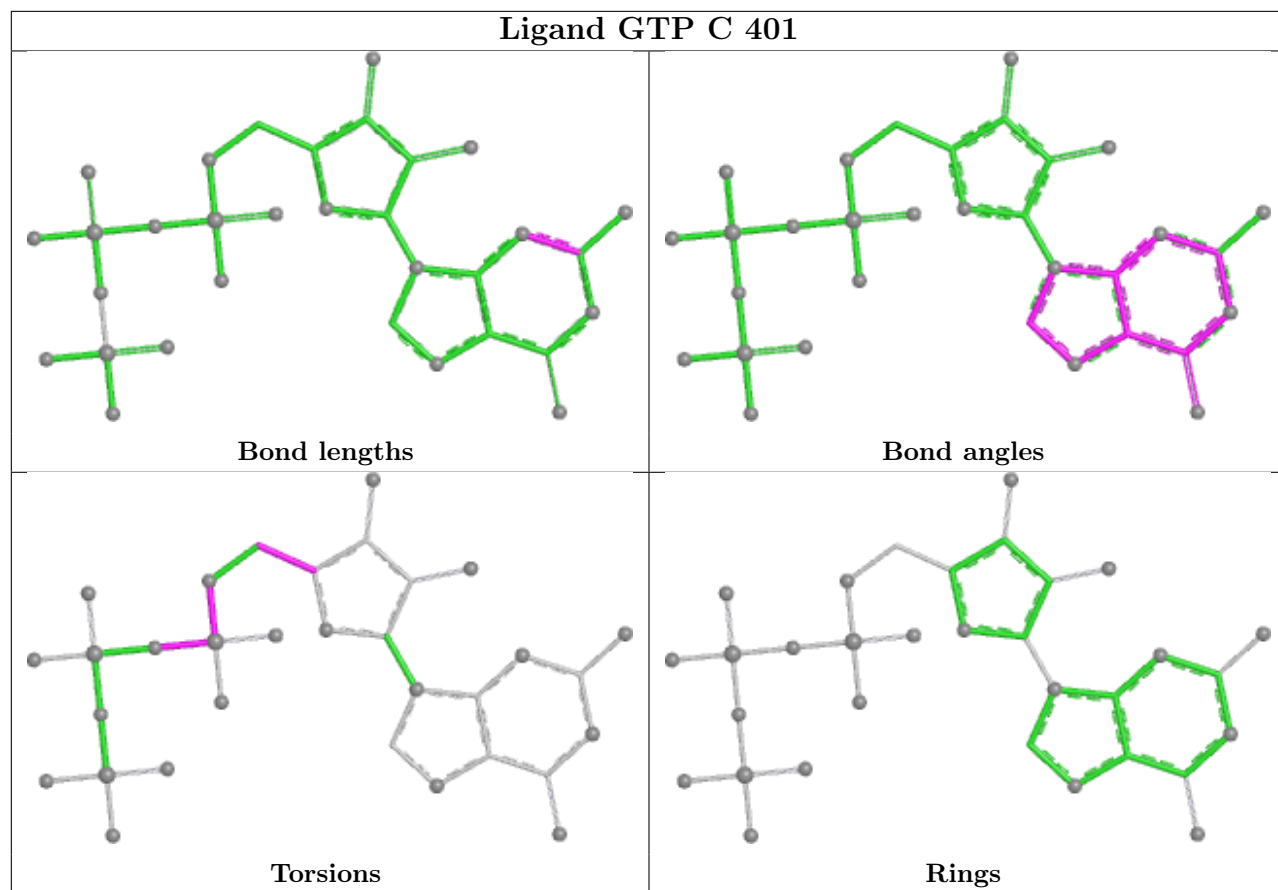
6 monomers are involved in 21 short contacts:

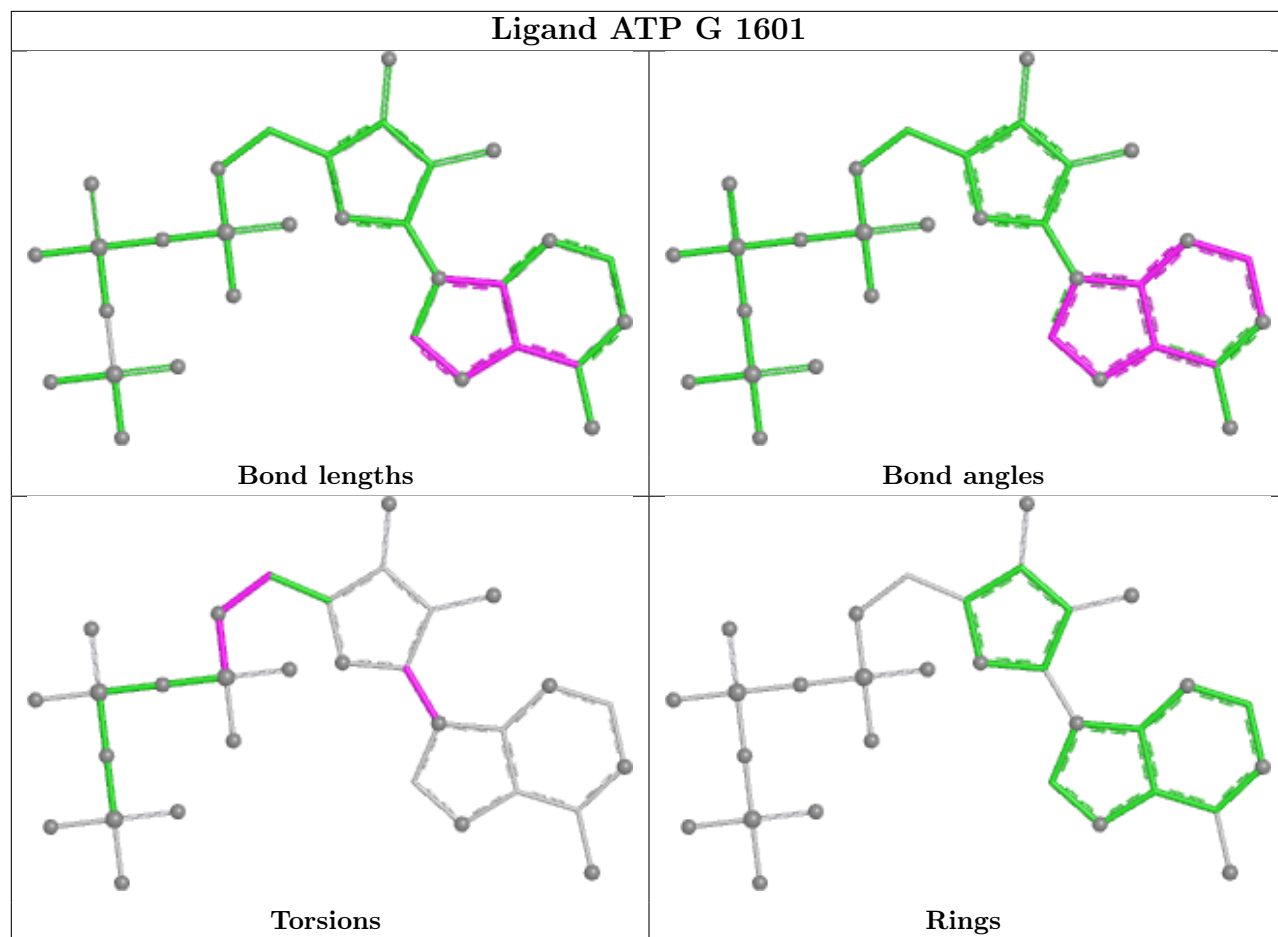
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	J	1601	ATP	4	0
6	C	401	GTP	4	0
4	D	1601	ATP	1	0
6	I	401	GTP	4	0
6	F	401	GTP	4	0
6	L	401	GTP	4	0

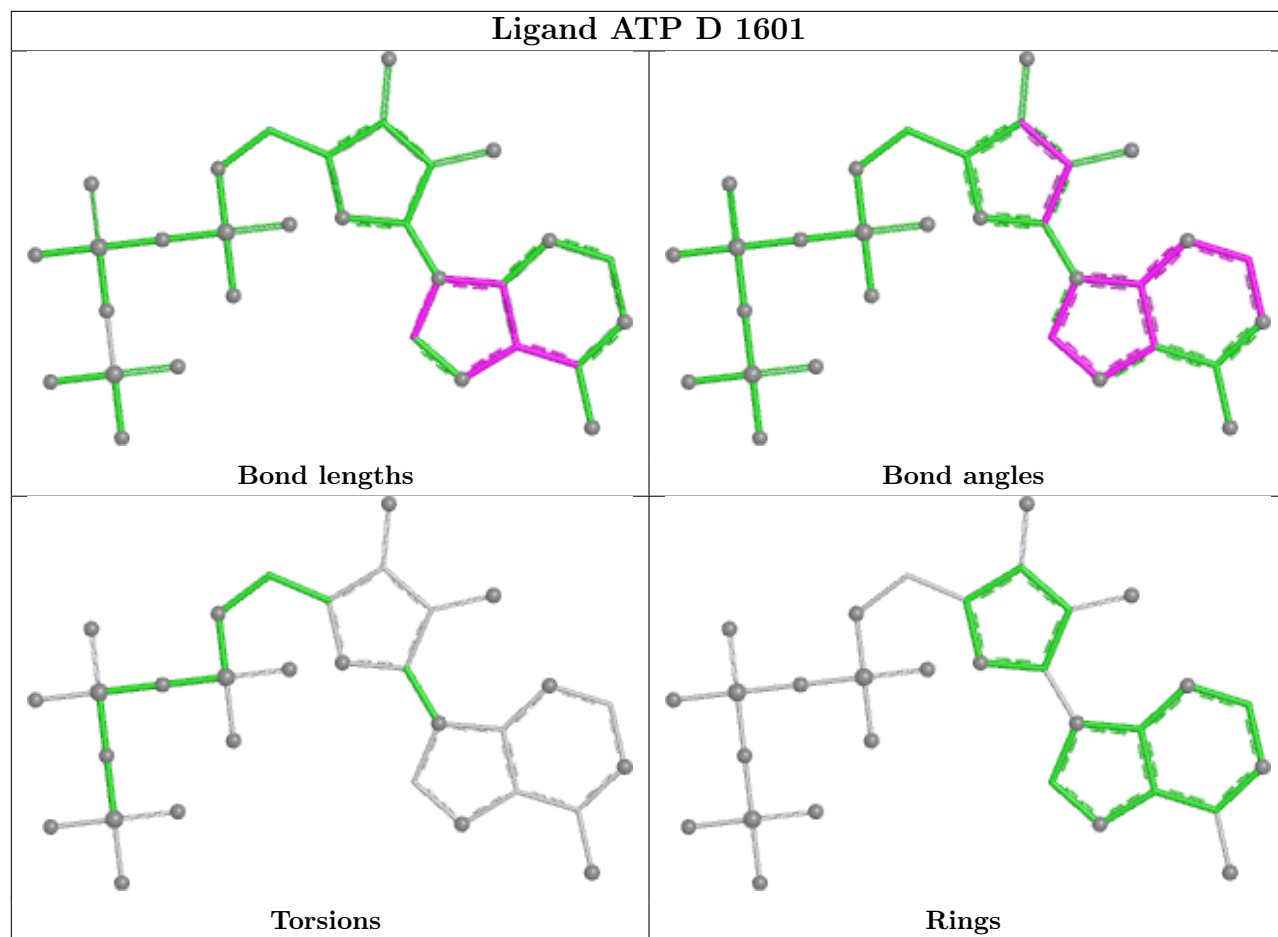
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



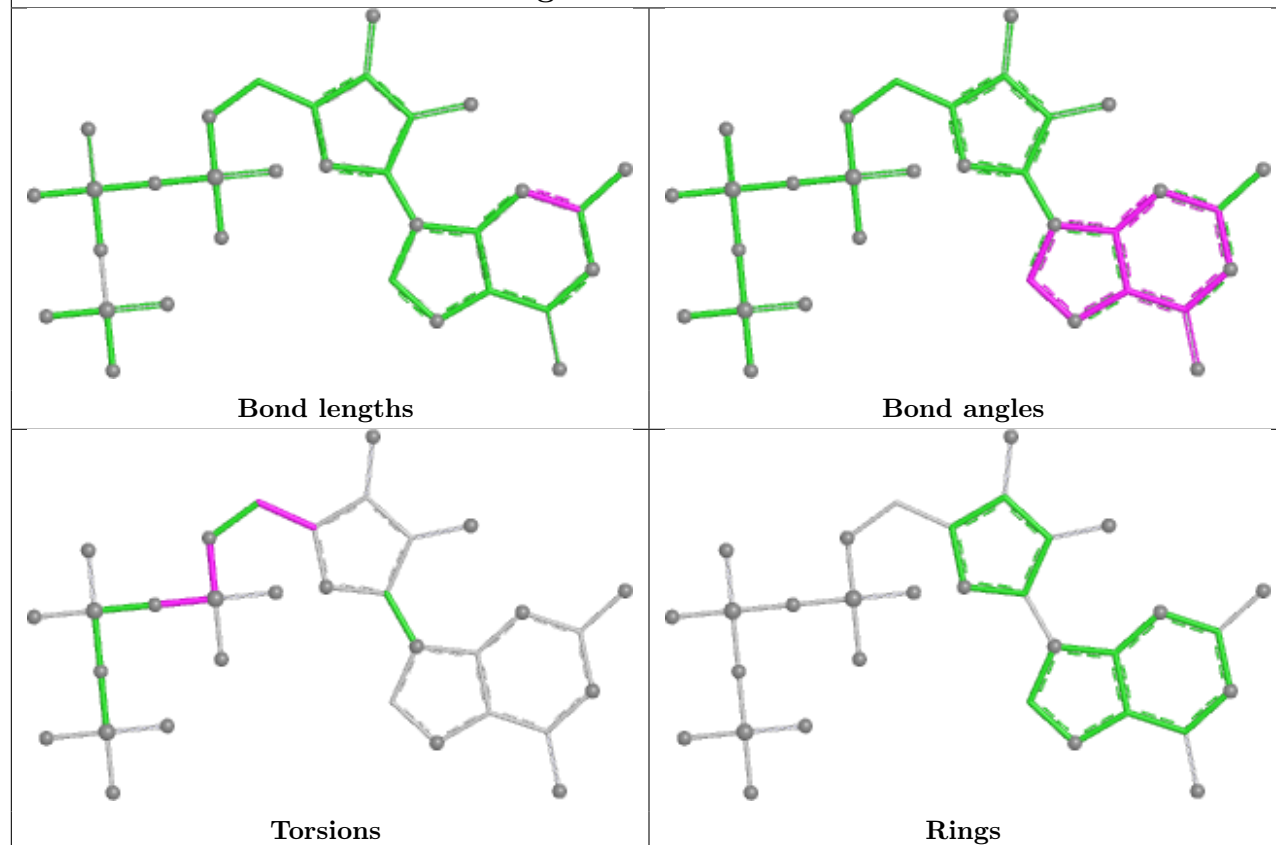




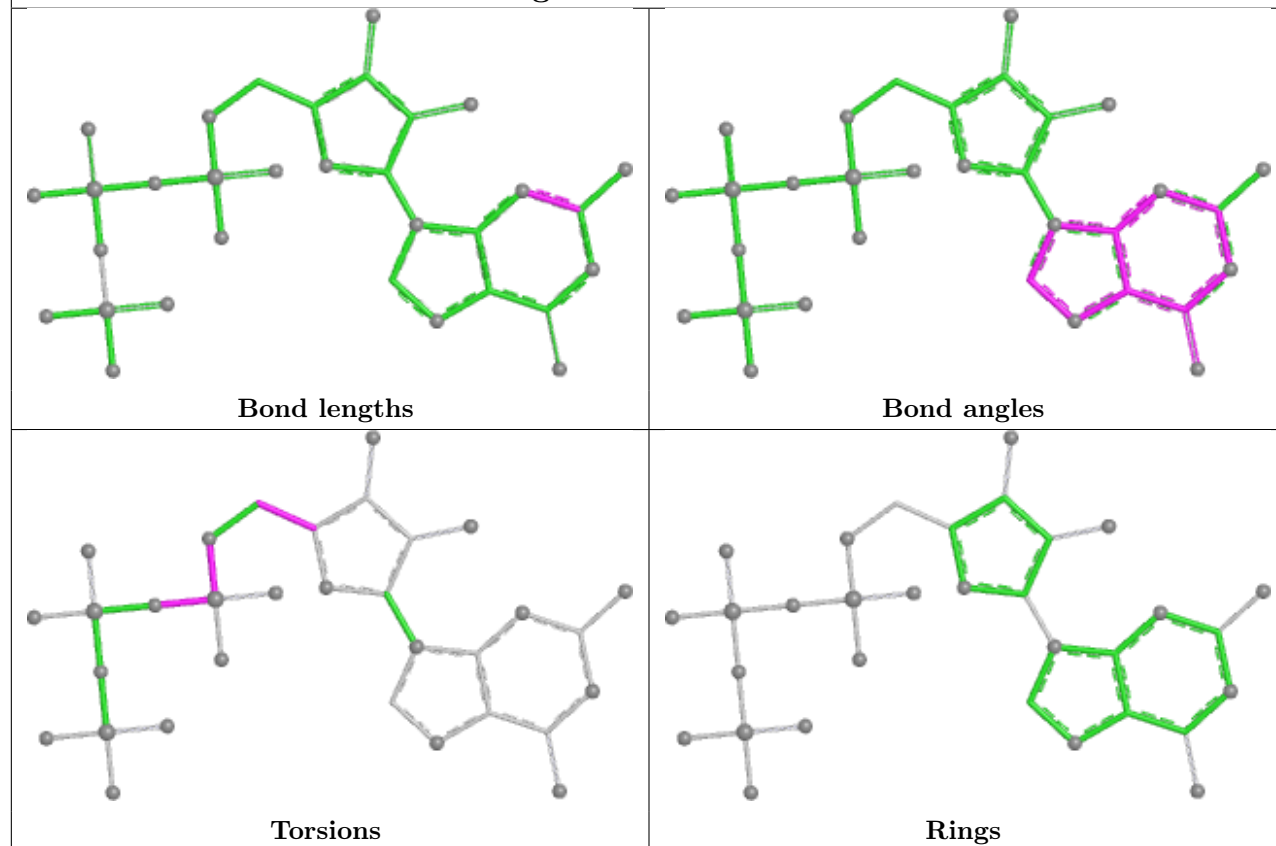


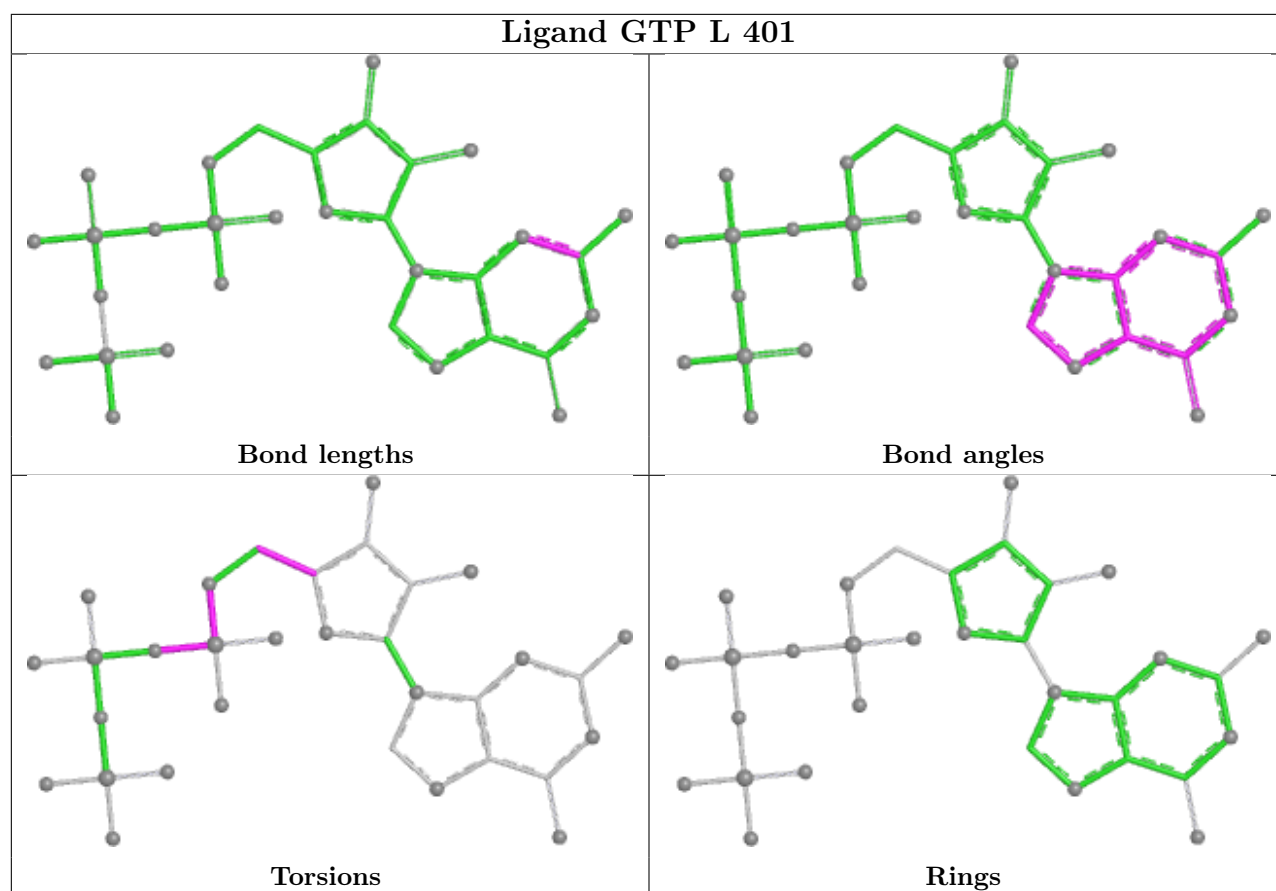


Ligand GTP I 401



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.

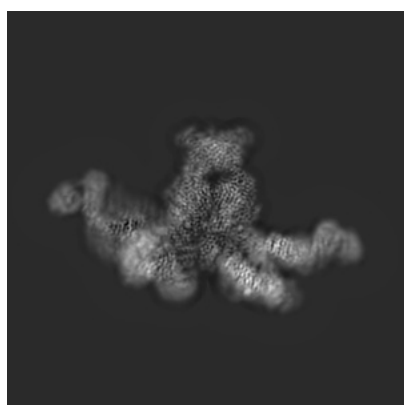
6 Map visualisation [i](#)

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.

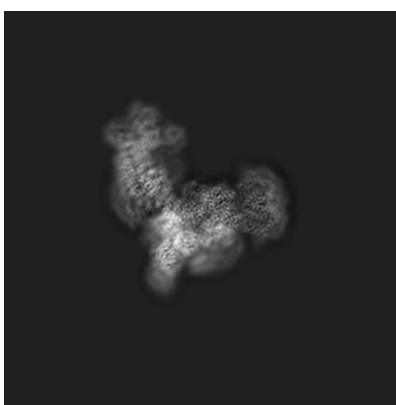
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

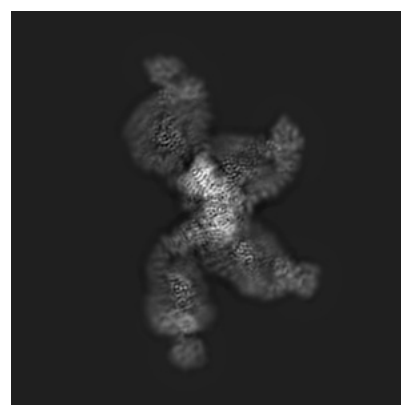
6.1.1 Primary map



X



Y

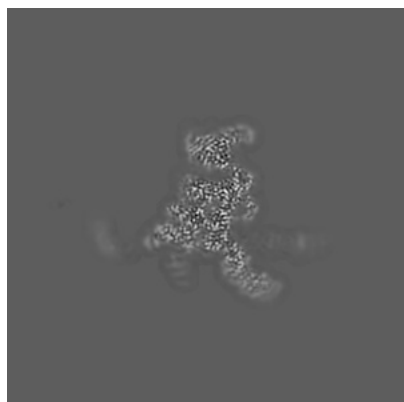


Z

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

6.2 Central slices [i](#)

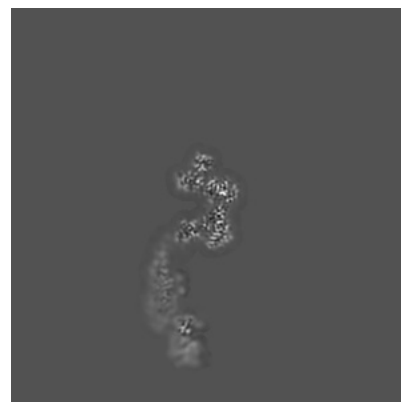
6.2.1 Primary map



X Index: 240



Y Index: 240

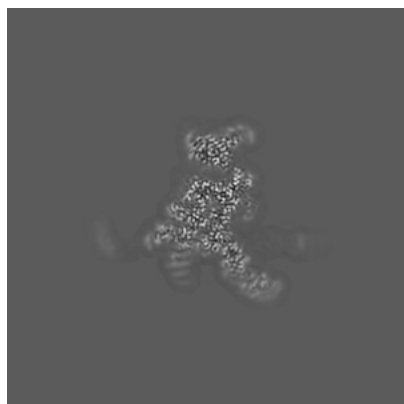


Z Index: 240

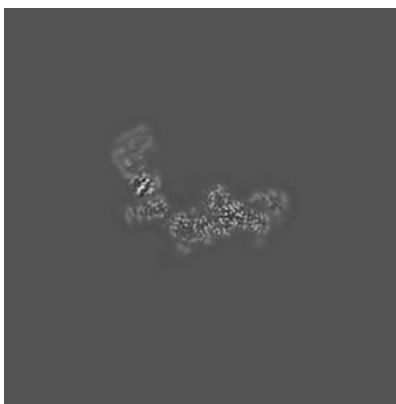
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 242



Y Index: 276

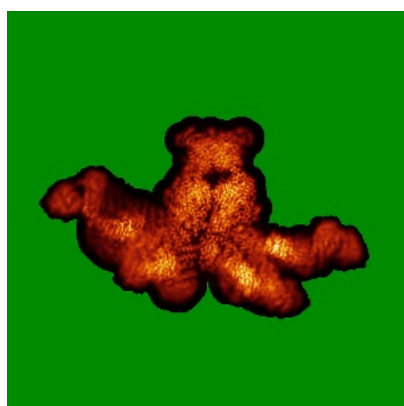


Z Index: 194

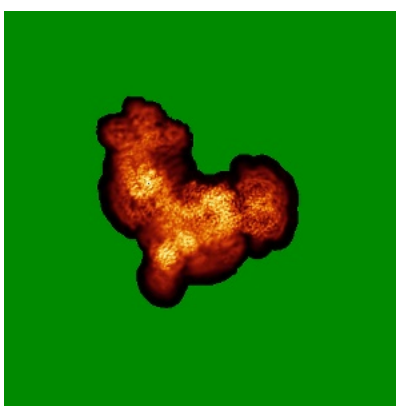
The images above show the largest variance slices of the map in three orthogonal directions.

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

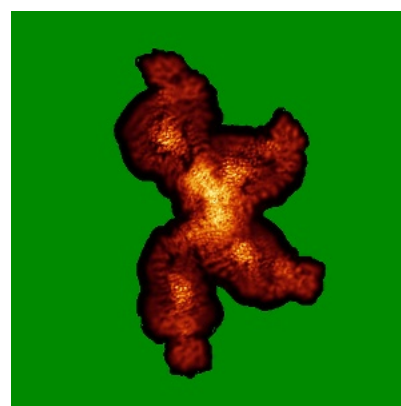
6.4.1 Primary map



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.

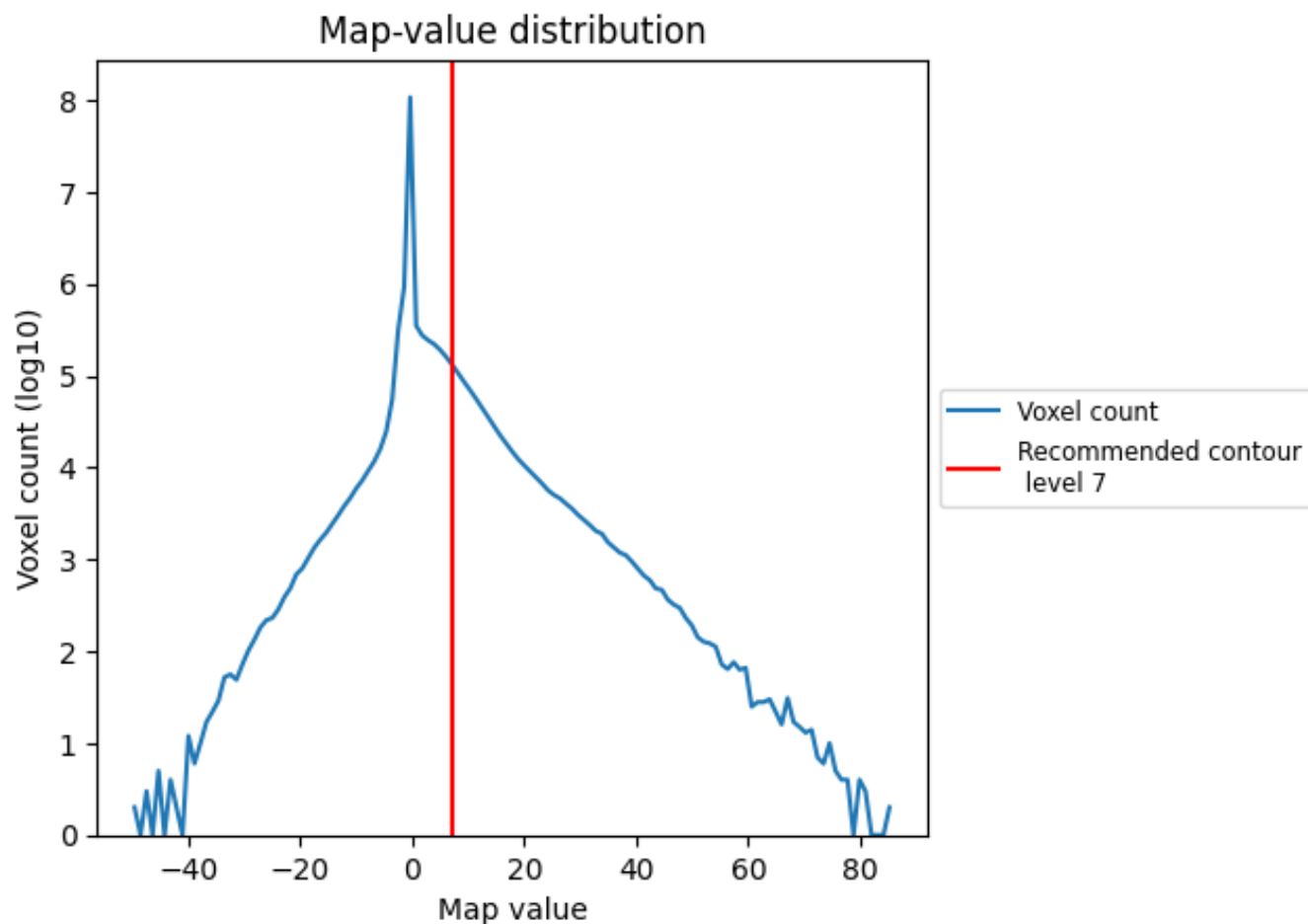
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

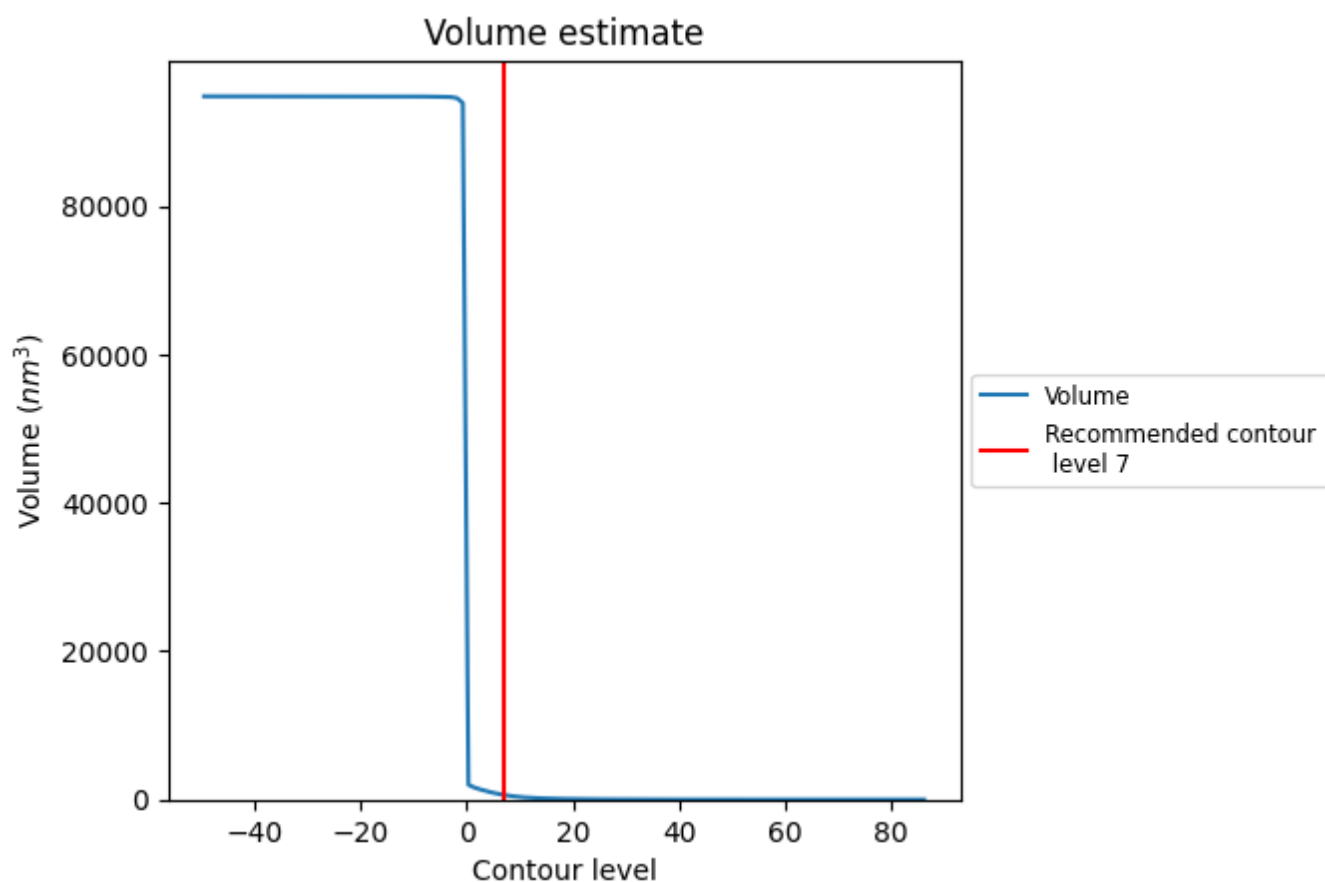
This section contains the results of statistical analysis of the map.

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.

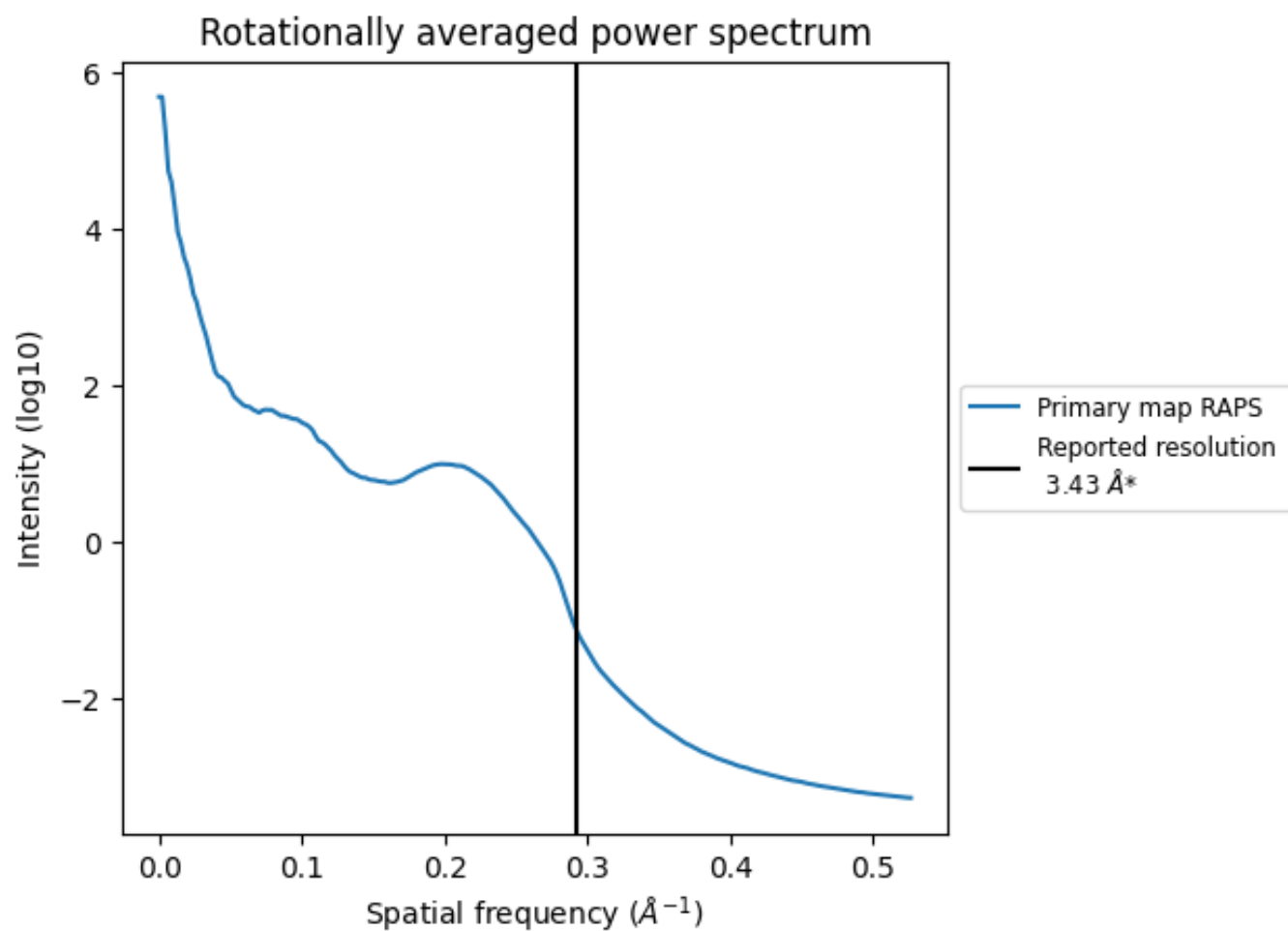
7.2 Volume estimate [i](#)



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

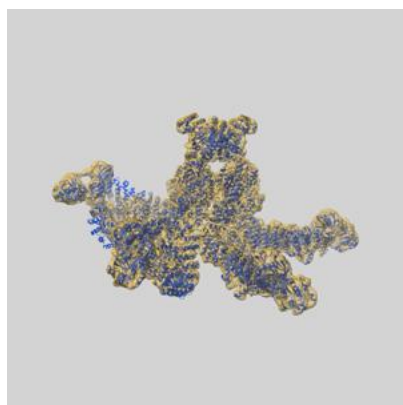
8 Fourier-Shell correlation

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

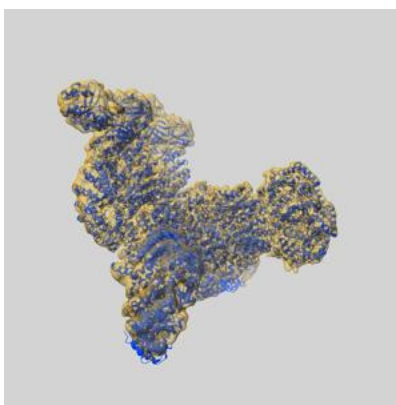
9 Map-model fit [i](#)

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](#).

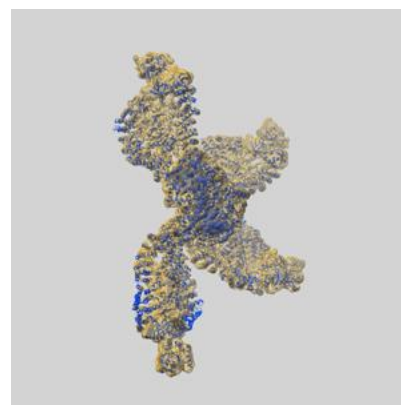
9.1 Map-model overlay [i](#)



X



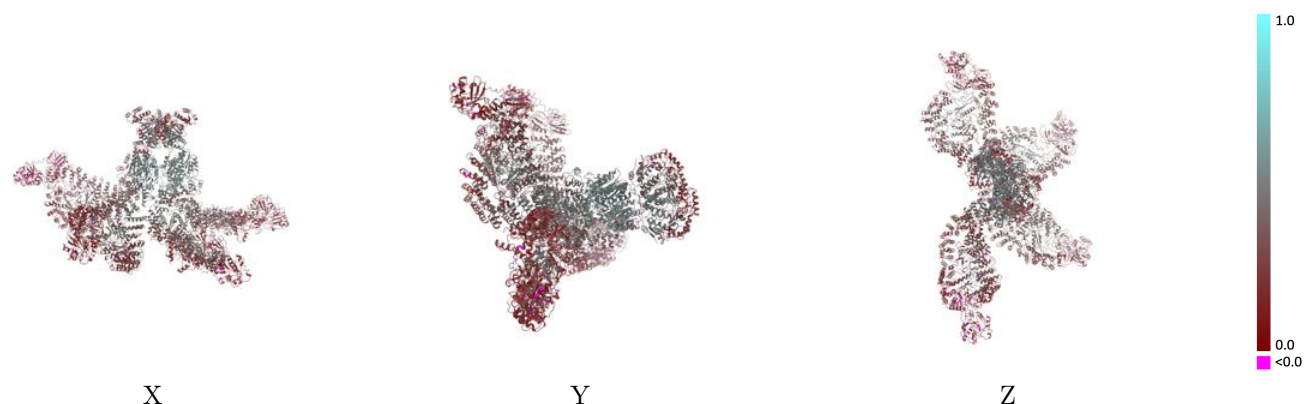
Y



Z

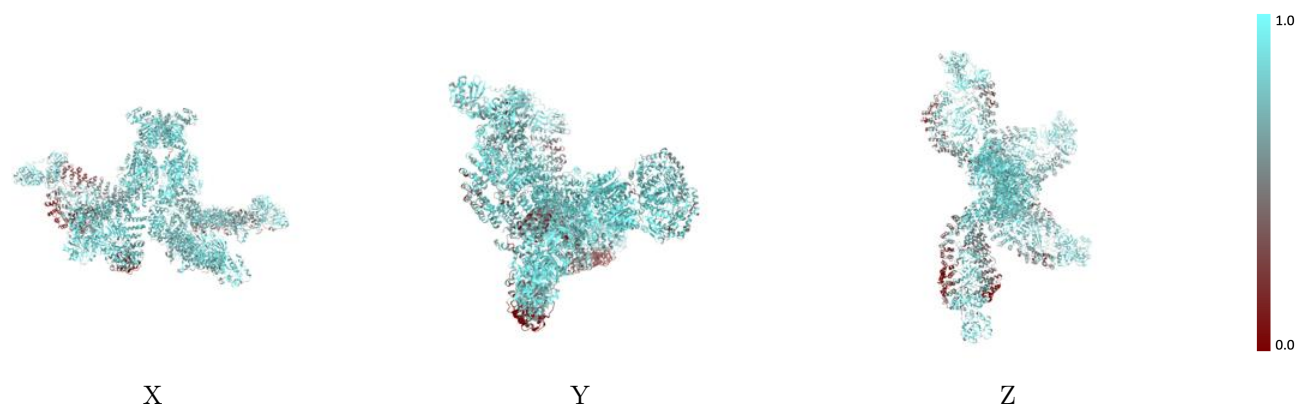
The images above show the 3D surface view of the map at the recommended contour level 7.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



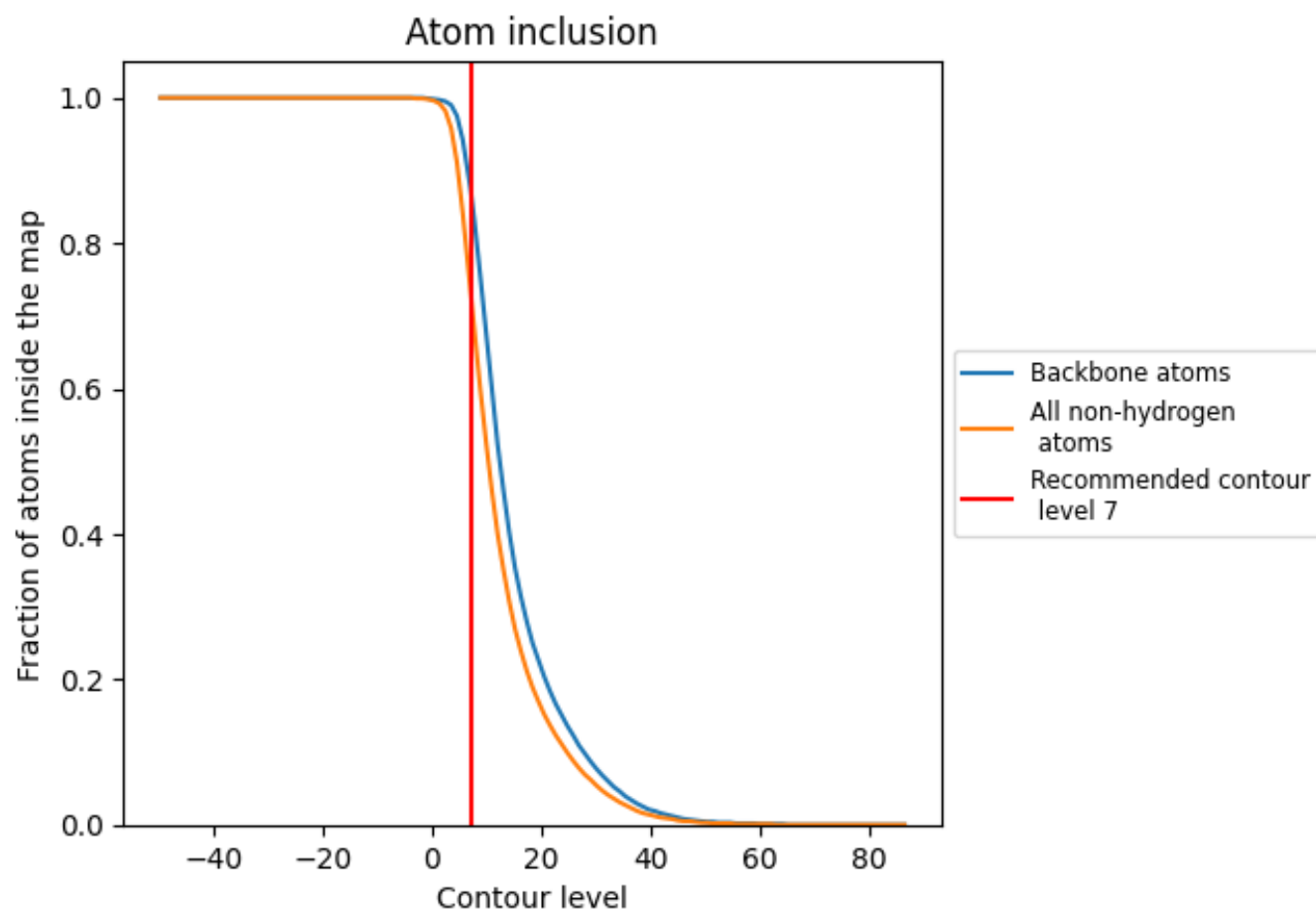
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

1.0

0.0

<0.0