



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 05:31 AM UTC

PDB ID : 3ZVJ / pdb_00003zvj
Title : Crystal structure of high molecular weight (HMW) form of Peroxiredoxin I from *Schistosoma mansoni*
Authors : Saccoccia, F.; Angelucci, F.; Bellelli, A.; Boumis, G.; Brunori, M.; Miele, A.E.
Deposited on : 2011-07-25
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

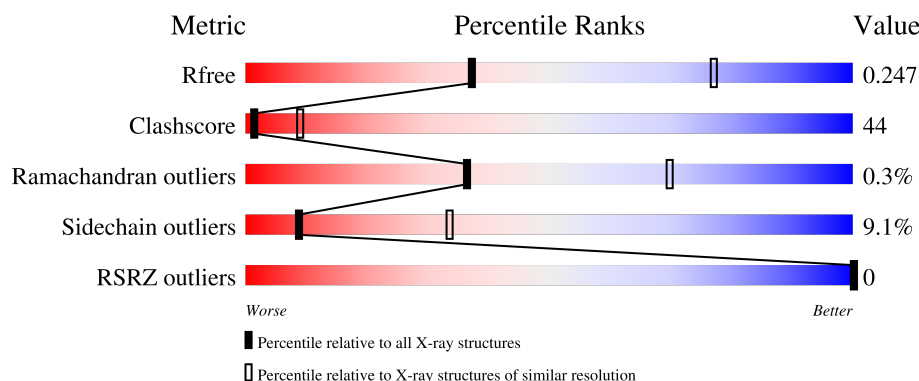
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



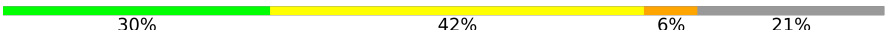
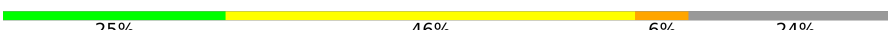
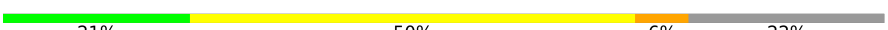
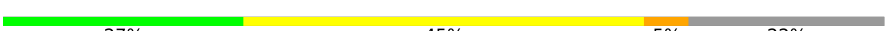
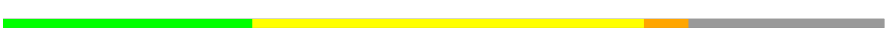
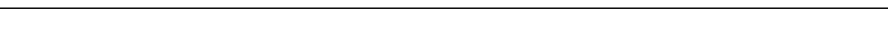
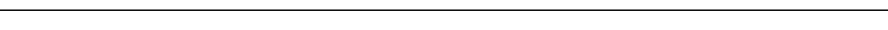
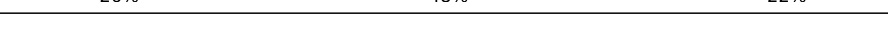
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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

Mol	Chain	Length	Quality of chain
1	A	219	28% 42% 5% 25%
1	B	219	22% 48% 5% 24%
1	C	219	25% 50% 5% 21%
1	E	219	26% 45% 5% 23%
1	F	219	29% 42% 8% 21%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	219	
1	H	219	
1	I	219	
1	J	219	
1	K	219	
1	L	219	
1	M	219	
1	N	219	
1	O	219	
1	P	219	
1	Q	219	
1	R	219	
1	S	219	
1	T	219	
2	D	219	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 26988 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called THIOREDOXIN PEROXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	165	Total	C	N	O	S	0	0	0
			1324	848	224	246	6			
1	B	166	Total	C	N	O	S	0	0	0
			1331	852	225	248	6			
1	C	174	Total	C	N	O	S	0	0	0
			1385	884	234	260	7			
1	E	169	Total	C	N	O	S	0	0	0
			1351	864	229	253	5			
1	F	172	Total	C	N	O	S	0	0	0
			1367	872	231	257	7			
1	G	172	Total	C	N	O	S	0	0	0
			1372	877	232	256	7			
1	H	171	Total	C	N	O	S	0	0	0
			1364	873	230	254	7			
1	I	167	Total	C	N	O	S	0	0	0
			1337	855	226	250	6			
1	J	171	Total	C	N	O	S	0	0	0
			1364	873	230	254	7			
1	K	170	Total	C	N	O	S	0	0	0
			1357	867	229	254	7			
1	L	171	Total	C	N	O	S	0	0	0
			1364	872	230	255	7			
1	M	171	Total	C	N	O	S	0	0	0
			1361	869	230	256	6			
1	N	165	Total	C	N	O	S	0	0	0
			1322	845	224	248	5			
1	O	167	Total	C	N	O	S	0	0	0
			1337	854	226	251	6			
1	P	167	Total	C	N	O	S	0	0	0
			1335	854	226	249	6			
1	Q	163	Total	C	N	O	S	0	0	0
			1311	840	222	244	5			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	R	168	Total	C	N	O	S	0	0	0
			1338	854	227	251	6			
1	S	172	Total	C	N	O	S	0	0	0
			1367	872	231	257	7			
1	T	170	Total	C	N	O	S	0	0	0
			1357	867	229	254	7			

There are 646 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-33	MET	-	expression tag	UNP O97161
A	-32	ARG	-	expression tag	UNP O97161
A	-31	GLY	-	expression tag	UNP O97161
A	-30	SER	-	expression tag	UNP O97161
A	-29	HIS	-	expression tag	UNP O97161
A	-28	HIS	-	expression tag	UNP O97161
A	-27	HIS	-	expression tag	UNP O97161
A	-26	HIS	-	expression tag	UNP O97161
A	-25	HIS	-	expression tag	UNP O97161
A	-24	HIS	-	expression tag	UNP O97161
A	-23	GLY	-	expression tag	UNP O97161
A	-22	MET	-	expression tag	UNP O97161
A	-21	ALA	-	expression tag	UNP O97161
A	-20	SER	-	expression tag	UNP O97161
A	-19	MET	-	expression tag	UNP O97161
A	-18	THR	-	expression tag	UNP O97161
A	-17	GLY	-	expression tag	UNP O97161
A	-16	GLY	-	expression tag	UNP O97161
A	-15	GLN	-	expression tag	UNP O97161
A	-14	GLN	-	expression tag	UNP O97161
A	-13	MET	-	expression tag	UNP O97161
A	-12	GLY	-	expression tag	UNP O97161
A	-11	ARG	-	expression tag	UNP O97161
A	-10	ASP	-	expression tag	UNP O97161
A	-9	LEU	-	expression tag	UNP O97161
A	-8	TYR	-	expression tag	UNP O97161
A	-7	ASP	-	expression tag	UNP O97161
A	-6	ASP	-	expression tag	UNP O97161
A	-5	ASP	-	expression tag	UNP O97161
A	-4	ASP	-	expression tag	UNP O97161
A	-3	LYS	-	expression tag	UNP O97161
A	-2	GLY	-	expression tag	UNP O97161

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	expression tag	UNP O97161
A	0	THR	-	expression tag	UNP O97161
B	-33	MET	-	expression tag	UNP O97161
B	-32	ARG	-	expression tag	UNP O97161
B	-31	GLY	-	expression tag	UNP O97161
B	-30	SER	-	expression tag	UNP O97161
B	-29	HIS	-	expression tag	UNP O97161
B	-28	HIS	-	expression tag	UNP O97161
B	-27	HIS	-	expression tag	UNP O97161
B	-26	HIS	-	expression tag	UNP O97161
B	-25	HIS	-	expression tag	UNP O97161
B	-24	HIS	-	expression tag	UNP O97161
B	-23	GLY	-	expression tag	UNP O97161
B	-22	MET	-	expression tag	UNP O97161
B	-21	ALA	-	expression tag	UNP O97161
B	-20	SER	-	expression tag	UNP O97161
B	-19	MET	-	expression tag	UNP O97161
B	-18	THR	-	expression tag	UNP O97161
B	-17	GLY	-	expression tag	UNP O97161
B	-16	GLY	-	expression tag	UNP O97161
B	-15	GLN	-	expression tag	UNP O97161
B	-14	GLN	-	expression tag	UNP O97161
B	-13	MET	-	expression tag	UNP O97161
B	-12	GLY	-	expression tag	UNP O97161
B	-11	ARG	-	expression tag	UNP O97161
B	-10	ASP	-	expression tag	UNP O97161
B	-9	LEU	-	expression tag	UNP O97161
B	-8	TYR	-	expression tag	UNP O97161
B	-7	ASP	-	expression tag	UNP O97161
B	-6	ASP	-	expression tag	UNP O97161
B	-5	ASP	-	expression tag	UNP O97161
B	-4	ASP	-	expression tag	UNP O97161
B	-3	LYS	-	expression tag	UNP O97161
B	-2	GLY	-	expression tag	UNP O97161
B	-1	SER	-	expression tag	UNP O97161
B	0	THR	-	expression tag	UNP O97161
C	-33	MET	-	expression tag	UNP O97161
C	-32	ARG	-	expression tag	UNP O97161
C	-31	GLY	-	expression tag	UNP O97161
C	-30	SER	-	expression tag	UNP O97161
C	-29	HIS	-	expression tag	UNP O97161
C	-28	HIS	-	expression tag	UNP O97161

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	-27	HIS	-	expression tag	UNP O97161
C	-26	HIS	-	expression tag	UNP O97161
C	-25	HIS	-	expression tag	UNP O97161
C	-24	HIS	-	expression tag	UNP O97161
C	-23	GLY	-	expression tag	UNP O97161
C	-22	MET	-	expression tag	UNP O97161
C	-21	ALA	-	expression tag	UNP O97161
C	-20	SER	-	expression tag	UNP O97161
C	-19	MET	-	expression tag	UNP O97161
C	-18	THR	-	expression tag	UNP O97161
C	-17	GLY	-	expression tag	UNP O97161
C	-16	GLY	-	expression tag	UNP O97161
C	-15	GLN	-	expression tag	UNP O97161
C	-14	GLN	-	expression tag	UNP O97161
C	-13	MET	-	expression tag	UNP O97161
C	-12	GLY	-	expression tag	UNP O97161
C	-11	ARG	-	expression tag	UNP O97161
C	-10	ASP	-	expression tag	UNP O97161
C	-9	LEU	-	expression tag	UNP O97161
C	-8	TYR	-	expression tag	UNP O97161
C	-7	ASP	-	expression tag	UNP O97161
C	-6	ASP	-	expression tag	UNP O97161
C	-5	ASP	-	expression tag	UNP O97161
C	-4	ASP	-	expression tag	UNP O97161
C	-3	LYS	-	expression tag	UNP O97161
C	-2	GLY	-	expression tag	UNP O97161
C	-1	SER	-	expression tag	UNP O97161
C	0	THR	-	expression tag	UNP O97161
E	-33	MET	-	expression tag	UNP O97161
E	-32	ARG	-	expression tag	UNP O97161
E	-31	GLY	-	expression tag	UNP O97161
E	-30	SER	-	expression tag	UNP O97161
E	-29	HIS	-	expression tag	UNP O97161
E	-28	HIS	-	expression tag	UNP O97161
E	-27	HIS	-	expression tag	UNP O97161
E	-26	HIS	-	expression tag	UNP O97161
E	-25	HIS	-	expression tag	UNP O97161
E	-24	HIS	-	expression tag	UNP O97161
E	-23	GLY	-	expression tag	UNP O97161
E	-22	MET	-	expression tag	UNP O97161
E	-21	ALA	-	expression tag	UNP O97161
E	-20	SER	-	expression tag	UNP O97161

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	-19	MET	-	expression tag	UNP O97161
E	-18	THR	-	expression tag	UNP O97161
E	-17	GLY	-	expression tag	UNP O97161
E	-16	GLY	-	expression tag	UNP O97161
E	-15	GLN	-	expression tag	UNP O97161
E	-14	GLN	-	expression tag	UNP O97161
E	-13	MET	-	expression tag	UNP O97161
E	-12	GLY	-	expression tag	UNP O97161
E	-11	ARG	-	expression tag	UNP O97161
E	-10	ASP	-	expression tag	UNP O97161
E	-9	LEU	-	expression tag	UNP O97161
E	-8	TYR	-	expression tag	UNP O97161
E	-7	ASP	-	expression tag	UNP O97161
E	-6	ASP	-	expression tag	UNP O97161
E	-5	ASP	-	expression tag	UNP O97161
E	-4	ASP	-	expression tag	UNP O97161
E	-3	LYS	-	expression tag	UNP O97161
E	-2	GLY	-	expression tag	UNP O97161
E	-1	SER	-	expression tag	UNP O97161
E	0	THR	-	expression tag	UNP O97161
F	-33	MET	-	expression tag	UNP O97161
F	-32	ARG	-	expression tag	UNP O97161
F	-31	GLY	-	expression tag	UNP O97161
F	-30	SER	-	expression tag	UNP O97161
F	-29	HIS	-	expression tag	UNP O97161
F	-28	HIS	-	expression tag	UNP O97161
F	-27	HIS	-	expression tag	UNP O97161
F	-26	HIS	-	expression tag	UNP O97161
F	-25	HIS	-	expression tag	UNP O97161
F	-24	HIS	-	expression tag	UNP O97161
F	-23	GLY	-	expression tag	UNP O97161
F	-22	MET	-	expression tag	UNP O97161
F	-21	ALA	-	expression tag	UNP O97161
F	-20	SER	-	expression tag	UNP O97161
F	-19	MET	-	expression tag	UNP O97161
F	-18	THR	-	expression tag	UNP O97161
F	-17	GLY	-	expression tag	UNP O97161
F	-16	GLY	-	expression tag	UNP O97161
F	-15	GLN	-	expression tag	UNP O97161
F	-14	GLN	-	expression tag	UNP O97161
F	-13	MET	-	expression tag	UNP O97161
F	-12	GLY	-	expression tag	UNP O97161

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	-11	ARG	-	expression tag	UNP O97161
F	-10	ASP	-	expression tag	UNP O97161
F	-9	LEU	-	expression tag	UNP O97161
F	-8	TYR	-	expression tag	UNP O97161
F	-7	ASP	-	expression tag	UNP O97161
F	-6	ASP	-	expression tag	UNP O97161
F	-5	ASP	-	expression tag	UNP O97161
F	-4	ASP	-	expression tag	UNP O97161
F	-3	LYS	-	expression tag	UNP O97161
F	-2	GLY	-	expression tag	UNP O97161
F	-1	SER	-	expression tag	UNP O97161
F	0	THR	-	expression tag	UNP O97161
G	-33	MET	-	expression tag	UNP O97161
G	-32	ARG	-	expression tag	UNP O97161
G	-31	GLY	-	expression tag	UNP O97161
G	-30	SER	-	expression tag	UNP O97161
G	-29	HIS	-	expression tag	UNP O97161
G	-28	HIS	-	expression tag	UNP O97161
G	-27	HIS	-	expression tag	UNP O97161
G	-26	HIS	-	expression tag	UNP O97161
G	-25	HIS	-	expression tag	UNP O97161
G	-24	HIS	-	expression tag	UNP O97161
G	-23	GLY	-	expression tag	UNP O97161
G	-22	MET	-	expression tag	UNP O97161
G	-21	ALA	-	expression tag	UNP O97161
G	-20	SER	-	expression tag	UNP O97161
G	-19	MET	-	expression tag	UNP O97161
G	-18	THR	-	expression tag	UNP O97161
G	-17	GLY	-	expression tag	UNP O97161
G	-16	GLY	-	expression tag	UNP O97161
G	-15	GLN	-	expression tag	UNP O97161
G	-14	GLN	-	expression tag	UNP O97161
G	-13	MET	-	expression tag	UNP O97161
G	-12	GLY	-	expression tag	UNP O97161
G	-11	ARG	-	expression tag	UNP O97161
G	-10	ASP	-	expression tag	UNP O97161
G	-9	LEU	-	expression tag	UNP O97161
G	-8	TYR	-	expression tag	UNP O97161
G	-7	ASP	-	expression tag	UNP O97161
G	-6	ASP	-	expression tag	UNP O97161
G	-5	ASP	-	expression tag	UNP O97161
G	-4	ASP	-	expression tag	UNP O97161

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
G	-3	LYS	-	expression tag	UNP O97161
G	-2	GLY	-	expression tag	UNP O97161
G	-1	SER	-	expression tag	UNP O97161
G	0	THR	-	expression tag	UNP O97161
H	-33	MET	-	expression tag	UNP O97161
H	-32	ARG	-	expression tag	UNP O97161
H	-31	GLY	-	expression tag	UNP O97161
H	-30	SER	-	expression tag	UNP O97161
H	-29	HIS	-	expression tag	UNP O97161
H	-28	HIS	-	expression tag	UNP O97161
H	-27	HIS	-	expression tag	UNP O97161
H	-26	HIS	-	expression tag	UNP O97161
H	-25	HIS	-	expression tag	UNP O97161
H	-24	HIS	-	expression tag	UNP O97161
H	-23	GLY	-	expression tag	UNP O97161
H	-22	MET	-	expression tag	UNP O97161
H	-21	ALA	-	expression tag	UNP O97161
H	-20	SER	-	expression tag	UNP O97161
H	-19	MET	-	expression tag	UNP O97161
H	-18	THR	-	expression tag	UNP O97161
H	-17	GLY	-	expression tag	UNP O97161
H	-16	GLY	-	expression tag	UNP O97161
H	-15	GLN	-	expression tag	UNP O97161
H	-14	GLN	-	expression tag	UNP O97161
H	-13	MET	-	expression tag	UNP O97161
H	-12	GLY	-	expression tag	UNP O97161
H	-11	ARG	-	expression tag	UNP O97161
H	-10	ASP	-	expression tag	UNP O97161
H	-9	LEU	-	expression tag	UNP O97161
H	-8	TYR	-	expression tag	UNP O97161
H	-7	ASP	-	expression tag	UNP O97161
H	-6	ASP	-	expression tag	UNP O97161
H	-5	ASP	-	expression tag	UNP O97161
H	-4	ASP	-	expression tag	UNP O97161
H	-3	LYS	-	expression tag	UNP O97161
H	-2	GLY	-	expression tag	UNP O97161
H	-1	SER	-	expression tag	UNP O97161
H	0	THR	-	expression tag	UNP O97161
I	-33	MET	-	expression tag	UNP O97161
I	-32	ARG	-	expression tag	UNP O97161
I	-31	GLY	-	expression tag	UNP O97161
I	-30	SER	-	expression tag	UNP O97161

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
I	-29	HIS	-	expression tag	UNP O97161
I	-28	HIS	-	expression tag	UNP O97161
I	-27	HIS	-	expression tag	UNP O97161
I	-26	HIS	-	expression tag	UNP O97161
I	-25	HIS	-	expression tag	UNP O97161
I	-24	HIS	-	expression tag	UNP O97161
I	-23	GLY	-	expression tag	UNP O97161
I	-22	MET	-	expression tag	UNP O97161
I	-21	ALA	-	expression tag	UNP O97161
I	-20	SER	-	expression tag	UNP O97161
I	-19	MET	-	expression tag	UNP O97161
I	-18	THR	-	expression tag	UNP O97161
I	-17	GLY	-	expression tag	UNP O97161
I	-16	GLY	-	expression tag	UNP O97161
I	-15	GLN	-	expression tag	UNP O97161
I	-14	GLN	-	expression tag	UNP O97161
I	-13	MET	-	expression tag	UNP O97161
I	-12	GLY	-	expression tag	UNP O97161
I	-11	ARG	-	expression tag	UNP O97161
I	-10	ASP	-	expression tag	UNP O97161
I	-9	LEU	-	expression tag	UNP O97161
I	-8	TYR	-	expression tag	UNP O97161
I	-7	ASP	-	expression tag	UNP O97161
I	-6	ASP	-	expression tag	UNP O97161
I	-5	ASP	-	expression tag	UNP O97161
I	-4	ASP	-	expression tag	UNP O97161
I	-3	LYS	-	expression tag	UNP O97161
I	-2	GLY	-	expression tag	UNP O97161
I	-1	SER	-	expression tag	UNP O97161
I	0	THR	-	expression tag	UNP O97161
J	-33	MET	-	expression tag	UNP O97161
J	-32	ARG	-	expression tag	UNP O97161
J	-31	GLY	-	expression tag	UNP O97161
J	-30	SER	-	expression tag	UNP O97161
J	-29	HIS	-	expression tag	UNP O97161
J	-28	HIS	-	expression tag	UNP O97161
J	-27	HIS	-	expression tag	UNP O97161
J	-26	HIS	-	expression tag	UNP O97161
J	-25	HIS	-	expression tag	UNP O97161
J	-24	HIS	-	expression tag	UNP O97161
J	-23	GLY	-	expression tag	UNP O97161
J	-22	MET	-	expression tag	UNP O97161

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
J	-21	ALA	-	expression tag	UNP O97161
J	-20	SER	-	expression tag	UNP O97161
J	-19	MET	-	expression tag	UNP O97161
J	-18	THR	-	expression tag	UNP O97161
J	-17	GLY	-	expression tag	UNP O97161
J	-16	GLY	-	expression tag	UNP O97161
J	-15	GLN	-	expression tag	UNP O97161
J	-14	GLN	-	expression tag	UNP O97161
J	-13	MET	-	expression tag	UNP O97161
J	-12	GLY	-	expression tag	UNP O97161
J	-11	ARG	-	expression tag	UNP O97161
J	-10	ASP	-	expression tag	UNP O97161
J	-9	LEU	-	expression tag	UNP O97161
J	-8	TYR	-	expression tag	UNP O97161
J	-7	ASP	-	expression tag	UNP O97161
J	-6	ASP	-	expression tag	UNP O97161
J	-5	ASP	-	expression tag	UNP O97161
J	-4	ASP	-	expression tag	UNP O97161
J	-3	LYS	-	expression tag	UNP O97161
J	-2	GLY	-	expression tag	UNP O97161
J	-1	SER	-	expression tag	UNP O97161
J	0	THR	-	expression tag	UNP O97161
K	-33	MET	-	expression tag	UNP O97161
K	-32	ARG	-	expression tag	UNP O97161
K	-31	GLY	-	expression tag	UNP O97161
K	-30	SER	-	expression tag	UNP O97161
K	-29	HIS	-	expression tag	UNP O97161
K	-28	HIS	-	expression tag	UNP O97161
K	-27	HIS	-	expression tag	UNP O97161
K	-26	HIS	-	expression tag	UNP O97161
K	-25	HIS	-	expression tag	UNP O97161
K	-24	HIS	-	expression tag	UNP O97161
K	-23	GLY	-	expression tag	UNP O97161
K	-22	MET	-	expression tag	UNP O97161
K	-21	ALA	-	expression tag	UNP O97161
K	-20	SER	-	expression tag	UNP O97161
K	-19	MET	-	expression tag	UNP O97161
K	-18	THR	-	expression tag	UNP O97161
K	-17	GLY	-	expression tag	UNP O97161
K	-16	GLY	-	expression tag	UNP O97161
K	-15	GLN	-	expression tag	UNP O97161
K	-14	GLN	-	expression tag	UNP O97161

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
K	-13	MET	-	expression tag	UNP O97161
K	-12	GLY	-	expression tag	UNP O97161
K	-11	ARG	-	expression tag	UNP O97161
K	-10	ASP	-	expression tag	UNP O97161
K	-9	LEU	-	expression tag	UNP O97161
K	-8	TYR	-	expression tag	UNP O97161
K	-7	ASP	-	expression tag	UNP O97161
K	-6	ASP	-	expression tag	UNP O97161
K	-5	ASP	-	expression tag	UNP O97161
K	-4	ASP	-	expression tag	UNP O97161
K	-3	LYS	-	expression tag	UNP O97161
K	-2	GLY	-	expression tag	UNP O97161
K	-1	SER	-	expression tag	UNP O97161
K	0	THR	-	expression tag	UNP O97161
L	-33	MET	-	expression tag	UNP O97161
L	-32	ARG	-	expression tag	UNP O97161
L	-31	GLY	-	expression tag	UNP O97161
L	-30	SER	-	expression tag	UNP O97161
L	-29	HIS	-	expression tag	UNP O97161
L	-28	HIS	-	expression tag	UNP O97161
L	-27	HIS	-	expression tag	UNP O97161
L	-26	HIS	-	expression tag	UNP O97161
L	-25	HIS	-	expression tag	UNP O97161
L	-24	HIS	-	expression tag	UNP O97161
L	-23	GLY	-	expression tag	UNP O97161
L	-22	MET	-	expression tag	UNP O97161
L	-21	ALA	-	expression tag	UNP O97161
L	-20	SER	-	expression tag	UNP O97161
L	-19	MET	-	expression tag	UNP O97161
L	-18	THR	-	expression tag	UNP O97161
L	-17	GLY	-	expression tag	UNP O97161
L	-16	GLY	-	expression tag	UNP O97161
L	-15	GLN	-	expression tag	UNP O97161
L	-14	GLN	-	expression tag	UNP O97161
L	-13	MET	-	expression tag	UNP O97161
L	-12	GLY	-	expression tag	UNP O97161
L	-11	ARG	-	expression tag	UNP O97161
L	-10	ASP	-	expression tag	UNP O97161
L	-9	LEU	-	expression tag	UNP O97161
L	-8	TYR	-	expression tag	UNP O97161
L	-7	ASP	-	expression tag	UNP O97161
L	-6	ASP	-	expression tag	UNP O97161

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
L	-5	ASP	-	expression tag	UNP O97161
L	-4	ASP	-	expression tag	UNP O97161
L	-3	LYS	-	expression tag	UNP O97161
L	-2	GLY	-	expression tag	UNP O97161
L	-1	SER	-	expression tag	UNP O97161
L	0	THR	-	expression tag	UNP O97161
M	-33	MET	-	expression tag	UNP O97161
M	-32	ARG	-	expression tag	UNP O97161
M	-31	GLY	-	expression tag	UNP O97161
M	-30	SER	-	expression tag	UNP O97161
M	-29	HIS	-	expression tag	UNP O97161
M	-28	HIS	-	expression tag	UNP O97161
M	-27	HIS	-	expression tag	UNP O97161
M	-26	HIS	-	expression tag	UNP O97161
M	-25	HIS	-	expression tag	UNP O97161
M	-24	HIS	-	expression tag	UNP O97161
M	-23	GLY	-	expression tag	UNP O97161
M	-22	MET	-	expression tag	UNP O97161
M	-21	ALA	-	expression tag	UNP O97161
M	-20	SER	-	expression tag	UNP O97161
M	-19	MET	-	expression tag	UNP O97161
M	-18	THR	-	expression tag	UNP O97161
M	-17	GLY	-	expression tag	UNP O97161
M	-16	GLY	-	expression tag	UNP O97161
M	-15	GLN	-	expression tag	UNP O97161
M	-14	GLN	-	expression tag	UNP O97161
M	-13	MET	-	expression tag	UNP O97161
M	-12	GLY	-	expression tag	UNP O97161
M	-11	ARG	-	expression tag	UNP O97161
M	-10	ASP	-	expression tag	UNP O97161
M	-9	LEU	-	expression tag	UNP O97161
M	-8	TYR	-	expression tag	UNP O97161
M	-7	ASP	-	expression tag	UNP O97161
M	-6	ASP	-	expression tag	UNP O97161
M	-5	ASP	-	expression tag	UNP O97161
M	-4	ASP	-	expression tag	UNP O97161
M	-3	LYS	-	expression tag	UNP O97161
M	-2	GLY	-	expression tag	UNP O97161
M	-1	SER	-	expression tag	UNP O97161
M	0	THR	-	expression tag	UNP O97161
N	-33	MET	-	expression tag	UNP O97161
N	-32	ARG	-	expression tag	UNP O97161

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
N	-31	GLY	-	expression tag	UNP O97161
N	-30	SER	-	expression tag	UNP O97161
N	-29	HIS	-	expression tag	UNP O97161
N	-28	HIS	-	expression tag	UNP O97161
N	-27	HIS	-	expression tag	UNP O97161
N	-26	HIS	-	expression tag	UNP O97161
N	-25	HIS	-	expression tag	UNP O97161
N	-24	HIS	-	expression tag	UNP O97161
N	-23	GLY	-	expression tag	UNP O97161
N	-22	MET	-	expression tag	UNP O97161
N	-21	ALA	-	expression tag	UNP O97161
N	-20	SER	-	expression tag	UNP O97161
N	-19	MET	-	expression tag	UNP O97161
N	-18	THR	-	expression tag	UNP O97161
N	-17	GLY	-	expression tag	UNP O97161
N	-16	GLY	-	expression tag	UNP O97161
N	-15	GLN	-	expression tag	UNP O97161
N	-14	GLN	-	expression tag	UNP O97161
N	-13	MET	-	expression tag	UNP O97161
N	-12	GLY	-	expression tag	UNP O97161
N	-11	ARG	-	expression tag	UNP O97161
N	-10	ASP	-	expression tag	UNP O97161
N	-9	LEU	-	expression tag	UNP O97161
N	-8	TYR	-	expression tag	UNP O97161
N	-7	ASP	-	expression tag	UNP O97161
N	-6	ASP	-	expression tag	UNP O97161
N	-5	ASP	-	expression tag	UNP O97161
N	-4	ASP	-	expression tag	UNP O97161
N	-3	LYS	-	expression tag	UNP O97161
N	-2	GLY	-	expression tag	UNP O97161
N	-1	SER	-	expression tag	UNP O97161
N	0	THR	-	expression tag	UNP O97161
O	-33	MET	-	expression tag	UNP O97161
O	-32	ARG	-	expression tag	UNP O97161
O	-31	GLY	-	expression tag	UNP O97161
O	-30	SER	-	expression tag	UNP O97161
O	-29	HIS	-	expression tag	UNP O97161
O	-28	HIS	-	expression tag	UNP O97161
O	-27	HIS	-	expression tag	UNP O97161
O	-26	HIS	-	expression tag	UNP O97161
O	-25	HIS	-	expression tag	UNP O97161
O	-24	HIS	-	expression tag	UNP O97161

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
O	-23	GLY	-	expression tag	UNP O97161
O	-22	MET	-	expression tag	UNP O97161
O	-21	ALA	-	expression tag	UNP O97161
O	-20	SER	-	expression tag	UNP O97161
O	-19	MET	-	expression tag	UNP O97161
O	-18	THR	-	expression tag	UNP O97161
O	-17	GLY	-	expression tag	UNP O97161
O	-16	GLY	-	expression tag	UNP O97161
O	-15	GLN	-	expression tag	UNP O97161
O	-14	GLN	-	expression tag	UNP O97161
O	-13	MET	-	expression tag	UNP O97161
O	-12	GLY	-	expression tag	UNP O97161
O	-11	ARG	-	expression tag	UNP O97161
O	-10	ASP	-	expression tag	UNP O97161
O	-9	LEU	-	expression tag	UNP O97161
O	-8	TYR	-	expression tag	UNP O97161
O	-7	ASP	-	expression tag	UNP O97161
O	-6	ASP	-	expression tag	UNP O97161
O	-5	ASP	-	expression tag	UNP O97161
O	-4	ASP	-	expression tag	UNP O97161
O	-3	LYS	-	expression tag	UNP O97161
O	-2	GLY	-	expression tag	UNP O97161
O	-1	SER	-	expression tag	UNP O97161
O	0	THR	-	expression tag	UNP O97161
P	-33	MET	-	expression tag	UNP O97161
P	-32	ARG	-	expression tag	UNP O97161
P	-31	GLY	-	expression tag	UNP O97161
P	-30	SER	-	expression tag	UNP O97161
P	-29	HIS	-	expression tag	UNP O97161
P	-28	HIS	-	expression tag	UNP O97161
P	-27	HIS	-	expression tag	UNP O97161
P	-26	HIS	-	expression tag	UNP O97161
P	-25	HIS	-	expression tag	UNP O97161
P	-24	HIS	-	expression tag	UNP O97161
P	-23	GLY	-	expression tag	UNP O97161
P	-22	MET	-	expression tag	UNP O97161
P	-21	ALA	-	expression tag	UNP O97161
P	-20	SER	-	expression tag	UNP O97161
P	-19	MET	-	expression tag	UNP O97161
P	-18	THR	-	expression tag	UNP O97161
P	-17	GLY	-	expression tag	UNP O97161
P	-16	GLY	-	expression tag	UNP O97161

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
P	-15	GLN	-	expression tag	UNP O97161
P	-14	GLN	-	expression tag	UNP O97161
P	-13	MET	-	expression tag	UNP O97161
P	-12	GLY	-	expression tag	UNP O97161
P	-11	ARG	-	expression tag	UNP O97161
P	-10	ASP	-	expression tag	UNP O97161
P	-9	LEU	-	expression tag	UNP O97161
P	-8	TYR	-	expression tag	UNP O97161
P	-7	ASP	-	expression tag	UNP O97161
P	-6	ASP	-	expression tag	UNP O97161
P	-5	ASP	-	expression tag	UNP O97161
P	-4	ASP	-	expression tag	UNP O97161
P	-3	LYS	-	expression tag	UNP O97161
P	-2	GLY	-	expression tag	UNP O97161
P	-1	SER	-	expression tag	UNP O97161
P	0	THR	-	expression tag	UNP O97161
Q	-33	MET	-	expression tag	UNP O97161
Q	-32	ARG	-	expression tag	UNP O97161
Q	-31	GLY	-	expression tag	UNP O97161
Q	-30	SER	-	expression tag	UNP O97161
Q	-29	HIS	-	expression tag	UNP O97161
Q	-28	HIS	-	expression tag	UNP O97161
Q	-27	HIS	-	expression tag	UNP O97161
Q	-26	HIS	-	expression tag	UNP O97161
Q	-25	HIS	-	expression tag	UNP O97161
Q	-24	HIS	-	expression tag	UNP O97161
Q	-23	GLY	-	expression tag	UNP O97161
Q	-22	MET	-	expression tag	UNP O97161
Q	-21	ALA	-	expression tag	UNP O97161
Q	-20	SER	-	expression tag	UNP O97161
Q	-19	MET	-	expression tag	UNP O97161
Q	-18	THR	-	expression tag	UNP O97161
Q	-17	GLY	-	expression tag	UNP O97161
Q	-16	GLY	-	expression tag	UNP O97161
Q	-15	GLN	-	expression tag	UNP O97161
Q	-14	GLN	-	expression tag	UNP O97161
Q	-13	MET	-	expression tag	UNP O97161
Q	-12	GLY	-	expression tag	UNP O97161
Q	-11	ARG	-	expression tag	UNP O97161
Q	-10	ASP	-	expression tag	UNP O97161
Q	-9	LEU	-	expression tag	UNP O97161
Q	-8	TYR	-	expression tag	UNP O97161

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
Q	-7	ASP	-	expression tag	UNP O97161
Q	-6	ASP	-	expression tag	UNP O97161
Q	-5	ASP	-	expression tag	UNP O97161
Q	-4	ASP	-	expression tag	UNP O97161
Q	-3	LYS	-	expression tag	UNP O97161
Q	-2	GLY	-	expression tag	UNP O97161
Q	-1	SER	-	expression tag	UNP O97161
Q	0	THR	-	expression tag	UNP O97161
R	-33	MET	-	expression tag	UNP O97161
R	-32	ARG	-	expression tag	UNP O97161
R	-31	GLY	-	expression tag	UNP O97161
R	-30	SER	-	expression tag	UNP O97161
R	-29	HIS	-	expression tag	UNP O97161
R	-28	HIS	-	expression tag	UNP O97161
R	-27	HIS	-	expression tag	UNP O97161
R	-26	HIS	-	expression tag	UNP O97161
R	-25	HIS	-	expression tag	UNP O97161
R	-24	HIS	-	expression tag	UNP O97161
R	-23	GLY	-	expression tag	UNP O97161
R	-22	MET	-	expression tag	UNP O97161
R	-21	ALA	-	expression tag	UNP O97161
R	-20	SER	-	expression tag	UNP O97161
R	-19	MET	-	expression tag	UNP O97161
R	-18	THR	-	expression tag	UNP O97161
R	-17	GLY	-	expression tag	UNP O97161
R	-16	GLY	-	expression tag	UNP O97161
R	-15	GLN	-	expression tag	UNP O97161
R	-14	GLN	-	expression tag	UNP O97161
R	-13	MET	-	expression tag	UNP O97161
R	-12	GLY	-	expression tag	UNP O97161
R	-11	ARG	-	expression tag	UNP O97161
R	-10	ASP	-	expression tag	UNP O97161
R	-9	LEU	-	expression tag	UNP O97161
R	-8	TYR	-	expression tag	UNP O97161
R	-7	ASP	-	expression tag	UNP O97161
R	-6	ASP	-	expression tag	UNP O97161
R	-5	ASP	-	expression tag	UNP O97161
R	-4	ASP	-	expression tag	UNP O97161
R	-3	LYS	-	expression tag	UNP O97161
R	-2	GLY	-	expression tag	UNP O97161
R	-1	SER	-	expression tag	UNP O97161
R	0	THR	-	expression tag	UNP O97161

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
S	-33	MET	-	expression tag	UNP O97161
S	-32	ARG	-	expression tag	UNP O97161
S	-31	GLY	-	expression tag	UNP O97161
S	-30	SER	-	expression tag	UNP O97161
S	-29	HIS	-	expression tag	UNP O97161
S	-28	HIS	-	expression tag	UNP O97161
S	-27	HIS	-	expression tag	UNP O97161
S	-26	HIS	-	expression tag	UNP O97161
S	-25	HIS	-	expression tag	UNP O97161
S	-24	HIS	-	expression tag	UNP O97161
S	-23	GLY	-	expression tag	UNP O97161
S	-22	MET	-	expression tag	UNP O97161
S	-21	ALA	-	expression tag	UNP O97161
S	-20	SER	-	expression tag	UNP O97161
S	-19	MET	-	expression tag	UNP O97161
S	-18	THR	-	expression tag	UNP O97161
S	-17	GLY	-	expression tag	UNP O97161
S	-16	GLY	-	expression tag	UNP O97161
S	-15	GLN	-	expression tag	UNP O97161
S	-14	GLN	-	expression tag	UNP O97161
S	-13	MET	-	expression tag	UNP O97161
S	-12	GLY	-	expression tag	UNP O97161
S	-11	ARG	-	expression tag	UNP O97161
S	-10	ASP	-	expression tag	UNP O97161
S	-9	LEU	-	expression tag	UNP O97161
S	-8	TYR	-	expression tag	UNP O97161
S	-7	ASP	-	expression tag	UNP O97161
S	-6	ASP	-	expression tag	UNP O97161
S	-5	ASP	-	expression tag	UNP O97161
S	-4	ASP	-	expression tag	UNP O97161
S	-3	LYS	-	expression tag	UNP O97161
S	-2	GLY	-	expression tag	UNP O97161
S	-1	SER	-	expression tag	UNP O97161
S	0	THR	-	expression tag	UNP O97161
T	-33	MET	-	expression tag	UNP O97161
T	-32	ARG	-	expression tag	UNP O97161
T	-31	GLY	-	expression tag	UNP O97161
T	-30	SER	-	expression tag	UNP O97161
T	-29	HIS	-	expression tag	UNP O97161
T	-28	HIS	-	expression tag	UNP O97161
T	-27	HIS	-	expression tag	UNP O97161
T	-26	HIS	-	expression tag	UNP O97161

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
T	-25	HIS	-	expression tag	UNP O97161
T	-24	HIS	-	expression tag	UNP O97161
T	-23	GLY	-	expression tag	UNP O97161
T	-22	MET	-	expression tag	UNP O97161
T	-21	ALA	-	expression tag	UNP O97161
T	-20	SER	-	expression tag	UNP O97161
T	-19	MET	-	expression tag	UNP O97161
T	-18	THR	-	expression tag	UNP O97161
T	-17	GLY	-	expression tag	UNP O97161
T	-16	GLY	-	expression tag	UNP O97161
T	-15	GLN	-	expression tag	UNP O97161
T	-14	GLN	-	expression tag	UNP O97161
T	-13	MET	-	expression tag	UNP O97161
T	-12	GLY	-	expression tag	UNP O97161
T	-11	ARG	-	expression tag	UNP O97161
T	-10	ASP	-	expression tag	UNP O97161
T	-9	LEU	-	expression tag	UNP O97161
T	-8	TYR	-	expression tag	UNP O97161
T	-7	ASP	-	expression tag	UNP O97161
T	-6	ASP	-	expression tag	UNP O97161
T	-5	ASP	-	expression tag	UNP O97161
T	-4	ASP	-	expression tag	UNP O97161
T	-3	LYS	-	expression tag	UNP O97161
T	-2	GLY	-	expression tag	UNP O97161
T	-1	SER	-	expression tag	UNP O97161
T	0	THR	-	expression tag	UNP O97161

- Molecule 2 is a protein called THIOREDOXIN PEROXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	168	Total	C	N	O	S	0	0	0
			1344	860	227	251	6			

There are 35 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-33	MET	-	expression tag	UNP O97161
D	-32	ARG	-	expression tag	UNP O97161
D	-31	GLY	-	expression tag	UNP O97161
D	-30	SER	-	expression tag	UNP O97161
D	-29	HIS	-	expression tag	UNP O97161
D	-28	HIS	-	expression tag	UNP O97161

Continued on next page...

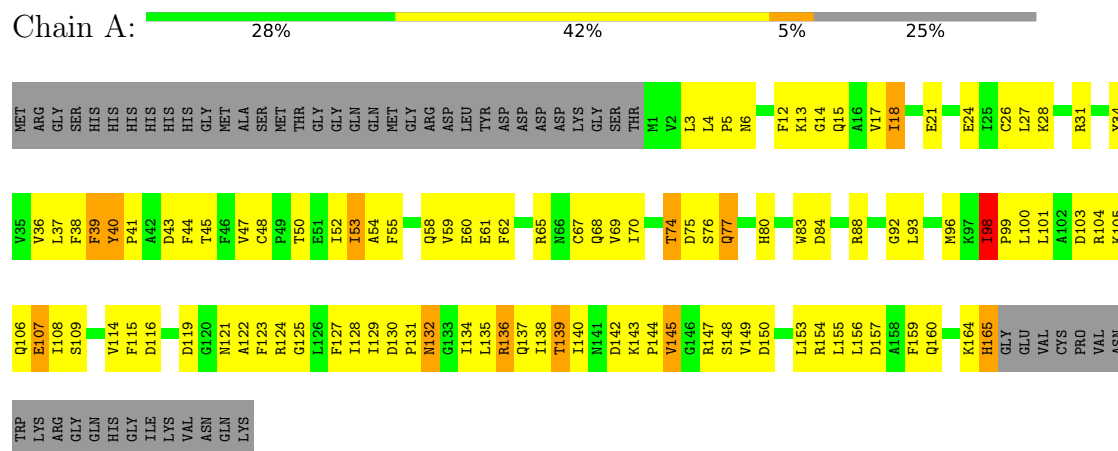
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	-27	HIS	-	expression tag	UNP O97161
D	-26	HIS	-	expression tag	UNP O97161
D	-25	HIS	-	expression tag	UNP O97161
D	-24	HIS	-	expression tag	UNP O97161
D	-23	GLY	-	expression tag	UNP O97161
D	-22	MET	-	expression tag	UNP O97161
D	-21	ALA	-	expression tag	UNP O97161
D	-20	SER	-	expression tag	UNP O97161
D	-19	MET	-	expression tag	UNP O97161
D	-18	THR	-	expression tag	UNP O97161
D	-17	GLY	-	expression tag	UNP O97161
D	-16	GLY	-	expression tag	UNP O97161
D	-15	GLN	-	expression tag	UNP O97161
D	-14	GLN	-	expression tag	UNP O97161
D	-13	MET	-	expression tag	UNP O97161
D	-12	GLY	-	expression tag	UNP O97161
D	-11	ARG	-	expression tag	UNP O97161
D	-10	ASP	-	expression tag	UNP O97161
D	-9	LEU	-	expression tag	UNP O97161
D	-8	TYR	-	expression tag	UNP O97161
D	-7	ASP	-	expression tag	UNP O97161
D	-6	ASP	-	expression tag	UNP O97161
D	-5	ASP	-	expression tag	UNP O97161
D	-4	ASP	-	expression tag	UNP O97161
D	-3	LYS	-	expression tag	UNP O97161
D	-2	GLY	-	expression tag	UNP O97161
D	-1	SER	-	expression tag	UNP O97161
D	0	THR	-	expression tag	UNP O97161
D	140	LEU	ILE	conflict	UNP O97161

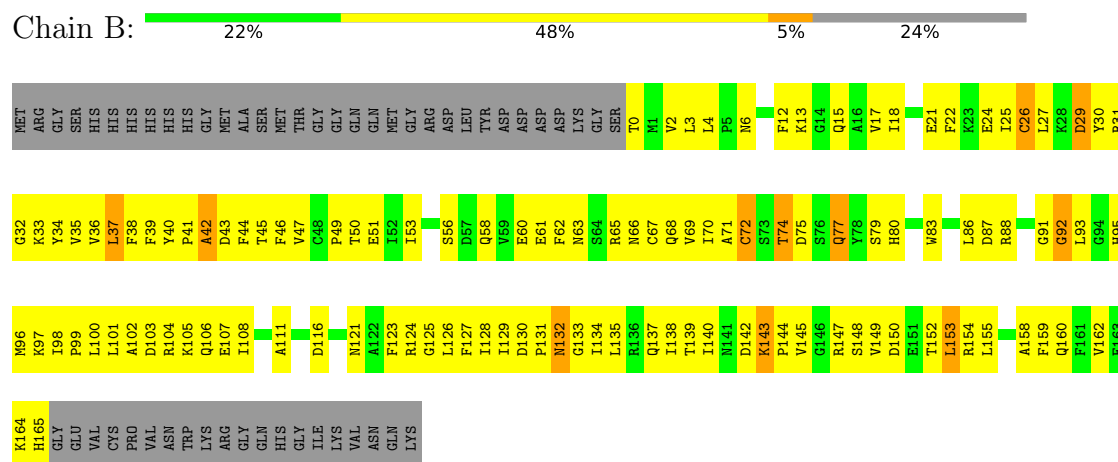
3 Residue-property plots

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

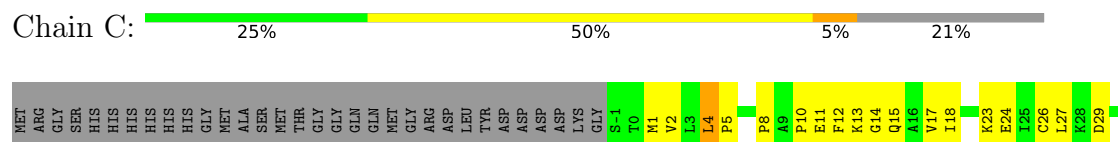
• Molecule 1: THIOREDOXIN PEROXIDASE

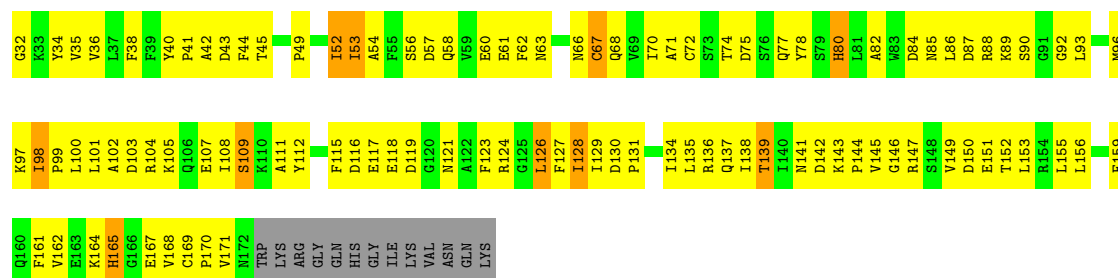


• Molecule 1: THIOREDOXIN PEROXIDASE

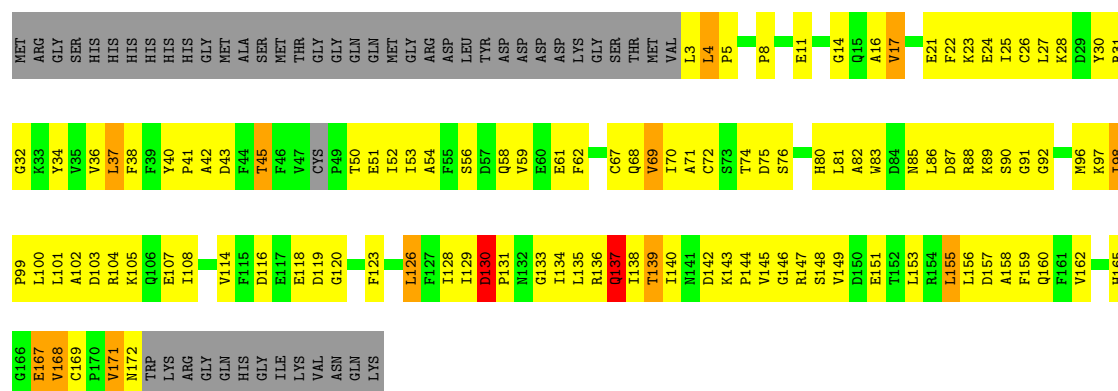
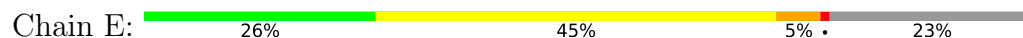


• Molecule 1: THIOREDOXIN PEROXIDASE

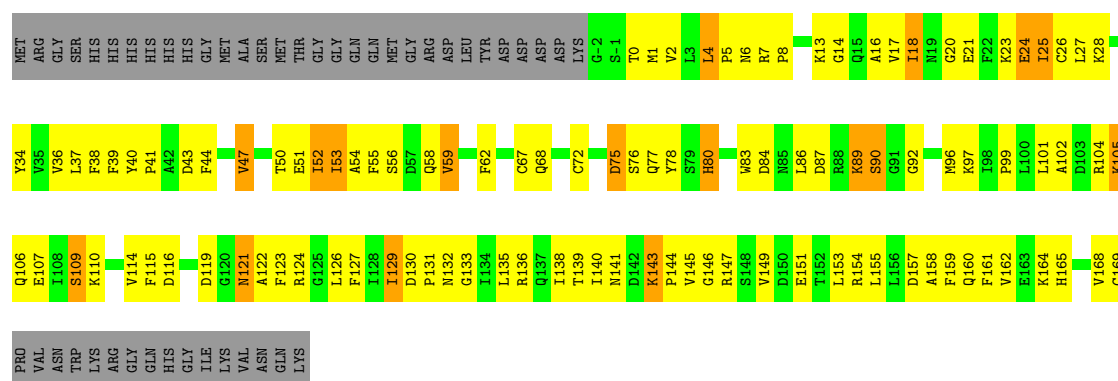




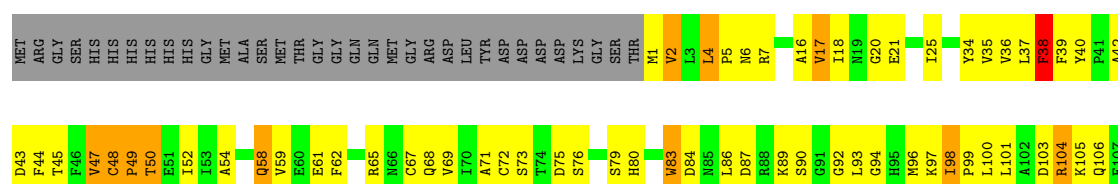
• Molecule 1: THIOREDOXIN PEROXIDASE

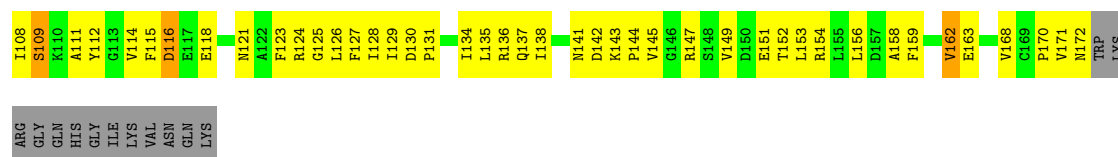


• Molecule 1: THIOREDOXIN PEROXIDASE

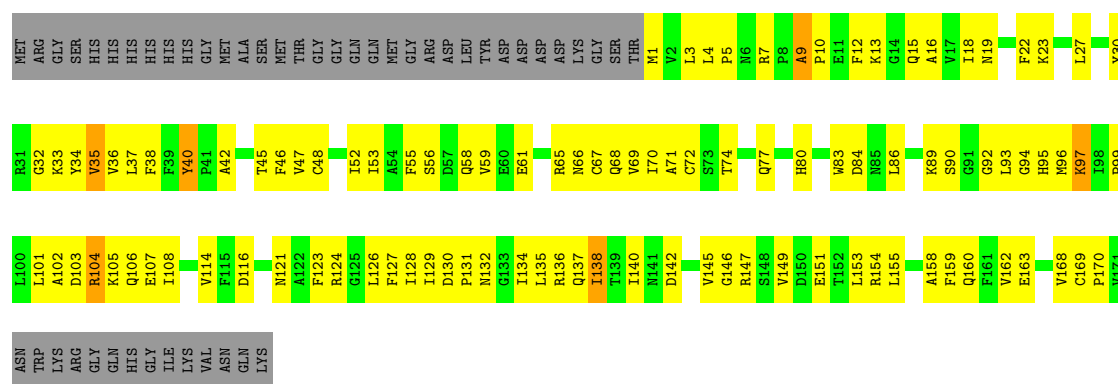


• Molecule 1: THIOREDOXIN PEROXIDASE

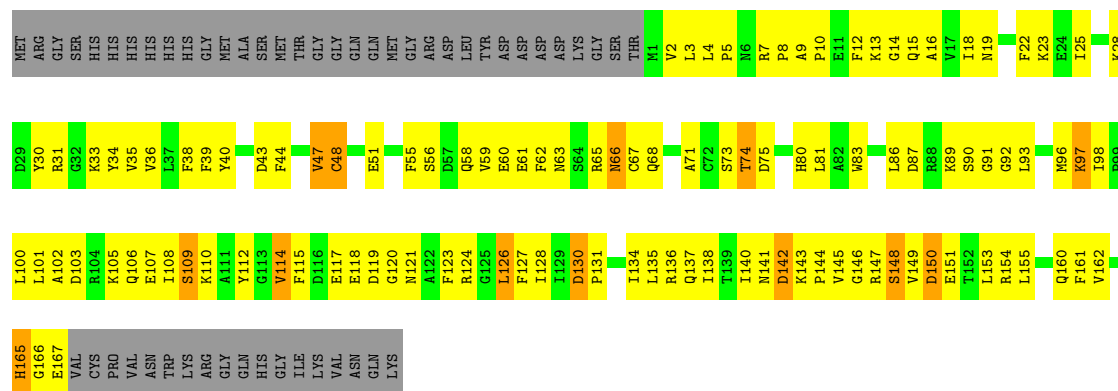




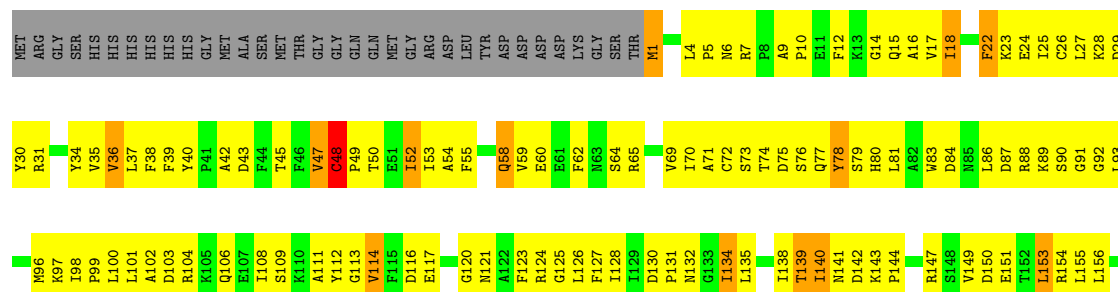
• Molecule 1: THIOREDOXIN PEROXIDASE

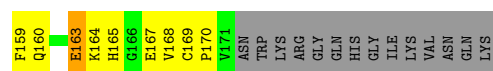


• Molecule 1: THIOREDOXIN PEROXIDASE



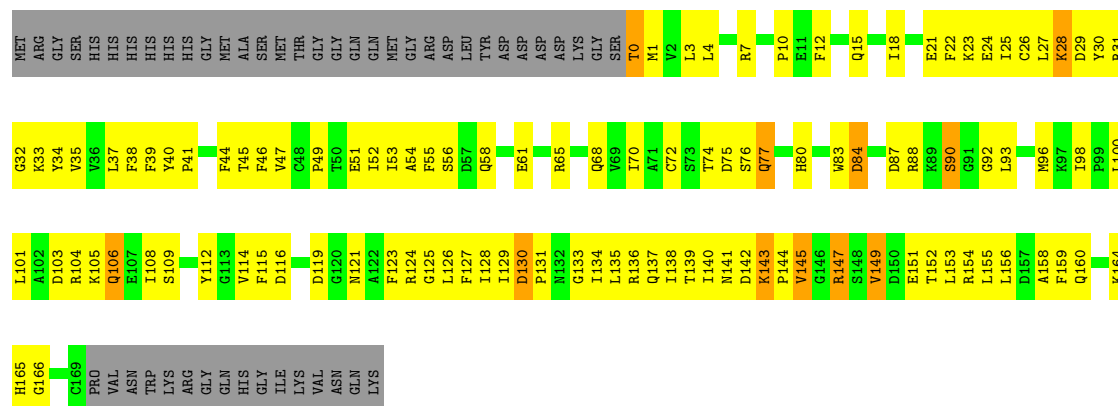
• Molecule 1: THIOREDOXIN PEROXIDASE





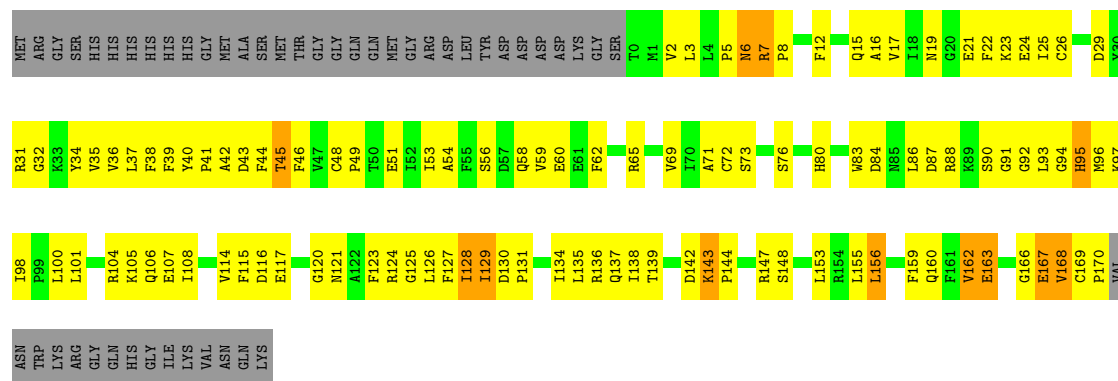
● Molecule 1: THIOREDOXIN PEROXIDASE

Chain K:  27% 45% 5% 22%

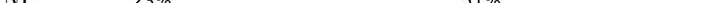


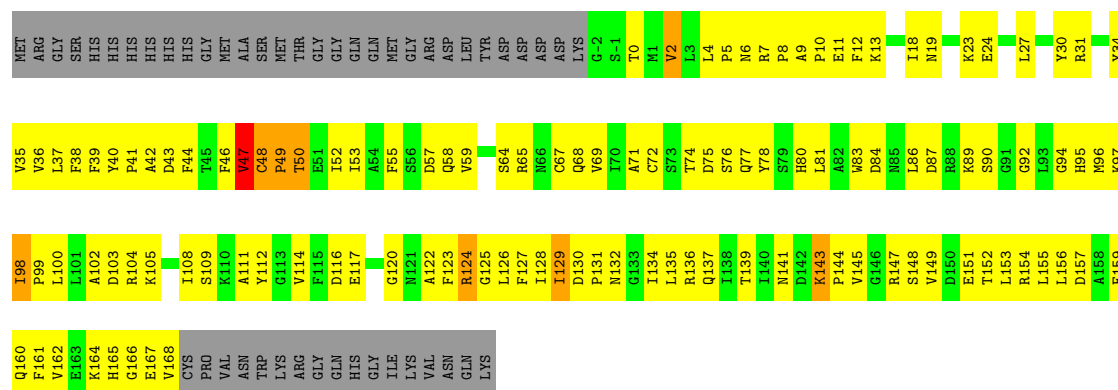
• Molecule 1: THIOREDOXIN PEROXIDASE

Chain L: 28% 44% 5% 22%

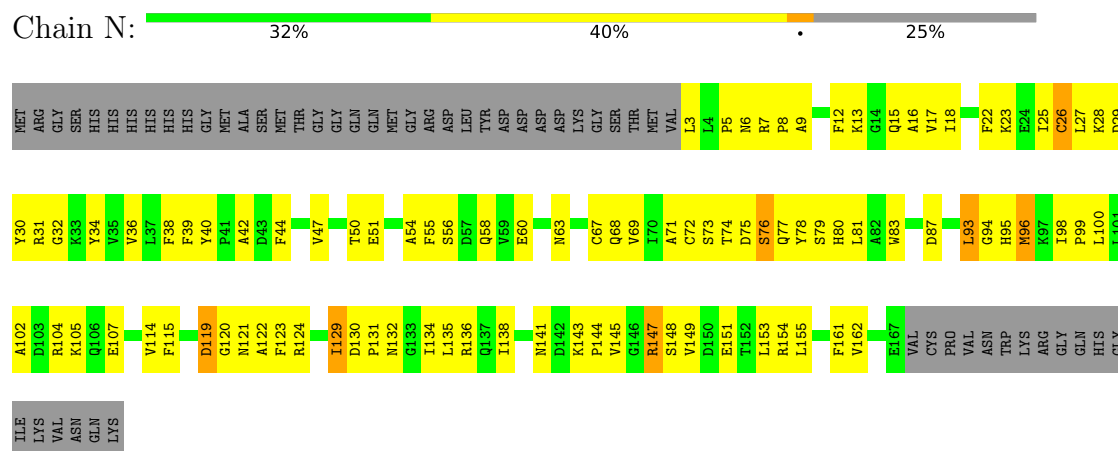


- Molecule 1: THIOREDOXIN PEROXIDASE

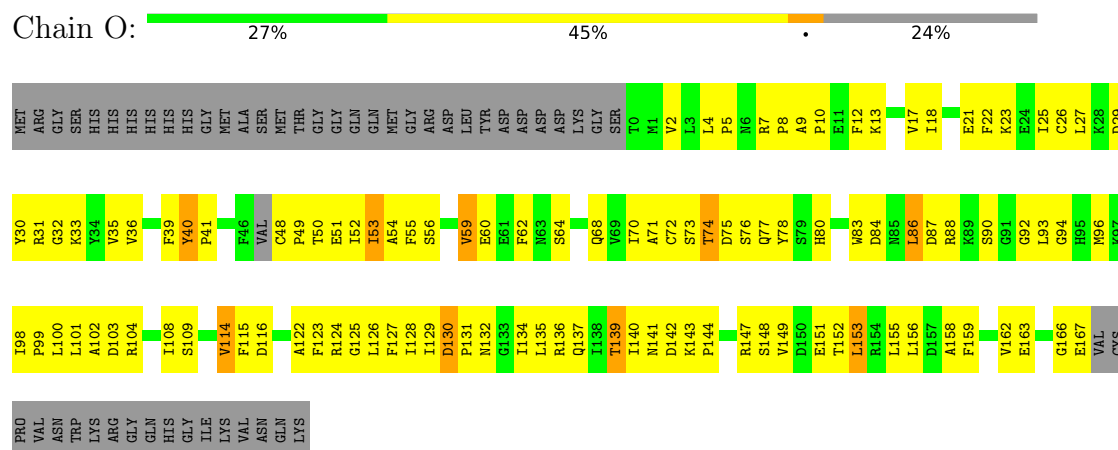
Chain M:  23% 51% . 22%



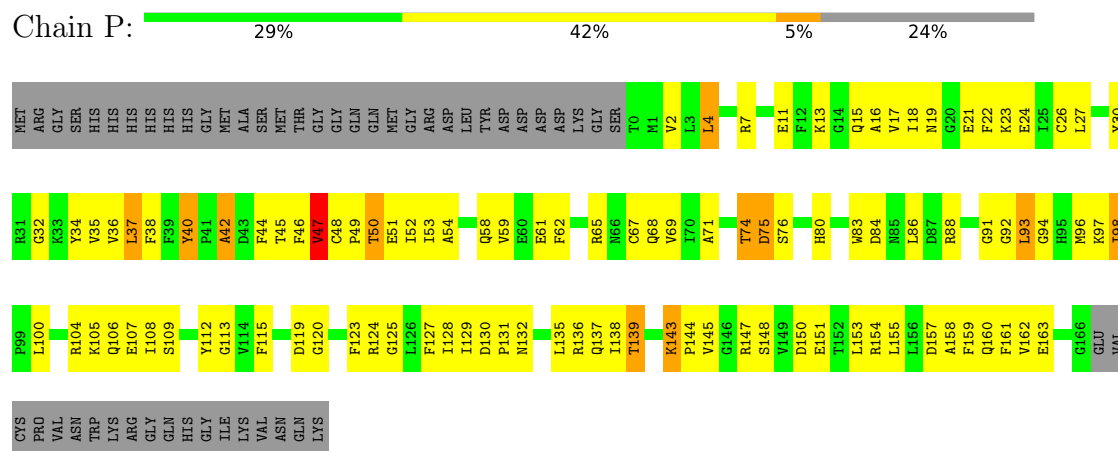
● Molecule 1: THIOREDOXIN PEROXIDASE



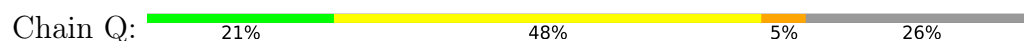
● Molecule 1: THIOREDOXIN PEROXIDASE

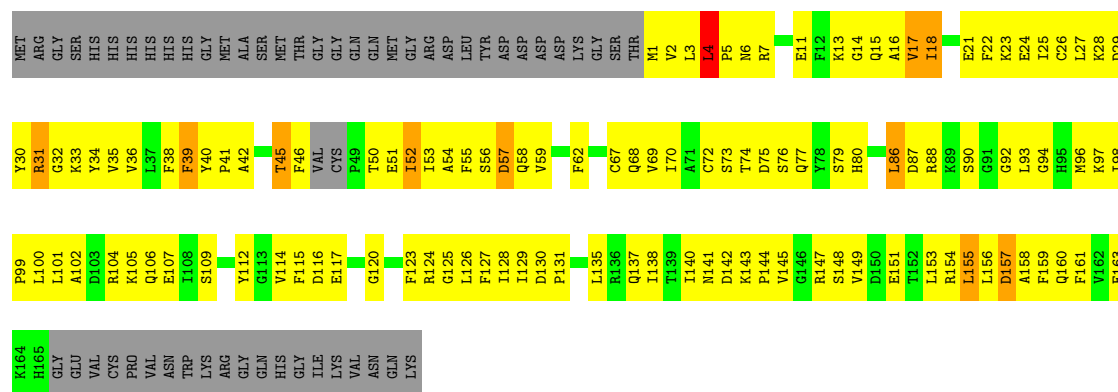


● Molecule 1: THIOREDOXIN PEROXIDASE

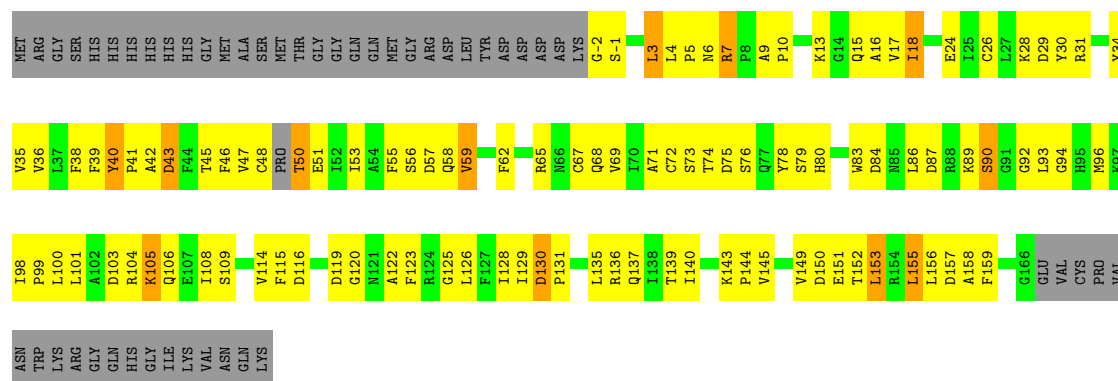


● Molecule 1: THIOREDOXIN PEROXIDASE

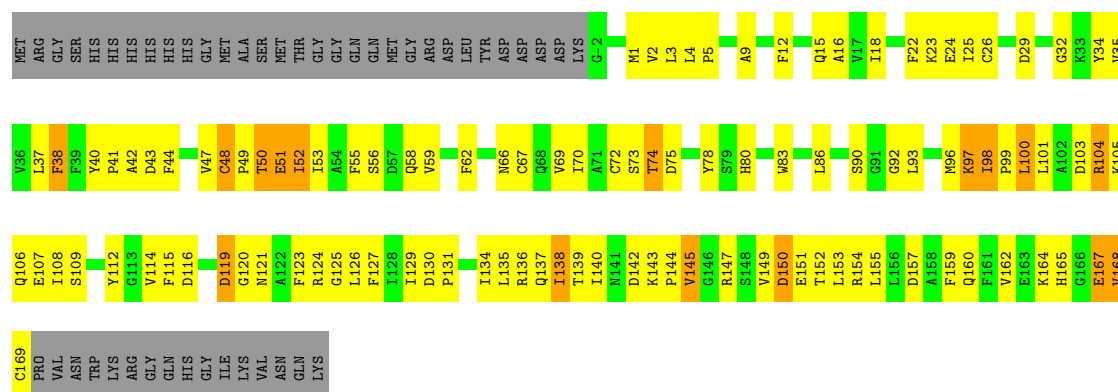




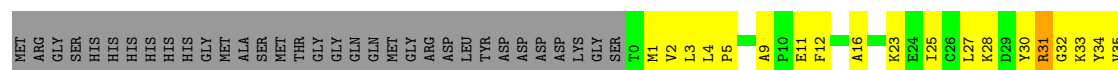
• Molecule 1: THIOREDOXIN PEROXIDASE

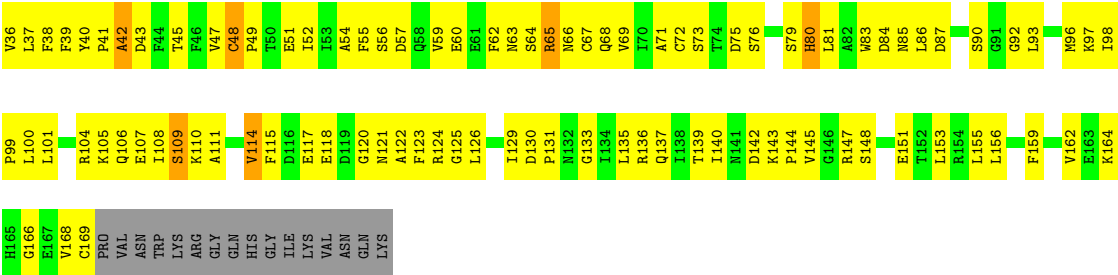


• Molecule 1: THIOREDOXIN PEROXIDASE

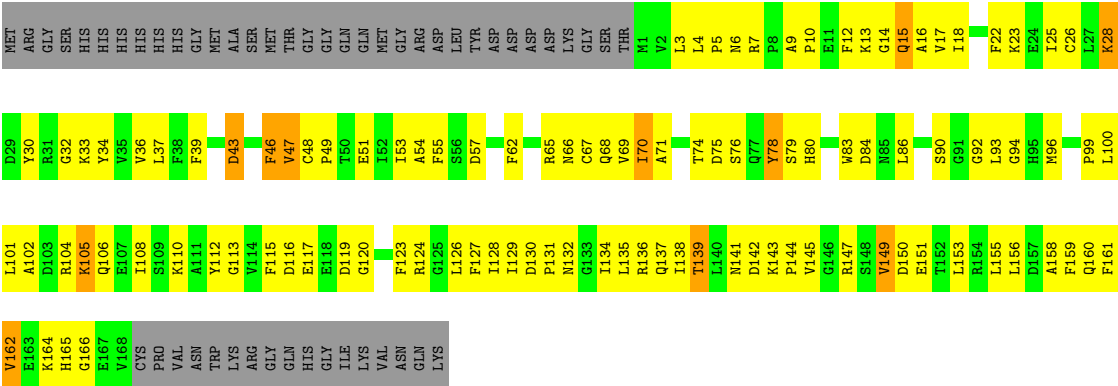
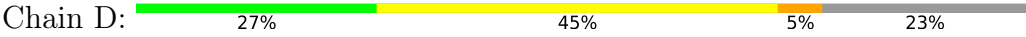


• Molecule 1: THIOREDOXIN PEROXIDASE





● Molecule 2: THIOREDOXIN PEROXIDASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	126.91Å 204.94Å 126.84Å 90.00° 114.60° 90.00°	Depositor
Resolution (Å)	29.86 – 3.00 29.86 – 3.00	Depositor EDS
% Data completeness (in resolution range)	95.7 (29.86-3.00) 95.5 (29.86-3.00)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.54 (at 3.00Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.219 , 0.270 0.212 , 0.247	Depositor DCC
R_{free} test set	5627 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	17.8	Xtriage
Anisotropy	0.459	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.35$, $\langle L^2 \rangle = 0.18$	Xtriage
Estimated twinning fraction	0.400 for l,-k,h	Xtriage
Reported twinning fraction	0.500 for L,-K,H	Depositor
Outliers	0 of 112406 reflections	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	26988	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.67% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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	0.45	0/1354	0.95	6/1829 (0.3%)
1	B	0.48	0/1361	0.90	3/1839 (0.2%)
1	C	0.44	0/1416	0.88	2/1915 (0.1%)
1	E	0.45	0/1381	0.92	5/1865 (0.3%)
1	F	0.46	0/1397	0.95	3/1887 (0.2%)
1	G	0.44	0/1403	0.95	5/1897 (0.3%)
1	H	0.43	0/1395	0.89	4/1886 (0.2%)
1	I	0.44	0/1367	0.93	2/1846 (0.1%)
1	J	0.47	0/1395	0.94	4/1886 (0.2%)
1	K	0.44	0/1387	0.91	4/1874 (0.2%)
1	L	0.44	0/1395	0.89	2/1886 (0.1%)
1	M	0.46	0/1391	0.95	5/1879 (0.3%)
1	N	0.43	0/1352	0.91	3/1826 (0.2%)
1	O	0.42	0/1366	0.90	2/1843 (0.1%)
1	P	0.45	0/1365	0.97	6/1844 (0.3%)
1	Q	0.41	0/1340	0.90	2/1807 (0.1%)
1	R	0.44	0/1366	0.98	8/1842 (0.4%)
1	S	0.45	0/1397	0.94	1/1887 (0.1%)
1	T	0.42	0/1387	0.92	4/1874 (0.2%)
2	D	0.44	0/1374	0.88	3/1856 (0.2%)
All	All	0.44	0/27589	0.92	74/37268 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	P	0	1

There are no bond length outliers.

All (74) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	50	THR	N-CA-C	-8.81	101.12	112.23
1	H	9	ALA	CA-C-N	7.67	128.12	119.92
1	H	9	ALA	C-N-CA	7.67	128.12	119.92
1	J	9	ALA	CA-C-N	7.63	127.69	119.90
1	J	9	ALA	C-N-CA	7.63	127.69	119.90
1	E	4	LEU	CA-C-N	7.33	126.59	118.97
1	E	4	LEU	C-N-CA	7.33	126.59	118.97
1	F	4	LEU	CA-C-N	7.14	126.82	119.82
1	F	4	LEU	C-N-CA	7.14	126.82	119.82
1	R	40	TYR	CA-C-N	6.98	126.50	119.24
1	R	40	TYR	C-N-CA	6.98	126.50	119.24
1	R	9	ALA	CA-C-N	6.85	127.26	119.93
1	R	9	ALA	C-N-CA	6.85	127.26	119.93
1	A	98	ILE	CA-C-N	6.66	127.05	119.93
1	A	98	ILE	C-N-CA	6.66	127.05	119.93
1	T	42	ALA	N-CA-C	6.66	117.37	108.38
1	C	169	CYS	CA-C-N	6.41	127.85	119.84
1	C	169	CYS	C-N-CA	6.41	127.85	119.84
1	G	98	ILE	CA-C-N	6.34	126.29	119.76
1	G	98	ILE	C-N-CA	6.34	126.29	119.76
1	K	130	ASP	CA-C-N	6.33	125.82	119.24
1	K	130	ASP	C-N-CA	6.33	125.82	119.24
1	P	4	LEU	CA-C-N	6.14	125.62	119.24
1	P	4	LEU	C-N-CA	6.14	125.62	119.24
1	S	145	VAL	N-CA-C	6.09	116.58	107.51
1	L	143	LYS	CA-C-N	6.05	126.21	119.32
1	L	143	LYS	C-N-CA	6.05	126.21	119.32
1	P	143	LYS	CA-C-N	6.02	125.57	119.19
1	P	143	LYS	C-N-CA	6.02	125.57	119.19
1	T	48	CYS	CA-C-N	-6.02	115.57	121.65
1	T	48	CYS	C-N-CA	-6.02	115.57	121.65
1	K	98	ILE	CA-C-N	6.01	126.03	119.90
1	K	98	ILE	C-N-CA	6.01	126.03	119.90
1	A	40	TYR	CA-C-N	5.94	125.15	118.97
1	A	40	TYR	C-N-CA	5.94	125.15	118.97
1	N	40	TYR	CA-C-N	5.91	125.38	119.24
1	N	40	TYR	C-N-CA	5.91	125.38	119.24
1	M	49	PRO	N-CA-C	5.88	121.21	113.86
1	H	40	TYR	CA-C-N	5.80	125.94	119.32
1	H	40	TYR	C-N-CA	5.80	125.94	119.32
1	A	48	CYS	CA-C-N	5.79	125.89	119.87
1	A	48	CYS	C-N-CA	5.79	125.89	119.87
1	M	98	ILE	CA-C-N	5.74	125.69	119.78

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	98	ILE	C-N-CA	5.74	125.69	119.78
1	R	7	ARG	CA-C-N	5.70	125.63	119.76
1	R	7	ARG	C-N-CA	5.70	125.63	119.76
1	M	48	CYS	CA-C-N	5.63	125.25	119.56
1	M	48	CYS	C-N-CA	5.63	125.25	119.56
1	J	9	ALA	N-CA-C	5.58	117.84	110.36
1	T	140	ILE	N-CA-C	5.51	116.21	108.17
1	Q	4	LEU	CA-C-N	5.48	125.68	120.31
1	Q	4	LEU	C-N-CA	5.48	125.68	120.31
1	B	92	GLY	N-CA-C	5.47	121.47	110.97
1	O	130	ASP	CA-C-N	5.39	126.58	119.84
1	O	130	ASP	C-N-CA	5.39	126.58	119.84
1	P	42	ALA	N-CA-C	5.32	116.23	108.14
1	F	25	ILE	N-CA-C	5.32	115.71	107.78
1	N	42	ALA	N-CA-C	5.29	115.34	107.88
2	D	9	ALA	CA-C-N	5.29	125.45	119.90
2	D	9	ALA	C-N-CA	5.29	125.45	119.90
1	I	48	CYS	CA-C-N	5.23	124.84	119.56
1	I	48	CYS	C-N-CA	5.23	124.84	119.56
2	D	162	VAL	N-CA-C	5.21	115.43	110.53
1	G	38	PHE	N-CA-C	5.20	116.89	108.26
1	G	17	VAL	N-CA-C	5.19	115.53	107.28
1	B	72	CYS	N-CA-C	5.15	117.21	109.23
1	R	130	ASP	CA-C-N	5.13	124.79	119.56
1	R	130	ASP	C-N-CA	5.13	124.79	119.56
1	J	14	GLY	N-CA-C	5.06	118.45	110.91
1	P	75	ASP	N-CA-C	5.05	116.45	110.19
1	E	137	GLN	N-CA-C	5.02	116.30	109.18
1	B	42	ALA	N-CA-C	5.01	114.94	107.88
1	E	130	ASP	CA-C-N	5.00	125.02	119.32
1	E	130	ASP	C-N-CA	5.00	125.02	119.32

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	P	49	PRO	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1324	0	1301	126	0
1	B	1331	0	1308	133	0
1	C	1385	0	1358	139	0
1	E	1351	0	1320	128	0
1	F	1367	0	1339	120	0
1	G	1372	0	1346	134	0
1	H	1364	0	1340	120	0
1	I	1337	0	1310	126	0
1	J	1364	0	1340	145	0
1	K	1357	0	1331	114	0
1	L	1364	0	1338	130	0
1	M	1361	0	1334	127	0
1	N	1322	0	1289	101	0
1	O	1337	0	1307	125	0
1	P	1335	0	1311	126	0
1	Q	1311	0	1287	129	0
1	R	1338	0	1311	114	0
1	S	1367	0	1339	133	0
1	T	1357	0	1331	131	0
2	D	1344	0	1319	143	0
All	All	26988	0	26459	2362	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 44.

All (2362) 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)
1:S:15:GLN:HG2	1:S:24:GLU:HG2	1.18	1.14
1:O:40:TYR:HE1	1:O:73:SER:HB3	1.05	1.12
1:S:51:GLU:OE1	1:S:51:GLU:HA	1.43	1.10
2:D:84:ASP:HA	2:D:93:LEU:HB2	1.28	1.10
1:T:60:GLU:HA	1:T:63:ASN:HB2	1.25	1.09
2:D:15:GLN:HA	2:D:15:GLN:HE21	1.17	1.08
1:A:61:GLU:HB3	1:A:65:ARG:HE	1.21	1.04

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:28:LYS:HA	1:I:31:ARG:HE	1.20	1.03
1:I:2:VAL:HA	1:J:1:MET:HA	1.41	1.01
1:O:40:TYR:CE1	1:O:73:SER:HB3	1.97	1.00
1:I:162:VAL:HA	1:I:166:GLY:HA3	1.41	1.00
1:O:41:PRO:HG3	1:O:143:LYS:HG2	1.43	0.99
1:S:47:VAL:CG2	1:S:51:GLU:HG2	1.92	0.98
1:H:93:LEU:HB3	1:H:96:MET:HG2	1.45	0.98
1:S:52:ILE:HD13	1:S:52:ILE:N	1.78	0.98
1:L:128:ILE:HG13	1:L:137:GLN:HB3	1.46	0.96
1:J:58:GLN:HE21	1:J:58:GLN:HA	1.31	0.95
1:L:40:TYR:HB2	1:L:41:PRO:HD2	1.48	0.95
1:O:86:LEU:HD11	1:O:90:SER:HB3	1.46	0.95
1:E:40:TYR:HB2	1:E:41:PRO:HD2	1.47	0.95
1:E:140:ILE:HB	1:F:138:ILE:HB	1.45	0.94
1:Q:128:ILE:HD12	1:Q:137:GLN:HB3	1.49	0.94
1:N:147:ARG:HE	1:N:147:ARG:H	1.16	0.94
1:J:47:VAL:HG22	1:J:48:CYS:H	1.32	0.93
1:K:109:SER:HB3	1:K:115:PHE:HB2	1.48	0.93
1:R:75:ASP:HB2	1:R:80:HIS:HE1	1.33	0.93
1:L:65:ARG:HG2	1:L:160:GLN:HE22	1.31	0.93
1:G:65:ARG:HH21	1:G:153:LEU:HD23	1.35	0.92
1:C:119:ASP:HB3	1:C:121:ASN:ND2	1.83	0.92
1:T:62:PHE:HB3	1:T:67:CYS:HB3	1.50	0.92
1:R:75:ASP:HB2	1:R:80:HIS:CE1	2.05	0.91
1:S:47:VAL:HG21	1:S:51:GLU:HG2	1.52	0.91
2:D:126:LEU:HD12	2:D:147:ARG:HD2	1.50	0.91
1:Q:11:GLU:HG2	1:Q:27:LEU:HB3	1.53	0.91
1:J:125:GLY:HA2	1:J:140:ILE:HA	1.49	0.90
1:S:4:LEU:HB3	1:T:123:PHE:HE2	1.32	0.90
1:K:58:GLN:OE1	1:K:61:GLU:HG3	1.72	0.90
1:R:48:CYS:HB2	1:R:51:GLU:H	1.36	0.90
1:C:119:ASP:HB3	1:C:121:ASN:HD21	1.36	0.89
2:D:47:VAL:HG12	2:D:48:CYS:H	1.36	0.89
1:N:56:SER:HB2	1:N:96:MET:HG3	1.53	0.89
1:O:84:ASP:HA	1:O:93:LEU:HB2	1.55	0.89
1:T:124:ARG:HB3	1:T:147:ARG:HH12	1.37	0.89
1:K:53:ILE:HA	1:K:56:SER:HB3	1.51	0.89
1:N:18:ILE:HD12	1:N:23:LYS:HB2	1.55	0.89
1:K:4:LEU:HB2	1:K:7:ARG:HD2	1.53	0.88
1:C:62:PHE:HB3	1:C:67:CYS:HB3	1.55	0.88
2:D:136:ARG:HB3	2:D:159:PHE:CE2	2.07	0.88

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:87:ASP:OD2	1:G:89:LYS:HB2	1.74	0.88
1:S:4:LEU:HB3	1:T:123:PHE:CE2	2.08	0.88
2:D:14:GLY:HA3	2:D:101:LEU:HD11	1.55	0.88
1:O:56:SER:HB3	1:O:96:MET:HE1	1.56	0.88
1:Q:22:PHE:HE1	1:Q:77:GLN:HB2	1.40	0.87
1:M:55:PHE:CE1	1:M:149:VAL:HG22	2.10	0.87
1:O:142:ASP:OD2	1:O:144:PRO:HD2	1.75	0.87
1:K:10:PRO:HB2	1:K:112:TYR:CE1	2.10	0.87
1:B:164:LYS:HD2	1:B:165:HIS:CE1	2.09	0.86
1:R:4:LEU:HD12	1:R:7:ARG:HE	1.39	0.86
1:T:32:GLY:HA2	1:T:131:PRO:HB3	1.55	0.86
1:A:132:ASN:HD22	1:A:132:ASN:H	1.24	0.86
1:R:130:ASP:HB2	1:R:131:PRO:HD2	1.58	0.86
1:K:143:LYS:HG3	1:K:144:PRO:HD3	1.56	0.86
1:L:124:ARG:HB3	1:L:147:ARG:NH2	1.91	0.85
1:E:76:SER:HA	1:E:102:ALA:HB1	1.56	0.85
1:J:24:GLU:HB3	1:K:24:GLU:HB3	1.56	0.85
1:A:34:TYR:HB2	1:A:67:CYS:HB2	1.58	0.85
1:P:53:ILE:HD13	1:P:88:ARG:HD3	1.58	0.85
1:O:86:LEU:HD12	1:O:87:ASP:N	1.90	0.85
2:D:124:ARG:HG2	2:D:147:ARG:HH12	1.42	0.84
1:A:28:LYS:HE3	1:A:31:ARG:HE	1.41	0.84
1:J:83:TRP:CD1	1:J:92:GLY:HA2	2.12	0.84
1:C:17:VAL:HB	1:C:100:LEU:HB2	1.60	0.84
1:F:41:PRO:O	1:F:121:ASN:HB3	1.78	0.84
1:T:12:PHE:HB2	1:T:108:ILE:HG13	1.58	0.84
1:A:104:ARG:HG3	1:J:120:GLY:O	1.78	0.83
1:I:75:ASP:HB2	1:I:80:HIS:HE1	1.42	0.83
1:J:86:LEU:HD21	1:J:90:SER:HB3	1.60	0.83
1:I:86:LEU:HB3	1:I:92:GLY:HA3	1.61	0.83
1:E:123:PHE:HE2	1:F:4:LEU:HD23	1.43	0.83
1:P:109:SER:HB2	1:P:115:PHE:HB2	1.61	0.83
1:S:126:LEU:HB3	1:S:139:THR:HB	1.59	0.83
1:B:104:ARG:O	1:B:106:GLN:HG3	1.79	0.83
1:E:74:THR:HG21	1:E:120:GLY:O	1.79	0.82
1:S:41:PRO:HD3	1:S:124:ARG:HG2	1.60	0.82
1:Q:93:LEU:HD13	1:Q:96:MET:HE3	1.62	0.82
1:C:35:VAL:HB	1:C:129:ILE:HB	1.61	0.82
1:P:4:LEU:HB2	1:P:7:ARG:HD3	1.58	0.82
1:A:75:ASP:HB2	1:A:80:HIS:HE1	1.45	0.82
1:J:150:ASP:HA	1:J:153:LEU:HD23	1.61	0.82

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:96:MET:HG3	1:B:100:LEU:HD11	1.60	0.82
1:Q:69:VAL:O	1:Q:99:PRO:HD2	1.80	0.82
1:I:28:LYS:O	1:I:31:ARG:HG2	1.80	0.81
1:E:17:VAL:HG21	1:E:80:HIS:HB3	1.61	0.81
2:D:34:TYR:CE1	2:D:131:PRO:HD3	2.16	0.81
1:N:149:VAL:O	1:N:153:LEU:HD13	1.81	0.81
1:C:53:ILE:HG23	1:C:96:MET:HE2	1.61	0.81
1:G:76:SER:HB3	1:G:104:ARG:NH2	1.95	0.81
1:Q:22:PHE:CE1	1:Q:77:GLN:HB2	2.16	0.81
1:N:8:PRO:HA	1:N:134:ILE:HA	1.63	0.81
1:E:30:TYR:HE2	1:E:68:GLN:HG2	1.45	0.80
1:H:4:LEU:HB2	1:H:7:ARG:HD3	1.60	0.80
1:Q:143:LYS:HB2	1:Q:144:PRO:HD3	1.63	0.80
1:B:0:THR:HB	1:B:2:VAL:HG13	1.62	0.80
1:I:8:PRO:HA	1:I:134:ILE:HA	1.63	0.80
1:T:126:LEU:HB3	1:T:139:THR:HB	1.62	0.80
1:I:25:ILE:HD11	1:I:101:LEU:HD13	1.64	0.80
1:L:69:VAL:HB	1:L:98:ILE:HG21	1.63	0.80
2:D:6:ASN:O	2:D:7:ARG:HD2	1.82	0.79
1:H:124:ARG:HH11	1:H:147:ARG:HH21	1.26	0.79
1:B:155:LEU:HB3	1:B:159:PHE:HE2	1.46	0.79
1:E:96:MET:HA	1:E:96:MET:HE2	1.64	0.79
1:L:76:SER:HB3	1:L:104:ARG:HH11	1.47	0.79
1:H:36:VAL:HG22	1:H:128:ILE:HG12	1.63	0.79
1:A:61:GLU:HB3	1:A:65:ARG:NE	1.98	0.79
1:S:169:CYS:HB3	1:T:48:CYS:SG	2.23	0.79
1:M:152:THR:HA	1:M:155:LEU:HG	1.63	0.78
1:O:162:VAL:HG21	1:P:145:VAL:HG22	1.63	0.78
1:P:120:GLY:HA3	1:Q:104:ARG:HG3	1.65	0.78
1:R:152:THR:HA	1:R:155:LEU:HD12	1.62	0.78
2:D:86:LEU:HG	2:D:92:GLY:HA3	1.62	0.78
1:I:83:TRP:HB3	1:I:93:LEU:HD12	1.66	0.78
1:C:18:ILE:HD13	1:C:23:LYS:HB2	1.65	0.78
1:H:168:VAL:HG12	1:H:169:CYS:H	1.47	0.78
1:S:26:CYS:HB3	1:S:29:ASP:OD1	1.83	0.78
1:T:28:LYS:HA	1:T:31:ARG:NE	1.98	0.78
2:D:135:LEU:HD12	2:D:136:ARG:H	1.47	0.78
1:G:84:ASP:HA	1:G:93:LEU:HB2	1.65	0.78
1:N:15:GLN:HE21	1:N:22:PHE:HB3	1.47	0.78
1:B:150:ASP:HA	1:B:153:LEU:HD22	1.65	0.78
1:L:65:ARG:HG2	1:L:160:GLN:NE2	1.99	0.78

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:167:GLU:HG2	1:L:169:CYS:SG	2.23	0.78
1:A:150:ASP:HA	1:A:153:LEU:HD13	1.65	0.77
1:S:53:ILE:HD11	1:S:93:LEU:HA	1.66	0.77
1:S:47:VAL:HG23	1:S:51:GLU:HG2	1.64	0.77
1:S:127:PHE:CE1	1:S:138:ILE:HG23	2.18	0.77
1:I:10:PRO:HG2	1:I:112:TYR:CZ	2.18	0.77
2:D:86:LEU:HD11	2:D:90:SER:HB2	1.66	0.77
1:G:76:SER:HB3	1:G:104:ARG:HH22	1.48	0.77
1:M:41:PRO:HA	1:M:122:ALA:H	1.49	0.77
1:N:119:ASP:HB2	1:N:121:ASN:OD1	1.85	0.77
1:P:148:SER:HB3	1:P:151:GLU:HB3	1.67	0.77
1:S:15:GLN:CG	1:S:24:GLU:HG2	2.07	0.77
1:E:138:ILE:HB	1:F:140:ILE:HB	1.65	0.77
1:R:59:VAL:HA	1:R:62:PHE:HD2	1.48	0.77
2:D:46:PHE:H	2:D:46:PHE:HD1	1.30	0.77
1:I:38:PHE:HB3	1:I:126:LEU:HG	1.67	0.77
1:I:22:PHE:O	1:I:23:LYS:HD2	1.85	0.77
1:N:15:GLN:NE2	1:N:22:PHE:HB3	1.98	0.77
1:T:28:LYS:O	1:T:31:ARG:HD3	1.83	0.77
1:S:96:MET:HE2	1:S:96:MET:HA	1.65	0.76
1:G:86:LEU:HG	1:G:92:GLY:HA3	1.66	0.76
2:D:5:PRO:O	2:D:135:LEU:HG	1.85	0.76
1:L:39:PHE:CE1	1:L:114:VAL:HG21	2.20	0.76
1:P:75:ASP:CG	1:Q:104:ARG:HH22	1.93	0.76
1:K:58:GLN:OE1	1:K:61:GLU:CG	2.34	0.76
1:E:5:PRO:HB3	1:E:136:ARG:O	1.85	0.76
1:I:28:LYS:HA	1:I:31:ARG:NE	1.97	0.76
1:S:55:PHE:CE2	1:S:149:VAL:HA	2.21	0.76
1:K:51:GLU:HG3	1:K:52:ILE:H	1.49	0.76
1:S:47:VAL:HG21	1:S:51:GLU:CG	2.15	0.76
1:S:127:PHE:HE1	1:S:138:ILE:HG23	1.51	0.76
1:T:162:VAL:HG13	1:T:166:GLY:HA2	1.67	0.76
1:C:56:SER:OG	1:C:96:MET:HB2	1.86	0.76
1:H:130:ASP:HB2	1:H:131:PRO:HD2	1.68	0.76
1:K:128:ILE:HG22	1:K:136:ARG:HB3	1.68	0.76
1:B:70:ILE:HG12	1:B:99:PRO:HG2	1.69	0.75
1:E:51:GLU:OE1	1:E:146:GLY:HA2	1.85	0.75
1:H:103:ASP:HB2	1:H:108:ILE:HD12	1.68	0.75
1:P:51:GLU:OE2	1:P:124:ARG:HD3	1.86	0.75
1:I:141:ASN:HD22	1:I:145:VAL:HG12	1.51	0.75
1:Q:6:ASN:O	1:Q:7:ARG:HG3	1.86	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:13:LYS:HE3	1:C:24:GLU:OE2	1.87	0.75
1:E:123:PHE:CE2	1:F:4:LEU:HD23	2.20	0.75
1:G:149:VAL:HG12	1:G:153:LEU:HD13	1.69	0.74
1:P:30:TYR:CE2	1:P:68:GLN:HG2	2.23	0.74
1:Q:57:ASP:HA	1:Q:97:LYS:HD3	1.69	0.74
1:E:30:TYR:CE2	1:E:68:GLN:HG2	2.21	0.74
1:Q:34:TYR:CD1	1:Q:130:ASP:HA	2.22	0.74
1:J:124:ARG:HB2	1:J:141:ASN:HB2	1.69	0.74
1:R:5:PRO:HA	1:R:135:LEU:HD23	1.69	0.74
1:H:22:PHE:CE1	1:H:77:GLN:HB2	2.22	0.74
1:J:80:HIS:CD2	1:J:102:ALA:HB2	2.22	0.74
2:D:17:VAL:HB	2:D:100:LEU:HB2	1.68	0.74
1:O:88:ARG:HH12	1:O:94:GLY:HA3	1.53	0.74
1:A:14:GLY:O	1:A:24:GLU:HG3	1.88	0.74
2:D:15:GLN:HA	2:D:15:GLN:NE2	1.99	0.74
1:K:7:ARG:HH11	1:K:7:ARG:HG3	1.51	0.74
1:T:124:ARG:CB	1:T:147:ARG:HH12	2.01	0.73
1:H:131:PRO:HG3	1:Q:163:GLU:HG3	1.70	0.73
1:I:35:VAL:HG22	1:I:68:GLN:HB3	1.69	0.73
1:A:109:SER:HB3	1:A:115:PHE:HB2	1.70	0.73
1:N:26:CYS:O	1:N:29:ASP:HB2	1.89	0.73
1:T:28:LYS:HA	1:T:31:ARG:HE	1.53	0.73
1:E:103:ASP:HB2	1:E:108:ILE:HD12	1.70	0.73
1:H:84:ASP:OD2	1:H:95:HIS:HA	1.88	0.73
1:O:130:ASP:OD2	1:O:134:ILE:HB	1.89	0.73
1:S:74:THR:HA	1:S:103:ASP:O	1.87	0.73
1:N:115:PHE:HA	1:N:122:ALA:HA	1.71	0.73
1:B:124:ARG:HE	1:B:143:LYS:HA	1.54	0.73
1:C:124:ARG:HH11	1:C:147:ARG:NH2	1.86	0.73
1:E:56:SER:O	1:E:59:VAL:HG23	1.88	0.73
1:H:36:VAL:HG13	1:H:126:LEU:HD21	1.71	0.73
1:K:0:THR:HG22	1:K:1:MET:H	1.54	0.73
1:B:83:TRP:CD1	1:B:92:GLY:HA2	2.24	0.73
1:K:105:LYS:HD3	1:T:118:GLU:O	1.89	0.73
1:O:13:LYS:HG2	1:O:25:ILE:O	1.89	0.73
1:B:32:GLY:CA	1:B:131:PRO:HB3	2.19	0.73
1:I:154:ARG:HH22	1:J:147:ARG:HA	1.53	0.73
1:I:126:LEU:HD12	1:I:147:ARG:HD2	1.71	0.72
1:T:30:TYR:O	1:T:31:ARG:HD2	1.89	0.72
1:F:50:THR:HA	1:F:54:ALA:HB2	1.69	0.72
1:N:7:ARG:H	1:N:7:ARG:HD2	1.54	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:88:ARG:NH1	1:O:94:GLY:HA3	2.04	0.72
1:Q:112:TYR:HB3	1:Q:127:PHE:CZ	2.23	0.72
1:F:129:ILE:HG22	1:F:133:GLY:HA2	1.69	0.72
1:O:22:PHE:CE2	1:O:77:GLN:HB3	2.23	0.72
1:G:130:ASP:OD2	1:G:134:ILE:HB	1.90	0.72
1:L:128:ILE:HB	1:L:136:ARG:HB2	1.71	0.72
1:S:116:ASP:HB2	1:S:123:PHE:CE1	2.25	0.72
1:F:62:PHE:HB3	1:F:67:CYS:O	1.89	0.72
1:N:7:ARG:H	1:N:7:ARG:CD	2.03	0.72
1:Q:116:ASP:HB2	1:Q:123:PHE:CE2	2.25	0.72
1:M:59:VAL:HG21	1:M:97:LYS:HB3	1.71	0.72
1:O:151:GLU:HG3	1:O:155:LEU:HD11	1.71	0.72
1:Q:13:LYS:HG3	1:Q:26:CYS:SG	2.29	0.72
1:Q:55:PHE:CZ	1:Q:149:VAL:HA	2.24	0.72
1:A:15:GLN:HG2	1:A:77:GLN:OE1	1.89	0.72
1:L:126:LEU:HB3	1:L:139:THR:HB	1.70	0.72
1:A:148:SER:HB2	1:B:154:ARG:CZ	2.20	0.72
1:G:39:PHE:CD2	1:G:114:VAL:HG21	2.25	0.72
1:C:98:ILE:HG13	1:C:99:PRO:HD2	1.72	0.72
1:O:5:PRO:HB3	1:O:136:ARG:O	1.90	0.72
1:O:158:ALA:O	1:O:162:VAL:HG23	1.90	0.72
1:O:162:VAL:O	1:O:166:GLY:HA2	1.90	0.72
1:S:51:GLU:OE1	1:S:51:GLU:CA	2.30	0.72
1:C:82:ALA:HA	1:C:85:ASN:HD22	1.53	0.71
1:Q:142:ASP:CG	1:Q:144:PRO:HD2	2.15	0.71
2:D:23:LYS:HE3	1:O:23:LYS:HB2	1.72	0.71
1:I:161:PHE:CE2	1:I:166:GLY:HA2	2.25	0.71
1:R:126:LEU:HB3	1:R:139:THR:HB	1.70	0.71
1:T:69:VAL:O	1:T:99:PRO:HD2	1.90	0.71
1:T:162:VAL:HA	1:T:166:GLY:H	1.54	0.71
1:H:16:ALA:HB2	1:H:101:LEU:HD12	1.71	0.71
1:F:4:LEU:O	1:F:135:LEU:HD23	1.91	0.71
1:R:4:LEU:HB2	1:R:7:ARG:HD3	1.72	0.71
1:T:124:ARG:HB3	1:T:147:ARG:NH1	2.06	0.71
1:F:106:GLN:HB3	1:F:110:LYS:HE3	1.72	0.71
1:I:75:ASP:HB2	1:I:80:HIS:CE1	2.25	0.71
1:Q:75:ASP:HB3	1:Q:79:SER:CB	2.21	0.71
1:T:32:GLY:CA	1:T:131:PRO:HB3	2.20	0.71
1:F:87:ASP:OD1	1:F:90:SER:HB3	1.91	0.71
1:R:36:VAL:HG22	1:R:128:ILE:HG12	1.70	0.71
1:T:41:PRO:HD3	1:T:124:ARG:HG2	1.73	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:GLN:HG3	1:A:155:LEU:HD13	1.72	0.71
1:K:15:GLN:HG2	1:K:77:GLN:NE2	2.05	0.71
1:R:73:SER:HB3	1:R:80:HIS:NE2	2.05	0.71
1:S:136:ARG:HB3	1:S:159:PHE:CE1	2.26	0.71
1:C:123:PHE:CD2	2:D:4:LEU:HD12	2.26	0.71
2:D:126:LEU:HD23	2:D:127:PHE:N	2.06	0.70
1:G:109:SER:HB3	1:G:115:PHE:HB2	1.72	0.70
1:L:59:VAL:HG21	1:L:97:LYS:HG2	1.71	0.70
1:E:67:CYS:HB2	1:E:156:LEU:HD21	1.73	0.70
1:E:162:VAL:HG12	1:E:167:GLU:HA	1.72	0.70
1:H:3:LEU:O	1:H:4:LEU:HD23	1.91	0.70
1:L:38:PHE:HB2	1:L:147:ARG:HH22	1.56	0.70
1:C:34:TYR:CE1	1:C:131:PRO:HD3	2.26	0.70
1:E:96:MET:HG3	1:E:100:LEU:HD21	1.73	0.70
1:Q:124:ARG:HB3	1:Q:147:ARG:HD3	1.73	0.70
1:B:75:ASP:HA	1:B:104:ARG:NH1	2.07	0.70
1:I:96:MET:HE2	1:I:96:MET:HA	1.73	0.70
2:D:117:GLU:O	1:E:105:LYS:HE3	1.90	0.70
1:E:123:PHE:CE2	1:F:5:PRO:HD2	2.27	0.70
1:M:144:PRO:HB2	1:N:162:VAL:HG21	1.73	0.70
1:T:130:ASP:OD1	1:T:131:PRO:HD2	1.91	0.70
1:J:40:TYR:CE2	1:J:73:SER:HB2	2.26	0.70
1:Q:148:SER:OG	1:Q:151:GLU:HB3	1.91	0.70
1:F:36:VAL:HG13	1:F:126:LEU:HD21	1.74	0.70
1:N:147:ARG:HE	1:N:147:ARG:N	1.88	0.70
1:T:39:PHE:HB2	1:T:125:GLY:H	1.56	0.70
1:C:127:PHE:CE2	1:C:138:ILE:HG23	2.27	0.69
1:E:80:HIS:CD2	1:E:102:ALA:HB2	2.27	0.69
1:F:51:GLU:HG2	1:F:147:ARG:HB2	1.73	0.69
1:L:48:CYS:HB2	1:L:49:PRO:HD3	1.74	0.69
1:N:75:ASP:HB2	1:N:80:HIS:NE2	2.07	0.69
1:O:86:LEU:HD12	1:O:87:ASP:H	1.57	0.69
1:I:10:PRO:HG2	1:I:112:TYR:CE2	2.27	0.69
1:R:50:THR:OG1	1:R:53:ILE:HB	1.93	0.69
1:P:135:LEU:HD12	1:P:136:ARG:H	1.55	0.69
1:C:12:PHE:CE1	1:C:27:LEU:HB2	2.27	0.69
1:S:103:ASP:HB2	1:S:108:ILE:HD12	1.75	0.69
1:F:80:HIS:HE1	1:F:102:ALA:HB2	1.55	0.69
1:P:50:THR:HA	1:P:53:ILE:HD12	1.75	0.69
1:C:149:VAL:HB	1:C:153:LEU:HD13	1.74	0.69
2:D:23:LYS:HG2	1:O:23:LYS:HD3	1.74	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:53:ILE:HD13	1:E:88:ARG:HD2	1.75	0.69
1:P:109:SER:CB	1:P:115:PHE:HB2	2.23	0.69
1:G:128:ILE:HD12	1:G:137:GLN:HB3	1.75	0.68
1:J:15:GLN:HE22	1:J:24:GLU:HB2	1.58	0.68
1:L:71:ALA:HB3	1:L:100:LEU:HD23	1.75	0.68
1:L:126:LEU:HB2	1:L:147:ARG:HH11	1.58	0.68
1:C:126:LEU:HB3	1:C:139:THR:HB	1.75	0.68
1:G:138:ILE:HB	1:H:140:ILE:HG22	1.74	0.68
1:S:52:ILE:N	1:S:52:ILE:CD1	2.49	0.68
1:C:15:GLN:NE2	1:C:24:GLU:HB2	2.08	0.68
1:M:148:SER:HB2	1:N:154:ARG:NE	2.08	0.68
1:T:72:CYS:HB2	1:T:101:LEU:HB3	1.75	0.68
1:G:47:VAL:C	1:G:49:PRO:HD2	2.18	0.68
1:G:149:VAL:HG12	1:G:153:LEU:CD1	2.24	0.68
1:H:105:LYS:O	1:H:106:GLN:HB2	1.93	0.68
1:I:34:TYR:CE1	1:I:131:PRO:HD3	2.29	0.68
1:H:169:CYS:HB3	1:H:170:PRO:HD2	1.74	0.68
1:J:12:PHE:CE2	1:J:27:LEU:HD13	2.28	0.68
1:R:40:TYR:CZ	1:R:73:SER:HB2	2.29	0.68
1:M:143:LYS:N	1:M:144:PRO:HD2	2.08	0.68
1:R:48:CYS:CB	1:R:51:GLU:H	2.05	0.68
1:G:159:PHE:HE1	1:H:142:ASP:HB2	1.60	0.67
1:J:60:GLU:OE1	1:J:60:GLU:HA	1.94	0.67
1:T:75:ASP:HB2	1:T:80:HIS:HE1	1.59	0.67
1:A:17:VAL:O	1:A:99:PRO:HA	1.93	0.67
1:E:3:LEU:HD12	1:E:4:LEU:H	1.59	0.67
1:E:123:PHE:CD2	1:F:5:PRO:HD2	2.29	0.67
1:O:22:PHE:HE2	1:O:77:GLN:HB3	1.57	0.67
1:Q:32:GLY:C	1:Q:131:PRO:HB3	2.19	0.67
1:I:55:PHE:CE1	1:I:149:VAL:HG22	2.28	0.67
1:I:145:VAL:HG21	1:J:159:PHE:CE1	2.29	0.67
1:H:53:ILE:HG23	1:H:96:MET:HE1	1.77	0.67
1:H:93:LEU:HD13	1:H:96:MET:HG3	1.75	0.67
1:I:135:LEU:HD11	1:I:137:GLN:O	1.93	0.67
1:S:5:PRO:HD3	1:S:138:ILE:CD1	2.24	0.67
1:C:93:LEU:HB3	1:C:96:MET:HE3	1.77	0.67
2:D:155:LEU:O	2:D:159:PHE:HD1	1.78	0.67
1:L:12:PHE:HB2	1:L:108:ILE:HG12	1.77	0.67
1:L:124:ARG:HB3	1:L:147:ARG:CZ	2.24	0.67
1:F:38:PHE:CE2	1:F:51:GLU:O	2.48	0.67
1:J:125:GLY:HA2	1:J:139:THR:O	1.95	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:155:LEU:O	1:M:159:PHE:HD2	1.78	0.67
1:O:80:HIS:ND1	1:O:100:LEU:HB3	2.08	0.67
1:A:39:PHE:O	1:A:124:ARG:HA	1.94	0.67
1:C:116:ASP:HB3	1:C:123:PHE:CE2	2.30	0.67
1:C:146:GLY:O	1:C:147:ARG:HG3	1.95	0.67
1:P:65:ARG:NH1	1:P:157:ASP:HB3	2.10	0.67
1:B:38:PHE:CZ	1:B:71:ALA:HB2	2.30	0.67
2:D:4:LEU:HB2	2:D:7:ARG:HD3	1.76	0.67
1:F:78:TYR:HB3	1:G:45:THR:HB	1.75	0.67
1:N:3:LEU:HB2	1:N:138:ILE:HD13	1.75	0.67
1:T:105:LYS:HB2	1:T:107:GLU:HG3	1.75	0.67
1:C:11:GLU:OE1	1:C:27:LEU:HB3	1.95	0.67
1:C:155:LEU:O	1:C:159:PHE:HD1	1.77	0.67
1:J:116:ASP:HB2	1:J:123:PHE:CE2	2.30	0.67
1:N:16:ALA:HA	1:N:100:LEU:O	1.95	0.67
2:D:33:LYS:O	2:D:131:PRO:HA	1.94	0.66
2:D:93:LEU:HD22	2:D:96:MET:CE	2.25	0.66
1:H:35:VAL:O	1:H:128:ILE:HA	1.96	0.66
1:T:129:ILE:HG12	1:T:135:LEU:HD13	1.77	0.66
1:L:32:GLY:HA2	1:L:131:PRO:HB3	1.77	0.66
1:M:162:VAL:HB	1:M:167:GLU:HB3	1.76	0.66
1:R:47:VAL:O	1:R:50:THR:HA	1.94	0.66
1:C:32:GLY:HA2	1:C:131:PRO:HB3	1.77	0.66
1:F:24:GLU:OE1	1:F:24:GLU:HA	1.93	0.66
1:K:15:GLN:HG2	1:K:77:GLN:HE21	1.59	0.66
1:P:11:GLU:OE1	1:P:27:LEU:HD23	1.95	0.66
1:F:52:ILE:HG22	1:F:53:ILE:N	2.09	0.66
1:H:86:LEU:HB3	1:H:92:GLY:HA3	1.76	0.66
1:I:9:ALA:HB2	1:I:135:LEU:HB2	1.76	0.66
1:B:13:LYS:HG3	1:B:25:ILE:O	1.96	0.66
1:B:70:ILE:HG23	1:B:99:PRO:HB2	1.78	0.66
1:B:42:ALA:O	1:B:45:THR:HG22	1.95	0.66
2:D:26:CYS:SG	2:D:28:LYS:HE3	2.35	0.66
1:G:48:CYS:O	1:G:50:THR:N	2.27	0.66
1:M:128:ILE:HB	1:M:137:GLN:HB3	1.78	0.66
1:B:88:ARG:HA	1:B:92:GLY:O	1.96	0.66
1:J:69:VAL:O	1:J:99:PRO:HD2	1.96	0.66
1:L:42:ALA:HB3	1:L:45:THR:HG23	1.78	0.66
1:N:76:SER:HB3	1:N:104:ARG:NE	2.10	0.66
1:S:145:VAL:HG21	1:T:159:PHE:CE1	2.31	0.66
2:D:127:PHE:HA	2:D:137:GLN:O	1.96	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:75:ASP:O	1:M:102:ALA:HB1	1.96	0.66
1:M:164:LYS:HG2	1:M:165:HIS:ND1	2.10	0.66
1:E:37:LEU:HD12	1:E:70:ILE:O	1.96	0.65
1:L:43:ASP:HA	1:L:83:TRP:CE3	2.31	0.65
1:S:75:ASP:HB2	1:S:80:HIS:CE1	2.32	0.65
1:B:33:LYS:HA	1:B:66:ASN:HD21	1.61	0.65
2:D:93:LEU:HD22	2:D:96:MET:HE3	1.78	0.65
1:M:4:LEU:HD21	1:N:114:VAL:HA	1.77	0.65
1:R:86:LEU:HG	1:R:87:ASP:H	1.60	0.65
1:B:17:VAL:HA	1:B:21:GLU:O	1.96	0.65
1:B:33:LYS:HA	1:B:66:ASN:ND2	2.11	0.65
1:H:93:LEU:HB3	1:H:96:MET:CG	2.22	0.65
1:K:103:ASP:OD2	1:K:108:ILE:HB	1.95	0.65
1:C:109:SER:HB3	1:C:115:PHE:HB2	1.78	0.65
2:D:76:SER:HB3	2:D:79:SER:OG	1.97	0.65
1:I:60:GLU:HA	1:I:63:ASN:HB2	1.77	0.65
1:A:5:PRO:O	1:A:6:ASN:HB3	1.96	0.65
1:A:105:LYS:HB3	1:A:107:GLU:OE2	1.96	0.65
1:B:12:PHE:HE1	1:B:27:LEU:HD13	1.61	0.65
1:B:61:GLU:O	1:B:65:ARG:HG3	1.97	0.65
1:C:11:GLU:OE2	1:C:27:LEU:HD23	1.96	0.65
1:L:37:LEU:HD12	1:L:38:PHE:N	2.12	0.65
1:O:148:SER:HB2	1:P:154:ARG:NE	2.12	0.65
1:M:59:VAL:HG21	1:M:97:LYS:CB	2.27	0.65
1:B:71:ALA:HB3	1:B:100:LEU:HD23	1.78	0.65
1:K:87:ASP:CG	1:K:90:SER:HB2	2.21	0.65
1:G:65:ARG:HD2	1:G:156:LEU:HD23	1.77	0.65
1:I:71:ALA:HB3	1:I:100:LEU:HD23	1.78	0.65
1:I:154:ARG:NH2	1:J:147:ARG:HA	2.11	0.65
1:T:86:LEU:HB3	1:T:92:GLY:HA3	1.78	0.65
1:B:74:THR:O	1:B:104:ARG:HD3	1.97	0.64
1:G:5:PRO:HG2	1:H:123:PHE:CD1	2.32	0.64
2:D:54:ALA:HA	2:D:57:ASP:OD2	1.97	0.64
1:E:43:ASP:HA	1:E:83:TRP:CZ3	2.31	0.64
1:I:144:PRO:HB3	1:J:167:GLU:HG3	1.79	0.64
1:N:31:ARG:HD3	1:N:131:PRO:O	1.96	0.64
1:E:129:ILE:HG23	1:E:134:ILE:O	1.97	0.64
1:F:136:ARG:HB3	1:F:159:PHE:CE2	2.32	0.64
1:O:41:PRO:CG	1:O:143:LYS:HG2	2.25	0.64
1:O:72:CYS:SG	1:O:101:LEU:HG	2.37	0.64
1:R:87:ASP:OD2	1:R:89:LYS:HB2	1.97	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:45:THR:O	1:T:49:PRO:HG3	1.97	0.64
1:H:96:MET:HE2	1:H:96:MET:HA	1.78	0.64
1:O:86:LEU:HG	1:O:92:GLY:N	2.12	0.64
1:P:65:ARG:HD2	1:P:160:GLN:HE22	1.62	0.64
1:S:52:ILE:HD13	1:S:52:ILE:H	1.61	0.64
1:S:164:LYS:HB3	1:S:165:HIS:CD2	2.32	0.64
1:O:159:PHE:CD2	1:P:145:VAL:HG21	2.33	0.64
1:Q:34:TYR:HD1	1:Q:130:ASP:HA	1.61	0.64
1:Q:55:PHE:CE2	1:Q:149:VAL:HA	2.32	0.64
1:S:12:PHE:HB2	1:S:108:ILE:HG12	1.79	0.64
1:H:126:LEU:HD23	1:H:127:PHE:N	2.12	0.64
1:L:163:GLU:O	1:L:163:GLU:HG2	1.97	0.64
1:P:65:ARG:HH21	1:P:153:LEU:HD23	1.62	0.64
1:S:55:PHE:HE2	1:S:149:VAL:HA	1.58	0.64
1:A:96:MET:HG2	1:A:100:LEU:HD21	1.80	0.64
1:H:168:VAL:HG12	1:H:169:CYS:N	2.12	0.64
1:S:5:PRO:HD3	1:S:138:ILE:HD12	1.80	0.64
1:S:75:ASP:HB2	1:S:80:HIS:HE1	1.63	0.64
1:H:137:GLN:NE2	1:H:155:LEU:HD13	2.12	0.64
1:I:34:TYR:CE1	1:I:160:GLN:HG2	2.32	0.64
1:J:25:ILE:HD12	1:J:70:ILE:HD13	1.80	0.64
1:K:28:LYS:HA	1:K:31:ARG:HB2	1.79	0.64
1:L:168:VAL:C	1:L:170:PRO:HD3	2.23	0.64
1:M:30:TYR:CE1	1:M:68:GLN:HG2	2.33	0.64
1:A:53:ILE:HG21	1:A:88:ARG:HH12	1.63	0.64
1:G:25:ILE:HD11	1:G:101:LEU:HD13	1.80	0.64
1:M:148:SER:HB2	1:N:154:ARG:CZ	2.28	0.64
1:A:127:PHE:CE1	1:A:138:ILE:HG23	2.33	0.64
1:E:8:PRO:HG3	1:E:134:ILE:CD1	2.28	0.64
1:G:16:ALA:HB2	1:G:101:LEU:HD12	1.79	0.64
1:H:34:TYR:HB2	1:H:67:CYS:HB2	1.80	0.64
1:I:167:GLU:OE1	1:I:167:GLU:HA	1.97	0.64
1:K:0:THR:HG22	1:L:2:VAL:HG12	1.79	0.64
1:M:80:HIS:CD2	1:M:102:ALA:HB2	2.33	0.64
1:N:104:ARG:HH22	1:O:75:ASP:HA	1.62	0.64
1:P:74:THR:HG21	1:P:120:GLY:O	1.98	0.64
1:P:119:ASP:HA	1:Q:105:LYS:HG2	1.79	0.64
1:B:60:GLU:HA	1:B:63:ASN:OD1	1.99	0.63
1:E:8:PRO:HG3	1:E:134:ILE:HD13	1.80	0.63
1:O:56:SER:CB	1:O:96:MET:HE1	2.27	0.63
1:P:44:PHE:CD1	1:P:83:TRP:HD1	2.16	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:155:LEU:HB3	1:B:159:PHE:CE2	2.30	0.63
1:E:25:ILE:HD12	1:E:70:ILE:HD13	1.80	0.63
1:L:137:GLN:HB2	1:L:159:PHE:HE2	1.63	0.63
1:T:33:LYS:HG2	1:T:66:ASN:OD1	1.98	0.63
1:K:65:ARG:HB3	1:K:160:GLN:HE22	1.64	0.63
1:S:32:GLY:O	1:S:131:PRO:HB3	1.99	0.63
1:I:58:GLN:HB3	1:I:61:GLU:OE1	1.97	0.63
1:K:112:TYR:HB2	1:K:114:VAL:HG22	1.80	0.63
1:G:151:GLU:HG2	1:H:151:GLU:HG2	1.80	0.63
1:G:61:GLU:HB3	1:G:153:LEU:HD21	1.81	0.63
1:G:159:PHE:HE1	1:H:142:ASP:CB	2.12	0.63
1:Q:55:PHE:HZ	1:Q:148:SER:O	1.81	0.63
1:A:34:TYR:CE1	1:A:130:ASP:HA	2.34	0.63
1:I:2:VAL:HG23	1:J:1:MET:H1	1.64	0.63
1:O:132:ASN:HB2	1:O:134:ILE:HG12	1.81	0.63
1:I:140:ILE:HG22	1:J:138:ILE:HB	1.79	0.63
1:N:72:CYS:SG	1:N:73:SER:N	2.72	0.63
1:P:143:LYS:N	1:P:144:PRO:HD2	2.13	0.63
1:Q:28:LYS:HA	1:Q:31:ARG:HH21	1.64	0.63
1:I:165:HIS:H	1:I:165:HIS:CD2	2.16	0.63
1:J:71:ALA:O	1:J:101:LEU:HB3	1.99	0.63
1:L:38:PHE:HB2	1:L:147:ARG:HH12	1.64	0.63
1:O:7:ARG:HB3	1:O:8:PRO:HD2	1.79	0.63
1:T:106:GLN:HB3	1:T:110:LYS:HG3	1.80	0.63
2:D:30:TYR:CE1	2:D:68:GLN:HG2	2.34	0.62
1:L:60:GLU:OE1	1:L:60:GLU:HA	1.99	0.62
1:Q:115:PHE:CZ	1:Q:120:GLY:HA2	2.34	0.62
1:R:65:ARG:HE	1:R:156:LEU:HD23	1.64	0.62
1:S:41:PRO:HD2	1:S:124:ARG:NH1	2.14	0.62
1:A:62:PHE:CE2	1:A:69:VAL:HG21	2.33	0.62
1:A:123:PHE:CE2	1:B:4:LEU:HD23	2.34	0.62
1:C:116:ASP:OD2	1:C:119:ASP:HB2	1.99	0.62
1:H:56:SER:O	1:H:59:VAL:HG23	1.98	0.62
1:A:34:TYR:CD1	1:A:130:ASP:HA	2.35	0.62
1:E:40:TYR:HB2	1:E:41:PRO:CD	2.26	0.62
1:H:70:ILE:HG12	1:H:99:PRO:HG2	1.80	0.62
1:O:51:GLU:O	1:O:55:PHE:HD1	1.82	0.62
1:C:34:TYR:HA	1:C:129:ILE:O	1.98	0.62
2:D:15:GLN:OE1	2:D:22:PHE:HB3	1.98	0.62
2:D:43:ASP:HA	2:D:83:TRP:CZ3	2.34	0.62
1:R:104:ARG:HG3	1:S:120:GLY:O	2.00	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:149:VAL:O	1:R:153:LEU:HD13	2.00	0.62
2:D:53:ILE:HA	2:D:96:MET:HE1	1.82	0.62
2:D:143:LYS:N	2:D:144:PRO:HD2	2.14	0.62
1:F:80:HIS:CE1	1:F:102:ALA:HB2	2.33	0.62
1:I:34:TYR:CZ	1:I:160:GLN:HG2	2.34	0.62
1:J:18:ILE:HD12	1:J:23:LYS:HB2	1.81	0.62
1:L:124:ARG:HB3	1:L:147:ARG:HH21	1.64	0.62
1:O:13:LYS:NZ	1:O:26:CYS:HB2	2.14	0.62
1:R:35:VAL:HB	1:R:129:ILE:HB	1.81	0.62
1:S:164:LYS:O	1:S:164:LYS:HD3	2.00	0.62
1:L:94:GLY:O	1:L:96:MET:HE3	1.99	0.62
1:M:7:ARG:HB3	1:M:8:PRO:HD2	1.82	0.62
1:M:12:PHE:HB2	1:M:108:ILE:HD13	1.80	0.62
1:M:136:ARG:HB3	1:M:159:PHE:CD1	2.34	0.62
1:N:74:THR:HG21	1:N:121:ASN:HA	1.81	0.62
1:A:124:ARG:HB3	1:A:147:ARG:HD3	1.80	0.62
1:C:34:TYR:CD1	1:C:130:ASP:HA	2.33	0.62
1:O:30:TYR:CD2	1:O:68:GLN:HG2	2.34	0.62
1:Q:156:LEU:O	1:Q:160:GLN:HG3	2.00	0.62
1:A:123:PHE:HE2	1:B:4:LEU:HD23	1.64	0.62
1:G:84:ASP:OD1	1:G:96:MET:HE3	2.00	0.62
1:J:112:TYR:HB3	1:J:127:PHE:CZ	2.35	0.62
1:L:43:ASP:HA	1:L:83:TRP:CZ3	2.35	0.62
1:P:32:GLY:C	1:P:131:PRO:HB3	2.25	0.62
1:R:41:PRO:HB2	1:R:46:PHE:CE2	2.35	0.62
1:S:107:GLU:HG2	1:S:108:ILE:N	2.15	0.62
1:B:40:TYR:HB2	1:B:41:PRO:HD2	1.82	0.62
2:D:15:GLN:HE21	2:D:15:GLN:CA	1.99	0.62
1:J:47:VAL:HG22	1:J:48:CYS:N	2.10	0.62
2:D:93:LEU:HB3	2:D:96:MET:HG2	1.82	0.62
1:N:148:SER:HB3	1:N:151:GLU:CB	2.30	0.62
1:Q:125:GLY:HA2	1:Q:140:ILE:HA	1.81	0.62
1:C:123:PHE:CD1	1:C:143:LYS:HG3	2.35	0.61
1:E:38:PHE:CZ	1:E:71:ALA:HB2	2.35	0.61
1:H:46:PHE:HZ	1:I:81:LEU:HD23	1.64	0.61
1:E:26:CYS:SG	1:E:28:LYS:HB2	2.40	0.61
1:J:26:CYS:HB3	1:J:29:ASP:CG	2.25	0.61
1:O:83:TRP:CE2	1:O:93:LEU:HD21	2.35	0.61
1:P:105:LYS:HB2	1:P:107:GLU:HG2	1.82	0.61
1:Q:140:ILE:O	1:R:137:GLN:HG3	1.99	0.61
1:F:26:CYS:O	1:F:27:LEU:HB3	1.98	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:17:VAL:HG22	1:G:21:GLU:O	2.00	0.61
1:B:12:PHE:CE1	1:B:27:LEU:HB2	2.35	0.61
1:E:88:ARG:HA	1:E:91:GLY:O	2.00	0.61
1:E:137:GLN:HB3	1:E:159:PHE:CZ	2.36	0.61
1:G:172:ASN:ND2	1:H:146:GLY:HA3	2.15	0.61
1:K:37:LEU:HD12	1:K:70:ILE:O	2.01	0.61
1:K:96:MET:HE2	1:K:96:MET:HA	1.81	0.61
1:N:56:SER:CB	1:N:96:MET:HG3	2.28	0.61
1:Q:86:LEU:HD11	1:Q:90:SER:HB3	1.82	0.61
1:T:86:LEU:C	1:T:92:GLY:HA3	2.25	0.61
1:B:130:ASP:OD2	1:B:134:ILE:HB	2.00	0.61
1:F:158:ALA:O	1:F:162:VAL:HG23	2.01	0.61
1:P:44:PHE:CE1	1:P:83:TRP:HD1	2.18	0.61
1:T:84:ASP:HA	1:T:93:LEU:HD12	1.82	0.61
1:A:74:THR:HG22	1:A:106:GLN:HG2	1.82	0.61
1:E:67:CYS:CB	1:E:156:LEU:HD21	2.31	0.61
1:F:106:GLN:O	1:F:110:LYS:HG3	2.01	0.61
1:J:124:ARG:CB	1:J:141:ASN:HB2	2.31	0.61
1:M:13:LYS:HG3	1:M:24:GLU:OE2	2.01	0.61
1:R:109:SER:HB3	1:R:114:VAL:HG23	1.83	0.61
1:F:80:HIS:HE1	1:F:102:ALA:CB	2.14	0.61
1:L:40:TYR:HB2	1:L:41:PRO:CD	2.28	0.61
1:R:30:TYR:CE1	1:R:68:GLN:HG2	2.36	0.61
1:T:35:VAL:HG22	1:T:68:GLN:HB3	1.81	0.61
1:H:124:ARG:HB3	1:H:147:ARG:CZ	2.31	0.61
1:Q:40:TYR:HB2	1:Q:41:PRO:HD2	1.82	0.61
1:S:47:VAL:CG2	1:S:51:GLU:CG	2.74	0.61
1:C:4:LEU:HB3	2:D:123:PHE:CD2	2.35	0.61
2:D:65:ARG:HB3	2:D:160:GLN:OE1	2.01	0.61
1:E:136:ARG:HD3	1:E:159:PHE:HD2	1.65	0.61
1:F:110:LYS:HE2	1:F:115:PHE:CE2	2.36	0.61
1:I:16:ALA:O	1:I:22:PHE:HA	2.01	0.61
1:K:105:LYS:O	1:K:106:GLN:HG3	2.01	0.61
1:P:21:GLU:HB2	1:P:23:LYS:HE3	1.82	0.61
1:L:39:PHE:CD2	1:L:72:CYS:HB3	2.36	0.61
1:M:126:LEU:HB3	1:M:139:THR:HB	1.82	0.61
1:Q:129:ILE:HG22	1:Q:130:ASP:O	2.01	0.61
1:C:143:LYS:N	1:C:144:PRO:HD2	2.15	0.60
1:A:130:ASP:OD2	1:A:136:ARG:NH1	2.33	0.60
1:J:87:ASP:O	1:J:88:ARG:HB2	2.00	0.60
1:L:38:PHE:HD2	1:L:147:ARG:NH2	2.00	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:93:LEU:HD13	1:G:96:MET:HE1	1.82	0.60
1:H:129:ILE:HG23	1:H:134:ILE:O	2.01	0.60
1:I:13:LYS:HA	1:I:25:ILE:O	2.02	0.60
1:I:15:GLN:O	1:I:101:LEU:HD12	2.02	0.60
1:J:128:ILE:O	1:J:135:LEU:HD12	2.02	0.60
1:O:12:PHE:CE2	1:O:27:LEU:HD22	2.37	0.60
2:D:65:ARG:NH1	2:D:153:LEU:HD11	2.15	0.60
1:F:130:ASP:HB2	1:F:131:PRO:HD2	1.83	0.60
1:S:130:ASP:HB2	1:S:131:PRO:HD2	1.83	0.60
1:C:149:VAL:HA	1:C:152:THR:OG1	2.01	0.60
2:D:104:ARG:HG3	1:E:120:GLY:H	1.67	0.60
1:F:105:LYS:N	1:F:105:LYS:HD2	2.17	0.60
1:G:84:ASP:O	1:G:94:GLY:O	2.18	0.60
1:L:41:PRO:HG2	1:L:45:THR:HG21	1.82	0.60
1:O:77:GLN:O	1:O:80:HIS:HB2	2.02	0.60
1:T:124:ARG:HB3	1:T:147:ARG:HH22	1.65	0.60
1:T:109:SER:HB2	1:T:115:PHE:HB2	1.84	0.60
1:B:128:ILE:HB	1:B:137:GLN:HB3	1.84	0.60
1:O:84:ASP:HA	1:O:93:LEU:CB	2.30	0.60
1:S:167:GLU:CD	1:S:167:GLU:H	2.10	0.60
1:T:9:ALA:CB	1:T:129:ILE:HD13	2.32	0.60
1:M:159:PHE:O	1:M:162:VAL:HG22	2.02	0.59
1:B:6:ASN:N	1:B:135:LEU:O	2.34	0.59
2:D:135:LEU:HD12	2:D:136:ARG:N	2.15	0.59
1:L:15:GLN:HG2	1:L:24:GLU:OE2	2.02	0.59
1:C:149:VAL:HB	1:C:153:LEU:CD1	2.32	0.59
1:E:83:TRP:HD1	1:E:92:GLY:HA2	1.67	0.59
1:O:128:ILE:HD12	1:O:137:GLN:HB3	1.84	0.59
1:H:124:ARG:HH11	1:H:147:ARG:NH2	1.98	0.59
1:S:164:LYS:HB3	1:S:165:HIS:HD2	1.67	0.59
1:T:60:GLU:CA	1:T:63:ASN:HB2	2.17	0.59
1:T:86:LEU:HB3	1:T:92:GLY:CA	2.31	0.59
1:B:38:PHE:HA	1:B:125:GLY:O	2.02	0.59
1:H:37:LEU:HD11	1:H:72:CYS:HB2	1.84	0.59
1:O:151:GLU:HG3	1:O:155:LEU:CD1	2.32	0.59
1:Q:105:LYS:O	1:Q:106:GLN:HB2	2.01	0.59
1:A:114:VAL:HB	1:A:123:PHE:HB2	1.85	0.59
1:H:127:PHE:CE2	1:H:138:ILE:HG23	2.38	0.59
1:L:65:ARG:NE	1:L:153:LEU:HD11	2.18	0.59
1:R:45:THR:HG21	1:S:78:TYR:CD1	2.37	0.59
1:A:132:ASN:HD22	1:A:132:ASN:N	1.98	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:83:TRP:CD2	1:N:93:LEU:HG	2.37	0.59
1:Q:116:ASP:HB2	1:Q:123:PHE:CZ	2.38	0.59
1:R:76:SER:HB3	1:R:79:SER:HB2	1.84	0.59
1:B:32:GLY:HA2	1:B:131:PRO:HB3	1.82	0.59
1:E:22:PHE:C	1:E:23:LYS:HD2	2.28	0.59
1:E:159:PHE:CD2	1:F:145:VAL:HG21	2.38	0.59
1:L:168:VAL:O	1:L:170:PRO:HD3	2.02	0.59
1:N:12:PHE:CE2	1:N:27:LEU:HD13	2.37	0.59
1:O:128:ILE:O	1:O:135:LEU:HD12	2.02	0.59
1:P:135:LEU:HD21	1:P:138:ILE:HD11	1.84	0.59
1:S:119:ASP:OD2	1:S:121:ASN:HB2	2.03	0.59
1:S:134:ILE:HG22	1:S:136:ARG:HD2	1.84	0.59
1:C:161:PHE:CD1	1:C:165:HIS:HE1	2.21	0.59
1:G:47:VAL:O	1:G:49:PRO:HD2	2.03	0.59
1:H:16:ALA:HB2	1:H:101:LEU:CD1	2.31	0.59
1:I:2:VAL:CA	1:J:1:MET:HA	2.26	0.59
1:M:36:VAL:HA	1:M:127:PHE:O	2.03	0.59
1:M:155:LEU:O	1:M:159:PHE:CD2	2.55	0.59
1:B:36:VAL:HB	1:B:69:VAL:HG22	1.85	0.58
2:D:116:ASP:OD2	2:D:119:ASP:HB2	2.03	0.58
1:M:96:MET:HA	1:M:96:MET:HE2	1.83	0.58
1:R:137:GLN:HE22	1:R:155:LEU:HD22	1.67	0.58
1:A:125:GLY:HA2	1:A:139:THR:O	2.03	0.58
1:B:132:ASN:H	1:B:132:ASN:HD22	1.51	0.58
1:A:53:ILE:HD13	1:A:88:ARG:NH1	2.19	0.58
1:B:126:LEU:HB3	1:B:139:THR:HB	1.84	0.58
1:C:53:ILE:HA	1:C:56:SER:HB3	1.85	0.58
1:F:34:TYR:CD1	1:F:130:ASP:HA	2.38	0.58
1:G:16:ALA:HB2	1:G:101:LEU:CD1	2.34	0.58
1:J:34:TYR:CE2	1:J:160:GLN:HG3	2.38	0.58
1:K:105:LYS:C	1:K:106:GLN:HG3	2.28	0.58
1:L:69:VAL:O	1:L:98:ILE:HB	2.02	0.58
1:M:148:SER:H	1:N:154:ARG:NH2	2.01	0.58
1:T:76:SER:HB3	1:T:104:ARG:NH1	2.18	0.58
1:B:41:PRO:O	1:B:121:ASN:HB3	2.03	0.58
1:J:83:TRP:HD1	1:J:92:GLY:HA2	1.65	0.58
1:J:164:LYS:HE3	1:J:165:HIS:NE2	2.19	0.58
1:M:96:MET:HG3	1:M:100:LEU:HD11	1.85	0.58
1:A:150:ASP:HA	1:A:153:LEU:CD1	2.34	0.58
1:B:12:PHE:CE1	1:B:27:LEU:HD13	2.38	0.58
1:B:30:TYR:HE1	1:B:68:GLN:OE1	1.86	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:45:THR:HA	1:C:78:TYR:CD2	2.38	0.58
1:F:87:ASP:OD2	1:F:89:LYS:HB2	2.03	0.58
1:G:65:ARG:NH2	1:G:153:LEU:HD23	2.13	0.58
1:G:130:ASP:HB2	1:G:131:PRO:HD2	1.84	0.58
1:J:5:PRO:O	1:J:7:ARG:HD3	2.03	0.58
1:K:124:ARG:HB3	1:K:147:ARG:NH1	2.19	0.58
1:C:53:ILE:HG22	1:C:57:ASP:OD2	2.04	0.58
2:D:4:LEU:HB2	2:D:7:ARG:CD	2.32	0.58
1:E:11:GLU:OE2	1:E:28:LYS:HE3	2.03	0.58
1:F:23:LYS:NZ	1:Q:23:LYS:HG2	2.19	0.58
1:I:109:SER:HB3	1:I:115:PHE:HB2	1.85	0.58
1:L:128:ILE:HD12	1:L:159:PHE:CD2	2.38	0.58
1:O:18:ILE:HD12	1:O:23:LYS:HE3	1.86	0.58
2:D:13:LYS:HD2	2:D:25:ILE:O	2.04	0.58
1:I:47:VAL:HG21	1:J:167:GLU:HG2	1.84	0.58
1:I:106:GLN:O	1:I:110:LYS:HG3	2.04	0.58
1:K:75:ASP:HB2	1:K:80:HIS:HE2	1.68	0.58
1:M:48:CYS:HG	1:N:161:PHE:HE2	1.51	0.58
1:P:62:PHE:CD2	1:P:69:VAL:HG21	2.37	0.58
1:S:62:PHE:O	1:S:67:CYS:HB3	2.03	0.58
1:A:4:LEU:O	1:A:135:LEU:HD23	2.04	0.58
1:F:105:LYS:HB3	1:F:107:GLU:HG3	1.86	0.58
1:M:112:TYR:HB2	1:M:114:VAL:HG22	1.86	0.58
1:O:115:PHE:HA	1:O:122:ALA:HA	1.86	0.58
1:Q:39:PHE:N	1:Q:39:PHE:CD1	2.72	0.58
1:C:123:PHE:CE2	2:D:4:LEU:HD12	2.39	0.58
1:C:124:ARG:HB3	1:C:147:ARG:CZ	2.34	0.58
1:E:31:ARG:CZ	1:E:133:GLY:HA3	2.34	0.58
1:F:59:VAL:HG11	1:F:97:LYS:HB3	1.85	0.58
1:K:22:PHE:HE2	1:K:77:GLN:HB2	1.69	0.58
1:L:7:ARG:HG3	1:L:8:PRO:HD2	1.85	0.58
1:S:153:LEU:HD12	1:S:153:LEU:H	1.69	0.58
1:J:10:PRO:HB2	1:J:112:TYR:CE1	2.38	0.58
1:L:58:GLN:O	1:L:62:PHE:HD1	1.86	0.58
1:M:36:VAL:HG23	1:M:67:CYS:SG	2.43	0.58
1:C:53:ILE:HG12	1:C:96:MET:HE1	1.86	0.57
1:H:124:ARG:NH1	1:H:147:ARG:HH21	1.99	0.57
1:O:109:SER:HB3	1:O:115:PHE:HB2	1.85	0.57
1:R:86:LEU:HD23	1:R:92:GLY:CA	2.34	0.57
1:T:28:LYS:HD2	1:T:31:ARG:HH21	1.69	0.57
1:A:34:TYR:HB2	1:A:67:CYS:CB	2.32	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:15:GLN:HE21	1:K:22:PHE:HB3	1.68	0.57
1:Q:56:SER:HA	1:Q:98:ILE:HG23	1.84	0.57
1:J:22:PHE:N	1:J:22:PHE:CD1	2.73	0.57
1:J:164:LYS:HG2	1:J:165:HIS:HD2	1.69	0.57
1:L:88:ARG:HA	1:L:92:GLY:O	2.04	0.57
1:P:11:GLU:OE1	1:P:11:GLU:HA	2.04	0.57
1:R:26:CYS:O	1:R:29:ASP:HB2	2.04	0.57
2:D:86:LEU:CG	2:D:92:GLY:HA3	2.32	0.57
1:G:61:GLU:O	1:G:65:ARG:HG3	2.04	0.57
1:P:36:VAL:HA	1:P:127:PHE:O	2.04	0.57
1:Q:14:GLY:HA3	1:Q:101:LEU:HD11	1.86	0.57
1:A:145:VAL:HG21	1:B:159:PHE:CE1	2.39	0.57
1:E:28:LYS:HA	1:E:31:ARG:HG2	1.84	0.57
1:J:42:ALA:HB3	1:J:45:THR:HG21	1.86	0.57
1:S:5:PRO:O	1:T:123:PHE:CZ	2.58	0.57
1:E:38:PHE:HB2	1:E:147:ARG:HH12	1.68	0.57
1:F:75:ASP:OD1	1:G:76:SER:HB3	2.04	0.57
1:K:65:ARG:CZ	1:K:153:LEU:HD11	2.34	0.57
1:N:34:TYR:CD1	1:N:130:ASP:HA	2.40	0.57
1:P:34:TYR:CD1	1:P:130:ASP:HA	2.39	0.57
1:Q:54:ALA:HB1	1:Q:58:GLN:OE1	2.05	0.57
1:Q:75:ASP:HB3	1:Q:79:SER:HB3	1.84	0.57
1:E:42:ALA:O	1:E:45:THR:HG22	2.04	0.57
1:F:34:TYR:CE2	1:F:160:GLN:HG2	2.39	0.57
1:T:3:LEU:O	1:T:4:LEU:HD12	2.04	0.57
1:C:101:LEU:HD12	1:C:102:ALA:H	1.70	0.57
1:H:105:LYS:HB2	1:H:107:GLU:HG2	1.87	0.57
1:J:117:GLU:HA	1:J:117:GLU:OE1	2.04	0.57
1:M:75:ASP:HB2	1:M:80:HIS:NE2	2.20	0.57
1:C:124:ARG:HD2	1:C:145:VAL:O	2.04	0.57
2:D:18:ILE:HG12	2:D:99:PRO:HB3	1.86	0.57
1:K:47:VAL:HG23	1:K:49:PRO:O	2.05	0.57
1:Q:34:TYR:CD1	1:Q:131:PRO:HD3	2.39	0.57
1:R:104:ARG:HG2	1:S:121:ASN:ND2	2.20	0.57
1:S:56:SER:HA	1:S:59:VAL:HG23	1.86	0.57
1:G:144:PRO:HB2	1:H:162:VAL:HG11	1.87	0.57
1:H:105:LYS:HE2	1:H:107:GLU:OE1	2.05	0.57
1:M:116:ASP:HB2	1:M:123:PHE:CE2	2.40	0.57
1:O:128:ILE:HD12	1:O:137:GLN:CB	2.34	0.57
1:P:65:ARG:NH2	1:P:153:LEU:HD23	2.18	0.57
1:P:88:ARG:HG2	1:P:92:GLY:O	2.05	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:158:ALA:O	1:P:161:PHE:HB3	2.04	0.57
1:S:124:ARG:HB3	1:S:147:ARG:NH2	2.19	0.57
1:A:61:GLU:OE1	1:A:61:GLU:HA	2.05	0.56
1:C:86:LEU:HD23	1:C:92:GLY:CA	2.35	0.56
1:G:18:ILE:HG13	1:G:99:PRO:HA	1.86	0.56
1:I:7:ARG:O	1:I:134:ILE:HG23	2.05	0.56
1:N:75:ASP:HB2	1:N:80:HIS:HE2	1.69	0.56
1:R:4:LEU:HB2	1:R:7:ARG:CD	2.35	0.56
1:T:40:TYR:CZ	1:T:73:SER:HB2	2.40	0.56
2:D:104:ARG:NH1	1:E:74:THR:HG23	2.20	0.56
1:E:61:GLU:OE1	1:E:153:LEU:HD21	2.04	0.56
1:G:123:PHE:CD2	1:H:5:PRO:HD2	2.40	0.56
1:Q:56:SER:HA	1:Q:98:ILE:CG2	2.35	0.56
1:A:36:VAL:HB	1:A:69:VAL:HG13	1.87	0.56
1:B:31:ARG:HD2	1:B:131:PRO:O	2.06	0.56
1:C:88:ARG:HG2	1:C:92:GLY:O	2.06	0.56
1:H:37:LEU:HD13	1:H:70:ILE:HG22	1.88	0.56
1:I:66:ASN:CG	1:I:66:ASN:O	2.48	0.56
1:J:58:GLN:HA	1:J:58:GLN:NE2	2.12	0.56
1:J:101:LEU:HD12	1:J:102:ALA:H	1.70	0.56
1:M:42:ALA:HA	1:M:75:ASP:OD1	2.06	0.56
1:M:46:PHE:HA	1:M:50:THR:OG1	2.05	0.56
1:N:22:PHE:CE1	1:N:77:GLN:HG2	2.40	0.56
1:O:35:VAL:HG22	1:O:68:GLN:HB3	1.86	0.56
1:A:127:PHE:HE1	1:A:138:ILE:HG23	1.69	0.56
1:E:105:LYS:HE2	1:E:107:GLU:OE1	2.05	0.56
1:K:7:ARG:HG3	1:K:7:ARG:NH1	2.20	0.56
1:N:135:LEU:HD21	1:N:138:ILE:HD11	1.87	0.56
1:O:126:LEU:HD12	1:O:147:ARG:HD2	1.87	0.56
2:D:46:PHE:CD1	2:D:46:PHE:N	2.62	0.56
1:E:158:ALA:O	1:E:162:VAL:HG22	2.05	0.56
1:I:34:TYR:CD1	1:I:131:PRO:HD3	2.41	0.56
1:L:128:ILE:CG1	1:L:137:GLN:HB3	2.28	0.56
1:M:86:LEU:HG	1:M:92:GLY:HA3	1.86	0.56
1:S:80:HIS:HD2	1:S:100:LEU:HB2	1.71	0.56
1:S:137:GLN:HG2	1:S:155:LEU:HD13	1.87	0.56
1:T:25:ILE:HD12	1:T:30:TYR:CE1	2.40	0.56
1:B:159:PHE:HA	1:B:162:VAL:HG22	1.86	0.56
2:D:108:ILE:H	2:D:108:ILE:HD12	1.70	0.56
1:E:96:MET:HA	1:E:96:MET:CE	2.35	0.56
1:N:148:SER:HB3	1:N:151:GLU:HB3	1.87	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:GLY:HA3	1:A:101:LEU:HD11	1.87	0.56
1:C:41:PRO:O	1:C:74:THR:HG22	2.06	0.56
1:J:88:ARG:HA	1:J:92:GLY:N	2.20	0.56
1:K:106:GLN:NE2	1:K:115:PHE:CE2	2.74	0.56
1:K:128:ILE:HB	1:K:137:GLN:HB3	1.88	0.56
1:N:60:GLU:HA	1:N:63:ASN:OD1	2.05	0.56
1:P:30:TYR:HE2	1:P:68:GLN:HG2	1.67	0.56
1:S:1:MET:HG2	1:T:1:MET:O	2.06	0.56
1:J:126:LEU:HD12	1:J:147:ARG:NH1	2.20	0.56
1:M:128:ILE:HD12	1:M:159:PHE:CE2	2.41	0.56
1:R:143:LYS:HB2	1:R:144:PRO:HD3	1.86	0.56
1:F:157:ASP:O	1:F:161:PHE:HB2	2.06	0.56
1:J:48:CYS:CB	1:J:49:PRO:HD2	2.35	0.56
1:L:38:PHE:HB2	1:L:147:ARG:NH2	2.20	0.56
1:N:58:GLN:OE1	1:N:149:VAL:HG11	2.06	0.56
1:P:30:TYR:CD2	1:P:68:GLN:HG2	2.41	0.56
1:P:88:ARG:HG2	1:P:93:LEU:HA	1.86	0.56
1:S:105:LYS:O	1:S:106:GLN:HB2	2.04	0.56
1:T:81:LEU:HD12	1:T:85:ASN:HD21	1.69	0.56
1:A:83:TRP:O	1:A:83:TRP:CD1	2.59	0.56
2:D:86:LEU:HG	2:D:92:GLY:CA	2.35	0.56
1:H:105:LYS:HE3	1:I:118:GLU:O	2.06	0.56
1:N:26:CYS:SG	1:N:28:LYS:HB2	2.46	0.56
1:P:88:ARG:HA	1:P:92:GLY:O	2.06	0.56
1:S:38:PHE:N	1:S:38:PHE:CD1	2.74	0.56
1:A:136:ARG:HA	1:A:136:ARG:HE	1.71	0.55
1:T:56:SER:HB3	1:T:96:MET:HE1	1.88	0.55
1:A:116:ASP:HB3	1:A:119:ASP:HB2	1.88	0.55
1:A:132:ASN:H	1:A:132:ASN:ND2	1.97	0.55
1:B:45:THR:HG23	1:B:46:PHE:CE1	2.42	0.55
2:D:65:ARG:CD	2:D:156:LEU:HD23	2.35	0.55
1:G:47:VAL:HB	1:G:49:PRO:HD3	1.87	0.55
1:H:12:PHE:CE2	1:H:27:LEU:HD13	2.41	0.55
1:I:12:PHE:HB2	1:I:108:ILE:HG12	1.88	0.55
1:M:4:LEU:HD13	1:N:123:PHE:CE2	2.41	0.55
1:M:86:LEU:HD12	1:M:87:ASP:H	1.71	0.55
1:O:123:PHE:CE2	1:P:4:LEU:HB3	2.41	0.55
1:P:65:ARG:CZ	1:P:157:ASP:HB3	2.36	0.55
1:P:65:ARG:HD3	1:P:157:ASP:HA	1.87	0.55
1:R:71:ALA:HB3	1:R:100:LEU:HA	1.87	0.55
1:T:76:SER:OG	1:T:79:SER:HB2	2.06	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:35:VAL:HG13	1:I:68:GLN:O	2.05	0.55
1:L:72:CYS:HB2	1:L:101:LEU:HB3	1.88	0.55
1:O:137:GLN:HE22	1:P:139:THR:HG22	1.71	0.55
1:Q:72:CYS:HA	1:Q:101:LEU:O	2.06	0.55
1:S:126:LEU:HD12	1:S:147:ARG:HG2	1.87	0.55
1:A:28:LYS:CE	1:A:31:ARG:HE	2.14	0.55
1:L:40:TYR:CZ	1:L:73:SER:HB2	2.41	0.55
1:R:-2:GLY:O	1:R:-1:SER:HB3	2.05	0.55
1:G:43:ASP:HB3	1:G:44:PHE:CD2	2.42	0.55
1:R:150:ASP:HA	1:R:153:LEU:HD22	1.87	0.55
2:D:36:VAL:HG23	2:D:67:CYS:SG	2.47	0.55
1:J:70:ILE:HG12	1:J:99:PRO:HB2	1.87	0.55
1:J:78:TYR:CD1	1:J:78:TYR:N	2.74	0.55
1:J:141:ASN:ND2	1:J:147:ARG:HG3	2.22	0.55
1:M:39:PHE:HE2	1:M:72:CYS:HG	1.53	0.55
1:M:40:TYR:O	1:M:122:ALA:HB3	2.07	0.55
1:G:18:ILE:HD12	1:G:18:ILE:N	2.22	0.55
1:G:38:PHE:O	1:G:38:PHE:CD1	2.60	0.55
1:G:65:ARG:CD	1:G:156:LEU:HD23	2.37	0.55
1:N:34:TYR:CE1	1:N:130:ASP:HA	2.42	0.55
1:P:37:LEU:HB3	1:P:127:PHE:HB2	1.88	0.55
1:S:15:GLN:HG2	1:S:24:GLU:CG	2.12	0.55
1:H:89:LYS:O	1:H:89:LYS:HD3	2.06	0.55
1:M:84:ASP:OD1	1:M:96:MET:HG2	2.06	0.55
1:M:136:ARG:HB3	1:M:159:PHE:CE1	2.42	0.55
1:Q:115:PHE:HE1	1:Q:117:GLU:HA	1.71	0.55
1:G:69:VAL:O	1:G:99:PRO:HD2	2.06	0.55
1:I:59:VAL:HG23	1:I:60:GLU:H	1.71	0.55
1:P:13:LYS:HG2	1:P:26:CYS:HB3	1.89	0.55
1:P:136:ARG:HB3	1:P:159:PHE:CE2	2.42	0.55
1:Q:16:ALA:O	1:Q:22:PHE:HA	2.07	0.55
1:R:84:ASP:O	1:R:94:GLY:O	2.25	0.55
1:T:54:ALA:O	1:T:57:ASP:HB2	2.07	0.55
1:C:103:ASP:HA	1:C:108:ILE:HD12	1.89	0.55
2:D:14:GLY:HA3	2:D:101:LEU:CD1	2.34	0.55
1:J:43:ASP:HA	1:J:83:TRP:CZ3	2.42	0.55
1:L:53:ILE:HD13	1:L:88:ARG:HG2	1.89	0.55
1:M:12:PHE:CZ	1:M:27:LEU:HD13	2.42	0.55
1:N:55:PHE:HZ	1:N:147:ARG:O	1.90	0.55
1:P:34:TYR:CE2	1:P:160:GLN:HG2	2.43	0.55
1:Q:142:ASP:OD2	1:Q:144:PRO:HD2	2.07	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:128:ILE:HG22	1:E:136:ARG:HB2	1.90	0.54
1:F:105:LYS:HD2	1:F:105:LYS:H	1.73	0.54
1:J:88:ARG:HG2	1:J:92:GLY:O	2.07	0.54
1:K:88:ARG:HA	1:K:92:GLY:O	2.07	0.54
1:M:130:ASP:OD2	1:M:132:ASN:HB2	2.07	0.54
1:A:83:TRP:O	1:A:83:TRP:HD1	1.89	0.54
1:C:13:LYS:NZ	1:C:24:GLU:HG2	2.21	0.54
1:F:164:LYS:HD3	1:F:165:HIS:CE1	2.42	0.54
1:H:151:GLU:OE2	1:H:155:LEU:HG	2.07	0.54
1:L:24:GLU:OE1	1:L:24:GLU:HA	2.07	0.54
1:Q:88:ARG:HA	1:Q:92:GLY:O	2.07	0.54
1:Q:157:ASP:O	1:Q:160:GLN:HB2	2.07	0.54
1:A:109:SER:OG	1:A:122:ALA:HB2	2.07	0.54
1:A:135:LEU:HD12	1:A:136:ARG:N	2.22	0.54
1:C:80:HIS:CD2	1:C:100:LEU:HB3	2.41	0.54
1:E:22:PHE:O	1:E:23:LYS:HD2	2.08	0.54
1:E:76:SER:CA	1:E:102:ALA:HB1	2.34	0.54
1:A:15:GLN:HG2	1:A:77:GLN:CD	2.32	0.54
1:C:86:LEU:HD11	1:C:90:SER:CB	2.37	0.54
2:D:105:LYS:H	2:D:105:LYS:HD3	1.72	0.54
1:L:34:TYR:HA	1:L:129:ILE:O	2.06	0.54
1:O:86:LEU:O	1:O:92:GLY:HA3	2.08	0.54
1:Q:80:HIS:HD2	1:Q:100:LEU:HB3	1.72	0.54
1:B:26:CYS:HB3	1:B:29:ASP:OD1	2.07	0.54
1:B:74:THR:HG22	1:B:106:GLN:HG2	1.88	0.54
2:D:105:LYS:O	2:D:106:GLN:HB2	2.07	0.54
1:F:80:HIS:CE1	1:F:102:ALA:CB	2.90	0.54
1:I:55:PHE:HE2	1:I:147:ARG:HE	1.56	0.54
1:N:32:GLY:C	1:N:131:PRO:HB3	2.33	0.54
1:B:95:HIS:O	1:B:96:MET:HE2	2.07	0.54
1:E:167:GLU:OE1	1:E:168:VAL:N	2.40	0.54
1:F:43:ASP:O	1:F:44:PHE:HB2	2.07	0.54
1:G:143:LYS:N	1:G:144:PRO:HD2	2.23	0.54
1:H:10:PRO:O	1:H:27:LEU:HD22	2.08	0.54
1:S:159:PHE:O	1:S:162:VAL:HG12	2.08	0.54
2:D:86:LEU:O	2:D:94:GLY:N	2.35	0.54
1:E:159:PHE:CE2	1:F:145:VAL:HG21	2.43	0.54
1:F:130:ASP:HB2	1:F:131:PRO:CD	2.38	0.54
1:H:22:PHE:HE1	1:H:77:GLN:HB2	1.70	0.54
1:H:160:GLN:O	1:H:163:GLU:HG2	2.08	0.54
1:K:119:ASP:HB3	1:K:121:ASN:ND2	2.22	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:104:ARG:HB3	1:M:120:GLY:HA3	1.88	0.54
1:C:34:TYR:HD1	1:C:130:ASP:HA	1.73	0.54
2:D:75:ASP:HB2	2:D:80:HIS:CE1	2.43	0.54
1:G:76:SER:O	1:G:79:SER:HB3	2.08	0.54
1:Q:18:ILE:HB	1:Q:23:LYS:HD3	1.89	0.54
1:S:74:THR:OG1	1:S:106:GLN:HG2	2.07	0.54
1:J:164:LYS:HG2	1:J:165:HIS:CD2	2.42	0.54
1:O:4:LEU:HD12	1:O:4:LEU:N	2.22	0.54
1:O:17:VAL:O	1:O:99:PRO:HA	2.08	0.54
1:P:107:GLU:HG3	1:P:108:ILE:HG13	1.90	0.54
1:Q:2:VAL:O	1:Q:4:LEU:HD23	2.07	0.54
1:Q:73:SER:OG	1:Q:80:HIS:HE1	1.91	0.54
1:A:69:VAL:O	1:A:98:ILE:HD13	2.07	0.54
1:A:157:ASP:HA	1:A:160:GLN:OE1	2.07	0.54
1:B:77:GLN:H	1:B:77:GLN:CD	2.15	0.54
1:F:127:PHE:HE1	1:F:138:ILE:HG23	1.72	0.54
1:R:28:LYS:O	1:R:31:ARG:HG2	2.08	0.54
1:R:103:ASP:HB2	1:R:108:ILE:HD12	1.89	0.54
1:B:15:GLN:O	1:B:101:LEU:HD12	2.08	0.53
1:J:164:LYS:HD2	1:S:164:LYS:HG3	1.90	0.53
1:M:18:ILE:O	1:M:19:ASN:HB3	2.06	0.53
1:R:83:TRP:CE3	1:R:93:LEU:HD11	2.43	0.53
1:C:137:GLN:HG2	2:D:141:ASN:OD1	2.08	0.53
1:J:36:VAL:HG12	1:J:69:VAL:HG13	1.91	0.53
1:J:106:GLN:HA	1:J:109:SER:OG	2.07	0.53
1:K:40:TYR:HB2	1:K:41:PRO:CD	2.38	0.53
1:K:72:CYS:HA	1:K:101:LEU:O	2.08	0.53
1:L:96:MET:HE2	1:L:96:MET:HA	1.90	0.53
1:P:38:PHE:HA	1:P:125:GLY:O	2.08	0.53
1:R:6:ASN:HB3	1:R:7:ARG:HD2	1.89	0.53
1:R:115:PHE:HA	1:R:122:ALA:HA	1.89	0.53
1:J:112:TYR:HD2	1:J:127:PHE:CD2	2.26	0.53
1:L:142:ASP:CG	1:L:144:PRO:HD2	2.32	0.53
1:Q:38:PHE:HB3	1:Q:126:LEU:HD12	1.90	0.53
1:T:16:ALA:HB3	1:T:23:LYS:O	2.09	0.53
1:A:98:ILE:HG23	1:A:99:PRO:HD2	1.90	0.53
1:F:105:LYS:O	1:F:106:GLN:HB2	2.08	0.53
1:I:59:VAL:HG11	1:I:97:LYS:HB3	1.91	0.53
1:J:48:CYS:CB	1:J:49:PRO:CD	2.86	0.53
1:P:17:VAL:HB	1:P:100:LEU:HB2	1.89	0.53
1:P:128:ILE:HG21	1:P:159:PHE:CD2	2.43	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:51:GLU:C	1:Q:52:ILE:HG13	2.33	0.53
1:B:26:CYS:O	1:B:29:ASP:HB2	2.09	0.53
2:D:39:PHE:O	2:D:124:ARG:HG3	2.08	0.53
2:D:130:ASP:HB3	2:D:136:ARG:HD3	1.89	0.53
1:E:145:VAL:HG21	1:F:159:PHE:CZ	2.44	0.53
1:G:71:ALA:HB3	1:G:100:LEU:HD23	1.89	0.53
1:H:4:LEU:HD12	1:H:7:ARG:CZ	2.38	0.53
1:H:53:ILE:HA	1:H:96:MET:SD	2.49	0.53
1:K:51:GLU:O	1:K:54:ALA:HB3	2.09	0.53
1:K:104:ARG:HH22	1:T:75:ASP:CG	2.16	0.53
1:M:18:ILE:HG12	1:M:99:PRO:HA	1.91	0.53
1:O:17:VAL:HB	1:O:100:LEU:HB2	1.90	0.53
1:Q:45:THR:O	1:Q:46:PHE:C	2.51	0.53
1:R:86:LEU:HD23	1:R:92:GLY:N	2.23	0.53
1:S:168:VAL:HG12	1:S:168:VAL:O	2.08	0.53
1:T:75:ASP:HB2	1:T:80:HIS:CE1	2.41	0.53
1:C:141:ASN:HD22	1:C:145:VAL:HG12	1.72	0.53
1:C:142:ASP:C	1:C:144:PRO:HD2	2.33	0.53
1:F:139:THR:HG22	1:F:141:ASN:HD21	1.73	0.53
1:G:44:PHE:H	1:G:83:TRP:NE1	2.06	0.53
1:O:141:ASN:ND2	1:O:147:ARG:HG3	2.23	0.53
1:S:72:CYS:HA	1:S:101:LEU:O	2.09	0.53
1:A:59:VAL:O	1:A:62:PHE:HB2	2.09	0.53
1:L:59:VAL:HG21	1:L:97:LYS:CG	2.39	0.53
1:L:126:LEU:HD23	1:L:126:LEU:C	2.34	0.53
1:P:42:ALA:O	1:P:45:THR:HG23	2.08	0.53
1:R:13:LYS:HG3	1:R:24:GLU:OE2	2.09	0.53
1:A:75:ASP:CB	1:A:80:HIS:HE1	2.19	0.53
1:G:54:ALA:O	1:G:58:GLN:HG3	2.08	0.53
1:I:51:GLU:OE2	1:I:146:GLY:HA2	2.09	0.53
1:R:71:ALA:O	1:R:101:LEU:HB3	2.09	0.53
1:T:2:VAL:HG12	1:T:4:LEU:HD13	1.91	0.53
1:A:103:ASP:HB2	1:A:108:ILE:HD12	1.90	0.53
1:E:53:ILE:O	1:E:56:SER:HB3	2.09	0.53
1:F:151:GLU:OE1	1:F:151:GLU:HA	2.09	0.53
1:G:108:ILE:O	1:G:112:TYR:HD1	1.91	0.53
1:J:125:GLY:CA	1:J:140:ILE:HA	2.31	0.53
1:R:59:VAL:HA	1:R:62:PHE:CD2	2.38	0.53
1:G:159:PHE:CE1	1:H:142:ASP:HB2	2.42	0.53
1:J:40:TYR:HE1	1:J:71:ALA:HB1	1.74	0.53
1:L:40:TYR:CE1	1:L:73:SER:HB2	2.44	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:116:ASP:HB2	1:P:7:ARG:HH12	1.74	0.53
1:P:124:ARG:HB3	1:P:147:ARG:NH1	2.24	0.53
1:R:4:LEU:HD12	1:R:7:ARG:NE	2.16	0.53
1:E:123:PHE:HE2	1:F:4:LEU:CD2	2.19	0.52
1:F:68:GLN:OE1	1:F:99:PRO:HD3	2.10	0.52
1:H:80:HIS:CE1	1:H:102:ALA:HB2	2.44	0.52
1:I:74:THR:HA	1:I:103:ASP:O	2.08	0.52
1:P:69:VAL:HG12	1:P:98:ILE:HD12	1.91	0.52
1:S:44:PHE:CD1	1:S:83:TRP:CD1	2.96	0.52
1:B:40:TYR:HB2	1:B:46:PHE:HZ	1.75	0.52
1:F:161:PHE:CE1	1:F:165:HIS:HB2	2.44	0.52
1:G:123:PHE:CE2	1:H:5:PRO:HD2	2.45	0.52
1:L:130:ASP:OD2	1:L:134:ILE:HB	2.09	0.52
1:O:60:GLU:OE1	1:O:60:GLU:HA	2.09	0.52
1:Q:34:TYR:OH	1:Q:160:GLN:HG2	2.09	0.52
1:S:41:PRO:HD2	1:S:124:ARG:HH11	1.73	0.52
1:S:125:GLY:O	1:S:147:ARG:NH1	2.42	0.52
1:T:31:ARG:HH12	1:T:133:GLY:CA	2.22	0.52
1:E:116:ASP:O	1:E:119:ASP:O	2.26	0.52
1:F:34:TYR:CZ	1:F:131:PRO:HD3	2.45	0.52
1:F:80:HIS:CD2	1:F:80:HIS:N	2.76	0.52
1:G:151:GLU:OE1	1:H:151:GLU:HB2	2.10	0.52
1:J:126:LEU:N	1:J:139:THR:O	2.37	0.52
1:L:115:PHE:CZ	1:L:120:GLY:HA2	2.44	0.52
1:P:68:GLN:OE1	1:P:68:GLN:HA	2.10	0.52
1:R:55:PHE:CD1	1:R:149:VAL:HG22	2.44	0.52
1:S:86:LEU:C	1:S:92:GLY:HA3	2.34	0.52
2:D:101:LEU:HD12	2:D:102:ALA:N	2.24	0.52
2:D:161:PHE:O	2:D:165:HIS:HB2	2.10	0.52
1:G:87:ASP:OD1	1:G:90:SER:HB2	2.09	0.52
1:H:15:GLN:O	1:H:101:LEU:HD12	2.09	0.52
1:O:40:TYR:HB2	1:O:41:PRO:HD2	1.91	0.52
1:R:3:LEU:CD2	1:R:10:PRO:HG2	2.40	0.52
1:C:43:ASP:O	1:C:44:PHE:HB2	2.09	0.52
1:C:103:ASP:OD2	1:C:109:SER:HB2	2.10	0.52
1:G:6:ASN:O	1:G:7:ARG:HD2	2.10	0.52
1:M:4:LEU:HB3	1:M:5:PRO:HD2	1.91	0.52
1:M:9:ALA:HB2	1:M:135:LEU:HB2	1.91	0.52
1:O:155:LEU:O	1:O:158:ALA:HB3	2.10	0.52
1:P:105:LYS:HD3	1:P:107:GLU:CD	2.35	0.52
1:B:149:VAL:O	1:B:153:LEU:HD13	2.10	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:93:LEU:O	1:H:96:MET:HE3	2.09	0.52
1:K:55:PHE:HE2	1:K:152:THR:OG1	1.93	0.52
1:L:86:LEU:HD23	1:L:92:GLY:N	2.24	0.52
1:L:105:LYS:C	1:L:107:GLU:H	2.17	0.52
1:B:80:HIS:CE1	1:B:101:LEU:O	2.62	0.52
1:C:87:ASP:OD2	1:C:89:LYS:HB2	2.10	0.52
1:K:154:ARG:NH2	1:L:148:SER:HB2	2.24	0.52
1:L:58:GLN:OE1	1:L:58:GLN:HA	2.10	0.52
1:M:108:ILE:O	1:M:111:ALA:HB3	2.10	0.52
1:N:38:PHE:CE1	1:N:71:ALA:HB2	2.44	0.52
1:R:48:CYS:HB3	1:R:50:THR:HA	1.92	0.52
1:B:39:PHE:HE1	1:B:127:PHE:CE2	2.27	0.52
1:C:155:LEU:O	1:C:159:PHE:CD1	2.61	0.52
2:D:43:ASP:HB3	2:D:83:TRP:CE3	2.45	0.52
1:E:83:TRP:CD1	1:E:92:GLY:HA2	2.44	0.52
1:K:68:GLN:HA	1:K:68:GLN:NE2	2.24	0.52
1:O:76:SER:O	1:O:80:HIS:HD2	1.92	0.52
1:Q:75:ASP:HB3	1:Q:79:SER:HB2	1.91	0.52
1:S:3:LEU:O	1:S:138:ILE:HD13	2.09	0.52
1:T:137:GLN:HB2	1:T:159:PHE:CE2	2.45	0.52
1:I:55:PHE:HE1	1:I:149:VAL:HG22	1.71	0.52
1:I:143:LYS:HB2	1:I:144:PRO:HD3	1.90	0.52
1:J:55:PHE:HD1	1:J:62:PHE:HZ	1.58	0.52
1:N:5:PRO:HG3	1:N:138:ILE:HD12	1.91	0.52
1:N:39:PHE:CE2	1:N:72:CYS:HB3	2.45	0.52
1:O:167:GLU:OE1	1:P:47:VAL:HG23	2.10	0.52
1:T:33:LYS:HA	1:T:66:ASN:ND2	2.25	0.52
1:T:84:ASP:HA	1:T:93:LEU:HB2	1.91	0.52
1:T:126:LEU:HD22	1:T:147:ARG:HD2	1.92	0.52
1:A:135:LEU:HD12	1:A:136:ARG:H	1.74	0.52
2:D:10:PRO:HD2	2:D:112:TYR:CZ	2.45	0.52
1:E:171:VAL:HG12	1:E:172:ASN:H	1.74	0.52
1:G:72:CYS:HA	1:G:101:LEU:O	2.10	0.52
1:L:72:CYS:CB	1:L:101:LEU:HB3	2.40	0.52
1:T:136:ARG:HD2	1:T:159:PHE:CG	2.44	0.52
1:B:38:PHE:HB2	1:B:147:ARG:HH22	1.76	0.51
1:B:155:LEU:O	1:B:159:PHE:CD2	2.63	0.51
1:F:86:LEU:HG	1:F:92:GLY:HA3	1.91	0.51
1:G:16:ALA:HB2	1:G:101:LEU:HA	1.92	0.51
1:G:69:VAL:HG11	1:G:98:ILE:HD13	1.92	0.51
1:K:124:ARG:HH11	1:K:147:ARG:HH22	1.58	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:48:CYS:N	1:M:49:PRO:CD	2.73	0.51
1:M:151:GLU:O	1:M:154:ARG:HB3	2.10	0.51
1:O:18:ILE:HD12	1:O:23:LYS:CE	2.40	0.51
1:T:2:VAL:CG1	1:T:4:LEU:HD13	2.41	0.51
1:T:69:VAL:HG11	1:T:98:ILE:HD13	1.91	0.51
1:A:119:ASP:HB3	1:A:143:LYS:HZ1	1.75	0.51
1:F:18:ILE:HG13	1:F:23:LYS:CB	2.40	0.51
1:I:134:ILE:CG2	1:I:136:ARG:HH12	2.23	0.51
1:J:130:ASP:HB2	1:J:131:PRO:HD2	1.90	0.51
1:J:151:GLU:O	1:J:155:LEU:HG	2.10	0.51
1:M:18:ILE:HD11	1:M:99:PRO:HB3	1.91	0.51
1:Q:39:PHE:O	1:Q:147:ARG:NH1	2.44	0.51
1:S:32:GLY:C	1:S:131:PRO:HB3	2.34	0.51
1:B:158:ALA:O	1:B:162:VAL:HG13	2.10	0.51
1:C:124:ARG:HH11	1:C:147:ARG:HH21	1.53	0.51
1:J:6:ASN:C	1:J:7:ARG:HD2	2.35	0.51
1:M:141:ASN:HD22	1:M:145:VAL:HG12	1.74	0.51
1:M:168:VAL:C	1:N:47:VAL:HG11	2.35	0.51
1:R:38:PHE:HE2	1:R:69:VAL:HG12	1.75	0.51
1:R:68:GLN:NE2	1:R:68:GLN:HA	2.25	0.51
1:B:45:THR:HG23	1:B:46:PHE:CD1	2.45	0.51
1:E:123:PHE:HZ	1:F:6:ASN:HB2	1.74	0.51
1:E:171:VAL:HG12	1:E:172:ASN:N	2.26	0.51
1:G:49:PRO:HB3	1:G:52:ILE:HB	1.93	0.51
1:K:142:ASP:OD1	1:K:143:LYS:N	2.44	0.51
1:Q:50:THR:HG23	1:Q:51:GLU:N	2.25	0.51
1:S:9:ALA:HB2	1:S:135:LEU:HB2	1.91	0.51
1:S:25:ILE:HD11	1:S:101:LEU:HD13	1.92	0.51
1:T:136:ARG:HD2	1:T:159:PHE:CD1	2.45	0.51
1:A:119:ASP:HB3	1:A:143:LYS:NZ	2.25	0.51
1:B:103:ASP:HB2	1:B:108:ILE:HD12	1.93	0.51
1:B:128:ILE:HD11	1:B:152:THR:HG23	1.92	0.51
1:B:143:LYS:HD3	1:B:143:LYS:H	1.76	0.51
1:C:130:ASP:HB2	1:C:131:PRO:HD2	1.91	0.51
2:D:71:ALA:HB3	2:D:100:LEU:HD23	1.93	0.51
1:G:158:ALA:O	1:G:162:VAL:HG23	2.10	0.51
1:S:12:PHE:O	1:S:12:PHE:CD1	2.63	0.51
1:T:84:ASP:CA	1:T:93:LEU:HD12	2.41	0.51
1:T:151:GLU:O	1:T:155:LEU:HG	2.11	0.51
1:A:83:TRP:NE1	1:A:93:LEU:HG	2.26	0.51
1:A:142:ASP:HB2	1:A:145:VAL:HG23	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:47:VAL:HG12	2:D:48:CYS:N	2.17	0.51
1:E:32:GLY:HA2	1:E:131:PRO:HB3	1.92	0.51
1:J:132:ASN:HB2	1:J:134:ILE:HG12	1.92	0.51
1:K:26:CYS:O	1:K:29:ASP:HB2	2.10	0.51
1:L:65:ARG:CG	1:L:160:GLN:HE22	2.14	0.51
1:T:30:TYR:C	1:T:31:ARG:HD2	2.35	0.51
1:A:130:ASP:HB2	1:A:131:PRO:HD2	1.93	0.51
1:B:39:PHE:CE1	1:B:127:PHE:HE2	2.28	0.51
1:I:134:ILE:HG21	1:I:136:ARG:HH12	1.76	0.51
1:M:151:GLU:HG2	1:N:151:GLU:OE1	2.10	0.51
1:P:75:ASP:HB2	1:P:80:HIS:CE1	2.46	0.51
1:Q:124:ARG:HB2	1:Q:141:ASN:O	2.10	0.51
1:R:83:TRP:CD1	1:R:92:GLY:HA2	2.46	0.51
1:T:40:TYR:CZ	1:T:73:SER:CB	2.94	0.51
1:A:55:PHE:CD1	1:A:149:VAL:HG22	2.46	0.51
1:B:17:VAL:HB	1:B:100:LEU:HB2	1.93	0.51
1:C:53:ILE:HG12	1:C:96:MET:CE	2.41	0.51
1:C:123:PHE:HD1	1:C:143:LYS:HG3	1.76	0.51
2:D:124:ARG:HG2	2:D:147:ARG:NH1	2.18	0.51
1:E:96:MET:O	1:E:97:LYS:HB2	2.10	0.51
1:F:110:LYS:HG2	1:F:115:PHE:CG	2.46	0.51
1:G:47:VAL:C	1:G:49:PRO:CD	2.84	0.51
1:I:56:SER:HA	1:I:98:ILE:HG23	1.93	0.51
1:J:150:ASP:HA	1:J:153:LEU:CD2	2.37	0.51
1:K:151:GLU:OE1	1:K:151:GLU:HA	2.11	0.51
1:L:56:SER:O	1:L:59:VAL:HG22	2.11	0.51
1:O:55:PHE:HB3	1:O:98:ILE:CD1	2.40	0.51
1:P:160:GLN:HA	1:P:163:GLU:HB3	1.91	0.51
1:B:143:LYS:HD3	1:B:143:LYS:N	2.26	0.51
1:L:6:ASN:HA	1:L:135:LEU:O	2.11	0.51
1:N:124:ARG:HB3	1:N:147:ARG:NH1	2.25	0.51
1:O:4:LEU:HD23	1:P:123:PHE:CE1	2.46	0.51
1:P:158:ALA:HA	1:P:161:PHE:HB3	1.92	0.51
1:R:116:ASP:OD2	1:R:119:ASP:HB2	2.11	0.51
1:B:75:ASP:HB3	1:B:79:SER:HB3	1.92	0.51
1:B:83:TRP:HD1	1:B:92:GLY:HA2	1.72	0.51
1:C:14:GLY:C	1:C:24:GLU:HG3	2.36	0.51
1:E:53:ILE:CD1	1:E:88:ARG:HD2	2.41	0.51
1:K:72:CYS:SG	1:K:101:LEU:HG	2.51	0.51
1:M:126:LEU:HD11	1:M:152:THR:OG1	2.11	0.51
1:R:34:TYR:HB2	1:R:67:CYS:HA	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:86:LEU:HD23	1:C:92:GLY:HA2	1.93	0.50
1:H:168:VAL:CG1	1:H:169:CYS:H	2.22	0.50
1:L:73:SER:HB3	1:L:80:HIS:CE1	2.46	0.50
1:L:116:ASP:N	1:L:121:ASN:O	2.44	0.50
1:Q:112:TYR:HB2	1:Q:114:VAL:HG22	1.93	0.50
1:T:43:ASP:HA	1:T:83:TRP:CZ3	2.46	0.50
1:G:105:LYS:O	1:G:106:GLN:HB2	2.11	0.50
1:H:23:LYS:HG3	1:S:23:LYS:HG3	1.93	0.50
1:N:15:GLN:HG2	1:N:77:GLN:OE1	2.11	0.50
1:N:76:SER:O	1:N:80:HIS:HD2	1.95	0.50
1:R:38:PHE:O	1:R:72:CYS:HB3	2.11	0.50
1:S:167:GLU:CD	1:S:167:GLU:N	2.69	0.50
1:T:11:GLU:OE1	1:T:11:GLU:HA	2.10	0.50
1:T:42:ALA:HB3	1:T:45:THR:CG2	2.41	0.50
1:A:13:LYS:NZ	1:A:26:CYS:HB2	2.26	0.50
2:D:39:PHE:HE1	2:D:127:PHE:CE1	2.30	0.50
1:F:51:GLU:HB3	1:F:147:ARG:HH21	1.75	0.50
1:L:104:ARG:O	1:M:120:GLY:HA3	2.12	0.50
1:Q:68:GLN:OE1	1:Q:68:GLN:HA	2.10	0.50
1:Q:76:SER:H	1:Q:104:ARG:HH11	1.59	0.50
1:R:109:SER:O	1:R:114:VAL:HG22	2.11	0.50
1:T:124:ARG:HB3	1:T:147:ARG:NH2	2.26	0.50
2:D:128:ILE:HG22	2:D:136:ARG:HB2	1.93	0.50
1:G:45:THR:HG23	1:G:47:VAL:HG22	1.93	0.50
1:G:125:GLY:C	1:G:147:ARG:HH12	2.19	0.50
1:I:36:VAL:HG22	1:I:128:ILE:HG23	1.93	0.50
1:L:39:PHE:HB2	1:L:123:PHE:O	2.12	0.50
1:L:65:ARG:CD	1:L:153:LEU:HD11	2.41	0.50
1:L:143:LYS:HB2	1:L:144:PRO:HD3	1.94	0.50
1:M:18:ILE:HD12	1:M:23:LYS:HD3	1.94	0.50
1:M:18:ILE:HD12	1:M:23:LYS:CD	2.41	0.50
1:O:26:CYS:O	1:O:29:ASP:HB2	2.12	0.50
1:O:32:GLY:O	1:O:33:LYS:CG	2.60	0.50
1:O:162:VAL:O	1:O:166:GLY:CA	2.59	0.50
1:S:38:PHE:HB2	1:S:125:GLY:O	2.11	0.50
1:S:99:PRO:C	1:S:100:LEU:HD23	2.36	0.50
1:S:145:VAL:HG21	1:T:159:PHE:CD1	2.45	0.50
1:T:81:LEU:CD1	1:T:85:ASN:HD21	2.24	0.50
1:T:168:VAL:O	1:T:169:CYS:C	2.55	0.50
1:F:104:ARG:HH22	1:G:75:ASP:HA	1.76	0.50
1:F:109:SER:HB3	1:F:114:VAL:HG23	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:30:TYR:O	1:M:31:ARG:HD3	2.10	0.50
1:N:154:ARG:NH2	1:N:155:LEU:HD21	2.27	0.50
1:Q:38:PHE:HA	1:Q:126:LEU:HA	1.93	0.50
1:Q:50:THR:O	1:Q:53:ILE:HG13	2.12	0.50
1:R:38:PHE:HB2	1:R:125:GLY:O	2.11	0.50
1:S:42:ALA:HA	1:S:75:ASP:OD2	2.11	0.50
1:S:150:ASP:N	1:S:150:ASP:OD1	2.45	0.50
1:A:84:ASP:OD1	1:A:96:MET:HB2	2.11	0.50
1:B:105:LYS:HD2	1:C:118:GLU:O	2.11	0.50
2:D:55:PHE:HD2	2:D:62:PHE:CZ	2.29	0.50
2:D:110:LYS:C	2:D:113:GLY:H	2.20	0.50
1:E:8:PRO:HA	1:E:134:ILE:HA	1.94	0.50
1:G:171:VAL:HB	1:H:48:CYS:SG	2.51	0.50
1:J:83:TRP:CG	1:J:93:LEU:HG	2.47	0.50
1:M:35:VAL:HB	1:M:129:ILE:HB	1.94	0.50
1:S:151:GLU:HB2	1:T:151:GLU:CD	2.37	0.50
1:T:40:TYR:CD2	1:T:42:ALA:O	2.64	0.50
2:D:108:ILE:HD12	2:D:108:ILE:N	2.27	0.50
1:K:123:PHE:CZ	1:K:143:LYS:HE2	2.47	0.50
1:O:137:GLN:NE2	1:P:139:THR:HG22	2.26	0.50
1:O:141:ASN:HD22	1:O:147:ARG:HG3	1.77	0.50
1:Q:16:ALA:HB2	1:Q:101:LEU:HA	1.94	0.50
1:Q:124:ARG:HG2	1:Q:143:LYS:HA	1.93	0.50
1:R:4:LEU:CD1	1:R:7:ARG:HE	2.20	0.50
1:R:15:GLN:C	1:R:101:LEU:HD12	2.36	0.50
1:A:68:GLN:OE1	1:A:98:ILE:HG12	2.12	0.50
1:C:86:LEU:HD11	1:C:90:SER:HB2	1.93	0.50
1:C:97:LYS:HD3	1:C:97:LYS:N	2.26	0.50
2:D:37:LEU:HD13	2:D:70:ILE:HB	1.93	0.50
2:D:128:ILE:O	2:D:136:ARG:N	2.43	0.50
1:E:128:ILE:HB	1:E:137:GLN:HG3	1.93	0.50
1:E:151:GLU:CD	1:F:151:GLU:HG2	2.36	0.50
1:I:22:PHE:C	1:I:23:LYS:HD2	2.37	0.50
1:J:76:SER:HB3	1:J:104:ARG:HE	1.76	0.50
1:L:38:PHE:HB2	1:L:147:ARG:NH1	2.26	0.50
1:M:76:SER:O	1:M:80:HIS:HD2	1.95	0.50
1:N:34:TYR:HB3	1:N:67:CYS:SG	2.52	0.50
1:Q:153:LEU:H	1:Q:153:LEU:HD12	1.76	0.50
1:T:51:GLU:OE2	1:T:147:ARG:NE	2.45	0.50
2:D:126:LEU:HB3	2:D:139:THR:HG22	1.94	0.50
1:F:20:GLY:O	1:F:21:GLU:HG3	2.12	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:129:ILE:HA	1:G:134:ILE:O	2.12	0.50
1:H:7:ARG:CD	1:H:7:ARG:N	2.75	0.50
1:I:161:PHE:CD2	1:I:166:GLY:HA2	2.47	0.50
1:M:86:LEU:HD11	1:M:90:SER:HB2	1.93	0.50
1:Q:17:VAL:HG12	1:Q:21:GLU:N	2.27	0.50
1:C:117:GLU:OE1	1:C:117:GLU:HA	2.12	0.49
1:C:153:LEU:O	1:C:156:LEU:HB3	2.12	0.49
1:H:7:ARG:N	1:H:7:ARG:HD2	2.27	0.49
1:I:40:TYR:CE1	1:I:71:ALA:HB1	2.47	0.49
1:I:87:ASP:HB2	1:I:90:SER:OG	2.11	0.49
1:J:97:LYS:HE2	1:J:97:LYS:HA	1.94	0.49
1:P:40:TYR:CG	1:P:52:ILE:HD11	2.47	0.49
1:P:44:PHE:CD1	1:P:83:TRP:CD1	2.99	0.49
1:S:38:PHE:N	1:S:38:PHE:HD1	2.08	0.49
1:S:86:LEU:HB3	1:S:92:GLY:CA	2.42	0.49
1:T:106:GLN:HG2	1:T:115:PHE:CE1	2.47	0.49
1:A:37:LEU:HA	1:A:70:ILE:O	2.12	0.49
1:E:130:ASP:HB2	1:E:131:PRO:HD2	1.94	0.49
1:F:41:PRO:HA	1:F:122:ALA:HB3	1.93	0.49
1:G:37:LEU:HD11	1:G:72:CYS:HB3	1.94	0.49
1:G:83:TRP:CE3	1:G:93:LEU:HD11	2.46	0.49
1:H:116:ASP:N	1:H:121:ASN:O	2.35	0.49
1:L:128:ILE:HD12	1:L:159:PHE:HD2	1.77	0.49
1:M:6:ASN:HB2	1:N:123:PHE:HZ	1.76	0.49
1:S:105:LYS:HB2	1:S:107:GLU:OE1	2.12	0.49
2:D:75:ASP:HB2	2:D:80:HIS:HE1	1.76	0.49
1:G:124:ARG:HE	1:G:143:LYS:HA	1.77	0.49
1:J:78:TYR:H	1:J:78:TYR:HD1	1.57	0.49
1:K:46:PHE:HA	1:K:51:GLU:OE2	2.13	0.49
1:M:34:TYR:CE1	1:M:131:PRO:HD2	2.47	0.49
1:Q:141:ASN:HD22	1:Q:147:ARG:HG2	1.77	0.49
1:R:87:ASP:HB3	1:R:90:SER:HB2	1.94	0.49
1:A:55:PHE:CE1	1:A:149:VAL:HG22	2.47	0.49
1:C:10:PRO:HD2	1:C:112:TYR:CE1	2.48	0.49
1:C:161:PHE:CE1	1:C:165:HIS:HE1	2.29	0.49
1:C:168:VAL:O	1:C:170:PRO:HD3	2.13	0.49
1:F:26:CYS:SG	1:F:28:LYS:HB3	2.52	0.49
1:N:56:SER:HA	1:N:98:ILE:HG13	1.93	0.49
1:N:120:GLY:O	1:O:104:ARG:HG3	2.13	0.49
1:R:38:PHE:CE1	1:R:71:ALA:HA	2.48	0.49
1:C:27:LEU:HD11	1:C:129:ILE:HG21	1.93	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:155:LEU:O	2:D:159:PHE:CD1	2.64	0.49
1:E:3:LEU:HD12	1:E:4:LEU:N	2.28	0.49
1:E:38:PHE:HE2	1:E:52:ILE:HD12	1.78	0.49
1:F:51:GLU:OE1	1:F:146:GLY:HA2	2.11	0.49
1:G:103:ASP:O	1:G:106:GLN:N	2.44	0.49
1:I:12:PHE:HB2	1:I:108:ILE:CD1	2.43	0.49
1:N:148:SER:HB3	1:N:151:GLU:HB2	1.92	0.49
1:A:17:VAL:HA	1:A:21:GLU:O	2.13	0.49
1:G:40:TYR:CE2	1:G:83:TRP:CZ3	3.00	0.49
1:K:51:GLU:HG3	1:K:52:ILE:N	2.24	0.49
1:L:59:VAL:HG21	1:L:97:LYS:CB	2.43	0.49
1:O:136:ARG:HH21	1:O:159:PHE:HD2	1.60	0.49
1:P:22:PHE:C	1:P:23:LYS:HD2	2.38	0.49
1:S:40:TYR:CZ	1:S:73:SER:HB3	2.46	0.49
1:A:137:GLN:HG2	1:B:140:ILE:O	2.12	0.49
1:C:49:PRO:O	1:C:52:ILE:N	2.44	0.49
1:C:98:ILE:HG13	1:C:99:PRO:CD	2.41	0.49
2:D:105:LYS:HD3	2:D:105:LYS:N	2.28	0.49
1:E:86:LEU:HB2	1:E:92:GLY:HA3	1.95	0.49
1:K:51:GLU:OE1	1:K:124:ARG:NH1	2.45	0.49
1:M:143:LYS:HD3	1:M:143:LYS:H	1.77	0.49
1:R:5:PRO:CA	1:R:135:LEU:HD23	2.39	0.49
1:S:104:ARG:O	1:S:106:GLN:HG3	2.13	0.49
2:D:4:LEU:HB2	2:D:7:ARG:NE	2.27	0.49
1:E:36:VAL:HG23	1:E:67:CYS:SG	2.52	0.49
1:E:50:THR:O	1:E:54:ALA:HB2	2.13	0.49
1:H:158:ALA:O	1:H:162:VAL:HG13	2.13	0.49
1:J:124:ARG:HB2	1:J:141:ASN:O	2.13	0.49
1:J:127:PHE:CE2	1:J:138:ILE:HG23	2.48	0.49
1:K:53:ILE:HA	1:K:56:SER:CB	2.35	0.49
1:L:38:PHE:HA	1:L:125:GLY:O	2.12	0.49
1:L:127:PHE:CE1	1:L:138:ILE:HG23	2.48	0.49
1:M:12:PHE:HB3	1:M:108:ILE:HG23	1.94	0.49
1:Q:141:ASN:ND2	1:Q:147:ARG:HG2	2.27	0.49
1:S:5:PRO:HB3	1:S:136:ARG:O	2.12	0.49
1:S:58:GLN:OE1	1:S:58:GLN:HA	2.12	0.49
1:A:124:ARG:CB	1:A:147:ARG:HD3	2.42	0.49
1:B:72:CYS:SG	1:B:101:LEU:HB3	2.53	0.49
1:E:128:ILE:HD12	1:E:137:GLN:CG	2.43	0.49
1:F:130:ASP:OD2	1:F:132:ASN:HB2	2.13	0.49
1:I:8:PRO:CA	1:I:134:ILE:HD13	2.42	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:50:THR:O	1:J:54:ALA:HB2	2.13	0.49
1:M:10:PRO:HD2	1:M:112:TYR:CE2	2.48	0.49
1:M:143:LYS:HB2	1:M:143:LYS:HZ2	1.78	0.49
1:O:31:ARG:HG3	1:O:131:PRO:O	2.12	0.49
1:O:86:LEU:HG	1:O:92:GLY:CA	2.43	0.49
1:S:16:ALA:HB2	1:S:101:LEU:HA	1.94	0.49
1:C:72:CYS:HB2	1:C:101:LEU:HB3	1.94	0.49
1:F:110:LYS:HE2	1:F:115:PHE:CZ	2.48	0.49
1:I:93:LEU:O	1:I:96:MET:HE3	2.13	0.49
1:N:105:LYS:HB2	1:N:107:GLU:HG3	1.94	0.49
1:S:130:ASP:HB2	1:S:131:PRO:CD	2.43	0.49
1:C:77:GLN:O	1:C:80:HIS:HB2	2.13	0.48
1:C:143:LYS:HB2	1:C:143:LYS:NZ	2.28	0.48
2:D:32:GLY:C	2:D:131:PRO:HB3	2.38	0.48
2:D:65:ARG:HD2	2:D:156:LEU:HD23	1.95	0.48
1:F:168:VAL:O	1:F:169:CYS:HB2	2.13	0.48
1:G:49:PRO:CB	1:G:52:ILE:HB	2.43	0.48
1:J:40:TYR:CZ	1:J:73:SER:HB2	2.48	0.48
1:K:34:TYR:CE1	1:K:130:ASP:HA	2.48	0.48
1:K:44:PHE:HA	1:K:83:TRP:NE1	2.28	0.48
1:N:83:TRP:O	1:N:93:LEU:HB2	2.12	0.48
1:O:149:VAL:O	1:O:153:LEU:HD13	2.12	0.48
1:R:34:TYR:O	1:R:68:GLN:N	2.41	0.48
1:A:132:ASN:N	1:A:132:ASN:ND2	2.57	0.48
1:B:32:GLY:C	1:B:131:PRO:HB3	2.38	0.48
1:F:1:MET:HG2	1:F:2:VAL:HG23	1.94	0.48
1:F:68:GLN:OE1	1:F:99:PRO:CD	2.61	0.48
1:F:80:HIS:CD2	1:F:80:HIS:H	2.31	0.48
1:G:48:CYS:HB2	1:G:124:ARG:CZ	2.43	0.48
1:I:16:ALA:CB	1:I:25:ILE:HD13	2.43	0.48
1:K:12:PHE:HB2	1:K:108:ILE:HD13	1.95	0.48
1:B:86:LEU:HD23	1:B:91:GLY:O	2.13	0.48
2:D:34:TYR:CD1	2:D:131:PRO:HD3	2.47	0.48
1:J:124:ARG:HB2	1:J:141:ASN:CB	2.40	0.48
1:O:116:ASP:CB	1:P:7:ARG:HH12	2.26	0.48
1:T:33:LYS:HA	1:T:66:ASN:HD21	1.78	0.48
1:E:149:VAL:O	1:E:153:LEU:HD13	2.12	0.48
1:F:39:PHE:CD2	1:F:72:CYS:HB3	2.48	0.48
1:G:2:VAL:O	1:G:4:LEU:HD13	2.12	0.48
1:G:108:ILE:O	1:G:111:ALA:HB3	2.12	0.48
1:K:34:TYR:HA	1:K:129:ILE:O	2.14	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:77:GLN:HG3	1:M:78:TYR:N	2.29	0.48
1:Q:26:CYS:O	1:Q:29:ASP:HB2	2.14	0.48
1:S:86:LEU:O	1:S:92:GLY:HA3	2.13	0.48
1:C:35:VAL:HB	1:C:129:ILE:HD12	1.95	0.48
1:C:41:PRO:HB3	1:C:121:ASN:HB2	1.95	0.48
2:D:46:PHE:HD1	2:D:46:PHE:N	2.07	0.48
1:E:28:LYS:O	1:E:31:ARG:HG2	2.14	0.48
1:F:34:TYR:CE1	1:F:130:ASP:HA	2.47	0.48
1:H:4:LEU:HB2	1:H:7:ARG:CD	2.38	0.48
1:H:61:GLU:O	1:H:65:ARG:N	2.43	0.48
1:J:59:VAL:HG11	1:J:97:LYS:HG3	1.96	0.48
1:S:37:LEU:O	1:S:127:PHE:HB2	2.13	0.48
1:T:38:PHE:C	1:T:38:PHE:CD1	2.91	0.48
1:B:68:GLN:HE21	1:B:99:PRO:HG3	1.77	0.48
1:C:151:GLU:OE2	2:D:151:GLU:HG2	2.13	0.48
1:C:159:PHE:CE1	2:D:145:VAL:HG21	2.49	0.48
2:D:16:ALA:HA	2:D:101:LEU:HA	1.95	0.48
2:D:23:LYS:HE3	1:O:23:LYS:CB	2.42	0.48
2:D:93:LEU:HD22	2:D:96:MET:HE2	1.96	0.48
2:D:104:ARG:HG3	1:E:120:GLY:N	2.28	0.48
1:G:17:VAL:HA	1:G:21:GLU:O	2.13	0.48
1:I:44:PHE:CE1	1:I:83:TRP:CG	3.02	0.48
1:J:28:LYS:O	1:J:31:ARG:HB2	2.13	0.48
1:J:101:LEU:HD12	1:J:102:ALA:N	2.27	0.48
1:K:126:LEU:HD23	1:K:126:LEU:C	2.38	0.48
1:L:127:PHE:CD1	1:L:138:ILE:HG12	2.48	0.48
1:O:32:GLY:O	1:O:33:LYS:HG2	2.14	0.48
1:Q:15:GLN:HG3	1:Q:77:GLN:HE21	1.78	0.48
1:S:103:ASP:OD2	1:S:108:ILE:HB	2.13	0.48
1:B:62:PHE:HB3	1:B:67:CYS:O	2.14	0.48
1:C:11:GLU:CD	1:C:27:LEU:HB3	2.38	0.48
1:E:136:ARG:NE	1:E:136:ARG:HA	2.29	0.48
1:I:39:PHE:HE2	1:I:127:PHE:CD1	2.32	0.48
1:I:60:GLU:O	1:I:63:ASN:HB2	2.14	0.48
1:I:142:ASP:HB3	1:I:144:PRO:HD2	1.96	0.48
1:K:34:TYR:CD1	1:K:129:ILE:O	2.67	0.48
1:K:47:VAL:HG22	1:K:51:GLU:CG	2.43	0.48
1:M:39:PHE:CE2	1:M:72:CYS:SG	3.07	0.48
1:M:86:LEU:HD11	1:M:90:SER:CB	2.43	0.48
1:O:39:PHE:HE1	1:O:127:PHE:CE2	2.31	0.48
1:P:59:VAL:HG21	1:P:97:LYS:HB2	1.94	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:18:ILE:HG12	1:R:99:PRO:HB3	1.96	0.48
1:R:86:LEU:HG	1:R:87:ASP:N	2.28	0.48
1:S:59:VAL:HG21	1:S:97:LYS:HB2	1.95	0.48
1:S:153:LEU:HD12	1:S:153:LEU:N	2.28	0.48
1:B:39:PHE:HE1	1:B:127:PHE:HE2	1.62	0.48
1:E:43:ASP:HB2	1:E:75:ASP:CG	2.39	0.48
1:H:84:ASP:HA	1:H:93:LEU:HB2	1.95	0.48
1:J:5:PRO:C	1:J:7:ARG:H	2.21	0.48
1:N:31:ARG:HD2	1:N:132:ASN:HA	1.96	0.48
1:O:17:VAL:HA	1:O:21:GLU:O	2.14	0.48
1:O:48:CYS:N	1:O:49:PRO:CD	2.76	0.48
1:P:34:TYR:CE1	1:P:130:ASP:HA	2.49	0.48
1:B:124:ARG:HD2	1:B:142:ASP:O	2.13	0.48
1:H:12:PHE:HE2	1:H:27:LEU:HD13	1.78	0.48
1:J:47:VAL:HG13	1:J:48:CYS:O	2.14	0.48
1:K:127:PHE:CE1	1:K:138:ILE:HG23	2.48	0.48
1:K:164:LYS:HD3	1:K:165:HIS:CE1	2.49	0.48
1:O:36:VAL:HA	1:O:127:PHE:O	2.13	0.48
1:S:143:LYS:HB3	1:S:144:PRO:HD3	1.96	0.48
1:T:60:GLU:HA	1:T:63:ASN:CB	2.18	0.48
1:F:40:TYR:HE1	1:F:43:ASP:OD1	1.97	0.48
1:G:48:CYS:HB2	1:G:124:ARG:NH1	2.29	0.48
1:M:48:CYS:HB2	1:M:49:PRO:HD3	1.96	0.48
1:M:112:TYR:CB	1:M:114:VAL:HG22	2.44	0.48
1:N:36:VAL:HB	1:N:69:VAL:HG22	1.95	0.48
1:P:2:VAL:HG12	1:P:4:LEU:HD22	1.96	0.48
1:Q:16:ALA:CB	1:Q:101:LEU:HA	2.44	0.48
1:Q:87:ASP:HA	1:Q:94:GLY:HA2	1.96	0.48
1:R:15:GLN:OE1	1:R:24:GLU:HB2	2.13	0.48
1:R:65:ARG:NE	1:R:156:LEU:HD23	2.26	0.48
1:T:40:TYR:HD2	1:T:42:ALA:O	1.97	0.48
1:T:86:LEU:CB	1:T:92:GLY:HA3	2.43	0.48
1:A:140:ILE:HB	1:B:138:ILE:HB	1.95	0.47
1:E:14:GLY:O	1:E:24:GLU:HA	2.14	0.47
1:H:4:LEU:HB3	1:H:5:PRO:HD2	1.95	0.47
1:H:38:PHE:HB2	1:H:147:ARG:NH1	2.29	0.47
1:I:150:ASP:OD1	1:I:150:ASP:N	2.45	0.47
1:N:16:ALA:HB2	1:N:25:ILE:HD11	1.95	0.47
1:P:15:GLN:OE1	1:P:15:GLN:HA	2.13	0.47
1:S:126:LEU:HD12	1:S:147:ARG:CG	2.44	0.47
1:T:137:GLN:HB2	1:T:159:PHE:HE2	1.78	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:62:PHE:O	1:C:67:CYS:N	2.46	0.47
2:D:53:ILE:CA	2:D:96:MET:HE1	2.42	0.47
1:E:136:ARG:HD3	1:E:159:PHE:CD2	2.48	0.47
1:J:48:CYS:HB3	1:J:49:PRO:HD2	1.96	0.47
1:K:104:ARG:HG3	1:T:120:GLY:C	2.39	0.47
1:P:54:ALA:O	1:P:58:GLN:HG2	2.15	0.47
1:S:41:PRO:HG3	1:S:143:LYS:HD2	1.96	0.47
1:S:149:VAL:O	1:S:152:THR:HB	2.14	0.47
1:C:54:ALA:O	1:C:58:GLN:HB2	2.15	0.47
1:E:72:CYS:HB2	1:E:101:LEU:HB3	1.96	0.47
1:F:78:TYR:CB	1:G:45:THR:HB	2.43	0.47
1:H:89:LYS:HD3	1:H:89:LYS:C	2.39	0.47
1:K:25:ILE:HG22	1:K:29:ASP:OD2	2.13	0.47
1:M:44:PHE:N	1:M:83:TRP:CZ3	2.83	0.47
1:P:13:LYS:HG2	1:P:26:CYS:CB	2.44	0.47
1:A:13:LYS:HZ3	1:A:26:CYS:HB2	1.78	0.47
1:A:18:ILE:N	1:A:18:ILE:HD12	2.29	0.47
1:G:127:PHE:HD2	1:G:135:LEU:HD11	1.79	0.47
1:H:74:THR:HA	1:H:103:ASP:O	2.14	0.47
1:K:155:LEU:O	1:K:158:ALA:HB3	2.14	0.47
1:O:151:GLU:O	1:O:155:LEU:HD12	2.14	0.47
1:P:2:VAL:HG12	1:P:4:LEU:CD2	2.44	0.47
1:T:30:TYR:CE2	1:T:68:GLN:HG2	2.49	0.47
1:A:15:GLN:OE1	1:A:24:GLU:HB2	2.14	0.47
1:B:104:ARG:NH1	1:C:104:ARG:HH12	2.12	0.47
1:C:42:ALA:HB3	1:C:45:THR:HG21	1.96	0.47
1:I:8:PRO:HA	1:I:134:ILE:HD13	1.96	0.47
1:I:161:PHE:O	1:I:166:GLY:N	2.46	0.47
1:Q:145:VAL:HG21	1:R:159:PHE:CE1	2.50	0.47
1:R:17:VAL:C	1:R:18:ILE:HG13	2.39	0.47
1:R:153:LEU:O	1:R:157:ASP:CG	2.57	0.47
1:T:41:PRO:O	1:T:121:ASN:HB3	2.14	0.47
1:B:49:PRO:O	1:B:53:ILE:HG13	2.13	0.47
1:B:51:GLU:OE1	1:B:124:ARG:NH1	2.48	0.47
1:C:38:PHE:CZ	1:C:71:ALA:HB2	2.50	0.47
1:F:47:VAL:HG11	1:F:144:PRO:O	2.15	0.47
1:G:142:ASP:CG	1:G:144:PRO:HD2	2.40	0.47
1:L:12:PHE:CD1	1:L:108:ILE:HD13	2.50	0.47
1:L:46:PHE:HB2	1:L:49:PRO:HG2	1.96	0.47
1:L:115:PHE:CE1	1:L:121:ASN:N	2.78	0.47
1:L:127:PHE:HA	1:L:137:GLN:O	2.13	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:143:LYS:N	1:L:144:PRO:HD2	2.30	0.47
1:O:88:ARG:HA	1:O:92:GLY:O	2.14	0.47
1:O:128:ILE:HB	1:O:137:GLN:H	1.78	0.47
1:T:5:PRO:HB3	1:T:136:ARG:O	2.15	0.47
1:A:40:TYR:HH	1:A:80:HIS:CD2	2.32	0.47
1:B:132:ASN:N	1:B:132:ASN:ND2	2.63	0.47
1:B:142:ASP:OD1	1:B:144:PRO:HD2	2.15	0.47
2:D:151:GLU:O	2:D:155:LEU:HG	2.15	0.47
1:E:96:MET:HB3	1:E:98:ILE:HG13	1.97	0.47
1:F:121:ASN:CG	1:G:104:ARG:HE	2.23	0.47
1:G:149:VAL:O	1:G:152:THR:HB	2.14	0.47
1:H:127:PHE:HE2	1:H:138:ILE:HG23	1.77	0.47
1:I:106:GLN:HB2	1:I:110:LYS:HE3	1.96	0.47
1:I:109:SER:OG	1:I:114:VAL:HG23	2.15	0.47
1:J:22:PHE:N	1:J:22:PHE:HD1	2.12	0.47
1:J:154:ARG:NH2	1:J:155:LEU:HD21	2.30	0.47
1:K:127:PHE:CD1	1:K:138:ILE:HG23	2.49	0.47
1:L:65:ARG:HD2	1:L:153:LEU:HD11	1.96	0.47
1:M:18:ILE:O	1:M:19:ASN:CB	2.62	0.47
1:R:6:ASN:HB3	1:R:7:ARG:CD	2.44	0.47
1:B:3:LEU:C	1:B:4:LEU:HD12	2.39	0.47
1:B:50:THR:HG23	1:B:51:GLU:N	2.30	0.47
2:D:47:VAL:CG1	2:D:48:CYS:H	2.17	0.47
2:D:104:ARG:HG3	1:E:120:GLY:CA	2.45	0.47
1:E:25:ILE:HD11	1:E:101:LEU:HD22	1.96	0.47
1:F:23:LYS:HZ1	1:Q:23:LYS:HG2	1.80	0.47
1:G:59:VAL:HG11	1:G:97:LYS:HB2	1.96	0.47
1:H:40:TYR:CE1	1:H:71:ALA:HB1	2.50	0.47
1:K:35:VAL:HB	1:K:129:ILE:HB	1.97	0.47
1:M:95:HIS:O	1:M:96:MET:HE2	2.14	0.47
1:M:157:ASP:O	1:M:161:PHE:N	2.46	0.47
1:P:74:THR:HG23	1:Q:104:ARG:HH21	1.80	0.47
1:T:142:ASP:CG	1:T:143:LYS:H	2.23	0.47
1:A:41:PRO:HB3	1:A:121:ASN:HD22	1.80	0.47
2:D:34:TYR:CE1	2:D:130:ASP:HA	2.50	0.47
2:D:105:LYS:O	2:D:106:GLN:CB	2.63	0.47
1:G:40:TYR:CE2	1:G:83:TRP:HZ3	2.33	0.47
1:K:12:PHE:CE1	1:K:27:LEU:HB2	2.50	0.47
1:L:115:PHE:CD1	1:L:121:ASN:O	2.68	0.47
1:P:18:ILE:HB	1:P:23:LYS:HD3	1.96	0.47
1:P:148:SER:CB	1:P:151:GLU:HB3	2.42	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:40:TYR:CD2	1:Q:42:ALA:O	2.68	0.47
1:A:165:HIS:N	1:A:165:HIS:HD1	2.12	0.47
1:C:13:LYS:HZ1	1:C:24:GLU:HG2	1.78	0.47
2:D:104:ARG:HG3	1:E:120:GLY:HA3	1.97	0.47
1:E:126:LEU:HB3	1:E:139:THR:HB	1.97	0.47
1:H:36:VAL:HB	1:H:69:VAL:HG22	1.96	0.47
1:H:55:PHE:CE1	1:H:149:VAL:HG12	2.49	0.47
1:I:12:PHE:CB	1:I:108:ILE:HG12	2.46	0.47
1:I:25:ILE:HD11	1:I:101:LEU:HD22	1.96	0.47
1:P:86:LEU:HD23	1:P:91:GLY:O	2.15	0.47
1:Q:17:VAL:HG22	1:Q:22:PHE:CD1	2.50	0.47
1:Q:36:VAL:HG23	1:Q:67:CYS:SG	2.54	0.47
1:R:34:TYR:CB	1:R:67:CYS:HA	2.45	0.47
1:B:22:PHE:HE1	1:B:77:GLN:CG	2.28	0.46
1:B:36:VAL:HG12	1:B:69:VAL:HG13	1.98	0.46
2:D:65:ARG:HD3	2:D:156:LEU:HD23	1.96	0.46
1:F:131:PRO:HG2	1:O:163:GLU:HG2	1.96	0.46
1:I:123:PHE:CB	1:I:140:ILE:HD11	2.45	0.46
1:J:18:ILE:HG12	1:J:99:PRO:HA	1.96	0.46
1:J:31:ARG:HD3	1:J:131:PRO:O	2.14	0.46
1:J:69:VAL:HG12	1:J:70:ILE:N	2.30	0.46
1:J:126:LEU:HD23	1:J:127:PHE:N	2.30	0.46
1:K:27:LEU:CD2	1:K:31:ARG:HH21	2.27	0.46
1:P:59:VAL:HG21	1:P:97:LYS:CB	2.44	0.46
1:Q:39:PHE:N	1:Q:39:PHE:HD1	2.11	0.46
1:S:5:PRO:HD3	1:S:138:ILE:HD11	1.97	0.46
1:C:142:ASP:CG	1:C:144:PRO:HD2	2.41	0.46
1:G:40:TYR:HE2	1:G:83:TRP:CZ3	2.34	0.46
1:I:83:TRP:CD1	1:I:92:GLY:HA2	2.50	0.46
1:J:71:ALA:HB3	1:J:100:LEU:HA	1.97	0.46
1:K:55:PHE:CE1	1:K:149:VAL:HG22	2.50	0.46
1:K:80:HIS:ND1	1:K:100:LEU:HB3	2.30	0.46
1:K:124:ARG:HD2	1:K:145:VAL:O	2.15	0.46
1:N:83:TRP:CE3	1:N:93:LEU:HG	2.50	0.46
1:O:39:PHE:CE1	1:O:127:PHE:HE2	2.33	0.46
1:P:128:ILE:HG21	1:P:159:PHE:CE2	2.50	0.46
1:Q:38:PHE:HD2	1:Q:147:ARG:NH2	2.12	0.46
1:Q:96:MET:SD	1:Q:98:ILE:HG12	2.56	0.46
1:S:59:VAL:HG21	1:S:97:LYS:CB	2.46	0.46
1:T:54:ALA:HA	1:T:57:ASP:OD2	2.15	0.46
1:A:60:GLU:OE1	1:A:60:GLU:HA	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:86:LEU:CG	1:G:92:GLY:HA3	2.40	0.46
1:I:148:SER:HB3	1:I:151:GLU:HB3	1.97	0.46
1:K:38:PHE:HA	1:K:125:GLY:O	2.16	0.46
1:M:38:PHE:CZ	1:M:71:ALA:HA	2.50	0.46
1:M:69:VAL:HB	1:M:98:ILE:HG21	1.97	0.46
1:M:134:ILE:HG21	1:M:136:ARG:HH22	1.80	0.46
1:N:30:TYR:CE2	1:N:68:GLN:HG2	2.51	0.46
1:O:68:GLN:HE21	1:O:70:ILE:HG12	1.81	0.46
1:P:136:ARG:HB3	1:P:159:PHE:CZ	2.50	0.46
1:Q:34:TYR:CE1	1:Q:130:ASP:HA	2.49	0.46
1:H:56:SER:OG	1:H:97:LYS:HD3	2.15	0.46
1:I:40:TYR:O	1:I:73:SER:HB3	2.15	0.46
1:I:80:HIS:HD2	1:I:100:LEU:HB3	1.80	0.46
1:I:106:GLN:CB	1:I:110:LYS:HE3	2.46	0.46
1:J:116:ASP:HB3	1:J:121:ASN:O	2.15	0.46
1:L:127:PHE:O	1:L:128:ILE:HG12	2.15	0.46
1:M:40:TYR:HB2	1:M:41:PRO:HD2	1.97	0.46
1:N:76:SER:HB3	1:N:104:ARG:CD	2.45	0.46
1:S:153:LEU:H	1:S:153:LEU:CD1	2.26	0.46
1:A:83:TRP:CD1	1:A:93:LEU:HG	2.51	0.46
1:A:148:SER:HB2	1:B:154:ARG:NH2	2.31	0.46
1:B:22:PHE:HE1	1:B:77:GLN:HG2	1.80	0.46
1:E:27:LEU:HD11	1:E:129:ILE:HG21	1.96	0.46
1:K:44:PHE:CD2	1:K:83:TRP:CD1	3.04	0.46
1:M:12:PHE:HB3	1:M:108:ILE:CG2	2.46	0.46
1:M:124:ARG:HB3	1:M:147:ARG:CZ	2.46	0.46
1:P:71:ALA:HB2	1:P:98:ILE:HD11	1.97	0.46
1:Q:55:PHE:CE2	1:Q:149:VAL:HG13	2.51	0.46
1:R:55:PHE:CE1	1:R:149:VAL:HG22	2.51	0.46
1:C:40:TYR:HE2	1:C:43:ASP:OD1	1.98	0.46
1:E:82:ALA:O	1:E:85:ASN:N	2.49	0.46
1:J:16:ALA:HB2	1:J:25:ILE:HD13	1.98	0.46
1:J:164:LYS:CG	1:J:165:HIS:HD2	2.28	0.46
1:L:6:ASN:HD22	1:L:134:ILE:CG2	2.28	0.46
1:M:143:LYS:N	1:M:144:PRO:CD	2.77	0.46
1:N:13:LYS:HD3	1:N:26:CYS:HB2	1.98	0.46
1:Q:38:PHE:HB2	1:Q:147:ARG:NH1	2.31	0.46
1:R:3:LEU:HD23	1:R:10:PRO:HG2	1.97	0.46
1:R:18:ILE:HG12	1:R:99:PRO:CB	2.46	0.46
1:S:5:PRO:HD2	1:T:123:PHE:CD2	2.51	0.46
1:T:34:TYR:CD1	1:T:131:PRO:HD3	2.50	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:26:CYS:O	1:C:29:ASP:HB2	2.15	0.46
1:C:126:LEU:N	1:C:139:THR:O	2.49	0.46
1:F:17:VAL:HG21	1:F:80:HIS:HB2	1.98	0.46
1:F:55:PHE:O	1:F:59:VAL:N	2.49	0.46
1:H:123:PHE:CB	1:H:140:ILE:HD11	2.45	0.46
1:K:35:VAL:HB	1:K:129:ILE:HD12	1.97	0.46
1:N:143:LYS:N	1:N:144:PRO:HD2	2.31	0.46
1:O:13:LYS:HZ2	1:O:26:CYS:HB2	1.79	0.46
1:P:34:TYR:HA	1:P:129:ILE:O	2.16	0.46
1:P:46:PHE:O	1:P:47:VAL:HG12	2.15	0.46
1:P:104:ARG:HD3	1:P:104:ARG:HA	1.84	0.46
1:T:65:ARG:NH1	1:T:153:LEU:HB3	2.31	0.46
1:A:76:SER:HA	1:A:104:ARG:HD3	1.97	0.46
1:B:132:ASN:HD22	1:B:132:ASN:N	2.13	0.46
1:F:13:LYS:HE3	1:F:13:LYS:HB2	1.78	0.46
1:F:52:ILE:HG23	1:F:96:MET:HE1	1.98	0.46
1:I:126:LEU:C	1:I:127:PHE:CD1	2.94	0.46
1:L:65:ARG:HD2	1:L:156:LEU:HD12	1.97	0.46
1:N:94:GLY:C	1:N:95:HIS:HD2	2.24	0.46
1:R:41:PRO:HB3	1:R:143:LYS:HZ2	1.80	0.46
1:R:48:CYS:HA	1:R:50:THR:HB	1.98	0.46
1:S:109:SER:CB	1:S:115:PHE:HB2	2.45	0.46
1:B:154:ARG:NH2	1:B:155:LEU:HD21	2.31	0.46
1:C:84:ASP:OD1	1:C:96:MET:HG2	2.16	0.46
1:F:154:ARG:NH2	1:F:155:LEU:HD21	2.30	0.46
1:I:16:ALA:HB2	1:I:25:ILE:HD13	1.97	0.46
1:I:130:ASP:HB3	1:I:136:ARG:HG2	1.97	0.46
1:P:65:ARG:HD2	1:P:160:GLN:NE2	2.29	0.46
1:A:39:PHE:N	1:A:39:PHE:CD1	2.84	0.46
1:C:70:ILE:HG12	1:C:99:PRO:HB2	1.97	0.46
2:D:78:TYR:N	2:D:78:TYR:CD1	2.84	0.46
1:F:56:SER:O	1:F:59:VAL:HB	2.16	0.46
1:F:116:ASP:OD2	1:F:119:ASP:HB2	2.16	0.46
1:G:35:VAL:HG22	1:G:68:GLN:HB3	1.98	0.46
1:G:71:ALA:O	1:G:101:LEU:N	2.48	0.46
1:H:136:ARG:HB3	1:H:159:PHE:CE1	2.51	0.46
1:J:76:SER:HB2	1:J:78:TYR:HD1	1.81	0.46
1:K:51:GLU:CG	1:K:52:ILE:H	2.24	0.46
1:K:53:ILE:CA	1:K:56:SER:HB3	2.33	0.46
1:K:154:ARG:CZ	1:L:148:SER:HB2	2.46	0.46
1:M:89:LYS:O	1:M:89:LYS:HD3	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:143:LYS:N	1:P:144:PRO:CD	2.79	0.46
1:T:108:ILE:O	1:T:111:ALA:HB3	2.15	0.46
1:T:162:VAL:HA	1:T:166:GLY:N	2.27	0.46
1:A:128:ILE:HD12	1:A:137:GLN:HB3	1.98	0.45
1:G:144:PRO:HB2	1:H:162:VAL:CG1	2.46	0.45
1:I:3:LEU:C	1:I:4:LEU:HD12	2.41	0.45
1:L:69:VAL:HB	1:L:98:ILE:CG2	2.42	0.45
1:M:65:ARG:HD2	1:M:156:LEU:HD22	1.97	0.45
1:O:139:THR:HG23	1:P:139:THR:HG23	1.97	0.45
1:Q:16:ALA:HB2	1:Q:101:LEU:HD12	1.98	0.45
2:D:7:ARG:C	2:D:134:ILE:HG23	2.42	0.45
2:D:126:LEU:HD22	2:D:137:GLN:OE1	2.16	0.45
1:F:51:GLU:HB3	1:F:147:ARG:NH2	2.32	0.45
1:H:40:TYR:HE1	1:H:71:ALA:HB1	1.81	0.45
1:J:17:VAL:HG21	1:J:80:HIS:HB2	1.97	0.45
1:J:38:PHE:HE1	1:J:40:TYR:HB3	1.81	0.45
1:K:33:LYS:O	1:K:131:PRO:HA	2.16	0.45
1:R:105:LYS:O	1:R:106:GLN:HB2	2.16	0.45
1:T:87:ASP:OD1	1:T:90:SER:HB3	2.17	0.45
1:T:130:ASP:CG	1:T:131:PRO:HD2	2.40	0.45
1:A:69:VAL:C	1:A:70:ILE:HG13	2.41	0.45
1:A:140:ILE:HD12	1:B:138:ILE:HB	1.97	0.45
1:C:82:ALA:HA	1:C:85:ASN:ND2	2.28	0.45
2:D:17:VAL:N	2:D:100:LEU:O	2.45	0.45
1:H:104:ARG:HB3	1:I:120:GLY:HA3	1.98	0.45
1:J:168:VAL:HG22	1:J:169:CYS:N	2.32	0.45
1:K:47:VAL:HG22	1:K:51:GLU:HG2	1.96	0.45
1:L:86:LEU:HB3	1:L:92:GLY:HA3	1.98	0.45
1:M:11:GLU:HA	1:M:11:GLU:OE1	2.16	0.45
1:S:15:GLN:HA	1:S:24:GLU:HA	1.97	0.45
1:T:65:ARG:HD3	1:T:156:LEU:HD23	1.99	0.45
1:A:41:PRO:HB3	1:A:121:ASN:ND2	2.31	0.45
1:A:75:ASP:HB2	1:A:80:HIS:CE1	2.36	0.45
1:A:145:VAL:HG21	1:B:159:PHE:HE1	1.79	0.45
1:C:126:LEU:HD13	1:C:139:THR:OG1	2.16	0.45
1:J:26:CYS:HB3	1:J:29:ASP:OD1	2.15	0.45
1:J:40:TYR:CE1	1:J:71:ALA:HB1	2.51	0.45
1:K:140:ILE:HG22	1:L:5:PRO:HG3	1.98	0.45
1:L:72:CYS:SG	1:L:101:LEU:HD23	2.57	0.45
1:M:137:GLN:NE2	1:M:139:THR:OG1	2.49	0.45
1:O:86:LEU:HD11	1:O:90:SER:CB	2.34	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:106:GLN:NE2	1:P:115:PHE:CZ	2.85	0.45
1:S:22:PHE:C	1:S:23:LYS:HD2	2.42	0.45
1:S:136:ARG:HB3	1:S:159:PHE:CZ	2.51	0.45
1:A:138:ILE:HB	1:B:140:ILE:HB	1.98	0.45
1:F:43:ASP:HA	1:F:83:TRP:CZ3	2.52	0.45
1:J:96:MET:HG2	1:J:100:LEU:HG	1.98	0.45
1:K:141:ASN:HD21	1:L:155:LEU:HD21	1.80	0.45
1:N:22:PHE:CZ	1:N:81:LEU:HD22	2.52	0.45
1:R:151:GLU:HG3	1:R:155:LEU:HD11	1.98	0.45
1:S:157:ASP:HA	1:S:160:GLN:HB2	1.97	0.45
1:A:96:MET:CG	1:A:100:LEU:HD21	2.46	0.45
2:D:142:ASP:C	2:D:144:PRO:HD2	2.42	0.45
1:F:116:ASP:HB3	1:F:123:PHE:HE1	1.82	0.45
1:I:18:ILE:O	1:I:19:ASN:HB2	2.16	0.45
1:J:74:THR:HA	1:J:103:ASP:O	2.17	0.45
1:K:44:PHE:HA	1:K:83:TRP:CE2	2.51	0.45
1:L:95:HIS:ND1	1:L:95:HIS:N	2.65	0.45
1:M:148:SER:N	1:N:154:ARG:NH2	2.65	0.45
1:N:38:PHE:C	1:N:39:PHE:CD1	2.95	0.45
1:O:140:ILE:O	1:P:137:GLN:HB2	2.17	0.45
1:S:34:TYR:HB2	1:S:66:ASN:O	2.17	0.45
1:T:39:PHE:CE2	1:T:114:VAL:HG21	2.51	0.45
1:A:53:ILE:HG13	1:A:93:LEU:HD22	1.98	0.45
1:A:119:ASP:O	1:A:121:ASN:OD1	2.35	0.45
1:E:69:VAL:O	1:E:99:PRO:HD2	2.17	0.45
1:H:22:PHE:CZ	1:H:77:GLN:HB2	2.50	0.45
1:H:67:CYS:SG	1:H:68:GLN:N	2.90	0.45
1:M:40:TYR:HB2	1:M:41:PRO:CD	2.47	0.45
1:O:40:TYR:HB2	1:O:41:PRO:CD	2.46	0.45
1:O:50:THR:OG1	1:O:53:ILE:HB	2.17	0.45
1:Q:39:PHE:HZ	1:Q:112:TYR:CD2	2.34	0.45
1:Q:68:GLN:CG	1:Q:70:ILE:HD11	2.46	0.45
1:R:16:ALA:HB2	1:R:101:LEU:CD1	2.47	0.45
1:R:39:PHE:HB2	1:R:123:PHE:O	2.17	0.45
1:S:86:LEU:HB3	1:S:92:GLY:HA3	1.98	0.45
1:T:105:LYS:C	1:T:107:GLU:H	2.23	0.45
1:C:149:VAL:O	1:C:150:ASP:C	2.57	0.45
1:F:14:GLY:O	1:F:24:GLU:OE1	2.34	0.45
1:F:18:ILE:HG13	1:F:23:LYS:HB2	1.97	0.45
1:H:128:ILE:O	1:H:135:LEU:HD12	2.16	0.45
1:H:134:ILE:HG22	1:H:135:LEU:N	2.31	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:124:ARG:HH11	1:K:147:ARG:NH2	2.14	0.45
1:M:41:PRO:HA	1:M:122:ALA:N	2.25	0.45
1:R:57:ASP:HB2	1:R:58:GLN:OE1	2.16	0.45
2:D:78:TYR:N	2:D:78:TYR:HD1	2.13	0.45
2:D:124:ARG:CG	2:D:147:ARG:HH12	2.20	0.45
1:E:87:ASP:C	1:E:89:LYS:H	2.25	0.45
1:F:105:LYS:HE2	1:G:118:GLU:O	2.17	0.45
1:J:47:VAL:CG2	1:J:48:CYS:H	2.12	0.45
1:K:55:PHE:CE1	1:K:147:ARG:O	2.70	0.45
1:L:116:ASP:CG	1:L:123:PHE:CZ	2.95	0.45
1:N:147:ARG:N	1:N:147:ARG:NE	2.62	0.45
1:O:59:VAL:O	1:O:62:PHE:HB2	2.17	0.45
1:O:78:TYR:CD1	1:O:78:TYR:N	2.84	0.45
1:P:58:GLN:O	1:P:61:GLU:HB2	2.17	0.45
1:B:34:TYR:CE1	1:B:131:PRO:HD3	2.52	0.45
1:B:34:TYR:HA	1:B:129:ILE:O	2.16	0.45
1:C:84:ASP:HB2	1:C:93:LEU:HD12	1.98	0.45
1:F:4:LEU:C	1:F:135:LEU:HD23	2.42	0.45
1:F:86:LEU:HD12	1:F:87:ASP:H	1.82	0.45
1:G:39:PHE:HA	1:G:72:CYS:O	2.18	0.45
1:I:39:PHE:O	1:I:124:ARG:HA	2.17	0.45
1:J:4:LEU:O	1:J:7:ARG:HB2	2.17	0.45
1:J:84:ASP:HA	1:J:93:LEU:HB2	1.99	0.45
1:M:128:ILE:O	1:M:135:LEU:HD12	2.16	0.45
1:O:55:PHE:CZ	1:O:149:VAL:HG22	2.52	0.45
1:P:7:ARG:HD2	1:P:7:ARG:N	2.32	0.45
1:P:35:VAL:HA	1:P:68:GLN:O	2.17	0.45
1:Q:25:ILE:HD12	1:Q:30:TYR:CE2	2.52	0.45
1:Q:73:SER:OG	1:Q:80:HIS:CE1	2.70	0.45
1:R:86:LEU:HB3	1:R:92:GLY:HA3	1.98	0.45
1:C:1:MET:HB3	1:C:2:VAL:H	1.55	0.44
1:C:82:ALA:O	1:C:85:ASN:HB2	2.17	0.44
1:F:136:ARG:HA	1:F:136:ARG:HD2	1.82	0.44
1:F:155:LEU:O	1:F:158:ALA:HB3	2.16	0.44
1:G:40:TYR:CE1	1:G:73:SER:HB3	2.52	0.44
1:G:43:ASP:CB	1:G:44:PHE:CD2	3.01	0.44
1:I:40:TYR:HE1	1:I:71:ALA:HB1	1.79	0.44
1:J:130:ASP:CG	1:J:132:ASN:H	2.26	0.44
1:J:143:LYS:HB2	1:J:144:PRO:HD3	1.99	0.44
1:L:22:PHE:C	1:L:23:LYS:HD2	2.42	0.44
1:L:143:LYS:N	1:L:144:PRO:CD	2.79	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:56:SER:HA	1:N:98:ILE:CD1	2.48	0.44
1:N:135:LEU:HD21	1:N:138:ILE:CD1	2.46	0.44
1:P:130:ASP:OD2	1:P:132:ASN:HB2	2.16	0.44
1:T:126:LEU:HD23	1:T:139:THR:HG21	1.98	0.44
1:B:69:VAL:O	1:B:99:PRO:HD2	2.17	0.44
1:F:24:GLU:HB3	1:Q:24:GLU:HB3	1.98	0.44
1:G:141:ASN:HD21	1:H:155:LEU:CD2	2.30	0.44
1:H:145:VAL:HG12	1:H:146:GLY:O	2.17	0.44
1:K:30:TYR:CD1	1:K:68:GLN:HG2	2.51	0.44
1:L:37:LEU:HD12	1:L:38:PHE:H	1.80	0.44
1:L:86:LEU:HD23	1:L:91:GLY:C	2.42	0.44
1:L:126:LEU:HB2	1:L:147:ARG:NH1	2.29	0.44
1:L:129:ILE:HA	1:L:134:ILE:O	2.17	0.44
1:N:17:VAL:O	1:N:99:PRO:HA	2.17	0.44
1:O:41:PRO:HB3	1:O:143:LYS:HE2	1.98	0.44
1:O:124:ARG:HB3	1:O:147:ARG:NH1	2.32	0.44
1:Q:68:GLN:HG3	1:Q:70:ILE:HD11	1.97	0.44
1:T:71:ALA:O	1:T:101:LEU:HB3	2.17	0.44
1:A:5:PRO:HA	1:A:135:LEU:HG	2.00	0.44
1:B:160:GLN:O	1:B:164:LYS:HB2	2.16	0.44
1:C:101:LEU:HD12	1:C:102:ALA:N	2.33	0.44
1:C:141:ASN:HD22	1:C:145:VAL:CG1	2.30	0.44
1:C:142:ASP:HB3	1:C:145:VAL:HG23	1.99	0.44
2:D:135:LEU:O	2:D:136:ARG:HD2	2.17	0.44
1:G:96:MET:SD	1:G:100:LEU:HD21	2.58	0.44
1:G:171:VAL:O	1:G:172:ASN:C	2.61	0.44
1:H:58:GLN:NE2	1:H:61:GLU:OE1	2.51	0.44
1:H:86:LEU:HD11	1:H:90:SER:OG	2.16	0.44
1:I:25:ILE:CD1	1:I:101:LEU:HD13	2.42	0.44
1:K:134:ILE:HG22	1:K:135:LEU:N	2.32	0.44
1:K:147:ARG:HE	1:K:147:ARG:N	2.15	0.44
1:L:126:LEU:HD22	1:L:139:THR:OG1	2.17	0.44
1:B:36:VAL:HG13	1:B:126:LEU:HD21	1.98	0.44
2:D:54:ALA:O	2:D:57:ASP:HB2	2.17	0.44
1:J:112:TYR:HD2	1:J:127:PHE:CE2	2.35	0.44
1:O:62:PHE:HE1	1:O:152:THR:HG21	1.82	0.44
1:Q:34:TYR:CZ	1:Q:160:GLN:HG2	2.53	0.44
1:R:115:PHE:HE1	1:R:120:GLY:C	2.25	0.44
1:B:66:ASN:HB2	1:K:166:GLY:HA3	1.99	0.44
1:F:78:TYR:CG	1:G:45:THR:HB	2.52	0.44
1:F:143:LYS:N	1:F:144:PRO:CD	2.81	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:42:ALA:HA	1:G:75:ASP:OD2	2.18	0.44
1:G:141:ASN:HD21	1:H:155:LEU:HD22	1.83	0.44
1:I:59:VAL:HG23	1:I:60:GLU:N	2.32	0.44
1:I:83:TRP:NE1	1:I:92:GLY:HA2	2.33	0.44
1:K:3:LEU:HD11	1:K:112:TYR:HA	1.98	0.44
1:K:116:ASP:HB2	1:K:123:PHE:CE1	2.53	0.44
1:L:84:ASP:OD1	1:L:95:HIS:HA	2.18	0.44
1:L:105:LYS:C	1:L:107:GLU:N	2.74	0.44
1:N:7:ARG:CD	1:N:7:ARG:N	2.78	0.44
1:N:76:SER:OG	1:N:79:SER:HB2	2.17	0.44
1:P:54:ALA:O	1:P:58:GLN:CG	2.66	0.44
1:P:135:LEU:HD12	1:P:136:ARG:N	2.29	0.44
1:S:48:CYS:SG	1:S:49:PRO:HD2	2.58	0.44
1:T:115:PHE:HE2	1:T:117:GLU:OE2	2.00	0.44
1:B:44:PHE:CZ	1:B:83:TRP:HB2	2.53	0.44
1:B:71:ALA:HB2	1:B:98:ILE:HD11	2.00	0.44
1:B:129:ILE:CG2	1:B:133:GLY:HA2	2.47	0.44
1:C:96:MET:HG3	1:C:96:MET:O	2.18	0.44
1:E:142:ASP:CG	1:E:144:PRO:HD2	2.43	0.44
1:F:44:PHE:N	1:F:83:TRP:CZ2	2.81	0.44
1:F:127:PHE:CD1	1:F:138:ILE:HA	2.53	0.44
1:G:37:LEU:HD11	1:G:72:CYS:CB	2.48	0.44
1:J:38:PHE:HE2	1:J:55:PHE:CE2	2.36	0.44
1:N:36:VAL:HG23	1:N:67:CYS:SG	2.57	0.44
1:Q:28:LYS:CA	1:Q:31:ARG:HH21	2.29	0.44
1:S:55:PHE:CE2	1:S:149:VAL:HG22	2.53	0.44
1:A:40:TYR:HA	1:A:41:PRO:HD3	1.82	0.44
1:B:143:LYS:HB2	1:B:144:PRO:CD	2.48	0.44
1:C:159:PHE:CZ	2:D:145:VAL:HG21	2.52	0.44
1:G:6:ASN:C	1:G:7:ARG:HD2	2.43	0.44
1:G:145:VAL:HG21	1:H:159:PHE:CD1	2.53	0.44
1:I:13:LYS:HG2	1:I:14:GLY:H	1.83	0.44
1:J:65:ARG:NE	1:J:153:LEU:HD12	2.33	0.44
1:J:77:GLN:HG2	1:J:78:TYR:CE1	2.52	0.44
1:K:55:PHE:CD2	1:K:149:VAL:HG13	2.53	0.44
1:L:105:LYS:O	1:L:106:GLN:HB2	2.18	0.44
1:M:47:VAL:HG12	1:M:48:CYS:H	1.82	0.44
1:O:74:THR:O	1:O:103:ASP:O	2.35	0.44
1:S:38:PHE:HD1	1:S:38:PHE:H	1.63	0.44
1:A:134:ILE:HG22	1:A:136:ARG:NH2	2.33	0.44
1:E:21:GLU:HB3	1:E:23:LYS:NZ	2.32	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:154:ARG:HH22	1:F:155:LEU:HD21	1.83	0.44
1:G:151:GLU:CD	1:H:151:GLU:HB2	2.42	0.44
1:I:55:PHE:HE2	1:I:147:ARG:HH21	1.66	0.44
1:I:105:LYS:HE2	1:I:107:GLU:CD	2.42	0.44
1:J:37:LEU:HG	1:J:39:PHE:CE1	2.53	0.44
1:K:34:TYR:CE2	1:K:131:PRO:HD3	2.53	0.44
1:L:120:GLY:H	1:M:105:LYS:HG3	1.83	0.44
1:M:12:PHE:CE2	1:M:27:LEU:HD13	2.52	0.44
1:M:38:PHE:HB2	1:M:147:ARG:NH1	2.32	0.44
1:N:143:LYS:HB2	1:N:144:PRO:HD3	1.99	0.44
1:Q:126:LEU:C	1:Q:126:LEU:HD23	2.42	0.44
1:T:12:PHE:CE1	1:T:27:LEU:HB2	2.53	0.44
1:A:124:ARG:HB3	1:A:147:ARG:NH1	2.33	0.44
1:B:24:GLU:HB2	1:M:24:GLU:HB3	2.00	0.44
1:B:38:PHE:HB2	1:B:147:ARG:HH12	1.83	0.44
1:F:14:GLY:O	1:F:101:LEU:CD1	2.66	0.44
1:J:87:ASP:OD2	1:J:89:LYS:HE3	2.18	0.44
1:M:4:LEU:HD13	1:N:123:PHE:HE2	1.83	0.44
1:M:65:ARG:HE	1:M:153:LEU:HD12	1.83	0.44
1:R:41:PRO:O	1:R:42:ALA:HB2	2.17	0.44
1:S:73:SER:OG	1:S:80:HIS:CE1	2.71	0.44
2:D:12:PHE:HB2	2:D:108:ILE:HG23	2.00	0.43
1:G:36:VAL:HG22	1:G:128:ILE:HG12	2.00	0.43
1:H:40:TYR:CE2	1:H:83:TRP:HZ3	2.36	0.43
1:H:68:GLN:OE1	1:H:68:GLN:HA	2.17	0.43
1:K:39:PHE:CE1	1:K:114:VAL:HG21	2.53	0.43
1:N:34:TYR:HD1	1:N:129:ILE:O	1.99	0.43
1:O:9:ALA:HA	1:O:10:PRO:HD3	1.86	0.43
1:R:83:TRP:CG	1:R:93:LEU:HG	2.52	0.43
1:R:86:LEU:HG	1:R:90:SER:HB3	2.00	0.43
1:T:97:LYS:HD2	1:T:97:LYS:N	2.33	0.43
1:B:37:LEU:HD12	1:B:38:PHE:N	2.33	0.43
1:C:58:GLN:HG3	1:C:61:GLU:HG3	1.99	0.43
2:D:4:LEU:HA	2:D:5:PRO:HD3	1.93	0.43
2:D:149:VAL:O	2:D:153:LEU:HB2	2.18	0.43
1:E:8:PRO:HA	1:E:135:LEU:H	1.83	0.43
1:G:62:PHE:CD2	1:G:69:VAL:HG21	2.54	0.43
1:I:5:PRO:HD3	1:I:138:ILE:HD12	1.98	0.43
1:I:119:ASP:OD2	1:I:121:ASN:HB2	2.18	0.43
1:J:25:ILE:HB	1:J:30:TYR:HE1	1.83	0.43
1:J:53:ILE:HG23	1:J:88:ARG:NH2	2.33	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:35:VAL:HB	1:L:129:ILE:HD12	1.99	0.43
1:P:38:PHE:HD2	1:P:147:ARG:NH2	2.16	0.43
1:Q:1:MET:HE3	1:Q:1:MET:HB2	1.92	0.43
2:D:53:ILE:HG13	2:D:96:MET:HE1	2.00	0.43
2:D:158:ALA:O	2:D:162:VAL:HG23	2.18	0.43
1:F:76:SER:HB3	1:F:104:ARG:NH1	2.33	0.43
1:I:93:LEU:HB3	1:I:96:MET:HE3	1.98	0.43
1:K:55:PHE:CD1	1:K:149:VAL:HG22	2.53	0.43
1:L:51:GLU:O	1:L:54:ALA:HB3	2.18	0.43
1:O:86:LEU:C	1:O:92:GLY:HA3	2.44	0.43
1:P:15:GLN:NE2	1:P:24:GLU:OE2	2.52	0.43
1:P:104:ARG:HH22	1:Q:104:ARG:NH1	2.15	0.43
1:Q:59:VAL:HA	1:Q:62:PHE:HD2	1.82	0.43
1:Q:159:PHE:CG	1:R:145:VAL:HG21	2.53	0.43
1:T:143:LYS:N	1:T:144:PRO:CD	2.81	0.43
1:A:154:ARG:NH2	1:B:148:SER:H	2.16	0.43
1:C:149:VAL:O	1:C:152:THR:N	2.51	0.43
1:I:145:VAL:HG21	1:J:159:PHE:HE1	1.78	0.43
1:J:35:VAL:HG12	1:J:36:VAL:N	2.32	0.43
1:K:126:LEU:N	1:K:139:THR:O	2.47	0.43
1:L:31:ARG:HD3	1:L:31:ARG:HA	1.89	0.43
1:L:34:TYR:CD1	1:L:130:ASP:HA	2.54	0.43
1:P:80:HIS:HB3	1:P:100:LEU:HD12	2.00	0.43
1:Q:16:ALA:HB1	1:Q:100:LEU:O	2.18	0.43
1:R:16:ALA:HA	1:R:101:LEU:HA	1.99	0.43
1:R:56:SER:HB2	1:R:96:MET:HE2	2.00	0.43
1:R:119:ASP:OD2	1:R:143:LYS:HE2	2.18	0.43
1:A:88:ARG:HA	1:A:92:GLY:O	2.18	0.43
1:B:53:ILE:HG12	1:B:93:LEU:HD22	2.00	0.43
1:B:160:GLN:OE1	1:K:164:LYS:O	2.36	0.43
1:C:136:ARG:HB3	1:C:159:PHE:CE2	2.54	0.43
1:F:16:ALA:HB2	1:F:101:LEU:CD1	2.49	0.43
1:H:46:PHE:O	1:H:47:VAL:C	2.61	0.43
1:L:162:VAL:O	1:L:166:GLY:HA2	2.17	0.43
1:P:75:ASP:HA	1:Q:104:ARG:NH2	2.33	0.43
1:Q:50:THR:HG23	1:Q:52:ILE:H	1.84	0.43
1:T:42:ALA:HB3	1:T:45:THR:HG21	2.01	0.43
1:A:38:PHE:O	1:A:38:PHE:CD1	2.72	0.43
1:A:145:VAL:HG11	1:B:159:PHE:CE1	2.53	0.43
1:A:160:GLN:O	1:A:164:LYS:HB3	2.19	0.43
1:E:105:LYS:HB2	1:E:107:GLU:HG2	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:151:GLU:OE2	1:G:154:ARG:NH2	2.52	0.43
1:J:38:PHE:O	1:J:72:CYS:N	2.52	0.43
1:J:112:TYR:HB2	1:J:114:VAL:HG22	1.99	0.43
1:M:11:GLU:OE1	1:M:27:LEU:HB3	2.19	0.43
1:M:94:GLY:O	1:M:96:MET:HE3	2.18	0.43
1:P:88:ARG:HA	1:P:92:GLY:H	1.83	0.43
1:P:137:GLN:HG2	1:P:155:LEU:HD13	2.01	0.43
1:R:3:LEU:H	1:R:3:LEU:HG	1.62	0.43
1:R:116:ASP:CG	1:R:119:ASP:HB2	2.44	0.43
1:A:50:THR:O	1:A:54:ALA:HB2	2.19	0.43
1:B:43:ASP:O	1:B:44:PHE:HB2	2.18	0.43
1:C:5:PRO:HD2	2:D:123:PHE:CD1	2.54	0.43
2:D:110:LYS:HG2	2:D:115:PHE:HB2	1.99	0.43
1:G:136:ARG:HB3	1:G:159:PHE:CE1	2.54	0.43
1:H:130:ASP:OD1	1:H:132:ASN:N	2.52	0.43
1:J:75:ASP:HB2	1:J:80:HIS:HE1	1.83	0.43
1:L:16:ALA:O	1:L:22:PHE:HA	2.18	0.43
1:M:58:GLN:NE2	1:M:58:GLN:HA	2.32	0.43
1:Q:105:LYS:HE3	1:Q:107:GLU:OE1	2.19	0.43
1:Q:137:GLN:HG3	1:Q:155:LEU:HD22	2.00	0.43
1:F:40:TYR:HA	1:F:124:ARG:HG2	2.01	0.43
1:G:168:VAL:CG2	1:G:170:PRO:HD2	2.49	0.43
1:H:30:TYR:O	1:H:33:LYS:HB2	2.19	0.43
1:H:34:TYR:HB2	1:H:66:ASN:O	2.19	0.43
1:I:48:CYS:SG	1:J:169:CYS:HA	2.58	0.43
1:M:48:CYS:N	1:M:49:PRO:HD3	2.34	0.43
1:O:126:LEU:HD23	1:O:127:PHE:N	2.33	0.43
1:O:162:VAL:HG21	1:P:145:VAL:CG2	2.44	0.43
1:A:137:GLN:HB2	1:A:159:PHE:HZ	1.84	0.43
1:B:35:VAL:HB	1:B:129:ILE:HB	2.00	0.43
2:D:49:PRO:O	2:D:53:ILE:HB	2.19	0.43
1:E:58:GLN:HB2	1:E:149:VAL:HG11	2.00	0.43
1:E:82:ALA:O	1:E:85:ASN:HB2	2.19	0.43
1:F:105:LYS:CB	1:F:107:GLU:HG3	2.49	0.43
1:G:2:VAL:HG12	1:G:4:LEU:CD1	2.48	0.43
1:I:25:ILE:HD11	1:I:101:LEU:CD1	2.43	0.43
1:K:18:ILE:O	1:K:21:GLU:N	2.52	0.43
1:L:39:PHE:CD1	1:L:114:VAL:HG21	2.54	0.43
1:L:117:GLU:OE1	1:L:117:GLU:HA	2.18	0.43
1:M:143:LYS:H	1:M:143:LYS:CD	2.31	0.43
1:O:53:ILE:H	1:O:53:ILE:HG13	1.54	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:116:ASP:OD1	1:O:116:ASP:O	2.36	0.43
1:Q:76:SER:HB3	1:Q:104:ARG:HB2	2.00	0.43
1:S:49:PRO:C	1:S:50:THR:OG1	2.58	0.43
1:S:53:ILE:HA	1:S:96:MET:HE1	2.00	0.43
1:T:124:ARG:HB3	1:T:147:ARG:CZ	2.48	0.43
1:A:44:PHE:CD2	1:J:79:SER:HA	2.54	0.43
1:B:41:PRO:HD2	1:B:46:PHE:HZ	1.84	0.43
1:C:4:LEU:HB3	2:D:123:PHE:CE2	2.54	0.43
1:E:21:GLU:HB3	1:E:23:LYS:HZ2	1.83	0.43
1:E:128:ILE:O	1:E:135:LEU:HD12	2.18	0.43
1:E:129:ILE:HG22	1:E:130:ASP:O	2.19	0.43
1:G:40:TYR:CD1	1:G:73:SER:HB3	2.54	0.43
1:G:168:VAL:HG23	1:G:170:PRO:HD2	2.00	0.43
1:I:89:LYS:O	1:I:89:LYS:HG3	2.19	0.43
1:J:15:GLN:HE22	1:J:24:GLU:CB	2.30	0.43
1:J:149:VAL:O	1:J:153:LEU:HD22	2.19	0.43
1:K:23:LYS:HB3	1:K:23:LYS:HE2	1.91	0.43
1:M:2:VAL:O	1:M:4:LEU:HG	2.19	0.43
1:P:53:ILE:HG23	1:P:88:ARG:CZ	2.49	0.43
1:S:43:ASP:O	1:S:44:PHE:HB2	2.19	0.43
1:T:51:GLU:HG2	1:T:55:PHE:HE2	1.83	0.43
1:B:50:THR:CG2	1:B:51:GLU:N	2.82	0.42
1:C:58:GLN:HG3	1:C:61:GLU:CG	2.49	0.42
1:C:68:GLN:OE1	1:C:68:GLN:HA	2.18	0.42
1:E:130:ASP:CB	1:E:131:PRO:HD2	2.47	0.42
1:E:157:ASP:O	1:E:160:GLN:HB2	2.19	0.42
1:H:154:ARG:NH2	1:H:155:LEU:HD21	2.34	0.42
1:I:130:ASP:HB3	1:I:136:ARG:CG	2.49	0.42
1:K:80:HIS:O	1:K:84:ASP:HB2	2.18	0.42
1:M:55:PHE:CZ	1:M:149:VAL:HG22	2.52	0.42
1:P:36:VAL:HG23	1:P:67:CYS:SG	2.59	0.42
1:Q:145:VAL:HG21	1:R:159:PHE:CD1	2.54	0.42
1:R:5:PRO:HB3	1:R:136:ARG:O	2.19	0.42
1:S:69:VAL:HG12	1:S:98:ILE:HD13	2.02	0.42
1:A:38:PHE:HE1	1:A:52:ILE:HG23	1.84	0.42
1:C:164:LYS:HB3	1:C:165:HIS:CD2	2.54	0.42
2:D:164:LYS:HG3	1:M:160:GLN:OE1	2.20	0.42
1:E:4:LEU:N	1:E:4:LEU:HD22	2.33	0.42
1:E:62:PHE:CE2	1:E:69:VAL:HG21	2.55	0.42
1:F:37:LEU:O	1:F:126:LEU:HA	2.19	0.42
1:F:164:LYS:CD	1:F:165:HIS:CE1	3.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:98:ILE:HG23	1:G:99:PRO:HD2	2.01	0.42
1:G:151:GLU:OE2	1:G:154:ARG:NE	2.51	0.42
1:I:58:GLN:OE1	1:I:58:GLN:HA	2.19	0.42
1:J:130:ASP:OD1	1:J:134:ILE:HG12	2.19	0.42
1:J:142:ASP:CG	1:J:144:PRO:HD2	2.44	0.42
1:K:55:PHE:CE2	1:K:149:VAL:HA	2.54	0.42
1:K:100:LEU:HD23	1:K:100:LEU:HA	1.80	0.42
1:O:134:ILE:HD13	1:O:134:ILE:N	2.33	0.42
1:R:153:LEU:CD1	1:R:153:LEU:H	2.32	0.42
1:S:44:PHE:CE1	1:S:83:TRP:HA	2.54	0.42
1:A:18:ILE:O	1:A:21:GLU:HB2	2.19	0.42
1:A:116:ASP:CB	1:A:119:ASP:HB2	2.49	0.42
1:C:105:LYS:HD3	1:C:107:GLU:CD	2.44	0.42
1:C:134:ILE:HG22	1:C:135:LEU:N	2.34	0.42
1:C:162:VAL:O	1:C:167:GLU:HA	2.20	0.42
1:G:38:PHE:CE1	1:G:71:ALA:HA	2.54	0.42
1:I:44:PHE:HE1	1:I:83:TRP:CD1	2.36	0.42
1:J:15:GLN:NE2	1:J:24:GLU:HB2	2.31	0.42
1:J:40:TYR:HE2	1:J:43:ASP:OD1	2.03	0.42
1:L:44:PHE:N	1:L:83:TRP:CE2	2.78	0.42
1:O:143:LYS:N	1:O:144:PRO:HD2	2.35	0.42
1:S:109:SER:HB2	1:S:115:PHE:HB2	2.01	0.42
1:S:154:ARG:NH1	1:T:148:SER:HB2	2.35	0.42
1:A:36:VAL:HB	1:A:69:VAL:HA	2.00	0.42
1:C:143:LYS:N	1:C:144:PRO:CD	2.82	0.42
1:E:16:ALA:O	1:E:22:PHE:HA	2.19	0.42
1:F:149:VAL:O	1:F:153:LEU:HD13	2.19	0.42
1:H:32:GLY:N	1:H:131:PRO:O	2.50	0.42
1:H:130:ASP:HB2	1:H:131:PRO:CD	2.45	0.42
1:M:43:ASP:HB3	1:M:83:TRP:CE3	2.53	0.42
1:N:135:LEU:HD12	1:N:136:ARG:N	2.35	0.42
1:O:101:LEU:HD12	1:O:102:ALA:H	1.84	0.42
1:Q:38:PHE:HB3	1:Q:126:LEU:CG	2.50	0.42
1:R:128:ILE:HG22	1:R:136:ARG:CG	2.50	0.42
1:S:34:TYR:CE1	1:S:131:PRO:HD3	2.54	0.42
1:B:96:MET:HE2	1:B:96:MET:HA	2.00	0.42
1:B:105:LYS:O	1:B:107:GLU:N	2.53	0.42
2:D:105:LYS:HD2	1:E:118:GLU:O	2.20	0.42
1:G:126:LEU:HD23	1:G:127:PHE:N	2.34	0.42
1:H:9:ALA:HA	1:H:10:PRO:HD3	1.81	0.42
1:J:159:PHE:O	1:J:163:GLU:HG3	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:115:PHE:HE1	1:L:121:ASN:H	1.61	0.42
1:O:86:LEU:CD1	1:O:90:SER:HB3	2.34	0.42
1:P:112:TYR:CD1	1:P:127:PHE:CZ	3.08	0.42
1:Q:18:ILE:CG1	1:Q:23:LYS:HD3	2.49	0.42
1:Q:137:GLN:HB2	1:Q:159:PHE:CE2	2.54	0.42
1:C:13:LYS:HA	1:C:13:LYS:HD2	1.84	0.42
1:E:5:PRO:CB	1:E:136:ARG:O	2.63	0.42
1:E:31:ARG:NH1	1:E:133:GLY:HA3	2.34	0.42
1:J:52:ILE:H	1:J:52:ILE:HG13	1.25	0.42
1:J:69:VAL:HB	1:J:98:ILE:HD12	2.02	0.42
1:K:32:GLY:C	1:K:131:PRO:HB3	2.45	0.42
1:M:83:TRP:HE1	1:M:92:GLY:HA2	1.83	0.42
1:M:87:ASP:OD1	1:M:89:LYS:HB3	2.20	0.42
1:R:58:GLN:OE1	1:R:58:GLN:N	2.51	0.42
1:S:143:LYS:HB3	1:S:144:PRO:CD	2.50	0.42
1:C:8:PRO:HA	1:C:134:ILE:HA	2.02	0.42
1:C:36:VAL:HG22	1:C:128:ILE:HG12	2.01	0.42
1:C:62:PHE:HB3	1:C:67:CYS:O	2.18	0.42
1:G:103:ASP:OD1	1:G:106:GLN:HA	2.18	0.42
1:H:103:ASP:HB2	1:H:108:ILE:CD1	2.43	0.42
1:I:43:ASP:HA	1:I:83:TRP:CZ3	2.55	0.42
1:K:123:PHE:CE2	1:K:143:LYS:HE2	2.55	0.42
1:K:136:ARG:HG3	1:K:159:PHE:CD1	2.55	0.42
1:M:74:THR:HA	1:M:103:ASP:O	2.19	0.42
1:O:5:PRO:HD2	1:P:123:PHE:CE2	2.54	0.42
1:P:129:ILE:HG22	1:P:130:ASP:O	2.20	0.42
1:Q:145:VAL:HG13	1:R:158:ALA:HB1	2.01	0.42
1:B:68:GLN:NE2	1:B:99:PRO:HG3	2.35	0.42
1:C:146:GLY:C	1:C:147:ARG:HG3	2.44	0.42
1:G:17:VAL:HG13	1:G:20:GLY:C	2.44	0.42
1:J:111:ALA:C	1:J:113:GLY:H	2.27	0.42
1:K:55:PHE:HE1	1:K:147:ARG:O	2.01	0.42
1:N:39:PHE:CD2	1:N:72:CYS:HB3	2.55	0.42
1:N:44:PHE:N	1:N:83:TRP:CE2	2.88	0.42
1:N:51:GLU:O	1:N:54:ALA:N	2.53	0.42
1:P:19:ASN:O	1:P:21:GLU:HG3	2.20	0.42
1:P:24:GLU:HA	1:P:24:GLU:OE1	2.20	0.42
1:P:93:LEU:HD13	1:P:96:MET:CE	2.49	0.42
1:T:51:GLU:OE2	1:T:147:ARG:CZ	2.67	0.42
1:A:98:ILE:HA	1:A:99:PRO:HD3	1.88	0.42
1:A:143:LYS:N	1:A:144:PRO:HD2	2.35	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:108:ILE:O	1:C:111:ALA:HB3	2.20	0.42
1:C:126:LEU:HB3	1:C:139:THR:CB	2.46	0.42
2:D:105:LYS:HD2	1:E:119:ASP:HA	2.02	0.42
2:D:135:LEU:HD21	2:D:138:ILE:HD11	2.01	0.42
1:F:14:GLY:O	1:F:101:LEU:HD11	2.20	0.42
1:I:165:HIS:CD2	1:I:165:HIS:N	2.85	0.42
1:J:25:ILE:HB	1:J:30:TYR:CE1	2.55	0.42
1:J:83:TRP:NE1	1:J:92:GLY:HA2	2.34	0.42
1:K:141:ASN:HA	1:L:137:GLN:OE1	2.20	0.42
1:M:50:THR:O	1:M:50:THR:HG22	2.19	0.42
1:N:147:ARG:H	1:N:147:ARG:NE	1.99	0.42
1:O:114:VAL:HG11	1:O:125:GLY:HA3	2.02	0.42
1:P:4:LEU:HD22	1:P:4:LEU:N	2.35	0.42
1:P:105:LYS:HD3	1:P:107:GLU:OE1	2.19	0.42
1:P:138:ILE:HD12	1:P:138:ILE:N	2.34	0.42
1:Q:80:HIS:CD2	1:Q:100:LEU:HB3	2.54	0.42
1:S:35:VAL:CG1	1:S:70:ILE:HD12	2.50	0.42
1:T:84:ASP:OD1	1:T:96:MET:HB2	2.19	0.42
1:C:60:GLU:HA	1:C:63:ASN:ND2	2.35	0.42
1:I:30:TYR:CE1	1:I:68:GLN:HG2	2.55	0.42
1:J:34:TYR:CD2	1:J:156:LEU:HD21	2.55	0.42
1:L:72:CYS:SG	1:L:73:SER:N	2.93	0.42
1:M:130:ASP:OD1	1:M:134:ILE:O	2.38	0.42
1:N:6:ASN:HB3	1:N:7:ARG:HD2	2.02	0.42
1:N:78:TYR:O	1:N:81:LEU:HB3	2.20	0.42
1:P:158:ALA:HA	1:P:161:PHE:CB	2.49	0.42
1:R:38:PHE:HE2	1:R:69:VAL:CG1	2.33	0.42
1:R:76:SER:OG	1:R:78:TYR:N	2.53	0.42
1:S:37:LEU:HD23	1:S:112:TYR:CZ	2.55	0.42
1:S:105:LYS:HB3	1:S:105:LYS:HE2	1.67	0.42
1:A:5:PRO:O	1:A:6:ASN:CB	2.67	0.41
1:A:36:VAL:O	1:A:70:ILE:N	2.53	0.41
1:A:116:ASP:CG	1:A:119:ASP:HB2	2.45	0.41
1:B:75:ASP:O	1:B:102:ALA:HB1	2.20	0.41
1:L:105:LYS:HE3	1:M:117:GLU:O	2.20	0.41
1:L:127:PHE:HD1	1:L:138:ILE:HG12	1.85	0.41
1:P:38:PHE:HB2	1:P:147:ARG:NH1	2.35	0.41
1:P:65:ARG:CD	1:P:160:GLN:HE22	2.31	0.41
1:Q:88:ARG:HG3	1:Q:94:GLY:N	2.35	0.41
1:S:168:VAL:O	1:S:169:CYS:C	2.63	0.41
1:T:65:ARG:HE	1:T:65:ARG:HB3	1.53	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:LEU:C	1:A:4:LEU:HD22	2.45	0.41
1:B:105:LYS:C	1:B:107:GLU:H	2.28	0.41
1:B:127:PHE:HE1	1:B:138:ILE:HG23	1.85	0.41
1:B:143:LYS:N	1:B:144:PRO:HD2	2.34	0.41
1:E:51:GLU:O	1:E:54:ALA:HB3	2.20	0.41
1:E:87:ASP:O	1:E:88:ARG:HG2	2.20	0.41
1:F:135:LEU:HD12	1:F:136:ARG:H	1.84	0.41
1:I:62:PHE:O	1:I:67:CYS:N	2.50	0.41
1:I:75:ASP:O	1:I:102:ALA:HB1	2.20	0.41
1:J:71:ALA:CB	1:J:100:LEU:HD22	2.51	0.41
1:L:46:PHE:C	1:L:49:PRO:HD2	2.44	0.41
1:N:87:ASP:HA	1:N:95:HIS:NE2	2.35	0.41
1:Q:126:LEU:HD23	1:Q:127:PHE:N	2.35	0.41
1:Q:158:ALA:O	1:Q:161:PHE:HB3	2.20	0.41
1:T:40:TYR:CE1	1:T:73:SER:HB2	2.55	0.41
1:T:126:LEU:CB	1:T:139:THR:HB	2.41	0.41
1:B:58:GLN:NE2	1:B:149:VAL:HG21	2.35	0.41
1:E:22:PHE:CZ	1:E:81:LEU:HD22	2.55	0.41
1:G:1:MET:HB3	1:H:1:MET:SD	2.60	0.41
1:G:34:TYR:CD1	1:G:130:ASP:HA	2.55	0.41
1:G:96:MET:SD	1:G:100:LEU:HD11	2.60	0.41
1:I:56:SER:O	1:I:97:LYS:HB2	2.20	0.41
1:L:125:GLY:O	1:L:147:ARG:NH1	2.53	0.41
1:M:71:ALA:HB3	1:M:100:LEU:HA	2.01	0.41
1:P:130:ASP:HB3	1:P:136:ARG:HH11	1.85	0.41
1:Q:76:SER:HA	1:Q:102:ALA:HB1	2.02	0.41
1:S:34:TYR:CD1	1:S:131:PRO:HD3	2.55	0.41
1:T:62:PHE:HB3	1:T:67:CYS:CB	2.35	0.41
1:T:86:LEU:HG	1:T:92:GLY:N	2.35	0.41
1:A:34:TYR:CE1	1:A:131:PRO:HD3	2.56	0.41
2:D:51:GLU:HG3	2:D:147:ARG:H	1.85	0.41
2:D:93:LEU:HD13	2:D:96:MET:HG3	2.01	0.41
2:D:126:LEU:HD23	2:D:126:LEU:C	2.44	0.41
1:E:143:LYS:N	1:E:144:PRO:HD2	2.35	0.41
1:F:7:ARG:HB3	1:F:8:PRO:HD2	2.02	0.41
1:F:161:PHE:CD1	1:F:161:PHE:C	2.97	0.41
1:H:154:ARG:HH22	1:H:155:LEU:HD21	1.85	0.41
1:I:44:PHE:HE1	1:I:83:TRP:CG	2.38	0.41
1:J:169:CYS:HA	1:J:170:PRO:HD3	1.83	0.41
1:M:18:ILE:CD1	1:M:99:PRO:HB3	2.50	0.41
1:M:76:SER:O	1:M:80:HIS:CD2	2.73	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:68:GLN:OE1	1:N:68:GLN:HA	2.19	0.41
1:N:132:ASN:HB2	1:N:134:ILE:HG13	2.01	0.41
1:O:74:THR:HA	1:O:103:ASP:HB2	2.02	0.41
1:P:23:LYS:HD2	1:P:23:LYS:N	2.35	0.41
2:D:110:LYS:HG2	2:D:115:PHE:CB	2.50	0.41
2:D:130:ASP:OD2	2:D:134:ILE:HB	2.20	0.41
1:E:34:TYR:O	1:E:67:CYS:HA	2.21	0.41
1:E:159:PHE:CE1	1:F:145:VAL:HG11	2.54	0.41
1:G:75:ASP:O	1:G:80:HIS:HE1	2.03	0.41
1:I:65:ARG:NE	1:I:153:LEU:HD12	2.35	0.41
1:J:75:ASP:HB3	1:J:79:SER:HB2	2.02	0.41
1:O:2:VAL:HG22	1:P:113:GLY:HA3	2.02	0.41
1:S:150:ASP:O	1:S:154:ARG:HB2	2.21	0.41
1:B:116:ASP:HB2	1:B:123:PHE:CE2	2.56	0.41
1:E:51:GLU:OE2	1:E:147:ARG:HB2	2.21	0.41
1:F:146:GLY:O	1:F:147:ARG:HG3	2.21	0.41
1:I:2:VAL:HG23	1:J:1:MET:N	2.34	0.41
1:J:60:GLU:OE1	1:J:60:GLU:CA	2.64	0.41
1:M:37:LEU:HG	1:M:39:PHE:CE1	2.55	0.41
1:O:26:CYS:SG	1:O:27:LEU:N	2.93	0.41
1:Q:115:PHE:CE1	1:Q:117:GLU:HA	2.54	0.41
1:Q:124:ARG:HG3	1:Q:142:ASP:O	2.21	0.41
1:R:36:VAL:CG2	1:R:128:ILE:HG12	2.44	0.41
1:R:43:ASP:OD1	1:R:80:HIS:CE1	2.74	0.41
1:S:48:CYS:O	1:S:49:PRO:C	2.63	0.41
1:T:3:LEU:C	1:T:4:LEU:HD12	2.46	0.41
1:A:12:PHE:CE1	1:A:27:LEU:HD22	2.55	0.41
1:A:58:GLN:C	1:A:60:GLU:N	2.77	0.41
1:B:137:GLN:OE1	1:B:137:GLN:HA	2.20	0.41
1:C:93:LEU:HD13	1:C:96:MET:SD	2.61	0.41
1:F:54:ALA:O	1:F:58:GLN:HG3	2.20	0.41
1:G:34:TYR:CE1	1:G:131:PRO:HD3	2.56	0.41
1:I:154:ARG:HH21	1:I:155:LEU:HD21	1.85	0.41
1:L:21:GLU:HB2	1:L:23:LYS:HE3	2.02	0.41
1:M:47:VAL:HB	1:M:49:PRO:HD2	2.03	0.41
1:M:77:GLN:O	1:M:81:LEU:N	2.54	0.41
1:O:123:PHE:CD2	1:P:4:LEU:HD12	2.56	0.41
1:Q:59:VAL:HA	1:Q:62:PHE:CD2	2.55	0.41
1:Q:138:ILE:HB	1:R:140:ILE:HB	2.03	0.41
1:B:3:LEU:HD21	1:B:111:ALA:O	2.21	0.41
1:B:36:VAL:O	1:B:69:VAL:HA	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:58:GLN:HG2	1:C:149:VAL:HG21	2.01	0.41
1:C:61:GLU:CB	1:C:153:LEU:HD21	2.50	0.41
2:D:123:PHE:HA	2:D:143:LYS:HE2	2.02	0.41
1:E:103:ASP:HB2	1:E:108:ILE:CD1	2.46	0.41
1:G:2:VAL:H	1:H:1:MET:HB2	1.86	0.41
1:H:13:LYS:O	1:H:101:LEU:HD11	2.20	0.41
1:H:42:ALA:O	1:H:45:THR:HG23	2.21	0.41
1:K:46:PHE:CE2	1:K:83:TRP:HZ2	2.39	0.41
1:P:53:ILE:HG12	1:P:93:LEU:HD23	2.01	0.41
1:P:84:ASP:O	1:P:94:GLY:N	2.54	0.41
1:Q:33:LYS:C	1:Q:131:PRO:HG3	2.45	0.41
1:T:68:GLN:OE1	1:T:68:GLN:HA	2.19	0.41
1:A:61:GLU:CG	1:A:65:ARG:HH21	2.34	0.41
1:A:165:HIS:N	1:A:165:HIS:ND1	2.69	0.41
1:B:36:VAL:HG23	1:B:67:CYS:SG	2.61	0.41
1:B:104:ARG:NH2	1:C:75:ASP:HA	2.36	0.41
1:C:66:ASN:O	1:C:66:ASN:CG	2.64	0.41
2:D:16:ALA:HA	2:D:100:LEU:O	2.21	0.41
2:D:17:VAL:O	2:D:99:PRO:HA	2.21	0.41
2:D:66:ASN:HB2	1:M:166:GLY:HA2	2.03	0.41
2:D:120:GLY:HA3	1:E:104:ARG:HB3	2.03	0.41
1:E:155:LEU:O	1:E:159:PHE:HD1	2.03	0.41
1:F:43:ASP:OD1	1:F:83:TRP:CZ3	2.74	0.41
1:G:76:SER:O	1:G:80:HIS:CE1	2.74	0.41
1:G:163:GLU:O	1:G:163:GLU:HG2	2.20	0.41
1:H:123:PHE:HB3	1:H:140:ILE:HD11	2.02	0.41
1:I:33:LYS:HD2	1:I:66:ASN:OD1	2.21	0.41
1:K:31:ARG:CZ	1:K:133:GLY:HA3	2.51	0.41
1:K:65:ARG:HG2	1:K:156:LEU:HG	2.01	0.41
1:K:104:ARG:HG2	1:T:121:ASN:ND2	2.35	0.41
1:L:25:ILE:HD11	1:L:101:LEU:HD13	2.02	0.41
1:L:38:PHE:CD2	1:L:147:ARG:NH2	2.85	0.41
1:L:87:ASP:O	1:L:90:SER:N	2.54	0.41
1:N:9:ALA:HB2	1:N:135:LEU:HB2	2.03	0.41
1:N:77:GLN:HE21	1:N:77:GLN:HB3	1.71	0.41
1:N:80:HIS:CD2	1:N:102:ALA:HB2	2.56	0.41
1:N:98:ILE:HA	1:N:99:PRO:HD3	1.88	0.41
1:N:104:ARG:HH22	1:O:75:ASP:CA	2.32	0.41
1:O:12:PHE:CE2	1:O:27:LEU:HD13	2.56	0.41
1:O:68:GLN:HG3	1:O:70:ILE:HG13	2.03	0.41
1:R:3:LEU:HD12	1:R:3:LEU:O	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:68:GLN:HA	1:R:68:GLN:HE21	1.84	0.41
1:S:41:PRO:CD	1:S:124:ARG:HG2	2.42	0.41
1:S:126:LEU:HD23	1:S:127:PHE:N	2.36	0.41
1:T:126:LEU:HB2	1:T:147:ARG:HD3	2.03	0.41
1:A:76:SER:HB3	1:A:104:ARG:CZ	2.51	0.41
2:D:34:TYR:CD1	2:D:130:ASP:HA	2.55	0.41
2:D:129:ILE:HG23	2:D:134:ILE:C	2.46	0.41
1:E:4:LEU:HA	1:E:5:PRO:HD3	1.82	0.41
1:G:112:TYR:HB3	1:G:127:PHE:CZ	2.56	0.41
1:J:81:LEU:O	1:J:84:ASP:HB3	2.21	0.41
1:J:139:THR:O	1:J:139:THR:HG22	2.21	0.41
1:K:39:PHE:O	1:K:40:TYR:HB3	2.21	0.41
1:O:116:ASP:HB2	1:P:7:ARG:HH22	1.85	0.41
1:O:124:ARG:HB3	1:O:147:ARG:CZ	2.52	0.41
1:R:39:PHE:CD1	1:R:39:PHE:N	2.89	0.41
1:R:47:VAL:O	1:R:47:VAL:HG23	2.20	0.41
1:T:115:PHE:HA	1:T:122:ALA:HB2	2.03	0.41
1:A:150:ASP:O	1:A:153:LEU:HB2	2.21	0.40
1:B:153:LEU:O	1:B:154:ARG:C	2.64	0.40
2:D:34:TYR:HA	2:D:129:ILE:O	2.20	0.40
2:D:126:LEU:HB3	2:D:139:THR:CG2	2.52	0.40
1:G:98:ILE:HA	1:G:99:PRO:HD3	1.85	0.40
1:H:18:ILE:O	1:H:19:ASN:C	2.64	0.40
1:H:40:TYR:CG	1:H:52:ILE:HD11	2.56	0.40
1:J:38:PHE:CD1	1:J:38:PHE:C	2.99	0.40
1:J:127:PHE:N	1:J:127:PHE:CD1	2.88	0.40
1:N:18:ILE:HD12	1:N:23:LYS:CB	2.39	0.40
1:N:105:LYS:HD2	1:N:107:GLU:OE2	2.21	0.40
1:O:48:CYS:O	1:O:48:CYS:SG	2.79	0.40
1:O:51:GLU:O	1:O:54:ALA:HB3	2.20	0.40
1:O:71:ALA:O	1:O:101:LEU:HB3	2.21	0.40
1:O:130:ASP:HB2	1:O:131:PRO:HD2	2.02	0.40
1:P:16:ALA:HA	1:P:100:LEU:O	2.20	0.40
1:Q:4:LEU:HA	1:Q:5:PRO:HD3	1.73	0.40
1:T:105:LYS:C	1:T:107:GLU:N	2.80	0.40
1:T:126:LEU:HB3	1:T:139:THR:CB	2.41	0.40
1:T:164:LYS:HE3	1:T:164:LYS:HB2	1.89	0.40
1:C:105:LYS:HD3	1:C:107:GLU:OE1	2.22	0.40
2:D:10:PRO:HD2	2:D:112:TYR:OH	2.20	0.40
2:D:127:PHE:CE2	2:D:138:ILE:HG23	2.55	0.40
1:E:128:ILE:HD12	1:E:137:GLN:HG3	2.03	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:156:LEU:HA	1:E:156:LEU:HD12	1.84	0.40
1:J:88:ARG:C	1:J:91:GLY:H	2.29	0.40
1:K:61:GLU:O	1:K:65:ARG:HD3	2.21	0.40
1:K:124:ARG:HD3	1:K:147:ARG:NH2	2.36	0.40
1:L:137:GLN:HG2	1:L:155:LEU:HD13	2.03	0.40
1:M:112:TYR:C	1:M:114:VAL:H	2.30	0.40
1:Q:4:LEU:O	1:Q:135:LEU:HD23	2.22	0.40
1:Q:35:VAL:HB	1:Q:129:ILE:HD12	2.02	0.40
1:S:142:ASP:HB2	1:T:136:ARG:HG2	2.04	0.40
1:T:71:ALA:HB3	1:T:100:LEU:CD2	2.52	0.40
1:C:2:VAL:CG2	2:D:3:LEU:HB3	2.51	0.40
1:C:61:GLU:HB3	1:C:153:LEU:HD21	2.04	0.40
2:D:53:ILE:HG13	2:D:96:MET:CE	2.51	0.40
2:D:69:VAL:HG12	2:D:70:ILE:N	2.37	0.40
1:G:16:ALA:CB	1:G:101:LEU:HA	2.52	0.40
1:G:34:TYR:CE1	1:G:130:ASP:HA	2.56	0.40
1:G:40:TYR:OH	1:G:80:HIS:HD2	2.04	0.40
1:H:4:LEU:HB3	1:H:5:PRO:CD	2.51	0.40
1:H:86:LEU:HD12	1:H:86:LEU:HA	1.89	0.40
1:M:108:ILE:O	1:M:112:TYR:HD1	2.05	0.40
1:N:123:PHE:CE1	1:N:143:LYS:HG2	2.57	0.40
1:N:141:ASN:ND2	1:N:145:VAL:HG12	2.36	0.40
1:P:157:ASP:OD1	1:P:158:ALA:N	2.54	0.40
1:Q:40:TYR:CE2	1:Q:42:ALA:O	2.75	0.40
1:T:124:ARG:HD2	1:T:145:VAL:O	2.21	0.40
1:A:28:LYS:HE3	1:A:31:ARG:NE	2.23	0.40
1:A:43:ASP:OD1	1:A:83:TRP:CZ3	2.74	0.40
1:A:74:THR:CG2	1:A:106:GLN:HG2	2.49	0.40
1:C:126:LEU:HD23	1:C:127:PHE:N	2.37	0.40
1:C:161:PHE:CE1	1:C:165:HIS:CE1	3.10	0.40
1:E:4:LEU:O	1:E:135:LEU:HD23	2.21	0.40
1:E:32:GLY:HA2	1:E:131:PRO:CB	2.51	0.40
1:G:121:ASN:OD1	1:G:121:ASN:N	2.55	0.40
1:I:12:PHE:HB2	1:I:108:ILE:CG1	2.51	0.40
1:L:44:PHE:HA	1:L:83:TRP:NE1	2.37	0.40
1:L:168:VAL:O	1:L:168:VAL:HG12	2.20	0.40
1:Q:145:VAL:HG13	1:R:158:ALA:CB	2.50	0.40
1:T:38:PHE:HB2	1:T:125:GLY:O	2.21	0.40
1:T:59:VAL:HG13	1:T:63:ASN:OD1	2.21	0.40
1:A:5:PRO:HD3	1:B:140:ILE:HG21	2.04	0.40
1:B:77:GLN:CD	1:B:77:GLN:N	2.79	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:155:LEU:O	1:B:158:ALA:N	2.55	0.40
1:C:35:VAL:CG1	1:C:129:ILE:HD12	2.52	0.40
1:C:84:ASP:CB	1:C:93:LEU:HD12	2.52	0.40
2:D:142:ASP:CG	2:D:144:PRO:HD2	2.47	0.40
2:D:162:VAL:O	2:D:166:GLY:N	2.54	0.40
1:E:159:PHE:CG	1:F:145:VAL:HG21	2.56	0.40
1:G:25:ILE:CD1	1:G:101:LEU:HD13	2.49	0.40
1:G:116:ASP:OD1	1:G:118:GLU:HB3	2.21	0.40
1:H:74:THR:O	1:H:74:THR:HG22	2.22	0.40
1:H:84:ASP:O	1:H:94:GLY:N	2.54	0.40
1:I:25:ILE:O	1:I:25:ILE:HG13	2.21	0.40
1:I:86:LEU:HD23	1:I:91:GLY:O	2.22	0.40
1:I:105:LYS:O	1:I:106:GLN:HB2	2.20	0.40
1:M:38:PHE:HA	1:M:125:GLY:O	2.22	0.40
1:N:12:PHE:CZ	1:N:27:LEU:HD13	2.57	0.40
1:R:36:VAL:HG23	1:R:67:CYS:SG	2.62	0.40
1:R:98:ILE:HA	1:R:99:PRO:HD3	1.97	0.40
1:R:109:SER:HB3	1:R:114:VAL:CG2	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	163/219 (74%)	154 (94%)	9 (6%)	0	100	100
1	B	164/219 (75%)	154 (94%)	10 (6%)	0	100	100
1	C	172/219 (78%)	157 (91%)	15 (9%)	0	100	100
1	E	165/219 (75%)	155 (94%)	8 (5%)	2 (1%)	10	40
1	F	170/219 (78%)	149 (88%)	21 (12%)	0	100	100
1	G	170/219 (78%)	157 (92%)	11 (6%)	2 (1%)	10	40

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	169/219 (77%)	151 (89%)	18 (11%)	0	100	100
1	I	165/219 (75%)	154 (93%)	11 (7%)	0	100	100
1	J	169/219 (77%)	155 (92%)	12 (7%)	2 (1%)	10	40
1	K	168/219 (77%)	156 (93%)	12 (7%)	0	100	100
1	L	169/219 (77%)	155 (92%)	13 (8%)	1 (1%)	21	56
1	M	169/219 (77%)	156 (92%)	12 (7%)	1 (1%)	21	56
1	N	163/219 (74%)	147 (90%)	16 (10%)	0	100	100
1	O	163/219 (74%)	153 (94%)	10 (6%)	0	100	100
1	P	165/219 (75%)	152 (92%)	12 (7%)	1 (1%)	21	56
1	Q	159/219 (73%)	145 (91%)	14 (9%)	0	100	100
1	R	164/219 (75%)	147 (90%)	17 (10%)	0	100	100
1	S	170/219 (78%)	150 (88%)	19 (11%)	1 (1%)	21	56
1	T	168/219 (77%)	151 (90%)	17 (10%)	0	100	100
2	D	166/219 (76%)	156 (94%)	10 (6%)	0	100	100
All	All	3331/4380 (76%)	3054 (92%)	267 (8%)	10 (0%)	36	70

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	P	47	VAL
1	M	47	VAL
1	E	171	VAL
1	J	47	VAL
1	J	48	CYS
1	E	168	VAL
1	G	2	VAL
1	L	168	VAL
1	G	49	PRO
1	S	168	VAL

5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	144/188 (77%)	128 (89%)	16 (11%)	6	25
1	B	145/188 (77%)	131 (90%)	14 (10%)	8	30
1	C	152/188 (81%)	140 (92%)	12 (8%)	11	39
1	E	147/188 (78%)	131 (89%)	16 (11%)	6	26
1	F	149/188 (79%)	130 (87%)	19 (13%)	4	19
1	G	150/188 (80%)	139 (93%)	11 (7%)	13	42
1	H	149/188 (79%)	143 (96%)	6 (4%)	28	62
1	I	145/188 (77%)	132 (91%)	13 (9%)	9	34
1	J	149/188 (79%)	133 (89%)	16 (11%)	6	26
1	K	148/188 (79%)	134 (90%)	14 (10%)	8	31
1	L	149/188 (79%)	132 (89%)	17 (11%)	5	24
1	M	148/188 (79%)	135 (91%)	13 (9%)	9	35
1	N	143/188 (76%)	135 (94%)	8 (6%)	19	52
1	O	145/188 (77%)	132 (91%)	13 (9%)	9	34
1	P	145/188 (77%)	133 (92%)	12 (8%)	10	37
1	Q	142/188 (76%)	127 (89%)	15 (11%)	6	27
1	R	145/188 (77%)	135 (93%)	10 (7%)	14	45
1	S	149/188 (79%)	129 (87%)	20 (13%)	4	18
1	T	148/188 (79%)	138 (93%)	10 (7%)	14	45
2	D	146/188 (78%)	133 (91%)	13 (9%)	9	34
All	All	2938/3760 (78%)	2670 (91%)	268 (9%)	9	33

All (268) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	ILE
1	A	39	PHE
1	A	45	THR
1	A	47	VAL
1	A	53	ILE
1	A	74	THR
1	A	77	GLN
1	A	98	ILE
1	A	107	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	129	ILE
1	A	132	ASN
1	A	136	ARG
1	A	139	THR
1	A	145	VAL
1	A	156	LEU
1	A	165	HIS
1	B	18	ILE
1	B	26	CYS
1	B	29	ASP
1	B	37	LEU
1	B	47	VAL
1	B	56	SER
1	B	74	THR
1	B	77	GLN
1	B	87	ASP
1	B	97	LYS
1	B	132	ASN
1	B	143	LYS
1	B	145	VAL
1	B	153	LEU
1	C	4	LEU
1	C	52	ILE
1	C	53	ILE
1	C	67	CYS
1	C	80	HIS
1	C	98	ILE
1	C	109	SER
1	C	126	LEU
1	C	128	ILE
1	C	139	THR
1	C	165	HIS
1	C	171	VAL
2	D	15	GLN
2	D	28	LYS
2	D	43	ASP
2	D	46	PHE
2	D	47	VAL
2	D	70	ILE
2	D	74	THR
2	D	78	TYR
2	D	105	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	D	132	ASN
2	D	139	THR
2	D	149	VAL
2	D	150	ASP
1	E	17	VAL
1	E	37	LEU
1	E	45	THR
1	E	69	VAL
1	E	90	SER
1	E	98	ILE
1	E	114	VAL
1	E	126	LEU
1	E	130	ASP
1	E	137	GLN
1	E	139	THR
1	E	148	SER
1	E	155	LEU
1	E	165	HIS
1	E	167	GLU
1	E	169	CYS
1	F	0	THR
1	F	18	ILE
1	F	24	GLU
1	F	25	ILE
1	F	47	VAL
1	F	52	ILE
1	F	53	ILE
1	F	59	VAL
1	F	75	ASP
1	F	77	GLN
1	F	80	HIS
1	F	84	ASP
1	F	89	LYS
1	F	90	SER
1	F	105	LYS
1	F	109	SER
1	F	121	ASN
1	F	129	ILE
1	F	143	LYS
1	G	4	LEU
1	G	38	PHE
1	G	47	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	48	CYS
1	G	58	GLN
1	G	67	CYS
1	G	83	TRP
1	G	104	ARG
1	G	109	SER
1	G	116	ASP
1	G	162	VAL
1	H	35	VAL
1	H	97	LYS
1	H	104	ARG
1	H	114	VAL
1	H	138	ILE
1	H	153	LEU
1	I	47	VAL
1	I	66	ASN
1	I	74	THR
1	I	97	LYS
1	I	109	SER
1	I	114	VAL
1	I	117	GLU
1	I	126	LEU
1	I	130	ASP
1	I	142	ASP
1	I	148	SER
1	I	150	ASP
1	I	165	HIS
1	J	1	MET
1	J	18	ILE
1	J	22	PHE
1	J	36	VAL
1	J	48	CYS
1	J	52	ILE
1	J	58	GLN
1	J	64	SER
1	J	78	TYR
1	J	108	ILE
1	J	114	VAL
1	J	134	ILE
1	J	139	THR
1	J	140	ILE
1	J	153	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	J	163	GLU
1	K	0	THR
1	K	28	LYS
1	K	45	THR
1	K	74	THR
1	K	76	SER
1	K	77	GLN
1	K	84	ASP
1	K	90	SER
1	K	93	LEU
1	K	106	GLN
1	K	143	LYS
1	K	145	VAL
1	K	147	ARG
1	K	149	VAL
1	L	3	LEU
1	L	6	ASN
1	L	7	ARG
1	L	17	VAL
1	L	19	ASN
1	L	26	CYS
1	L	29	ASP
1	L	36	VAL
1	L	45	THR
1	L	93	LEU
1	L	95	HIS
1	L	128	ILE
1	L	129	ILE
1	L	156	LEU
1	L	162	VAL
1	L	163	GLU
1	L	167	GLU
1	M	0	THR
1	M	2	VAL
1	M	47	VAL
1	M	50	THR
1	M	52	ILE
1	M	53	ILE
1	M	57	ASP
1	M	64	SER
1	M	104	ARG
1	M	109	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	M	124	ARG
1	M	129	ILE
1	M	143	LYS
1	N	26	CYS
1	N	50	THR
1	N	76	SER
1	N	93	LEU
1	N	96	MET
1	N	119	ASP
1	N	129	ILE
1	N	147	ARG
1	O	40	TYR
1	O	52	ILE
1	O	53	ILE
1	O	59	VAL
1	O	64	SER
1	O	74	THR
1	O	86	LEU
1	O	108	ILE
1	O	114	VAL
1	O	129	ILE
1	O	139	THR
1	O	153	LEU
1	O	156	LEU
1	P	37	LEU
1	P	40	TYR
1	P	47	VAL
1	P	48	CYS
1	P	50	THR
1	P	74	THR
1	P	76	SER
1	P	93	LEU
1	P	98	ILE
1	P	139	THR
1	P	150	ASP
1	P	162	VAL
1	Q	3	LEU
1	Q	4	LEU
1	Q	17	VAL
1	Q	18	ILE
1	Q	31	ARG
1	Q	39	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	Q	45	THR
1	Q	52	ILE
1	Q	57	ASP
1	Q	74	THR
1	Q	86	LEU
1	Q	109	SER
1	Q	154	ARG
1	Q	155	LEU
1	Q	157	ASP
1	R	3	LEU
1	R	18	ILE
1	R	43	ASP
1	R	50	THR
1	R	59	VAL
1	R	74	THR
1	R	90	SER
1	R	105	LYS
1	R	153	LEU
1	R	155	LEU
1	S	2	VAL
1	S	18	ILE
1	S	38	PHE
1	S	48	CYS
1	S	50	THR
1	S	51	GLU
1	S	52	ILE
1	S	74	THR
1	S	90	SER
1	S	97	LYS
1	S	98	ILE
1	S	100	LEU
1	S	104	ARG
1	S	114	VAL
1	S	119	ASP
1	S	129	ILE
1	S	138	ILE
1	S	140	ILE
1	S	150	ASP
1	S	167	GLU
1	T	31	ARG
1	T	36	VAL
1	T	37	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	T	47	VAL
1	T	52	ILE
1	T	64	SER
1	T	65	ARG
1	T	80	HIS
1	T	109	SER
1	T	114	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (86) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	80	HIS
1	A	85	ASN
1	A	132	ASN
1	A	165	HIS
1	B	66	ASN
1	B	77	GLN
1	B	132	ASN
1	C	63	ASN
1	C	85	ASN
1	C	121	ASN
1	C	141	ASN
1	C	165	HIS
2	D	6	ASN
2	D	15	GLN
2	D	68	GLN
2	D	80	HIS
2	D	165	HIS
1	E	80	HIS
1	E	137	GLN
1	F	6	ASN
1	F	15	GLN
1	F	80	HIS
1	F	141	ASN
1	F	165	HIS
1	G	15	GLN
1	G	58	GLN
1	G	77	GLN
1	G	80	HIS
1	G	132	ASN
1	G	141	ASN
1	G	160	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	H	19	ASN
1	H	58	GLN
1	H	66	ASN
1	I	80	HIS
1	I	141	ASN
1	I	165	HIS
1	J	19	ASN
1	J	58	GLN
1	J	80	HIS
1	J	132	ASN
1	J	165	HIS
1	K	15	GLN
1	K	68	GLN
1	K	77	GLN
1	K	85	ASN
1	K	106	GLN
1	K	165	HIS
1	L	6	ASN
1	L	19	ASN
1	L	63	ASN
1	L	85	ASN
1	L	160	GLN
1	M	15	GLN
1	M	58	GLN
1	M	66	ASN
1	M	80	HIS
1	M	141	ASN
1	N	95	HIS
1	N	141	ASN
1	O	6	ASN
1	O	68	GLN
1	O	137	GLN
1	O	141	ASN
1	P	63	ASN
1	P	66	ASN
1	P	80	HIS
1	P	106	GLN
1	Q	77	GLN
1	Q	80	HIS
1	R	6	ASN
1	R	68	GLN
1	R	121	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	R	137	GLN
1	R	141	ASN
1	S	19	ASN
1	S	77	GLN
1	S	80	HIS
1	S	85	ASN
1	S	121	ASN
1	S	165	HIS
1	T	63	ASN
1	T	85	ASN
1	T	121	ASN
1	T	160	GLN
1	T	165	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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	165/219 (75%)	-1.66	0 100 100	32, 41, 45, 47	0
1	B	166/219 (75%)	-1.68	0 100 100	34, 41, 45, 49	0
1	C	174/219 (79%)	-1.66	0 100 100	34, 41, 46, 49	0
1	E	169/219 (77%)	-1.68	0 100 100	32, 39, 44, 48	0
1	F	172/219 (78%)	-1.68	0 100 100	32, 40, 45, 46	0
1	G	172/219 (78%)	-1.66	0 100 100	34, 41, 45, 47	0
1	H	171/219 (78%)	-1.67	0 100 100	31, 40, 45, 50	0
1	I	167/219 (76%)	-1.68	0 100 100	30, 40, 46, 49	0
1	J	171/219 (78%)	-1.69	0 100 100	30, 40, 44, 49	0
1	K	170/219 (77%)	-1.71	0 100 100	27, 39, 42, 45	0
1	L	171/219 (78%)	-1.68	0 100 100	31, 40, 44, 48	0
1	M	171/219 (78%)	-1.65	0 100 100	32, 41, 46, 49	0
1	N	165/219 (75%)	-1.69	0 100 100	31, 40, 47, 50	0
1	O	167/219 (76%)	-1.67	0 100 100	27, 41, 44, 46	0
1	P	167/219 (76%)	-1.65	0 100 100	33, 42, 45, 49	0
1	Q	163/219 (74%)	-1.69	0 100 100	31, 40, 45, 46	0
1	R	168/219 (76%)	-1.69	0 100 100	31, 42, 46, 50	0
1	S	172/219 (78%)	-1.67	0 100 100	31, 41, 45, 49	0
1	T	170/219 (77%)	-1.66	0 100 100	35, 41, 47, 57	0
2	D	168/219 (76%)	-1.68	0 100 100	32, 40, 45, 50	0
All	All	3379/4380 (77%)	-1.67	0 100 100	27, 40, 45, 57	0

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.