



Full wwPDB EM Validation Report ⓘ

Mar 30, 2026 – 11:28 AM UTC

PDB ID : 6ZXL / pdb_00006zxl
EMDB ID : EMD-11524
Title : Fully-loaded anthrax lethal toxin in its heptameric pre-pore state and PA7LF(2+1A) arrangement
Authors : Quentin, D.; Antoni, C.; Gatsogiannis, C.; Raunser, S.
Deposited on : 2020-07-29
Resolution : 4.20 Å(reported)
Based on initial model : 6ZXK

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

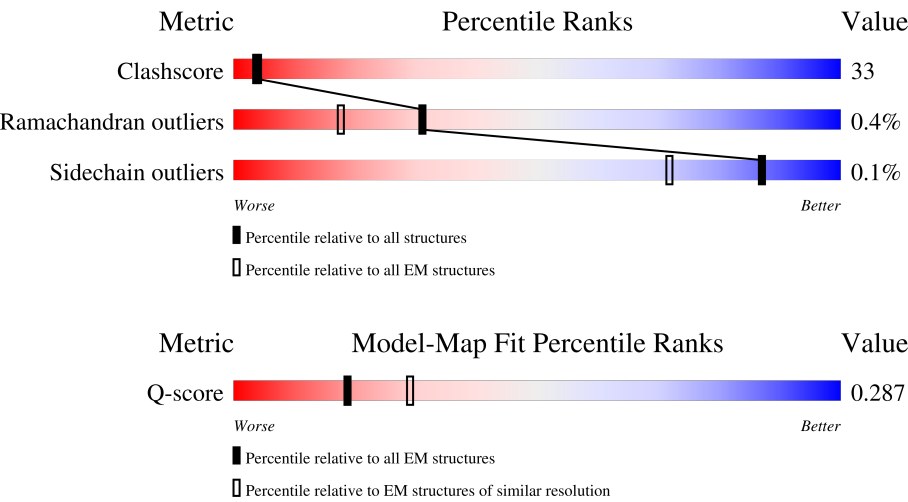
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5410 (3.70 - 4.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	759	6% 35% 34% 30%
1	B	759	35% 35% 30%
1	C	759	32% 37% 30%
1	D	759	35% 34% 30%

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Mol	Chain	Length	Quality of chain
1	E	759	5% 36%33%30%
1	F	759	37%32%30%
1	G	759	37%32%30%
2	H	809	8% 43%42%14%
2	I	809	27% 60%28%12%
2	J	809	58% 62%20%18%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 42172 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Protective antigen.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	529	Total	C	N	O	S	0	0
			3961	2477	691	789	4		
1	B	529	Total	C	N	O	S	0	0
			3977	2488	692	793	4		
1	C	529	Total	C	N	O	S	0	0
			3977	2488	692	793	4		
1	D	528	Total	C	N	O	S	0	0
			3970	2483	691	792	4		
1	E	529	Total	C	N	O	S	0	0
			3977	2488	692	793	4		
1	F	529	Total	C	N	O	S	0	0
			3977	2488	692	793	4		
1	G	529	Total	C	N	O	S	0	0
			3977	2488	692	793	4		

There are 161 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MET	-	initiating methionine	UNP Q68GS1
A	-22	GLY	-	expression tag	UNP Q68GS1
A	-21	HIS	-	expression tag	UNP Q68GS1
A	-20	HIS	-	expression tag	UNP Q68GS1
A	-19	HIS	-	expression tag	UNP Q68GS1
A	-18	HIS	-	expression tag	UNP Q68GS1
A	-17	HIS	-	expression tag	UNP Q68GS1
A	-16	HIS	-	expression tag	UNP Q68GS1
A	-15	HIS	-	expression tag	UNP Q68GS1
A	-14	HIS	-	expression tag	UNP Q68GS1
A	-13	HIS	-	expression tag	UNP Q68GS1
A	-12	HIS	-	expression tag	UNP Q68GS1
A	-11	SER	-	expression tag	UNP Q68GS1
A	-10	SER	-	expression tag	UNP Q68GS1
A	-9	GLY	-	expression tag	UNP Q68GS1
A	-8	HIS	-	expression tag	UNP Q68GS1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	ILE	-	expression tag	UNP Q68GS1
A	-6	ASP	-	expression tag	UNP Q68GS1
A	-5	ASP	-	expression tag	UNP Q68GS1
A	-4	ASP	-	expression tag	UNP Q68GS1
A	-3	ASP	-	expression tag	UNP Q68GS1
A	-2	LYS	-	expression tag	UNP Q68GS1
A	-1	HIS	-	expression tag	UNP Q68GS1
B	-23	MET	-	initiating methionine	UNP Q68GS1
B	-22	GLY	-	expression tag	UNP Q68GS1
B	-21	HIS	-	expression tag	UNP Q68GS1
B	-20	HIS	-	expression tag	UNP Q68GS1
B	-19	HIS	-	expression tag	UNP Q68GS1
B	-18	HIS	-	expression tag	UNP Q68GS1
B	-17	HIS	-	expression tag	UNP Q68GS1
B	-16	HIS	-	expression tag	UNP Q68GS1
B	-15	HIS	-	expression tag	UNP Q68GS1
B	-14	HIS	-	expression tag	UNP Q68GS1
B	-13	HIS	-	expression tag	UNP Q68GS1
B	-12	HIS	-	expression tag	UNP Q68GS1
B	-11	SER	-	expression tag	UNP Q68GS1
B	-10	SER	-	expression tag	UNP Q68GS1
B	-9	GLY	-	expression tag	UNP Q68GS1
B	-8	HIS	-	expression tag	UNP Q68GS1
B	-7	ILE	-	expression tag	UNP Q68GS1
B	-6	ASP	-	expression tag	UNP Q68GS1
B	-5	ASP	-	expression tag	UNP Q68GS1
B	-4	ASP	-	expression tag	UNP Q68GS1
B	-3	ASP	-	expression tag	UNP Q68GS1
B	-2	LYS	-	expression tag	UNP Q68GS1
B	-1	HIS	-	expression tag	UNP Q68GS1
C	-23	MET	-	initiating methionine	UNP Q68GS1
C	-22	GLY	-	expression tag	UNP Q68GS1
C	-21	HIS	-	expression tag	UNP Q68GS1
C	-20	HIS	-	expression tag	UNP Q68GS1
C	-19	HIS	-	expression tag	UNP Q68GS1
C	-18	HIS	-	expression tag	UNP Q68GS1
C	-17	HIS	-	expression tag	UNP Q68GS1
C	-16	HIS	-	expression tag	UNP Q68GS1
C	-15	HIS	-	expression tag	UNP Q68GS1
C	-14	HIS	-	expression tag	UNP Q68GS1
C	-13	HIS	-	expression tag	UNP Q68GS1
C	-12	HIS	-	expression tag	UNP Q68GS1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-11	SER	-	expression tag	UNP Q68GS1
C	-10	SER	-	expression tag	UNP Q68GS1
C	-9	GLY	-	expression tag	UNP Q68GS1
C	-8	HIS	-	expression tag	UNP Q68GS1
C	-7	ILE	-	expression tag	UNP Q68GS1
C	-6	ASP	-	expression tag	UNP Q68GS1
C	-5	ASP	-	expression tag	UNP Q68GS1
C	-4	ASP	-	expression tag	UNP Q68GS1
C	-3	ASP	-	expression tag	UNP Q68GS1
C	-2	LYS	-	expression tag	UNP Q68GS1
C	-1	HIS	-	expression tag	UNP Q68GS1
D	-23	MET	-	initiating methionine	UNP Q68GS1
D	-22	GLY	-	expression tag	UNP Q68GS1
D	-21	HIS	-	expression tag	UNP Q68GS1
D	-20	HIS	-	expression tag	UNP Q68GS1
D	-19	HIS	-	expression tag	UNP Q68GS1
D	-18	HIS	-	expression tag	UNP Q68GS1
D	-17	HIS	-	expression tag	UNP Q68GS1
D	-16	HIS	-	expression tag	UNP Q68GS1
D	-15	HIS	-	expression tag	UNP Q68GS1
D	-14	HIS	-	expression tag	UNP Q68GS1
D	-13	HIS	-	expression tag	UNP Q68GS1
D	-12	HIS	-	expression tag	UNP Q68GS1
D	-11	SER	-	expression tag	UNP Q68GS1
D	-10	SER	-	expression tag	UNP Q68GS1
D	-9	GLY	-	expression tag	UNP Q68GS1
D	-8	HIS	-	expression tag	UNP Q68GS1
D	-7	ILE	-	expression tag	UNP Q68GS1
D	-6	ASP	-	expression tag	UNP Q68GS1
D	-5	ASP	-	expression tag	UNP Q68GS1
D	-4	ASP	-	expression tag	UNP Q68GS1
D	-3	ASP	-	expression tag	UNP Q68GS1
D	-2	LYS	-	expression tag	UNP Q68GS1
D	-1	HIS	-	expression tag	UNP Q68GS1
E	-23	MET	-	initiating methionine	UNP Q68GS1
E	-22	GLY	-	expression tag	UNP Q68GS1
E	-21	HIS	-	expression tag	UNP Q68GS1
E	-20	HIS	-	expression tag	UNP Q68GS1
E	-19	HIS	-	expression tag	UNP Q68GS1
E	-18	HIS	-	expression tag	UNP Q68GS1
E	-17	HIS	-	expression tag	UNP Q68GS1
E	-16	HIS	-	expression tag	UNP Q68GS1

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-15	HIS	-	expression tag	UNP Q68GS1
E	-14	HIS	-	expression tag	UNP Q68GS1
E	-13	HIS	-	expression tag	UNP Q68GS1
E	-12	HIS	-	expression tag	UNP Q68GS1
E	-11	SER	-	expression tag	UNP Q68GS1
E	-10	SER	-	expression tag	UNP Q68GS1
E	-9	GLY	-	expression tag	UNP Q68GS1
E	-8	HIS	-	expression tag	UNP Q68GS1
E	-7	ILE	-	expression tag	UNP Q68GS1
E	-6	ASP	-	expression tag	UNP Q68GS1
E	-5	ASP	-	expression tag	UNP Q68GS1
E	-4	ASP	-	expression tag	UNP Q68GS1
E	-3	ASP	-	expression tag	UNP Q68GS1
E	-2	LYS	-	expression tag	UNP Q68GS1
E	-1	HIS	-	expression tag	UNP Q68GS1
F	-23	MET	-	initiating methionine	UNP Q68GS1
F	-22	GLY	-	expression tag	UNP Q68GS1
F	-21	HIS	-	expression tag	UNP Q68GS1
F	-20	HIS	-	expression tag	UNP Q68GS1
F	-19	HIS	-	expression tag	UNP Q68GS1
F	-18	HIS	-	expression tag	UNP Q68GS1
F	-17	HIS	-	expression tag	UNP Q68GS1
F	-16	HIS	-	expression tag	UNP Q68GS1
F	-15	HIS	-	expression tag	UNP Q68GS1
F	-14	HIS	-	expression tag	UNP Q68GS1
F	-13	HIS	-	expression tag	UNP Q68GS1
F	-12	HIS	-	expression tag	UNP Q68GS1
F	-11	SER	-	expression tag	UNP Q68GS1
F	-10	SER	-	expression tag	UNP Q68GS1
F	-9	GLY	-	expression tag	UNP Q68GS1
F	-8	HIS	-	expression tag	UNP Q68GS1
F	-7	ILE	-	expression tag	UNP Q68GS1
F	-6	ASP	-	expression tag	UNP Q68GS1
F	-5	ASP	-	expression tag	UNP Q68GS1
F	-4	ASP	-	expression tag	UNP Q68GS1
F	-3	ASP	-	expression tag	UNP Q68GS1
F	-2	LYS	-	expression tag	UNP Q68GS1
F	-1	HIS	-	expression tag	UNP Q68GS1
G	-23	MET	-	initiating methionine	UNP Q68GS1
G	-22	GLY	-	expression tag	UNP Q68GS1
G	-21	HIS	-	expression tag	UNP Q68GS1
G	-20	HIS	-	expression tag	UNP Q68GS1

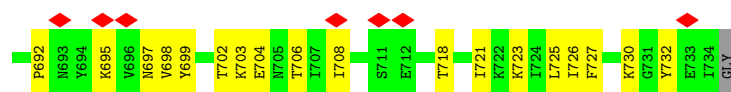
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Chain	Residue	Modelled	Actual	Comment	Reference
G	-19	HIS	-	expression tag	UNP Q68GS1
G	-18	HIS	-	expression tag	UNP Q68GS1
G	-17	HIS	-	expression tag	UNP Q68GS1
G	-16	HIS	-	expression tag	UNP Q68GS1
G	-15	HIS	-	expression tag	UNP Q68GS1
G	-14	HIS	-	expression tag	UNP Q68GS1
G	-13	HIS	-	expression tag	UNP Q68GS1
G	-12	HIS	-	expression tag	UNP Q68GS1
G	-11	SER	-	expression tag	UNP Q68GS1
G	-10	SER	-	expression tag	UNP Q68GS1
G	-9	GLY	-	expression tag	UNP Q68GS1
G	-8	HIS	-	expression tag	UNP Q68GS1
G	-7	ILE	-	expression tag	UNP Q68GS1
G	-6	ASP	-	expression tag	UNP Q68GS1
G	-5	ASP	-	expression tag	UNP Q68GS1
G	-4	ASP	-	expression tag	UNP Q68GS1
G	-3	ASP	-	expression tag	UNP Q68GS1
G	-2	LYS	-	expression tag	UNP Q68GS1
G	-1	HIS	-	expression tag	UNP Q68GS1

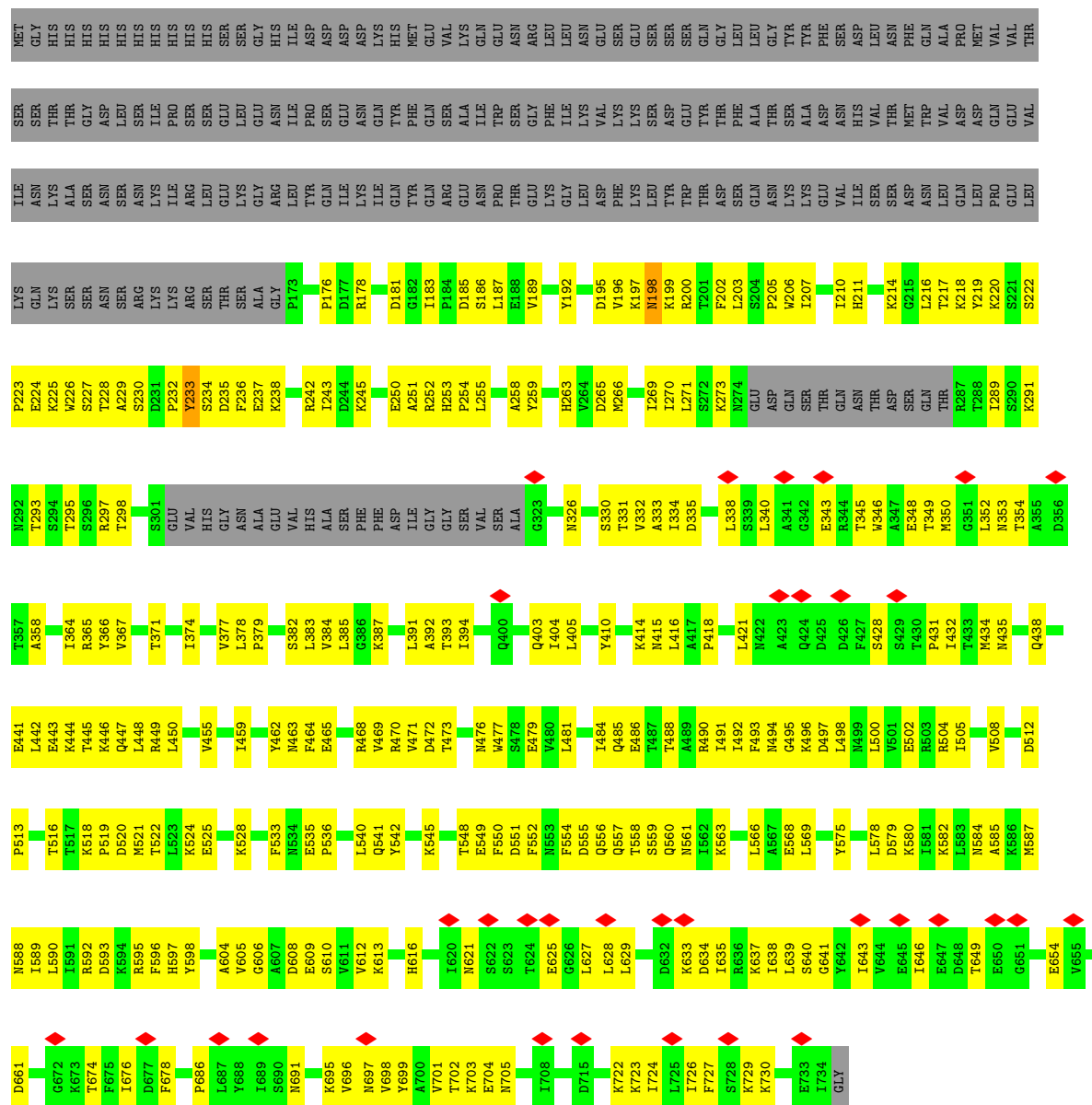
- Molecule 2 is a protein called Lethal factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	699	Total	C	N	O	S	0	0
			5378	3404	913	1055	6		
2	I	710	Total	C	N	O	S	0	0
			4739	2982	841	912	4		
2	J	661	Total	C	N	O	S	0	0
			4239	2655	752	830	2		



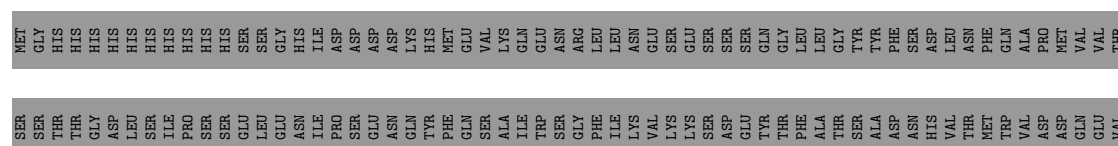
• Molecule 1: Protective antigen

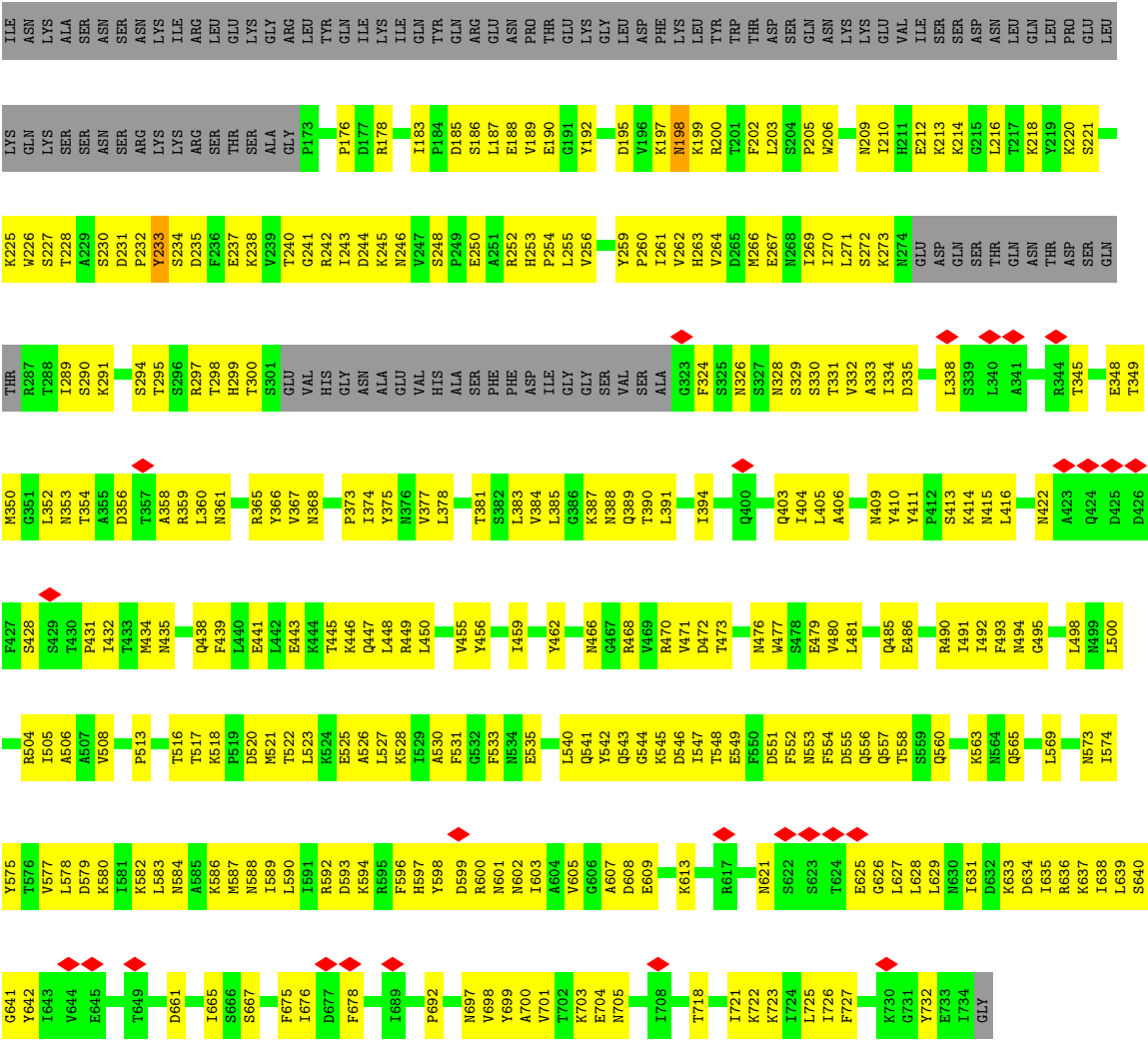
Chain B: 35% 35% 30%



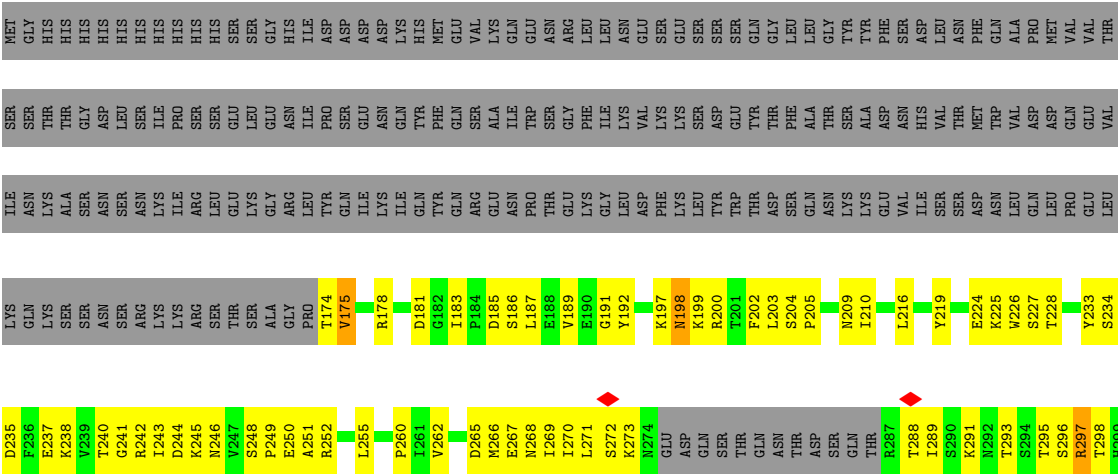
• Molecule 1: Protective antigen

Chain C: 32% 37% 30%





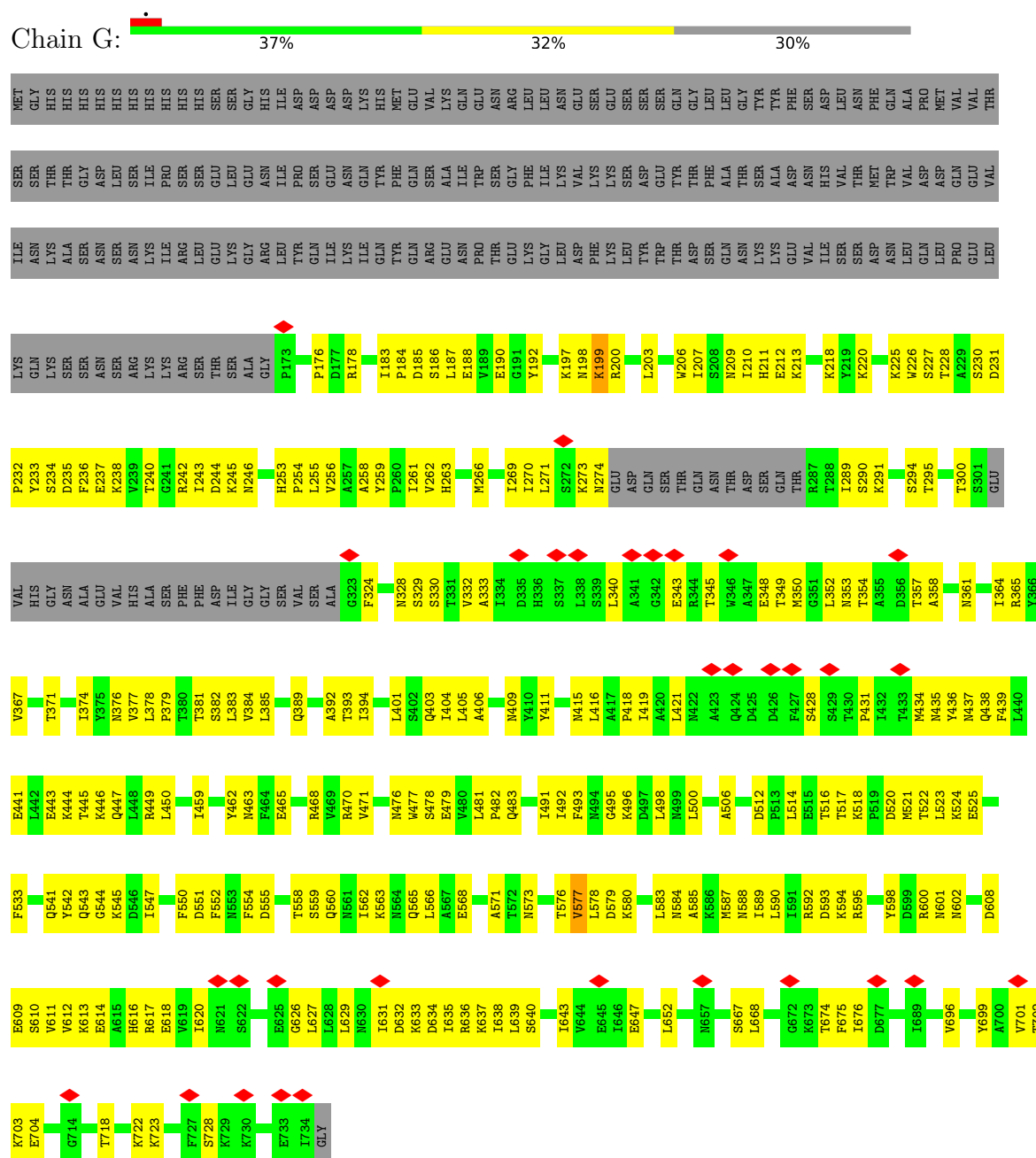
● Molecule 1: Protective antigen





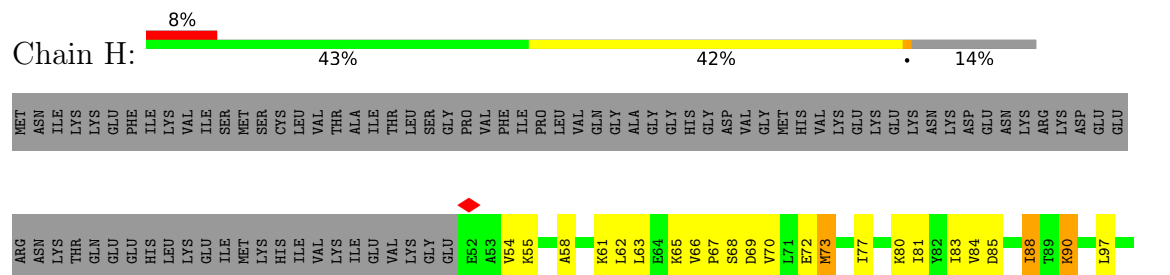
- Molecule 1: Protective antigen

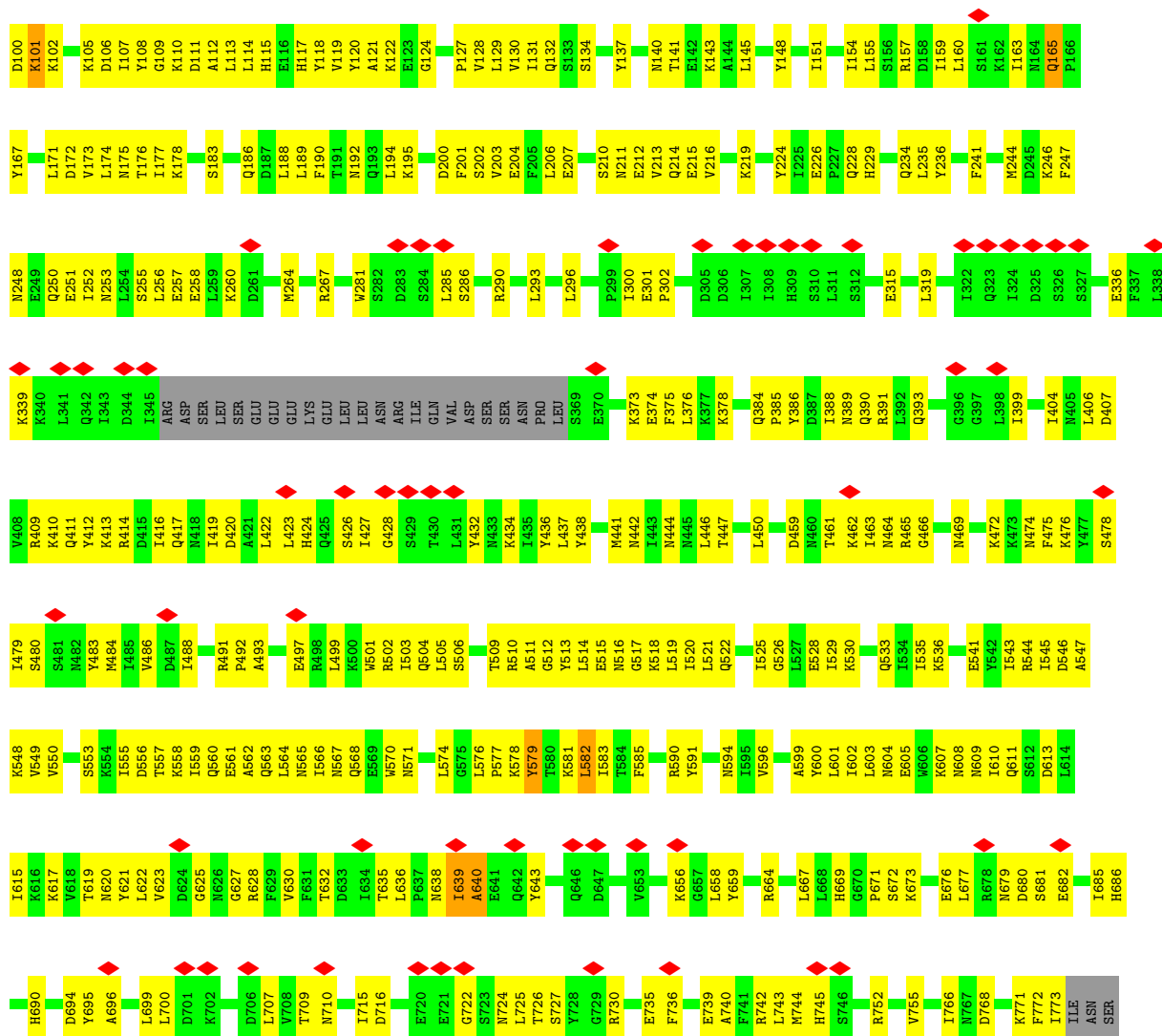
Chain G:



- Molecule 2: Lethal factor

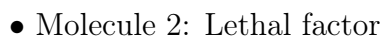
Chain H:





• Molecule 2: Lethal factor





Response	Percentage
Current government	58%
Opposition	62%
Neither	20%
Don't know	18%



Y728	G729	R730	T731	N732	E733	A734	E735	F736	F737	A738	E739	A740	F741	R742	L743	M744	H745	S746	T747	D748	H749	A750	E751	R752	L753	K754	V755	Q756	K757	N758	A759	F760	K761	T762	F763	Q764	F765	I766	N767	D768	Q769	I770	K771	F772	I773	ILE	ASN	SER													
L668	H669	G670	P671	S672	K673	G674	V675	E676	L677	R678	N679	D680	S681	E682	G683	F684	I685	H686	E687	F688	G689	H690	A691	V692	D693	D694	Y695	A696	G697	Y698	L699	L700	D701	K702	N703	Q704	S705	D706	L707	V708	T709	N710	S711	K712	K713	F714	I715	L716	I717	F718	K719	E720	E721	G722	S723	N724	L725	T726	S727		
N608	N609	I610	Q611	S612	D613	L614	I615	K616	K617	V618	T619	N620	Y621	L622	V623	D624	G625	N626	G627	R628	F629	V630	F631	T632	D633	I634	T635	L636	P637	N638	I639	A640	E641	Q642	Y643	T644	H645	Q646	D647	E648	I649	Y650	E651	Q652	V653	H654	S655	K656	G657	L658	Y659	V660	P661	E662	S663	R664	E665	L666	I667		
K548	V549	V550	P551	K552	S553	K554	I555	D556	T557	K558	I559	Q560	E561	A562	Q563	L564	N565	I566	N567	Q568	E569	H570	N571	K572	A573	L574	G575	L576	P577	K578	Y579	T580	K581	L582	I583	T584	F585	N586	V587	H588	N589	R590	Y591	A592	S593	N594	I595	V596	E597	S598	A599	Y600	L601	I602	L603	N604	E605	W606	K607		
I485	V486	D487	I488	P492	A493	L494	D495	M496	E497	R498	L499	K500	H501	R502	I503	Q504	L505	S506	P507	D508	T509	G512	Y513	L514	E515	N516	G517	K518	L519	I520	L521	Q522	R523	N524	I525	G526	L527	E528	I529	K530	D531	V532	Q533	I534	I535	K536	Q537	S538	E539	K540	E541	Y542	I543	R544	I545	D546	A547				
A421	L422	L423	H424	Q425	S426	I427	G428	SER	THR	LEU	TYR	M433	K434	I435	Y436	L437	Y438	E439	M440	M441	M442	I443	M444	N445	L446	T447	A448	T449	L450	G451	A452	D453	L454	V455	D456	S457	T458	D459	N460	T461	K462	I463	N464	N469	E470	F471	M474	F475	K476	Y477	S478	I479	S480	S481	N482	Y483	M484				
GLN	VAL	ASP	SER	SER	ASN	PRO	L368	S369	E370	K371	E372	K373	E374	F375	L376	K377	K378	L379	K380	L381	D382	I383	Q384	P385	Y386	D387	I388	N389	Q390	R391	L392	Q393	D394	T395	G396	G397	LEU	ILE	GLN	ASP	SER	PRO	ILE	SER	ARG	ASP	SER	LEU	SER	GLU	GLU	GLU	LYS	GLU	GLU	LEU	LEU	ASN	ARG	ILE	
E301	PRO	LYS	LYS	ASP	ASP	ILE	ILE	H309	S310	L311	S312	Q313	E314	E315	K316	E317	L318	L319	K320	ARG	ILE	GLN	ILE	ASP	SER	SER	ASP	PHE	LEU	SER	T332	E333	E334	K335	E336	F337	L338	LYS	LYS	LEU	GLN	ILE	ASP	ASP	ILE	ARG	ASP	SER	LEU	SER	GLU	GLU	GLU	LYS	GLU	GLU	LEU	LEU	ASN	ARG	ILE

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	44000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	74.4	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.098	Depositor
Minimum map value	-0.772	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	359.52002, 359.52002, 359.52002	wwPDB
Map dimensions	336, 336, 336	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

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	0.61	0/4029	0.79	3/5491 (0.1%)
1	B	0.68	0/4045	0.83	0/5511
1	C	0.68	0/4045	0.84	0/5511
1	D	0.68	0/4037	0.88	4/5500 (0.1%)
1	E	0.65	0/4045	0.83	1/5511 (0.0%)
1	F	0.64	0/4045	0.80	0/5511
1	G	0.62	0/4045	0.77	0/5511
2	H	0.45	0/5476	0.79	4/7434 (0.1%)
2	I	0.41	0/4804	0.69	0/6565
2	J	0.24	0/4294	0.60	4/5903 (0.1%)
All	All	0.58	0/42865	0.78	16/58448 (0.0%)

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
2	H	0	1

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	582	LEU	CA-CB-CG	6.62	139.48	116.30
2	J	127	PRO	N-CD-CG	-6.47	93.50	103.20
2	H	88	ILE	CA-C-N	6.40	144.10	122.20
2	H	88	ILE	C-N-CA	6.40	144.10	122.20
2	J	127	PRO	CA-N-CD	-6.31	103.17	112.00
1	D	297	ARG	CA-CB-CG	-6.09	101.93	114.10
2	H	73	MET	CB-CG-SD	-5.97	94.80	112.70
1	A	203	LEU	CA-CB-CG	-5.92	95.59	116.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	411	TYR	CA-CB-CG	-5.79	103.48	113.90
1	A	450	LEU	CA-CB-CG	-5.53	96.95	116.30
1	D	297	ARG	NE-CZ-NH1	-5.52	115.98	121.50
1	A	411	TYR	CA-CB-CG	-5.52	103.96	113.90
2	J	67	PRO	CA-N-CD	-5.48	104.33	112.00
2	J	543	ILE	N-CA-C	5.43	115.40	107.37
1	E	456	TYR	CA-CB-CG	-5.39	104.20	113.90
1	D	297	ARG	CB-CG-CD	5.07	122.97	111.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	165	GLN	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3961	0	3728	255	0
1	B	3977	0	3761	320	0
1	C	3977	0	3760	334	0
1	D	3970	0	3753	297	0
1	E	3977	0	3761	285	0
1	F	3977	0	3761	260	0
1	G	3977	0	3760	245	0
2	H	5378	0	5005	369	0
2	I	4739	0	3782	229	0
2	J	4239	0	3182	128	0
All	All	42172	0	38253	2669	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 33.

All (2669) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:89:THR:CG2	2:I:115:HIS:HA	1.55	1.35
1:C:233:TYR:CD1	1:C:243:ILE:HD11	1.74	1.23
2:H:117:HIS:NE2	2:H:119:VAL:HG23	1.56	1.21
2:I:89:THR:HG21	2:I:115:HIS:CB	1.72	1.19
2:H:578:LYS:HD3	2:H:579:TYR:HE1	1.04	1.16
1:B:233:TYR:HD2	1:B:243:ILE:HD11	1.01	1.14
1:E:643:ILE:HG21	1:E:723:LYS:HZ2	1.10	1.13
2:H:578:LYS:CD	2:H:579:TYR:HE1	1.63	1.11
2:I:89:THR:HG22	2:I:115:HIS:HA	1.23	1.10
2:H:117:HIS:NE2	2:H:119:VAL:CG2	2.13	1.10
1:C:233:TYR:HD1	1:C:243:ILE:CD1	1.65	1.09
1:C:232:PRO:HD2	1:C:233:TYR:CD2	1.88	1.09
1:B:233:TYR:CD2	1:B:243:ILE:HD11	1.86	1.08
1:E:721:ILE:HD11	1:E:723:LYS:HD2	1.29	1.07
1:C:584:ASN:H	1:C:587:MET:HE1	1.12	1.06
1:G:643:ILE:HG12	1:G:723:LYS:HE2	1.35	1.05
2:I:89:THR:CG2	2:I:115:HIS:CA	2.34	1.05
1:E:721:ILE:HG13	1:E:723:LYS:HG3	1.38	1.04
1:E:643:ILE:HG21	1:E:723:LYS:NZ	1.71	1.03
2:J:89:THR:CG2	2:J:115:HIS:HA	1.86	1.03
2:H:578:LYS:HD3	2:H:579:TYR:CE1	1.94	1.02
1:D:266:MET:HE1	1:D:364:ILE:HG22	1.39	1.01
1:A:210:ILE:O	1:A:214:LYS:NZ	1.95	1.00
1:G:643:ILE:HG12	1:G:723:LYS:CE	1.94	0.98
1:B:428:SER:HB2	1:B:431:PRO:HG3	1.46	0.97
2:H:446:LEU:HD11	2:H:590:ARG:HB2	1.47	0.97
1:E:232:PRO:HD2	1:E:233:TYR:CE1	2.00	0.95
2:H:563:GLN:HE22	2:H:585:PHE:H	1.08	0.95
1:E:428:SER:HB2	1:E:431:PRO:HG3	1.49	0.94
1:E:232:PRO:HD2	1:E:233:TYR:CD1	2.02	0.94
1:C:721:ILE:HB	1:C:723:LYS:HE2	1.50	0.93
1:E:524:LYS:HD2	1:E:579:ASP:HB3	1.48	0.92
1:E:524:LYS:HE3	1:E:578:LEU:HB3	1.51	0.92
2:H:157:ARG:NH2	2:H:211:ASN:OD1	2.02	0.92
1:E:721:ILE:CD1	1:E:723:LYS:HD2	1.98	0.92
1:E:176:PRO:HB2	1:E:178:ARG:HH12	1.33	0.92
1:A:428:SER:HB2	1:A:431:PRO:HG3	1.51	0.92
1:C:233:TYR:CD1	1:C:243:ILE:CD1	2.45	0.91
2:H:578:LYS:CD	2:H:579:TYR:CE1	2.53	0.91
1:G:273:LYS:HA	1:G:358:ALA:HA	1.53	0.91
1:B:238:LYS:HZ3	1:B:254:PRO:HA	1.35	0.91
2:I:81:ILE:HG22	2:I:129:LEU:HB3	1.51	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:639:ILE:HG13	2:H:640:ALA:H	1.35	0.90
1:C:232:PRO:HD2	1:C:233:TYR:CE2	2.06	0.90
1:B:366:TYR:HE1	1:B:378:LEU:CG	1.85	0.89
1:A:265:ASP:OD1	1:A:295:THR:OG1	1.90	0.89
1:B:233:TYR:HD2	1:B:243:ILE:CD1	1.85	0.89
1:G:428:SER:HB2	1:G:431:PRO:HG3	1.53	0.89
2:I:89:THR:HG21	2:I:115:HIS:HB2	1.54	0.89
2:H:117:HIS:CE1	2:H:119:VAL:HG22	2.08	0.89
1:C:233:TYR:CE1	1:C:243:ILE:HD11	2.08	0.88
1:G:584:ASN:H	1:G:587:MET:HE3	1.36	0.88
2:J:502:ARG:HH22	2:J:544:ARG:HB3	1.38	0.88
1:C:232:PRO:HD2	1:C:233:TYR:HD2	1.37	0.88
1:B:394:ILE:HD12	1:B:421:LEU:HD11	1.54	0.87
1:B:185:ASP:OD1	1:B:186:SER:N	2.06	0.87
1:E:502:GLU:O	1:E:503:ARG:NH1	2.07	0.87
1:C:584:ASN:N	1:C:587:MET:HE1	1.87	0.87
1:B:291:LYS:HZ1	1:B:335:ASP:H	1.19	0.87
2:I:89:THR:CG2	2:I:115:HIS:CB	2.53	0.87
1:A:365:ARG:HE	1:A:418:PRO:HB3	1.39	0.87
1:B:643:ILE:HB	1:B:699:TYR:HB2	1.55	0.86
1:B:497:ASP:O	1:B:637:LYS:NZ	2.08	0.86
2:I:226:GLU:OE2	2:I:229:HIS:ND1	2.09	0.86
1:F:297:ARG:HH12	1:F:328:ASN:HB3	1.41	0.86
1:C:705:ASN:ND2	1:C:722:LYS:O	2.08	0.86
1:E:234:SER:N	1:E:237:GLU:OE2	2.08	0.85
1:E:291:LYS:HZ1	1:E:335:ASP:H	1.24	0.85
2:H:117:HIS:CD2	2:H:119:VAL:O	2.30	0.85
1:F:185:ASP:OD1	1:F:186:SER:N	2.09	0.85
1:E:721:ILE:HG13	1:E:723:LYS:CG	2.07	0.85
1:B:365:ARG:HH21	1:B:418:PRO:HD3	1.42	0.85
1:E:189:VAL:O	1:E:220:LYS:NZ	2.10	0.85
2:I:768:ASP:HA	2:I:771:LYS:HD2	1.59	0.85
1:G:541:GLN:OE1	1:G:544:GLY:N	2.09	0.84
1:F:249:PRO:HA	1:F:252:ARG:HH11	1.43	0.84
1:G:523:LEU:HD22	1:G:578:LEU:HD11	1.60	0.84
1:G:198:ASN:HB2	1:G:200:ARG:HH12	1.41	0.84
2:J:89:THR:HG22	2:J:115:HIS:HA	1.56	0.83
1:A:599:ASP:OD1	1:A:600:ARG:N	2.08	0.83
1:D:365:ARG:NH1	1:D:412:PRO:O	2.11	0.83
1:C:234:SER:OG	1:C:237:GLU:OE1	1.96	0.83
1:C:262:VAL:O	1:C:328:ASN:ND2	2.11	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:89:THR:HG22	2:I:115:HIS:CA	2.04	0.83
1:A:497:ASP:O	1:A:637:LYS:NZ	2.11	0.83
1:A:189:VAL:O	1:A:220:LYS:NZ	2.10	0.83
1:B:346:TRP:HZ3	1:B:446:LYS:HZ1	1.27	0.82
1:D:326:ASN:OD1	1:D:490:ARG:NH2	2.13	0.82
2:H:578:LYS:CG	2:H:579:TYR:CE1	2.63	0.82
2:H:707:LEU:HD23	2:H:709:THR:HG22	1.62	0.82
2:I:451:GLY:HA2	2:I:454:LEU:HD23	1.61	0.82
1:D:331:THR:HG23	1:D:447:GLN:HE21	1.45	0.82
1:G:718:THR:CB	1:G:723:LYS:NZ	2.43	0.82
1:B:297:ARG:NH1	1:B:298:THR:O	2.12	0.82
1:B:584:ASN:H	1:B:587:MET:HE1	1.44	0.81
1:G:435:ASN:CG	1:G:438:GLN:HE22	1.87	0.81
2:H:117:HIS:CE1	2:H:119:VAL:CG2	2.63	0.81
2:H:578:LYS:HG2	2:H:579:TYR:CE1	2.15	0.81
1:C:447:GLN:HB3	1:C:449:ARG:HH22	1.46	0.81
2:H:424:HIS:O	2:H:510:ARG:NH2	2.13	0.81
2:H:244:MET:HE3	2:H:248:ASN:HB3	1.63	0.81
2:H:635:THR:OG1	2:H:638:ASN:ND2	2.14	0.80
1:C:259:TYR:HE2	1:C:261:ILE:HD11	1.46	0.80
1:D:202:PHE:HE2	1:D:204:SER:HB2	1.45	0.80
1:A:262:VAL:O	1:A:328:ASN:ND2	2.14	0.80
1:G:718:THR:CB	1:G:723:LYS:HZ1	1.93	0.80
1:B:366:TYR:HE1	1:B:378:LEU:HD21	1.47	0.80
1:B:522:THR:OG1	1:B:525:GLU:OE1	1.98	0.80
1:C:490:ARG:HH21	1:C:504:ARG:HH22	1.29	0.79
1:D:459:ILE:HG13	1:D:477:TRP:NE1	1.96	0.79
1:B:552:PHE:HD2	1:B:554:PHE:HE2	1.30	0.79
1:G:492:ILE:HB	1:G:590:LEU:HD13	1.64	0.79
1:G:643:ILE:HB	1:G:699:TYR:HB2	1.63	0.79
2:J:81:ILE:HG22	2:J:129:LEU:HB3	1.65	0.79
2:I:570:TRP:CZ3	2:I:607:LYS:HE2	2.18	0.79
2:H:446:LEU:HD12	2:H:591:TYR:HB2	1.64	0.79
1:B:210:ILE:O	1:B:214:LYS:NZ	2.14	0.79
1:A:386:GLY:O	1:A:449:ARG:NH2	2.15	0.78
1:F:443:GLU:HA	1:F:446:LYS:HZ3	1.49	0.78
2:H:406:LEU:HG	2:H:410:LYS:HE2	1.64	0.78
2:I:278:TYR:HB2	2:I:513:TYR:CZ	2.19	0.78
1:F:643:ILE:CD1	1:F:723:LYS:HE2	2.13	0.78
2:H:190:PHE:O	2:H:195:LYS:NZ	2.17	0.78
1:B:366:TYR:HE1	1:B:378:LEU:CD2	1.96	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:206:TRP:CD1	1:F:218:LYS:HZ3	2.02	0.78
1:E:599:ASP:HB3	1:E:605:VAL:HG21	1.65	0.78
1:G:253:HIS:CE1	1:G:255:LEU:HD13	2.18	0.78
1:F:360:LEU:HB3	1:F:432:ILE:HG21	1.66	0.77
1:C:428:SER:HB2	1:C:431:PRO:HG3	1.65	0.77
1:F:428:SER:HB2	1:F:431:PRO:HG3	1.66	0.77
1:B:391:LEU:HB3	1:B:432:ILE:HD11	1.65	0.77
1:G:212:GLU:OE1	1:G:212:GLU:N	2.17	0.77
2:I:89:THR:HG21	2:I:115:HIS:CA	2.07	0.77
2:H:117:HIS:NE2	2:H:119:VAL:HG22	1.97	0.77
1:C:721:ILE:CG2	1:C:723:LYS:HE2	2.15	0.77
2:I:115:HIS:CE1	2:I:116:GLU:HG3	2.20	0.77
1:C:721:ILE:CB	1:C:723:LYS:HE2	2.15	0.77
2:H:768:ASP:HA	2:H:771:LYS:HD2	1.66	0.77
2:I:169:LYS:HZ1	2:I:534:ILE:H	1.28	0.77
1:C:267:GLU:N	1:C:267:GLU:OE1	2.17	0.77
1:C:384:VAL:HG12	1:C:390:THR:HA	1.67	0.77
2:I:89:THR:HG21	2:I:115:HIS:HB3	1.61	0.77
1:G:435:ASN:OD1	1:G:437:ASN:ND2	2.18	0.77
1:C:248:SER:OG	1:C:250:GLU:OE1	2.02	0.77
1:D:297:ARG:HH21	1:D:499:ASN:HA	1.49	0.77
1:G:176:PRO:HB3	1:G:178:ARG:HH12	1.50	0.77
2:H:186:GLN:HB2	2:H:190:PHE:CZ	2.20	0.77
2:J:768:ASP:HA	2:J:771:LYS:HD2	1.66	0.77
1:E:185:ASP:OD1	1:E:186:SER:N	2.17	0.76
1:A:185:ASP:OD1	1:A:186:SER:N	2.18	0.76
1:F:643:ILE:HD12	1:F:723:LYS:HE2	1.65	0.76
1:G:263:HIS:HB3	1:G:328:ASN:HD21	1.51	0.76
1:B:365:ARG:HE	1:B:418:PRO:HB3	1.50	0.76
1:F:225:LYS:HD3	1:F:514:LEU:HD21	1.69	0.75
1:F:470:ARG:NH1	1:F:471:VAL:O	2.19	0.75
1:G:584:ASN:H	1:G:587:MET:CE	1.99	0.75
1:B:232:PRO:C	1:B:233:TYR:HD1	1.94	0.75
1:C:387:LYS:HD2	1:C:388:ASN:HB2	1.67	0.75
1:F:233:TYR:CD2	1:F:243:ILE:HD11	2.22	0.75
1:B:366:TYR:CE1	1:B:378:LEU:CG	2.68	0.75
1:A:341:ALA:O	1:A:344:ARG:NH1	2.19	0.75
1:B:238:LYS:NZ	1:B:254:PRO:HA	2.01	0.75
1:A:541:GLN:OE1	1:A:544:GLY:N	2.20	0.75
1:F:198:ASN:HB2	1:F:200:ARG:HH22	1.51	0.75
1:D:297:ARG:NH2	1:D:499:ASN:HA	2.01	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:548:THR:O	1:D:594:LYS:NZ	2.15	0.75
1:B:470:ARG:HA	1:C:479:GLU:OE1	1.87	0.75
1:D:439:PHE:HA	1:D:442:LEU:HD12	1.69	0.75
1:G:506:ALA:HB1	1:G:518:LYS:HZ2	1.51	0.75
2:H:579:TYR:N	2:H:579:TYR:HD1	1.84	0.75
1:B:609:GLU:HB2	1:B:724:ILE:HG21	1.69	0.74
1:C:541:GLN:OE1	1:C:544:GLY:N	2.20	0.74
1:B:568:GLU:HG2	1:B:569:LEU:HD12	1.67	0.74
1:F:592:ARG:HD2	1:F:598:TYR:CE2	2.21	0.74
2:I:469:ASN:HA	2:I:472:LYS:HZ3	1.52	0.74
1:D:633:LYS:O	1:D:637:LYS:NZ	2.17	0.74
1:E:326:ASN:HD22	1:E:485:GLN:HG3	1.52	0.74
1:E:541:GLN:HG2	1:E:546:ASP:HA	1.69	0.74
1:B:225:LYS:HD3	1:B:228:THR:HA	1.68	0.74
1:F:374:ILE:HD11	1:F:405:LEU:HD22	1.69	0.74
1:B:236:PHE:HE2	1:B:242:ARG:HH21	1.33	0.74
1:F:443:GLU:HA	1:F:446:LYS:NZ	2.02	0.74
2:J:197:HIS:HE2	2:J:199:THR:HG1	1.33	0.74
1:B:198:ASN:HD21	1:B:200:ARG:HH22	1.35	0.74
2:H:483:TYR:HB3	2:H:520:ILE:HD11	1.69	0.74
1:A:270:ILE:HD13	1:A:290:SER:HB3	1.69	0.74
2:H:427:ILE:O	2:H:432:TYR:OH	2.06	0.74
1:G:443:GLU:HA	1:G:446:LYS:HE2	1.69	0.74
1:F:445:THR:O	1:F:447:GLN:NE2	2.20	0.73
2:H:578:LYS:CG	2:H:579:TYR:HE1	2.01	0.73
1:C:698:VAL:HB	1:C:727:PHE:HB3	1.70	0.73
1:A:525:GLU:OE1	1:A:525:GLU:N	2.17	0.73
1:D:363:ASN:ND2	1:D:418:PRO:HG2	2.03	0.73
1:E:362:ALA:HB3	1:E:421:LEU:HD12	1.71	0.73
2:I:271:TRP:HE1	2:I:275:LYS:HE2	1.53	0.73
1:G:584:ASN:OD1	1:G:585:ALA:N	2.20	0.73
2:J:441:MET:HB3	2:J:499:LEU:HD22	1.70	0.73
1:A:374:ILE:HD11	1:A:405:LEU:HD22	1.68	0.73
1:C:326:ASN:HB3	1:C:490:ARG:HH22	1.54	0.73
1:C:490:ARG:HH21	1:C:504:ARG:NH2	1.86	0.73
2:H:253:ASN:O	2:H:256:LEU:HG	1.89	0.73
2:J:153:LYS:O	2:J:157:ARG:HG2	1.89	0.73
1:B:226:TRP:CZ2	1:B:234:SER:HB2	2.24	0.73
1:B:232:PRO:C	1:B:233:TYR:CD1	2.67	0.73
2:H:563:GLN:HE22	2:H:585:PHE:N	1.85	0.73
2:H:264:MET:HA	2:H:267:ARG:HD3	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:296:SER:O	1:D:331:THR:N	2.22	0.72
1:E:233:TYR:CD2	1:E:243:ILE:HD11	2.25	0.72
2:H:579:TYR:N	2:H:579:TYR:CD1	2.57	0.72
1:G:478:SER:OG	1:G:479:GLU:OE1	2.07	0.72
1:C:197:LYS:HB2	1:C:202:PHE:HE1	1.53	0.72
1:C:226:TRP:CZ2	1:C:234:SER:HB3	2.25	0.72
1:A:223:PRO:HG2	1:A:224:GLU:OE1	1.90	0.72
2:J:226:GLU:OE1	2:J:229:HIS:N	2.22	0.72
1:C:533:PHE:CE2	1:C:542:TYR:HB2	2.24	0.72
1:F:291:LYS:NZ	1:F:335:ASP:H	1.87	0.72
1:D:643:ILE:HB	1:D:699:TYR:HB2	1.71	0.72
1:B:548:THR:HA	1:B:575:TYR:CE1	2.25	0.72
1:C:555:ASP:OD1	1:C:556:GLN:N	2.22	0.72
2:H:563:GLN:NE2	2:H:585:PHE:H	1.87	0.72
1:E:721:ILE:HD11	1:E:723:LYS:CD	2.16	0.71
1:F:240:THR:HG21	1:F:242:ARG:HH22	1.55	0.71
1:A:522:THR:OG1	1:A:525:GLU:OE1	2.08	0.71
1:A:695:LYS:HA	1:A:730:LYS:HA	1.72	0.71
1:B:366:TYR:CE1	1:B:378:LEU:HD11	2.25	0.71
1:E:490:ARG:HH21	1:E:588:ASN:CG	1.98	0.71
1:E:592:ARG:HD3	1:E:598:TYR:CE2	2.25	0.71
2:J:226:GLU:OE1	2:J:229:HIS:ND1	2.20	0.71
1:G:209:ASN:O	1:G:213:LYS:NZ	2.23	0.71
1:E:443:GLU:HA	1:E:446:LYS:HZ3	1.56	0.71
1:G:185:ASP:OD1	1:G:186:SER:N	2.24	0.71
2:I:142:GLU:N	2:I:142:GLU:OE2	2.23	0.71
1:B:229:ALA:O	1:B:230:SER:OG	2.05	0.71
1:B:298:THR:HB	1:B:331:THR:HG22	1.73	0.71
2:H:160:LEU:HB3	2:H:165:GLN:O	1.91	0.71
2:J:500:LYS:O	2:J:502:ARG:NH1	2.22	0.71
1:C:200:ARG:HH22	1:D:189:VAL:HG11	1.56	0.71
2:H:73:MET:SD	2:H:73:MET:N	2.58	0.71
1:B:366:TYR:CE1	1:B:378:LEU:HG	2.26	0.71
1:C:189:VAL:HG13	1:C:190:GLU:HG3	1.71	0.71
1:E:466:ASN:HB2	1:F:226:TRP:CE3	2.26	0.71
1:B:584:ASN:N	1:B:587:MET:HE1	2.05	0.70
1:D:568:GLU:HG2	1:D:569:LEU:HD22	1.73	0.70
1:F:584:ASN:O	1:F:587:MET:HE2	1.91	0.70
1:C:272:SER:O	1:C:359:ARG:N	2.18	0.70
1:E:297:ARG:NH1	1:E:298:THR:O	2.23	0.70
1:F:341:ALA:O	1:F:344:ARG:NH1	2.23	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:560:GLN:O	1:F:563:LYS:HG3	1.92	0.70
2:I:281:TRP:HH2	2:I:423:LEU:HA	1.56	0.70
1:A:552:PHE:HB3	1:A:554:PHE:CZ	2.25	0.70
1:D:643:ILE:HG13	1:D:723:LYS:HE2	1.72	0.70
2:H:183:SER:HB2	2:H:186:GLN:HE22	1.56	0.70
1:G:234:SER:N	1:G:237:GLU:OE2	2.22	0.70
1:D:265:ASP:OD1	1:D:295:THR:OG1	2.08	0.70
1:D:490:ARG:NH2	1:D:504:ARG:HH22	1.90	0.70
2:I:42:HIS:O	2:I:45:LYS:NZ	2.25	0.70
1:C:631:ILE:O	1:C:636:ARG:NH2	2.23	0.70
1:E:206:TRP:CD1	1:E:218:LYS:HZ3	2.09	0.70
1:F:200:ARG:HH11	1:F:200:ARG:HG3	1.56	0.70
2:I:530:LYS:HE3	2:I:548:LYS:HE3	1.73	0.70
1:B:366:TYR:CE1	1:B:378:LEU:HD21	2.25	0.70
1:D:297:ARG:HD2	1:D:297:ARG:O	1.91	0.70
1:G:365:ARG:NH2	1:G:418:PRO:HD3	2.07	0.70
1:D:610:SER:HA	1:D:613:LYS:NZ	2.06	0.69
2:H:514:LEU:HD23	2:H:518:LYS:HB2	1.75	0.69
1:C:434:MET:HE1	1:C:439:PHE:HB2	1.75	0.69
2:I:278:TYR:HB2	2:I:513:TYR:CE2	2.27	0.69
1:C:185:ASP:OD1	1:C:186:SER:N	2.24	0.69
1:G:520:ASP:O	1:G:521:MET:HE2	1.92	0.69
1:B:234:SER:N	1:B:237:GLU:OE2	2.21	0.69
1:B:340:LEU:O	1:B:343:GLU:HG2	1.92	0.69
1:C:705:ASN:HD21	1:C:722:LYS:HB3	1.56	0.69
1:D:534:ASN:OD1	1:D:541:GLN:NE2	2.26	0.69
1:E:225:LYS:HD3	1:E:514:LEU:HD21	1.75	0.69
1:E:377:VAL:O	1:E:378:LEU:HD12	1.93	0.69
2:H:578:LYS:HG2	2:H:579:TYR:CD1	2.27	0.69
1:B:238:LYS:HE2	1:B:252:ARG:O	1.91	0.69
1:D:174:THR:O	1:D:175:VAL:HG22	1.93	0.69
1:E:360:LEU:HB3	1:E:432:ILE:HG21	1.75	0.69
1:G:198:ASN:HB2	1:G:200:ARG:NH1	2.07	0.69
1:B:552:PHE:HD2	1:B:554:PHE:CE2	2.10	0.68
1:E:490:ARG:HD3	1:E:504:ARG:NH2	2.08	0.68
1:C:527:LEU:HB3	1:C:533:PHE:HD1	1.58	0.68
1:F:562:ILE:HA	1:F:565:GLN:OE1	1.93	0.68
1:D:458:ASN:OD1	1:D:476:ASN:ND2	2.27	0.68
1:E:584:ASN:H	1:E:587:MET:HE2	1.58	0.68
2:H:117:HIS:HD2	2:H:119:VAL:O	1.75	0.68
2:I:192:ASN:OD1	2:I:193:GLN:N	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:118:TYR:OH	2:J:146:ASN:HB2	1.93	0.68
1:E:198:ASN:HD21	1:E:200:ARG:HH22	1.40	0.68
1:F:434:MET:HE1	1:F:439:PHE:HB2	1.75	0.68
1:G:524:LYS:HB2	1:G:578:LEU:HG	1.75	0.68
1:D:428:SER:HB2	1:D:431:PRO:HG3	1.75	0.68
1:A:528:LYS:NZ	1:A:535:GLU:HG2	2.08	0.68
1:C:198:ASN:ND2	2:I:139:GLU:OE2	2.24	0.68
1:F:273:LYS:HA	1:F:358:ALA:HA	1.75	0.68
2:H:600:TYR:O	2:H:604:ASN:ND2	2.27	0.68
1:B:273:LYS:HA	1:B:358:ALA:HA	1.76	0.68
1:C:233:TYR:HD1	1:C:243:ILE:HD12	1.57	0.68
1:A:551:ASP:OD1	1:A:552:PHE:N	2.26	0.68
2:H:556:ASP:O	2:H:559:ILE:HG12	1.94	0.68
1:C:187:LEU:HD11	1:C:205:PRO:HG3	1.76	0.68
1:D:612:VAL:O	1:D:616:HIS:ND1	2.24	0.67
1:A:527:LEU:HB3	1:A:533:PHE:HD2	1.60	0.67
1:C:197:LYS:O	1:C:200:ARG:N	2.26	0.67
1:C:415:ASN:ND2	1:D:325:SER:OG	2.27	0.67
1:F:533:PHE:CE2	1:F:542:TYR:HB2	2.28	0.67
1:G:262:VAL:O	1:G:328:ASN:ND2	2.28	0.67
2:I:468:PHE:HA	2:I:471:PHE:HD1	1.59	0.67
1:G:226:TRP:CZ2	1:G:234:SER:HB3	2.30	0.67
1:A:527:LEU:HB3	1:A:533:PHE:CD2	2.30	0.67
1:A:718:THR:O	1:A:723:LYS:HE3	1.94	0.67
1:D:200:ARG:HG3	1:D:200:ARG:HH11	1.60	0.67
1:F:183:ILE:HD11	1:F:236:PHE:HD1	1.59	0.67
2:H:437:LEU:HD22	2:H:488:ILE:HA	1.76	0.67
2:H:514:LEU:HG	2:H:516:ASN:H	1.59	0.67
2:I:252:ILE:O	2:I:255:SER:OG	2.13	0.67
1:G:382:SER:HA	1:G:393:THR:HA	1.76	0.67
1:A:267:GLU:N	1:A:267:GLU:OE2	2.26	0.67
2:H:427:ILE:HD11	2:H:506:SER:O	1.95	0.67
1:A:524:LYS:HG3	1:A:540:LEU:HD21	1.77	0.67
1:E:552:PHE:HB3	1:E:554:PHE:CZ	2.30	0.67
1:F:202:PHE:HE2	1:F:204:SER:HB2	1.60	0.67
1:G:374:ILE:HD11	1:G:405:LEU:HD22	1.77	0.67
2:J:451:GLY:HA2	2:J:454:LEU:HD23	1.77	0.67
1:A:502:GLU:O	1:A:503:ARG:NH1	2.24	0.67
1:C:493:PHE:CE2	1:C:495:GLY:HA3	2.30	0.67
1:E:365:ARG:NH1	1:E:414:LYS:HA	2.10	0.67
1:A:555:ASP:OD1	1:A:556:GLN:N	2.27	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:577:VAL:HG12	1:G:580:LYS:HB2	1.77	0.66
1:C:565:GLN:HE22	1:C:582:LYS:HB2	1.60	0.66
2:I:168:GLN:O	2:I:172:ASP:N	2.28	0.66
1:C:546:ASP:OD1	1:C:547:ILE:N	2.29	0.66
2:H:420:ASP:OD1	2:H:483:TYR:OH	2.13	0.66
1:C:270:ILE:HG12	1:C:361:ASN:O	1.95	0.66
2:J:762:THR:HA	2:J:765:PHE:CE1	2.29	0.66
1:D:262:VAL:HG21	1:D:379:PRO:HG2	1.78	0.66
1:D:297:ARG:HH22	1:D:500:LEU:HD23	1.60	0.66
1:F:189:VAL:O	1:F:220:LYS:NZ	2.24	0.66
1:G:403:GLN:H	1:G:403:GLN:CD	2.03	0.66
1:G:552:PHE:HB3	1:G:554:PHE:CZ	2.31	0.66
2:H:111:ASP:OD1	2:H:112:ALA:N	2.25	0.66
2:I:583:ILE:HD13	2:I:629:PHE:HB2	1.78	0.66
1:B:485:GLN:HA	1:B:504:ARG:HH12	1.59	0.66
1:C:231:ASP:HB2	1:C:232:PRO:HD3	1.75	0.66
1:C:244:ASP:OD1	1:C:246:ASN:ND2	2.28	0.66
2:H:106:ASP:OD1	2:H:108:TYR:N	2.27	0.66
2:H:226:GLU:OE1	2:H:229:HIS:N	2.29	0.66
1:F:561:ASN:OD1	1:F:565:GLN:NE2	2.29	0.66
1:C:273:LYS:HA	1:C:358:ALA:HA	1.78	0.66
1:D:226:TRP:CH2	1:D:234:SER:HB3	2.31	0.66
1:G:584:ASN:N	1:G:587:MET:HE3	2.07	0.66
2:I:619:THR:HA	2:I:622:LEU:HG	1.76	0.66
1:A:250:GLU:H	1:A:250:GLU:CD	2.04	0.66
1:D:293:THR:HG22	1:D:334:ILE:HD12	1.78	0.66
1:E:176:PRO:HB2	1:E:178:ARG:NH1	2.08	0.66
1:E:546:ASP:OD1	1:E:547:ILE:N	2.29	0.66
1:G:345:THR:O	1:G:348:GLU:HG3	1.95	0.66
1:E:295:THR:HA	1:E:332:VAL:HA	1.78	0.66
1:E:721:ILE:CG1	1:E:723:LYS:HD2	2.24	0.66
2:H:535:ILE:HD13	2:H:544:ARG:HD3	1.77	0.66
2:I:122:LYS:HE3	2:I:128:VAL:HB	1.77	0.66
1:A:614:GLU:OE2	1:A:617:ARG:HD3	1.96	0.65
1:E:540:LEU:HB3	1:E:547:ILE:HG21	1.76	0.65
1:F:636:ARG:HG3	1:F:637:LYS:NZ	2.11	0.65
2:H:441:MET:HE3	2:H:499:LEU:HD22	1.78	0.65
2:I:274:ILE:O	2:I:513:TYR:OH	2.05	0.65
1:F:249:PRO:HA	1:F:252:ARG:NH1	2.11	0.65
1:G:206:TRP:CD1	1:G:218:LYS:HZ3	2.14	0.65
1:G:226:TRP:CH2	1:G:234:SER:HB3	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:190:PHE:HB2	2:H:194:LEU:HD12	1.77	0.65
2:H:574:LEU:HD11	2:H:615:ILE:HG22	1.79	0.65
1:C:553:ASN:OD1	1:C:554:PHE:N	2.29	0.65
1:F:490:ARG:HB2	1:F:504:ARG:NH1	2.12	0.65
1:G:627:LEU:HB2	1:G:676:ILE:HD13	1.77	0.65
1:B:187:LEU:HD11	1:B:205:PRO:HG3	1.79	0.65
1:A:583:LEU:HD22	1:A:587:MET:HE1	1.77	0.65
1:C:718:THR:HA	1:C:721:ILE:HD13	1.77	0.65
1:G:383:LEU:N	1:G:392:ALA:O	2.30	0.65
2:H:226:GLU:OE1	2:H:229:HIS:ND1	2.26	0.65
1:C:297:ARG:NH1	1:C:329:SER:H	1.95	0.65
1:F:373:PRO:HB2	1:F:375:TYR:HE1	1.62	0.65
2:J:478:SER:OG	2:J:590:ARG:NE	2.26	0.65
1:D:610:SER:HA	1:D:613:LYS:HZ2	1.61	0.65
1:F:568:GLU:HG2	1:F:569:LEU:HD22	1.79	0.65
1:G:643:ILE:HG21	1:G:723:LYS:HZ2	1.61	0.65
2:H:578:LYS:C	2:H:579:TYR:HD1	2.04	0.65
1:B:471:VAL:HG12	1:C:479:GLU:OE2	1.96	0.65
1:C:558:THR:HG21	1:C:588:ASN:H	1.62	0.65
1:E:568:GLU:HG2	1:E:569:LEU:HD22	1.79	0.65
1:F:244:ASP:OD1	1:G:483:GLN:NE2	2.30	0.65
1:D:273:LYS:HA	1:D:358:ALA:HA	1.79	0.65
1:D:512:ASP:HB3	1:D:515:GLU:HB3	1.79	0.65
1:D:585:ALA:O	1:D:586:LYS:HG2	1.96	0.65
1:E:639:LEU:N	1:E:703:LYS:HZ3	1.95	0.65
2:H:639:ILE:HG13	2:H:640:ALA:N	2.11	0.65
1:D:249:PRO:HA	1:D:252:ARG:NH1	2.12	0.65
1:G:253:HIS:HE1	1:G:255:LEU:HD13	1.59	0.65
2:H:528:GLU:OE2	2:H:548:LYS:HB3	1.97	0.65
2:J:89:THR:CG2	2:J:115:HIS:CA	2.72	0.65
1:A:340:LEU:O	1:A:343:GLU:HG2	1.96	0.64
1:A:692:PRO:O	1:A:732:TYR:N	2.30	0.64
1:B:443:GLU:HA	1:B:446:LYS:HZ2	1.61	0.64
1:C:260:PRO:HD3	1:C:477:TRP:CH2	2.32	0.64
1:D:383:LEU:HD21	1:D:448:LEU:HD23	1.79	0.64
2:H:635:THR:HG1	2:H:638:ASN:ND2	1.95	0.64
1:B:266:MET:SD	1:B:269:ILE:HD11	2.37	0.64
1:B:269:ILE:HG22	1:B:270:ILE:N	2.12	0.64
2:J:89:THR:HG21	2:J:115:HIS:CB	2.27	0.64
1:B:485:GLN:HA	1:B:504:ARG:HH22	1.61	0.64
1:D:438:GLN:O	1:D:441:GLU:HG3	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:441:MET:SD	2:I:445:ASN:HB3	2.37	0.64
2:H:505:LEU:H	2:H:505:LEU:HD23	1.62	0.64
2:J:118:TYR:OH	2:J:143:LYS:O	2.15	0.64
1:A:248:SER:OG	1:A:250:GLU:OE1	2.14	0.64
1:F:240:THR:HG21	1:F:242:ARG:NH2	2.12	0.64
1:F:722:LYS:NZ	1:F:723:LYS:O	2.31	0.64
1:G:411:TYR:C	1:G:411:TYR:CD2	2.76	0.64
2:H:727:SER:HA	2:H:730:ARG:HD3	1.80	0.64
1:B:366:TYR:CD1	1:B:378:LEU:HD11	2.32	0.64
1:C:226:TRP:CE2	1:C:234:SER:HB3	2.32	0.64
1:E:405:LEU:HD11	1:E:411:TYR:HB2	1.78	0.64
2:J:137:TYR:HE1	2:J:143:LYS:HE3	1.62	0.64
2:H:121:ALA:HA	2:H:129:LEU:HA	1.79	0.64
1:A:270:ILE:HD11	1:A:288:THR:HB	1.79	0.64
1:C:270:ILE:HA	1:C:290:SER:HA	1.80	0.64
1:E:345:THR:O	1:E:348:GLU:HG3	1.97	0.64
1:F:612:VAL:O	1:F:616:HIS:ND1	2.30	0.64
2:I:89:THR:HG23	2:I:115:HIS:HA	1.71	0.64
2:I:535:ILE:HD13	2:I:544:ARG:HB2	1.78	0.64
1:C:552:PHE:HB3	1:C:554:PHE:CZ	2.33	0.64
1:G:547:ILE:HD12	1:G:550:PHE:HD2	1.62	0.64
1:A:234:SER:N	1:A:237:GLU:OE2	2.26	0.64
1:D:297:ARG:HH12	1:D:500:LEU:HD23	1.63	0.64
1:E:643:ILE:CG2	1:E:723:LYS:NZ	2.54	0.64
1:B:206:TRP:CD1	1:B:218:LYS:HZ3	2.16	0.63
1:B:225:LYS:NZ	1:B:228:THR:O	2.26	0.63
1:C:345:THR:O	1:C:348:GLU:HG3	1.97	0.63
1:G:381:THR:HG23	1:G:394:ILE:HD13	1.79	0.63
2:I:226:GLU:OE1	2:I:228:GLN:N	2.30	0.63
1:D:491:ILE:HD13	1:D:589:ILE:HB	1.79	0.63
1:D:633:LYS:HA	1:D:636:ARG:NH2	2.13	0.63
1:G:551:ASP:OD1	1:G:552:PHE:N	2.31	0.63
2:I:501:TRP:HD1	2:I:545:ILE:HB	1.63	0.63
1:G:340:LEU:O	1:G:343:GLU:HG2	1.98	0.63
1:G:403:GLN:OE1	1:G:403:GLN:N	2.32	0.63
2:H:710:ASN:HA	2:H:715:ILE:HD11	1.81	0.63
1:A:206:TRP:CD1	1:A:218:LYS:HZ2	2.17	0.63
1:C:206:TRP:CD1	1:C:218:LYS:HZ3	2.16	0.63
1:D:490:ARG:HH21	1:D:504:ARG:HH22	1.46	0.63
2:H:463:ILE:N	2:H:541:GLU:OE2	2.31	0.63
2:H:739:GLU:HA	2:H:742:ARG:NH1	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:LYS:O	1:A:200:ARG:N	2.32	0.63
2:I:167:TYR:HE2	2:I:534:ILE:HG12	1.62	0.63
1:E:695:LYS:HA	1:E:730:LYS:HA	1.79	0.63
1:G:523:LEU:HA	1:G:583:LEU:HD11	1.81	0.63
1:B:365:ARG:NH2	1:B:416:LEU:O	2.31	0.63
1:B:410:TYR:CE2	1:B:414:LYS:HE3	2.34	0.63
1:C:197:LYS:HB2	1:C:202:PHE:CE1	2.34	0.63
1:E:232:PRO:HD2	1:E:233:TYR:HE1	1.60	0.63
1:C:226:TRP:CH2	1:C:234:SER:HB3	2.33	0.63
1:C:508:VAL:HA	1:C:518:LYS:HD3	1.81	0.63
1:E:541:GLN:NE2	1:E:544:GLY:O	2.32	0.63
1:F:480:VAL:HG12	1:F:484:ILE:HD11	1.80	0.63
1:A:183:ILE:HD12	1:A:183:ILE:H	1.64	0.63
1:A:187:LEU:HD11	1:A:205:PRO:HG3	1.79	0.63
2:I:441:MET:HE3	2:I:499:LEU:HD22	1.81	0.63
1:F:626:GLY:HA2	1:F:678:PHE:CZ	2.34	0.62
1:C:459:ILE:HG12	1:C:477:TRP:NE1	2.14	0.62
1:E:273:LYS:O	1:E:359:ARG:NH1	2.32	0.62
1:F:209:ASN:O	1:F:213:LYS:NZ	2.25	0.62
2:J:104:ILE:O	2:J:112:ALA:N	2.32	0.62
2:J:252:ILE:O	2:J:255:SER:OG	2.17	0.62
1:C:527:LEU:HD12	1:C:533:PHE:CE1	2.34	0.62
1:F:240:THR:O	1:G:514:LEU:HB2	1.99	0.62
1:F:366:TYR:HD2	1:F:378:LEU:HD11	1.64	0.62
1:F:631:ILE:O	1:F:636:ARG:NH1	2.22	0.62
2:J:170:PHE:CE1	2:J:217:PHE:HD1	2.16	0.62
2:J:689:GLY:HA3	2:J:738:ALA:HA	1.81	0.62
1:A:373:PRO:HB2	1:A:375:TYR:HE1	1.62	0.62
1:C:260:PRO:HB2	1:C:456:TYR:CE2	2.34	0.62
1:E:523:LEU:HD22	1:E:578:LEU:HD11	1.82	0.62
1:B:217:THR:HG1	1:B:219:TYR:HE1	1.47	0.62
1:D:326:ASN:HD22	1:D:485:GLN:HE21	1.47	0.62
2:H:407:ASP:HA	2:H:410:LYS:HE3	1.82	0.62
2:H:504:GLN:NE2	2:H:505:LEU:O	2.32	0.62
1:B:250:GLU:OE1	1:B:250:GLU:N	2.27	0.62
2:H:578:LYS:NZ	2:H:579:TYR:CE1	2.67	0.62
2:I:226:GLU:OE2	2:I:229:HIS:N	2.33	0.62
1:C:721:ILE:HG21	1:C:723:LYS:NZ	2.14	0.62
1:D:345:THR:O	1:D:348:GLU:HG3	1.99	0.62
1:D:639:LEU:N	1:D:703:LYS:HZ3	1.97	0.62
1:G:345:THR:O	1:G:349:THR:HG23	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:522:THR:O	1:G:525:GLU:HG3	1.98	0.62
1:B:627:LEU:H	1:B:676:ILE:HG22	1.64	0.62
1:D:178:ARG:NE	1:D:224:GLU:OE1	2.33	0.62
1:D:552:PHE:HB3	1:D:554:PHE:CZ	2.34	0.62
1:D:705:ASN:HD21	1:D:722:LYS:HB3	1.65	0.62
1:E:231:ASP:HA	1:E:484:ILE:HD11	1.81	0.62
1:F:345:THR:O	1:F:348:GLU:HG3	2.00	0.62
1:A:496:LYS:HE2	1:A:542:TYR:OH	2.00	0.62
1:D:295:THR:HG22	1:D:332:VAL:HG23	1.80	0.62
1:E:232:PRO:HD2	1:E:233:TYR:HD1	1.64	0.62
1:E:233:TYR:HB2	1:E:238:LYS:HZ2	1.65	0.62
1:F:298:THR:HG21	1:F:331:THR:HB	1.79	0.62
1:F:524:LYS:NZ	1:F:525:GLU:OE2	2.21	0.62
2:J:231:ASP:O	2:J:234:GLN:HG3	1.99	0.62
1:B:226:TRP:CH2	1:B:234:SER:HB2	2.35	0.62
1:D:478:SER:OG	1:D:479:GLU:OE1	2.16	0.62
1:E:525:GLU:HA	1:E:528:LYS:HD2	1.81	0.62
2:H:255:SER:O	2:H:258:GLU:HG3	1.99	0.62
1:G:207:ILE:HB	1:G:210:ILE:HG12	1.82	0.61
2:J:542:TYR:CB	2:J:544:ARG:HH12	2.13	0.61
1:C:493:PHE:CZ	1:C:495:GLY:HA3	2.35	0.61
1:E:560:GLN:O	1:E:563:LYS:HG3	1.99	0.61
1:C:250:GLU:H	1:C:250:GLU:CD	2.08	0.61
1:G:468:ARG:CZ	1:G:470:ARG:HE	2.13	0.61
1:G:254:PRO:HB2	1:G:255:LEU:HD12	1.82	0.61
1:G:638:ILE:HG13	1:G:639:LEU:HD12	1.82	0.61
2:H:157:ARG:NH1	2:H:214:GLN:HG3	2.15	0.61
2:H:617:LYS:NZ	2:H:772:PHE:O	2.32	0.61
2:I:58:ALA:O	2:I:61:LYS:HG2	2.01	0.61
2:I:576:LEU:HD21	2:I:619:THR:HB	1.83	0.61
2:J:57:GLU:O	2:J:61:LYS:HG2	2.00	0.61
1:A:507:ALA:O	1:A:518:LYS:NZ	2.31	0.61
1:C:466:ASN:ND2	1:C:468:ARG:HE	1.97	0.61
1:D:490:ARG:HG3	1:D:502:GLU:OE1	2.01	0.61
1:A:698:VAL:HB	1:A:727:PHE:HB3	1.82	0.61
1:B:612:VAL:O	1:B:616:HIS:ND1	2.34	0.61
1:E:291:LYS:HZ1	1:E:335:ASP:N	1.98	0.61
1:E:459:ILE:HG12	1:E:477:TRP:NE1	2.15	0.61
1:E:476:ASN:N	1:E:476:ASN:OD1	2.30	0.61
1:F:291:LYS:HZ1	1:F:335:ASP:H	1.48	0.61
1:G:643:ILE:CG1	1:G:723:LYS:HE2	2.23	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:491:ARG:HG2	2:H:492:PRO:HD2	1.83	0.61
2:I:150:GLU:CD	2:I:153:LYS:HZ3	2.08	0.61
2:H:479:ILE:O	2:H:590:ARG:NH1	2.34	0.61
1:D:634:ASP:OD1	1:D:635:ILE:N	2.34	0.61
1:F:698:VAL:HB	1:F:727:PHE:HB3	1.83	0.61
1:B:449:ARG:HB3	1:B:449:ARG:HH11	1.66	0.61
1:C:368:ASN:ND2	1:C:405:LEU:O	2.34	0.61
1:D:471:VAL:HG12	1:E:479:GLU:OE2	2.00	0.61
2:H:285:LEU:O	2:H:290:ARG:NH2	2.34	0.61
1:A:493:PHE:CE2	1:A:495:GLY:HA3	2.36	0.61
1:F:265:ASP:OD2	1:F:295:THR:OG1	2.15	0.61
1:B:298:THR:HG22	1:B:330:SER:HA	1.83	0.60
1:D:436:TYR:CE2	1:D:440:LEU:HD11	2.35	0.60
2:H:427:ILE:CD1	2:H:505:LEU:HD12	2.29	0.60
1:C:627:LEU:H	1:C:676:ILE:HG22	1.66	0.60
1:E:491:ILE:HD12	1:E:589:ILE:HB	1.82	0.60
2:H:173:VAL:O	2:H:176:THR:OG1	2.17	0.60
2:H:388:ILE:HD11	2:H:416:ILE:HG13	1.82	0.60
2:I:63:LEU:O	2:I:66:VAL:HG12	2.02	0.60
1:C:233:TYR:CD2	1:C:233:TYR:N	2.69	0.60
1:C:295:THR:HG22	1:C:332:VAL:HG23	1.83	0.60
1:E:387:LYS:HG2	1:E:388:ASN:OD1	2.02	0.60
1:E:445:THR:HG22	1:E:447:GLN:OE1	2.01	0.60
1:F:297:ARG:NH2	1:F:328:ASN:OD1	2.34	0.60
1:F:551:ASP:OD1	1:F:552:PHE:N	2.34	0.60
2:H:247:PHE:HA	2:H:251:GLU:CD	2.25	0.60
2:H:479:ILE:C	2:H:590:ARG:HH22	2.08	0.60
2:I:188:LEU:HD11	2:I:223:TYR:HE2	1.65	0.60
2:J:60:GLU:O	2:J:64:GLU:HG3	2.01	0.60
1:A:270:ILE:HG22	1:A:361:ASN:O	2.01	0.60
1:A:353:ASN:OD1	1:A:354:THR:N	2.33	0.60
1:B:253:HIS:CE1	1:B:254:PRO:HD2	2.37	0.60
1:G:449:ARG:O	1:G:450:LEU:HD23	2.01	0.60
2:H:183:SER:CB	2:H:186:GLN:HE22	2.15	0.60
1:C:535:GLU:OE1	1:C:540:LEU:HD13	2.00	0.60
1:F:617:ARG:NH1	1:F:617:ARG:HB2	2.16	0.60
1:G:233:TYR:HB2	1:G:238:LYS:HE2	1.82	0.60
2:H:514:LEU:HB3	2:H:518:LYS:O	2.01	0.60
1:A:524:LYS:O	1:A:528:LYS:HG2	2.02	0.60
1:B:206:TRP:CG	1:B:218:LYS:HZ3	2.20	0.60
1:D:584:ASN:OD1	1:D:585:ALA:N	2.33	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:571:ASN:HA	2:J:576:LEU:HB2	1.84	0.60
1:A:365:ARG:HH21	1:A:418:PRO:HD3	1.66	0.60
1:B:625:GLU:HA	1:B:678:PHE:CE1	2.37	0.60
1:C:200:ARG:NH1	2:I:139:GLU:OE1	2.35	0.60
2:I:61:LYS:C	2:I:65:LYS:HZ3	2.09	0.60
1:B:269:ILE:HG22	1:B:270:ILE:H	1.67	0.60
1:F:353:ASN:OD1	1:F:354:THR:N	2.33	0.60
1:F:552:PHE:HB3	1:F:554:PHE:CZ	2.36	0.60
1:C:521:MET:HG2	1:C:525:GLU:OE2	2.02	0.60
1:E:233:TYR:HB2	1:E:238:LYS:NZ	2.17	0.60
1:F:639:LEU:N	1:F:703:LYS:HZ2	2.00	0.60
1:G:295:THR:HG22	1:G:332:VAL:HG23	1.83	0.60
2:H:286:SER:O	2:H:290:ARG:HG3	2.01	0.60
1:A:558:THR:HG21	1:A:588:ASN:H	1.67	0.59
2:H:427:ILE:HD12	2:H:505:LEU:HD12	1.83	0.59
1:B:271:LEU:HB2	1:B:289:ILE:HB	1.84	0.59
1:E:634:ASP:OD1	1:E:635:ILE:N	2.34	0.59
1:F:633:LYS:HA	1:F:636:ARG:HH11	1.66	0.59
2:J:170:PHE:O	2:J:174:LEU:HD23	2.02	0.59
1:A:533:PHE:CE1	1:A:542:TYR:HB2	2.38	0.59
1:B:233:TYR:CD1	1:B:233:TYR:N	2.69	0.59
1:B:333:ALA:HB2	1:B:447:GLN:HE22	1.67	0.59
1:D:493:PHE:CZ	1:D:495:GLY:HA3	2.37	0.59
1:F:444:LYS:HG3	1:F:445:THR:HG23	1.83	0.59
1:F:599:ASP:OD1	1:F:600:ARG:N	2.32	0.59
2:H:577:PRO:HA	2:I:82:TYR:HB3	1.84	0.59
1:C:242:ARG:HG3	1:C:242:ARG:HH11	1.68	0.59
1:D:242:ARG:HB3	1:D:462:TYR:CZ	2.38	0.59
1:E:678:PHE:HB3	1:E:687:LEU:HD11	1.83	0.59
1:F:193:THR:HG21	1:F:216:LEU:HB3	1.84	0.59
1:A:221:SER:OG	1:A:222:SER:N	2.34	0.59
1:F:366:TYR:CD2	1:F:378:LEU:HD11	2.37	0.59
1:G:225:LYS:HD3	1:G:514:LEU:HD21	1.85	0.59
2:H:465:ARG:HH11	2:H:465:ARG:HG2	1.67	0.59
1:A:289:ILE:HG21	1:A:346:TRP:CH2	2.37	0.59
1:A:718:THR:HA	1:A:721:ILE:HD13	1.83	0.59
1:B:266:MET:HB2	1:B:364:ILE:HG22	1.85	0.59
1:D:250:GLU:OE1	1:D:250:GLU:N	2.31	0.59
1:G:190:GLU:O	1:G:220:LYS:NZ	2.29	0.59
1:D:226:TRP:CZ2	1:D:234:SER:HB3	2.38	0.59
1:E:233:TYR:CD1	1:E:233:TYR:N	2.70	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:605:VAL:HG12	1:E:704:GLU:HB3	1.84	0.59
1:F:373:PRO:HB2	1:F:375:TYR:CE1	2.37	0.59
2:H:167:TYR:CZ	2:H:536:LYS:HE2	2.38	0.59
2:H:419:ILE:HD13	2:H:422:LEU:HD12	1.84	0.59
2:H:469:ASN:HA	2:H:472:LYS:NZ	2.18	0.59
1:C:466:ASN:HD21	1:C:468:ARG:HE	1.49	0.59
1:C:642:TYR:HD1	1:C:700:ALA:HA	1.66	0.59
1:G:403:GLN:HG3	1:G:411:TYR:HE1	1.68	0.59
2:I:72:GLU:HA	2:I:75:LYS:HZ3	1.67	0.59
1:B:695:LYS:HA	1:B:730:LYS:HA	1.83	0.59
1:E:580:LYS:HA	1:E:580:LYS:HE3	1.84	0.59
2:I:203:VAL:O	2:I:206:LEU:HG	2.02	0.59
2:I:467:ILE:HG22	2:I:471:PHE:CE1	2.37	0.59
1:A:238:LYS:NZ	1:A:254:PRO:HA	2.18	0.59
1:B:536:PRO:HG2	1:B:541:GLN:HE21	1.67	0.59
1:C:506:ALA:HB1	1:C:518:LYS:HZ1	1.68	0.59
1:D:266:MET:H	1:D:295:THR:HG21	1.66	0.59
1:F:489:ALA:N	1:F:505:ILE:O	2.33	0.59
2:H:203:VAL:O	2:H:206:LEU:HG	2.03	0.59
1:A:261:ILE:HG13	1:A:261:ILE:O	2.03	0.58
1:D:434:MET:HE1	1:D:439:PHE:HB2	1.85	0.58
1:D:459:ILE:HG13	1:D:477:TRP:CD1	2.38	0.58
2:H:300:ILE:HD13	2:H:386:TYR:HD2	1.65	0.58
1:A:468:ARG:CZ	1:A:468:ARG:HB2	2.32	0.58
1:A:568:GLU:HG2	1:A:569:LEU:HD22	1.85	0.58
1:C:486:GLU:HA	1:C:586:LYS:NZ	2.18	0.58
1:C:721:ILE:CG2	1:C:723:LYS:CE	2.81	0.58
1:D:643:ILE:N	1:D:699:TYR:O	2.29	0.58
1:E:699:TYR:CE1	1:E:725:LEU:HD13	2.39	0.58
1:G:633:LYS:HA	1:G:636:ARG:HH21	1.66	0.58
1:B:253:HIS:ND1	1:B:254:PRO:HD2	2.18	0.58
1:B:476:ASN:N	1:B:479:GLU:OE2	2.25	0.58
1:D:238:LYS:NZ	1:D:251:ALA:O	2.34	0.58
1:D:300:THR:O	1:D:324:PHE:HB3	2.04	0.58
1:E:447:GLN:C	1:E:448:LEU:HD22	2.28	0.58
1:F:238:LYS:NZ	1:F:252:ARG:HA	2.18	0.58
2:H:478:SER:OG	2:H:590:ARG:NH2	2.35	0.58
1:E:353:ASN:OD1	1:E:354:THR:N	2.36	0.58
1:C:244:ASP:CG	1:C:246:ASN:HD22	2.12	0.58
1:E:721:ILE:CD1	1:E:723:LYS:CD	2.79	0.58
1:G:543:GLN:HG2	1:G:545:LYS:NZ	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:739:GLU:HA	2:H:742:ARG:HH12	1.67	0.58
2:I:107:ILE:HA	2:I:219:LYS:HZ2	1.69	0.58
2:I:173:VAL:HG23	2:I:239:GLU:HG3	1.85	0.58
1:A:565:GLN:NE2	1:A:582:LYS:O	2.36	0.58
1:C:508:VAL:HG23	1:C:516:THR:HA	1.85	0.58
1:C:573:ASN:ND2	1:C:575:TYR:HB2	2.18	0.58
1:G:496:LYS:HE2	1:G:496:LYS:HA	1.86	0.58
1:A:494:ASN:HB2	1:A:498:LEU:HA	1.84	0.58
1:C:551:ASP:OD1	1:C:552:PHE:N	2.37	0.58
1:D:360:LEU:HB3	1:D:432:ILE:CG2	2.33	0.58
1:E:246:ASN:HD21	1:E:406:ALA:HB1	1.68	0.58
1:E:366:TYR:CE1	1:E:378:LEU:HD23	2.39	0.58
2:H:55:LYS:HE2	2:H:134:SER:HA	1.84	0.58
2:I:530:LYS:HB3	2:I:548:LYS:NZ	2.19	0.58
1:D:549:GLU:HB3	1:D:595:ARG:NH1	2.18	0.58
2:H:62:LEU:HD21	2:H:137:TYR:HB3	1.86	0.58
1:A:366:TYR:CZ	1:A:378:LEU:HD12	2.39	0.58
1:A:438:GLN:HA	1:A:441:GLU:OE1	2.04	0.58
1:B:291:LYS:HZ1	1:B:335:ASP:N	1.97	0.58
1:D:332:VAL:O	1:D:447:GLN:HG2	2.04	0.58
1:D:382:SER:HA	1:D:393:THR:HA	1.86	0.58
1:B:353:ASN:OD1	1:B:354:THR:N	2.37	0.57
1:C:233:TYR:HD2	1:C:233:TYR:N	2.02	0.57
1:E:291:LYS:HE3	1:E:335:ASP:O	2.04	0.57
2:J:454:LEU:HD12	2:J:455:VAL:HG13	1.86	0.57
1:B:326:ASN:ND2	1:B:485:GLN:HE21	2.02	0.57
1:G:234:SER:OG	1:G:237:GLU:HG2	2.04	0.57
2:I:113:LEU:HD23	2:I:115:HIS:NE2	2.18	0.57
2:J:91:HIS:CD2	2:J:93:SER:H	2.22	0.57
1:C:353:ASN:OD1	1:C:354:THR:N	2.37	0.57
1:C:634:ASP:OD1	1:C:635:ILE:N	2.37	0.57
1:C:639:LEU:N	1:C:703:LYS:HZ3	2.02	0.57
1:E:300:THR:O	1:E:324:PHE:HB3	2.03	0.57
1:F:667:SER:O	1:F:675:PHE:N	2.32	0.57
2:J:226:GLU:HB3	2:J:229:HIS:HB2	1.86	0.57
1:A:338:LEU:CD1	1:A:344:ARG:HH21	2.17	0.57
2:H:157:ARG:HD3	2:H:214:GLN:HG3	1.86	0.57
2:I:38:GLU:HG2	2:I:39:ILE:HD12	1.85	0.57
2:I:167:TYR:CE2	2:I:168:GLN:NE2	2.73	0.57
2:J:63:LEU:O	2:J:66:VAL:HG12	2.04	0.57
1:A:190:GLU:C	1:A:220:LYS:HZ2	2.13	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:TRP:CZ2	1:A:234:SER:HB3	2.39	0.57
1:A:249:PRO:HA	1:A:252:ARG:HG2	1.87	0.57
1:A:584:ASN:O	1:A:587:MET:HE2	2.04	0.57
1:B:366:TYR:CE1	1:B:378:LEU:CD1	2.87	0.57
1:B:468:ARG:HB3	1:B:470:ARG:NH2	2.19	0.57
1:C:225:LYS:HG2	1:C:228:THR:HA	1.86	0.57
1:C:334:ILE:CG2	1:C:446:LYS:HB3	2.34	0.57
1:C:403:GLN:O	1:C:404:ILE:HD13	2.04	0.57
1:C:513:PRO:O	1:C:516:THR:HG22	2.04	0.57
1:D:202:PHE:CE2	1:D:204:SER:HB2	2.35	0.57
1:E:524:LYS:HG2	1:E:540:LEU:HD21	1.87	0.57
1:F:202:PHE:CE2	1:F:204:SER:HB2	2.38	0.57
2:H:55:LYS:HG3	2:H:134:SER:O	2.05	0.57
2:H:194:LEU:HD11	2:H:212:GLU:HB3	1.85	0.57
1:A:210:ILE:HA	1:A:213:LYS:NZ	2.20	0.57
1:B:492:ILE:CG2	1:B:500:LEU:HD12	2.34	0.57
1:D:535:GLU:OE1	1:D:540:LEU:HD13	2.03	0.57
1:E:385:LEU:HD23	1:E:391:LEU:HD21	1.85	0.57
1:E:524:LYS:HZ2	1:E:579:ASP:H	1.53	0.57
1:F:233:TYR:HA	1:F:237:GLU:OE2	2.05	0.57
1:F:269:ILE:HG22	1:F:270:ILE:N	2.19	0.57
1:F:515:GLU:CD	1:F:515:GLU:N	2.63	0.57
1:F:485:GLN:HE22	1:F:504:ARG:CZ	2.18	0.57
2:H:202:SER:OG	2:H:204:GLU:HG3	2.04	0.57
2:I:159:ILE:O	2:I:162:LYS:HG2	2.04	0.57
1:B:383:LEU:N	1:B:392:ALA:O	2.36	0.57
1:D:643:ILE:HG13	1:D:723:LYS:CE	2.34	0.57
1:E:234:SER:O	1:E:237:GLU:HG2	2.05	0.57
1:F:253:HIS:O	1:F:256:VAL:HG22	2.04	0.57
1:F:350:MET:O	1:F:352:LEU:N	2.38	0.57
1:F:468:ARG:NH2	1:G:232:PRO:HB3	2.20	0.57
2:H:100:ASP:C	2:H:102:LYS:H	2.13	0.57
1:B:233:TYR:HD1	1:B:233:TYR:N	2.01	0.57
1:B:609:GLU:HB2	1:B:724:ILE:CG2	2.35	0.57
1:C:384:VAL:HG23	1:C:449:ARG:HB2	1.87	0.57
1:D:492:ILE:HD13	1:D:502:GLU:OE2	2.05	0.57
1:D:554:PHE:CE1	1:D:589:ILE:HD12	2.40	0.57
2:J:227:PRO:HB2	2:J:228:GLN:NE2	2.19	0.57
1:A:415:ASN:C	1:A:416:LEU:HD22	2.30	0.57
1:C:374:ILE:HG12	1:C:405:LEU:HB2	1.86	0.57
2:H:426:SER:HB3	2:H:510:ARG:CZ	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:409:ARG:O	2:I:413:LYS:HG3	2.05	0.57
1:B:463:ASN:ND2	1:B:465:GLU:OE2	2.37	0.56
1:B:555:ASP:OD1	1:B:556:GLN:N	2.36	0.56
1:D:197:LYS:HD3	1:D:198:ASN:OD1	2.05	0.56
1:D:628:LEU:HD12	1:D:628:LEU:O	2.05	0.56
1:G:233:TYR:HA	1:G:237:GLU:OE2	2.05	0.56
1:A:206:TRP:CG	1:A:218:LYS:HZ2	2.23	0.56
1:B:223:PRO:HG2	1:B:224:GLU:OE1	2.05	0.56
2:H:124:GLY:N	2:H:127:PRO:HG3	2.20	0.56
1:B:443:GLU:HA	1:B:446:LYS:NZ	2.20	0.56
1:B:627:LEU:HB3	1:B:629:LEU:HD23	1.87	0.56
1:D:483:GLN:OE1	1:D:483:GLN:N	2.39	0.56
1:D:535:GLU:OE2	1:D:540:LEU:HD22	2.05	0.56
1:D:577:VAL:HG12	1:D:580:LYS:HB2	1.87	0.56
1:E:271:LEU:HB2	1:E:289:ILE:HG13	1.88	0.56
1:E:301:SER:O	1:E:323:GLY:N	2.38	0.56
1:F:295:THR:HG22	1:F:332:VAL:HG23	1.88	0.56
1:F:634:ASP:OD1	1:F:635:ILE:N	2.38	0.56
1:G:271:LEU:HB2	1:G:289:ILE:HG23	1.86	0.56
2:J:589:ASN:OD1	2:J:590:ARG:N	2.34	0.56
1:B:225:LYS:HZ1	1:B:230:SER:HB3	1.70	0.56
1:B:488:THR:OG1	1:B:504:ARG:NH2	2.38	0.56
1:B:533:PHE:CZ	1:B:542:TYR:HB2	2.40	0.56
1:C:350:MET:O	1:C:352:LEU:N	2.38	0.56
1:D:362:ALA:HB3	1:D:421:LEU:HD13	1.86	0.56
1:E:610:SER:HA	1:E:613:LYS:HZ3	1.71	0.56
1:E:721:ILE:HG13	1:E:723:LYS:CD	2.34	0.56
1:F:187:LEU:HD11	1:F:205:PRO:HG3	1.86	0.56
1:F:297:ARG:HD2	1:F:298:THR:N	2.20	0.56
1:F:365:ARG:HE	1:F:418:PRO:HB3	1.70	0.56
2:H:155:LEU:HD13	2:H:159:ILE:HG13	1.88	0.56
2:H:183:SER:HB2	2:H:186:GLN:NE2	2.20	0.56
2:H:743:LEU:HB3	2:H:755:VAL:HG11	1.87	0.56
1:A:612:VAL:O	1:A:616:HIS:NE2	2.38	0.56
1:B:234:SER:HB3	1:B:237:GLU:HG2	1.87	0.56
1:C:203:LEU:HB3	2:I:44:VAL:HA	1.87	0.56
1:D:326:ASN:ND2	1:D:485:GLN:HB2	2.20	0.56
1:F:484:ILE:H	1:F:484:ILE:HD12	1.69	0.56
1:A:234:SER:OG	1:A:237:GLU:HG2	2.06	0.56
1:B:345:THR:O	1:B:348:GLU:HG3	2.06	0.56
1:F:468:ARG:HH21	1:G:232:PRO:HB3	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:291:LYS:NZ	1:B:335:ASP:H	1.97	0.56
1:B:550:PHE:O	1:B:575:TYR:OH	2.23	0.56
1:B:584:ASN:H	1:B:587:MET:CE	2.18	0.56
1:B:634:ASP:OD1	1:B:635:ILE:N	2.38	0.56
1:C:333:ALA:HA	1:C:447:GLN:HE22	1.71	0.56
1:F:198:ASN:O	1:F:199:LYS:HG2	2.06	0.56
1:G:353:ASN:OD1	1:G:354:THR:N	2.37	0.56
2:H:676:GLU:HG2	2:H:677:LEU:N	2.21	0.56
1:B:445:THR:O	1:B:447:GLN:HG2	2.05	0.56
1:B:552:PHE:HB2	1:B:554:PHE:CZ	2.41	0.56
1:C:264:VAL:HG21	1:C:381:THR:HG21	1.88	0.56
1:C:521:MET:HE1	1:C:583:LEU:HG	1.87	0.56
1:D:492:ILE:HG22	1:D:500:LEU:HD12	1.88	0.56
1:F:523:LEU:HD22	1:F:578:LEU:HD11	1.87	0.56
1:E:345:THR:O	1:E:349:THR:HG23	2.05	0.56
1:G:207:ILE:H	1:G:211:HIS:CE1	2.23	0.56
2:H:165:GLN:OE1	2:H:165:GLN:N	2.29	0.56
1:A:338:LEU:HD13	1:A:344:ARG:HH21	1.71	0.56
1:A:638:ILE:HG13	1:A:639:LEU:HD12	1.88	0.56
1:B:245:LYS:HB3	1:C:486:GLU:OE2	2.05	0.56
1:C:560:GLN:HA	1:C:563:LYS:HE3	1.88	0.56
1:D:434:MET:SD	1:D:438:GLN:HB2	2.45	0.56
1:E:459:ILE:HG12	1:E:477:TRP:CE2	2.40	0.56
1:F:549:GLU:C	1:F:594:LYS:HE3	2.30	0.56
1:G:560:GLN:HA	1:G:563:LYS:HE3	1.88	0.56
1:B:365:ARG:HH12	1:B:414:LYS:HA	1.71	0.55
1:D:183:ILE:HD12	1:D:183:ILE:H	1.71	0.55
1:D:373:PRO:HB2	1:D:375:TYR:HE1	1.71	0.55
1:E:341:ALA:O	1:E:344:ARG:NH1	2.34	0.55
1:E:593:ASP:OD1	1:E:595:ARG:NH2	2.39	0.55
2:H:63:LEU:O	2:H:66:VAL:HG12	2.06	0.55
1:A:403:GLN:CD	1:A:403:GLN:H	2.13	0.55
1:B:441:GLU:HA	1:B:444:LYS:NZ	2.21	0.55
1:B:584:ASN:OD1	1:B:585:ALA:N	2.38	0.55
1:C:250:GLU:OE1	1:C:250:GLU:N	2.24	0.55
1:C:573:ASN:HD21	1:C:575:TYR:HB2	1.70	0.55
1:D:508:VAL:HA	1:D:515:GLU:OE2	2.07	0.55
1:E:493:PHE:CZ	1:E:495:GLY:HA3	2.41	0.55
1:F:266:MET:H	1:F:295:THR:HG21	1.71	0.55
1:G:403:GLN:HG3	1:G:411:TYR:CE1	2.41	0.55
1:G:667:SER:N	1:G:675:PHE:O	2.26	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:556:GLN:OE1	1:A:557:GLN:NE2	2.40	0.55
1:B:634:ASP:O	1:B:637:LYS:HG2	2.06	0.55
1:C:577:VAL:HG22	1:C:580:LYS:HB2	1.88	0.55
1:G:493:PHE:CE2	1:G:495:GLY:HA3	2.41	0.55
1:G:722:LYS:NZ	1:G:723:LYS:O	2.40	0.55
2:H:83:ILE:HG22	2:H:131:ILE:HD11	1.87	0.55
2:I:531:ASP:OD1	2:I:532:VAL:N	2.40	0.55
2:I:533:GLN:OE1	2:I:533:GLN:N	2.39	0.55
1:A:325:SER:OG	1:G:415:ASN:ND2	2.39	0.55
1:A:555:ASP:O	1:A:558:THR:OG1	2.21	0.55
1:C:565:GLN:NE2	1:C:582:LYS:HB2	2.21	0.55
1:E:233:TYR:O	1:E:238:LYS:NZ	2.39	0.55
1:E:645:GLU:HA	1:E:655:VAL:HA	1.89	0.55
1:F:468:ARG:NH1	1:F:468:ARG:HB2	2.21	0.55
2:H:550:VAL:HG23	2:H:555:ILE:HD11	1.89	0.55
2:I:480:SER:CB	2:I:590:ARG:HE	2.19	0.55
2:J:248:ASN:ND2	2:J:248:ASN:O	2.38	0.55
1:A:634:ASP:OD1	1:A:635:ILE:N	2.40	0.55
1:C:485:GLN:HG2	1:C:504:ARG:NH2	2.22	0.55
1:D:242:ARG:HB3	1:D:462:TYR:CE2	2.41	0.55
2:I:498:ARG:NH2	2:I:541:GLU:O	2.37	0.55
1:A:266:MET:H	1:A:295:THR:HG21	1.69	0.55
1:A:328:ASN:HD21	1:A:452:THR:HB	1.72	0.55
1:A:359:ARG:NH2	1:A:429:SER:O	2.40	0.55
1:A:620:ILE:HG13	1:A:630:ASN:HD22	1.72	0.55
1:C:260:PRO:HB2	1:C:456:TYR:HE2	1.70	0.55
1:D:358:ALA:HB3	1:D:434:MET:HE3	1.87	0.55
1:E:442:LEU:O	1:E:446:LYS:HD2	2.06	0.55
1:G:206:TRP:CG	1:G:218:LYS:HZ3	2.24	0.55
2:H:696:ALA:O	2:H:699:LEU:HG	2.06	0.55
2:I:463:ILE:HB	2:I:465:ARG:HH22	1.72	0.55
2:I:477:TYR:HA	2:I:529:ILE:H	1.71	0.55
1:A:233:TYR:HA	1:A:237:GLU:OE2	2.06	0.55
1:A:350:MET:O	1:A:352:LEU:N	2.37	0.55
1:A:629:LEU:O	1:A:674:THR:N	2.40	0.55
1:B:698:VAL:HB	1:B:727:PHE:HB3	1.88	0.55
1:C:190:GLU:O	1:C:220:LYS:HE2	2.07	0.55
1:C:266:MET:H	1:C:295:THR:HG21	1.70	0.55
1:C:447:GLN:HB3	1:C:449:ARG:NH2	2.18	0.55
1:C:520:ASP:OD1	1:C:521:MET:N	2.39	0.55
1:C:639:LEU:HD12	1:C:639:LEU:O	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:636:ARG:HG3	1:D:639:LEU:HD21	1.89	0.55
2:H:264:MET:N	2:H:264:MET:SD	2.79	0.55
2:I:211:ASN:O	2:I:214:GLN:HG2	2.06	0.55
2:J:594:ASN:OD1	2:J:595:ILE:N	2.39	0.55
1:B:223:PRO:HG2	1:B:224:GLU:CD	2.32	0.55
1:D:297:ARG:NH2	1:D:500:LEU:HD23	2.21	0.55
1:E:540:LEU:HB2	1:E:547:ILE:HD13	1.89	0.55
1:F:297:ARG:HD2	1:F:298:THR:H	1.72	0.55
2:H:605:GLU:O	2:H:609:ASN:ND2	2.38	0.55
1:A:260:PRO:HB2	1:A:456:TYR:CE2	2.42	0.55
1:C:560:GLN:O	1:C:563:LYS:HG2	2.05	0.55
1:D:667:SER:O	1:D:675:PHE:N	2.33	0.55
1:F:242:ARG:HB3	1:F:462:TYR:CE2	2.42	0.55
1:F:643:ILE:HD13	1:F:723:LYS:HE2	1.89	0.55
2:H:108:TYR:O	2:H:110:LYS:HE2	2.07	0.55
2:I:40:MET:O	2:I:44:VAL:HG12	2.07	0.55
2:I:170:PHE:HD1	2:I:243:TYR:CE2	2.24	0.55
2:I:487:ASP:HA	2:I:518:LYS:HG3	1.88	0.55
1:C:228:THR:HG23	1:C:235:ASP:OD1	2.07	0.55
1:D:198:ASN:O	1:D:199:LYS:HD2	2.05	0.55
1:D:668:LEU:HA	1:D:674:THR:HA	1.89	0.55
1:F:599:ASP:CG	1:F:600:ARG:H	2.15	0.55
2:H:171:LEU:O	2:H:175:ASN:ND2	2.38	0.55
2:H:386:TYR:CE1	2:H:412:TYR:HE1	2.25	0.55
2:J:136:ASP:OD1	2:J:136:ASP:N	2.39	0.55
1:A:546:ASP:OD1	1:A:547:ILE:N	2.40	0.54
1:A:610:SER:O	1:A:613:LYS:HG2	2.07	0.54
1:B:558:THR:HG21	1:B:588:ASN:H	1.72	0.54
1:D:507:ALA:C	1:D:518:LYS:HD2	2.32	0.54
2:H:296:LEU:HD23	2:H:388:ILE:HG21	1.88	0.54
1:A:634:ASP:O	1:A:637:LYS:HG2	2.06	0.54
1:B:382:SER:HA	1:B:393:THR:HA	1.90	0.54
1:C:244:ASP:C	1:C:246:ASN:H	2.14	0.54
1:C:383:LEU:HD11	1:C:448:LEU:HD12	1.89	0.54
1:C:546:ASP:HB3	1:C:548:THR:HG22	1.89	0.54
1:D:233:TYR:HA	1:D:237:GLU:OE2	2.07	0.54
1:D:411:TYR:CD1	1:D:412:PRO:HA	2.42	0.54
1:D:471:VAL:N	1:E:479:GLU:OE1	2.39	0.54
1:G:620:ILE:HD12	1:G:620:ILE:H	1.72	0.54
2:H:247:PHE:HA	2:H:251:GLU:OE2	2.07	0.54
2:H:480:SER:HA	2:H:590:ARG:HH12	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:578:LYS:C	2:H:579:TYR:CD1	2.85	0.54
2:I:135:GLU:CD	2:I:135:GLU:H	2.15	0.54
2:I:136:ASP:OD1	2:I:136:ASP:N	2.34	0.54
1:C:245:LYS:HE2	1:C:245:LYS:HA	1.89	0.54
1:D:209:ASN:OD1	1:D:210:ILE:HG12	2.08	0.54
1:E:291:LYS:HZ2	1:E:334:ILE:HB	1.71	0.54
1:E:549:GLU:C	1:E:594:LYS:HE3	2.33	0.54
1:E:643:ILE:CG2	1:E:723:LYS:HZ2	2.00	0.54
1:G:212:GLU:OE2	1:G:213:LYS:NZ	2.38	0.54
2:H:129:LEU:HD23	2:H:129:LEU:H	1.71	0.54
2:J:203:VAL:O	2:J:206:LEU:HG	2.06	0.54
1:B:582:LYS:HE2	1:B:582:LYS:HA	1.88	0.54
1:C:221:SER:HB2	1:C:228:THR:HG21	1.89	0.54
1:C:635:ILE:C	1:C:637:LYS:H	2.15	0.54
1:D:542:TYR:O	1:D:545:LYS:HE2	2.07	0.54
1:E:209:ASN:OD1	1:E:210:ILE:HG12	2.06	0.54
1:F:542:TYR:O	1:F:545:LYS:HE2	2.08	0.54
1:F:583:LEU:CD1	1:F:587:MET:HE1	2.37	0.54
1:G:634:ASP:OD1	1:G:635:ILE:N	2.40	0.54
2:H:478:SER:OG	2:H:590:ARG:HA	2.07	0.54
1:C:291:LYS:HE2	1:C:335:ASP:O	2.07	0.54
1:E:659:ARG:HA	1:E:716:THR:O	2.07	0.54
1:F:234:SER:N	1:F:237:GLU:OE2	2.38	0.54
1:G:200:ARG:HG3	1:G:200:ARG:HH11	1.72	0.54
1:A:479:GLU:N	1:A:479:GLU:CD	2.66	0.54
1:B:224:GLU:OE1	1:B:224:GLU:N	2.40	0.54
1:B:295:THR:HG22	1:B:332:VAL:HG23	1.90	0.54
1:E:244:ASP:C	1:E:246:ASN:H	2.15	0.54
1:G:573:ASN:ND2	1:G:576:THR:OG1	2.41	0.54
2:I:176:THR:HB	2:I:239:GLU:OE2	2.07	0.54
2:I:264:MET:HA	2:I:267:ARG:NH2	2.23	0.54
2:I:533:GLN:HE21	2:I:544:ARG:HG3	1.73	0.54
1:D:590:LEU:HD21	1:D:592:ARG:HG3	1.89	0.54
1:E:326:ASN:OD1	1:E:490:ARG:NH1	2.41	0.54
1:E:562:ILE:HD13	1:E:565:GLN:OE1	2.07	0.54
1:G:258:ALA:HA	1:G:371:THR:OG1	2.07	0.54
2:H:656:LYS:HD2	2:H:672:SER:OG	2.08	0.54
1:A:446:LYS:NZ	1:A:708:ILE:O	2.30	0.54
1:E:231:ASP:HB2	1:E:232:PRO:HD3	1.90	0.54
1:E:350:MET:O	1:E:352:LEU:N	2.40	0.54
2:H:411:GLN:HA	2:H:414:ARG:NH1	2.21	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:261:ILE:HD11	1:A:369:THR:HG23	1.90	0.54
1:C:192:TYR:CD1	1:C:192:TYR:C	2.86	0.54
1:D:552:PHE:HB3	1:D:554:PHE:CE2	2.43	0.54
1:F:266:MET:HE2	1:F:269:ILE:HD11	1.89	0.54
1:F:485:GLN:OE1	1:F:504:ARG:NH1	2.41	0.54
1:G:245:LYS:HA	1:G:245:LYS:HE3	1.89	0.54
1:G:266:MET:H	1:G:295:THR:HG21	1.73	0.54
2:H:190:PHE:CD1	2:H:194:LEU:HB2	2.42	0.54
2:H:301:GLU:HG2	2:H:302:PRO:HD2	1.90	0.54
2:J:107:ILE:HD13	2:J:149:TYR:CD2	2.42	0.54
1:A:291:LYS:HB3	1:A:335:ASP:OD1	2.07	0.54
1:B:195:ASP:OD2	2:H:236:TYR:OH	2.25	0.54
1:E:646:ILE:N	1:E:654:GLU:O	2.37	0.54
1:G:198:ASN:H	1:G:200:ARG:HH22	1.56	0.54
1:G:593:ASP:OD2	1:G:595:ARG:HB3	2.08	0.54
1:G:617:ARG:HH11	1:G:617:ARG:HG2	1.73	0.54
2:H:434:LYS:HD3	2:H:436:TYR:CZ	2.43	0.54
1:E:490:ARG:HB2	1:E:504:ARG:NH1	2.23	0.53
2:H:447:THR:HG23	2:H:450:LEU:HB2	1.89	0.53
1:B:197:LYS:HZ1	2:H:236:TYR:HD1	1.53	0.53
1:D:267:GLU:OE1	1:D:267:GLU:N	2.40	0.53
1:D:297:ARG:NH1	1:D:500:LEU:HD23	2.23	0.53
1:E:462:TYR:CZ	1:E:467:GLY:HA2	2.43	0.53
1:E:565:GLN:HA	1:E:568:GLU:OE2	2.08	0.53
1:F:197:LYS:O	1:F:199:LYS:N	2.39	0.53
2:H:192:ASN:HA	2:H:195:LYS:HD2	1.90	0.53
2:H:447:THR:HG21	2:H:450:LEU:HD12	1.90	0.53
2:H:669:HIS:CE1	2:H:671:PRO:HB2	2.43	0.53
1:A:498:LEU:HB2	1:A:637:LYS:NZ	2.23	0.53
1:A:512:ASP:OD2	1:G:245:LYS:NZ	2.30	0.53
1:B:178:ARG:HA	1:B:178:ARG:NE	2.22	0.53
1:C:697:ASN:HA	1:C:727:PHE:O	2.09	0.53
1:D:459:ILE:HG13	1:D:477:TRP:CE2	2.44	0.53
1:D:509:ASN:H	1:D:515:GLU:CD	2.15	0.53
1:E:187:LEU:HD11	1:E:205:PRO:HG3	1.89	0.53
1:E:490:ARG:HD3	1:E:504:ARG:HH22	1.72	0.53
1:F:200:ARG:HG3	1:F:200:ARG:NH1	2.22	0.53
1:F:610:SER:O	1:F:613:LYS:HG2	2.08	0.53
1:G:667:SER:O	1:G:675:PHE:N	2.35	0.53
2:I:89:THR:HG22	2:I:114:LEU:HD12	1.90	0.53
2:J:115:HIS:CD2	2:J:116:GLU:HG3	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:583:LEU:HB3	1:A:587:MET:HE1	1.90	0.53
1:A:678:PHE:CZ	1:A:687:LEU:HD23	2.43	0.53
1:E:435:ASN:OD1	1:E:438:GLN:N	2.31	0.53
1:E:597:HIS:H	1:E:606:GLY:C	2.16	0.53
1:F:631:ILE:C	1:F:636:ARG:HH12	2.13	0.53
2:H:250:GLN:OE1	2:H:250:GLN:N	2.42	0.53
2:H:257:GLU:HA	2:H:260:LYS:HZ3	1.73	0.53
2:H:404:ILE:O	2:H:409:ARG:NH2	2.37	0.53
2:I:82:TYR:OH	2:I:91:HIS:CE1	2.62	0.53
2:I:273:LYS:O	2:I:276:GLN:HG3	2.08	0.53
2:J:502:ARG:NH1	2:J:544:ARG:HD3	2.23	0.53
1:A:174:THR:O	1:A:175:VAL:HB	2.08	0.53
1:C:197:LYS:O	1:C:198:ASN:C	2.51	0.53
1:C:202:PHE:HB2	2:I:45:LYS:HD3	1.91	0.53
1:D:353:ASN:OD1	1:D:354:THR:N	2.38	0.53
1:E:608:ASP:O	1:E:611:VAL:HG22	2.09	0.53
1:F:259:TYR:CE2	1:F:261:ILE:HD11	2.44	0.53
1:F:636:ARG:HG3	1:F:637:LYS:HZ1	1.73	0.53
1:G:617:ARG:NH1	1:G:617:ARG:O	2.41	0.53
2:H:105:LYS:HD2	2:H:109:GLY:O	2.07	0.53
1:D:297:ARG:CZ	1:D:500:LEU:H	2.21	0.53
1:D:385:LEU:HD13	1:D:448:LEU:HG	1.90	0.53
1:E:233:TYR:CD2	1:E:243:ILE:CD1	2.91	0.53
1:G:610:SER:O	1:G:613:LYS:HG2	2.08	0.53
2:I:762:THR:HA	2:I:765:PHE:CE1	2.44	0.53
1:A:227:SER:O	1:A:230:SER:N	2.41	0.53
1:A:455:VAL:O	1:A:455:VAL:HG13	2.08	0.53
1:B:533:PHE:CE2	1:B:542:TYR:HB2	2.44	0.53
1:C:297:ARG:NH1	1:C:329:SER:O	2.40	0.53
1:D:297:ARG:NH1	1:D:500:LEU:HB2	2.23	0.53
1:F:245:LYS:NZ	1:G:512:ASP:OD2	2.42	0.53
2:I:589:ASN:OD1	2:I:590:ARG:N	2.34	0.53
2:J:503:ILE:HG13	2:J:549:VAL:HG23	1.91	0.53
1:A:435:ASN:ND2	1:A:438:GLN:HG2	2.24	0.53
1:B:266:MET:CE	1:B:332:VAL:HG21	2.39	0.53
1:C:705:ASN:ND2	1:C:722:LYS:HB3	2.24	0.53
1:D:269:ILE:HG22	1:D:270:ILE:N	2.24	0.53
1:E:385:LEU:CD2	1:E:391:LEU:HD21	2.38	0.53
1:F:187:LEU:HD12	1:F:192:TYR:HB3	1.91	0.53
1:F:209:ASN:OD1	1:F:210:ILE:HG12	2.09	0.53
1:F:535:GLU:OE2	1:F:540:LEU:HD12	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:155:LEU:O	2:H:159:ILE:HB	2.09	0.53
1:A:245:LYS:HE2	1:A:245:LYS:HA	1.89	0.53
1:C:291:LYS:HE2	1:C:335:ASP:OD1	2.09	0.53
1:C:385:LEU:HG	1:C:391:LEU:HD21	1.91	0.53
1:G:263:HIS:CE1	1:G:367:VAL:HB	2.43	0.53
2:H:469:ASN:HA	2:H:472:LYS:HZ3	1.73	0.53
2:I:114:LEU:HD12	2:I:115:HIS:N	2.24	0.53
1:B:536:PRO:HG2	1:B:541:GLN:NE2	2.24	0.53
1:D:551:ASP:C	1:D:552:PHE:HD1	2.17	0.53
1:D:620:ILE:HD13	1:D:629:LEU:HA	1.91	0.53
1:E:226:TRP:CZ2	1:E:234:SER:HB3	2.44	0.53
1:E:406:ALA:HB1	1:E:407:PRO:HD2	1.90	0.53
1:G:244:ASP:C	1:G:246:ASN:H	2.16	0.53
1:G:438:GLN:HA	1:G:441:GLU:OE2	2.09	0.53
1:G:559:SER:HA	1:G:562:ILE:HG22	1.90	0.53
2:I:607:LYS:HA	2:I:615:ILE:HD11	1.91	0.53
2:J:89:THR:HG21	2:J:115:HIS:HA	1.82	0.53
1:A:470:ARG:HD3	1:A:471:VAL:H	1.73	0.52
1:B:392:ALA:HB2	1:B:432:ILE:HD13	1.91	0.52
1:C:405:LEU:HD21	1:C:411:TYR:HB2	1.92	0.52
1:E:610:SER:HA	1:E:613:LYS:NZ	2.24	0.52
1:E:721:ILE:CG1	1:E:723:LYS:CD	2.88	0.52
1:G:270:ILE:C	1:G:271:LEU:HD22	2.33	0.52
1:G:358:ALA:HB3	1:G:434:MET:HE3	1.90	0.52
2:I:137:TYR:CE2	2:I:143:LYS:HE3	2.44	0.52
2:J:110:LYS:HD3	2:J:110:LYS:N	2.23	0.52
2:J:145:LEU:HD21	2:J:226:GLU:HG3	1.91	0.52
2:J:204:GLU:O	2:J:207:GLU:HG2	2.08	0.52
1:A:197:LYS:O	1:A:198:ASN:C	2.52	0.52
1:B:183:ILE:HG13	1:B:236:PHE:HD1	1.75	0.52
1:B:449:ARG:HB3	1:B:449:ARG:NH1	2.23	0.52
1:C:447:GLN:C	1:C:448:LEU:HD22	2.35	0.52
1:D:635:ILE:HG23	1:D:636:ARG:HD3	1.91	0.52
2:H:80:LYS:H	2:H:128:VAL:HG12	1.74	0.52
2:H:567:ASN:OD1	2:H:568:GLN:N	2.42	0.52
2:I:115:HIS:ND1	2:I:116:GLU:HG3	2.23	0.52
2:J:443:ILE:HG21	2:J:454:LEU:HD21	1.91	0.52
1:A:360:LEU:HD12	1:A:361:ASN:H	1.74	0.52
1:C:459:ILE:HG12	1:C:477:TRP:CE2	2.44	0.52
1:C:486:GLU:HA	1:C:586:LYS:HZ1	1.75	0.52
1:E:470:ARG:HD2	1:E:471:VAL:N	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:628:LEU:HA	1:E:674:THR:O	2.10	0.52
1:F:635:ILE:C	1:F:637:LYS:H	2.17	0.52
1:G:459:ILE:HG13	1:G:477:TRP:NE1	2.24	0.52
1:B:263:HIS:CG	1:B:297:ARG:HG3	2.44	0.52
1:E:488:THR:HG22	1:E:506:ALA:HA	1.91	0.52
2:H:475:PHE:O	2:H:476:LYS:HD3	2.09	0.52
2:H:658:LEU:HD22	2:H:667:LEU:HD12	1.91	0.52
2:J:577:PRO:O	2:J:580:THR:HG22	2.09	0.52
1:A:360:LEU:HD12	1:A:361:ASN:N	2.24	0.52
1:D:705:ASN:ND2	1:D:722:LYS:O	2.42	0.52
1:E:240:THR:O	1:F:514:LEU:HB2	2.09	0.52
1:F:364:ILE:HG23	1:F:421:LEU:HD11	1.91	0.52
1:B:508:VAL:HA	1:B:518:LYS:HD3	1.92	0.52
1:C:435:ASN:N	1:C:438:GLN:OE1	2.42	0.52
1:D:234:SER:OG	1:D:237:GLU:HG2	2.10	0.52
1:G:270:ILE:HG13	1:G:361:ASN:OD1	2.10	0.52
1:G:696:VAL:O	1:G:728:SER:HA	2.08	0.52
2:H:591:TYR:CE2	2:H:594:ASN:HB3	2.45	0.52
2:H:640:ALA:HA	2:H:643:TYR:CE1	2.44	0.52
2:H:707:LEU:HD23	2:H:709:THR:CG2	2.37	0.52
2:I:686:HIS:O	2:I:738:ALA:HB1	2.10	0.52
2:J:237:ALA:HB1	2:J:240:ALA:HB3	1.90	0.52
1:A:697:ASN:HA	1:A:727:PHE:O	2.10	0.52
1:C:366:TYR:CD2	1:C:378:LEU:HD11	2.45	0.52
1:C:631:ILE:C	1:C:636:ARG:HH12	2.18	0.52
1:E:183:ILE:HD12	1:E:203:LEU:HD22	1.92	0.52
2:I:586:ASN:OD1	2:I:630:VAL:HG13	2.10	0.52
2:J:278:TYR:HB3	2:J:513:TYR:CE2	2.44	0.52
1:A:238:LYS:HD2	1:A:251:ALA:O	2.10	0.52
1:A:300:THR:O	1:A:324:PHE:HB3	2.09	0.52
1:A:528:LYS:HZ1	1:A:534:ASN:HA	1.75	0.52
1:D:535:GLU:HB3	1:D:538:GLY:HA2	1.91	0.52
1:E:197:LYS:O	1:E:198:ASN:C	2.53	0.52
1:E:508:VAL:HG23	1:E:516:THR:HA	1.92	0.52
1:E:562:ILE:HA	1:E:565:GLN:OE1	2.10	0.52
1:F:198:ASN:HB2	1:F:200:ARG:NH2	2.22	0.52
1:F:234:SER:OG	1:F:237:GLU:HG2	2.09	0.52
2:H:427:ILE:HG12	2:H:509:THR:O	2.09	0.52
2:H:427:ILE:HG13	2:H:428:GLY:N	2.25	0.52
2:I:118:TYR:OH	2:I:146:ASN:OD1	2.27	0.52
2:J:392:LEU:HD23	2:J:482:ASN:HA	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:513:TYR:HA	2:J:519:LEU:HD13	1.92	0.52
1:A:609:GLU:OE1	1:A:609:GLU:N	2.40	0.52
1:C:260:PRO:HD3	1:C:477:TRP:CZ3	2.45	0.52
1:C:578:LEU:HD12	1:C:579:ASP:N	2.25	0.52
1:E:365:ARG:HH12	1:E:414:LYS:HA	1.74	0.52
1:F:226:TRP:CZ2	1:F:234:SER:HB3	2.44	0.52
1:F:251:ALA:HA	1:F:256:VAL:HG21	1.92	0.52
2:H:204:GLU:O	2:H:207:GLU:HG3	2.10	0.52
2:H:555:ILE:H	2:H:555:ILE:HD12	1.74	0.52
1:B:197:LYS:O	1:B:198:ASN:C	2.53	0.52
1:B:435:ASN:OD1	1:B:438:GLN:N	2.31	0.52
1:B:485:GLN:HA	1:B:504:ARG:NH1	2.25	0.52
1:B:524:LYS:NZ	1:B:528:LYS:HE3	2.24	0.52
1:B:552:PHE:HB2	1:B:554:PHE:HZ	1.75	0.52
1:B:610:SER:HA	1:B:613:LYS:NZ	2.25	0.52
1:C:360:LEU:HD12	1:C:361:ASN:H	1.75	0.52
1:D:527:LEU:HD23	1:D:533:PHE:CE1	2.44	0.52
1:E:507:ALA:C	1:E:518:LYS:HD2	2.35	0.52
1:E:599:ASP:OD2	1:E:601:ASN:ND2	2.43	0.52
1:G:558:THR:HG21	1:G:588:ASN:H	1.75	0.52
2:H:171:LEU:HD22	2:H:206:LEU:HD23	1.92	0.52
2:I:615:ILE:O	2:I:619:THR:HG23	2.10	0.52
2:J:274:ILE:HD11	2:J:488:ILE:HD13	1.92	0.52
1:A:454:GLN:OE1	1:A:454:GLN:N	2.42	0.51
1:A:459:ILE:HG13	1:A:477:TRP:CE2	2.45	0.51
1:A:491:ILE:HG12	1:A:589:ILE:HB	1.93	0.51
1:A:528:LYS:NZ	1:A:534:ASN:HA	2.24	0.51
1:C:721:ILE:O	1:C:723:LYS:HG2	2.09	0.51
1:D:353:ASN:H	1:D:356:ASP:CG	2.19	0.51
1:F:232:PRO:O	1:F:233:TYR:HD1	1.92	0.51
1:F:506:ALA:C	1:F:518:LYS:HE3	2.35	0.51
1:G:639:LEU:N	1:G:703:LYS:HZ2	2.08	0.51
2:I:271:TRP:CD1	2:I:275:LYS:HG2	2.44	0.51
2:J:72:GLU:O	2:J:75:LYS:HG3	2.11	0.51
1:B:345:THR:O	1:B:349:THR:HG23	2.10	0.51
1:B:621:ASN:OD1	1:B:628:LEU:HG	2.09	0.51
1:C:345:THR:O	1:C:349:THR:HG23	2.11	0.51
1:D:550:PHE:CD1	1:D:593:ASP:HA	2.45	0.51
1:E:624:THR:O	1:E:687:LEU:HD13	2.10	0.51
1:F:291:LYS:NZ	1:F:292:ASN:O	2.43	0.51
1:F:362:ALA:HB3	1:F:421:LEU:HD12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:668:LEU:HA	1:F:674:THR:HA	1.93	0.51
1:G:199:LYS:H	1:G:200:ARG:NH1	2.08	0.51
2:H:526:GLY:HA3	2:H:555:ILE:HD13	1.92	0.51
2:J:502:ARG:HH12	2:J:544:ARG:HD3	1.75	0.51
1:A:226:TRP:CH2	1:A:234:SER:HB3	2.46	0.51
1:B:334:ILE:HD11	1:B:446:LYS:HE3	1.92	0.51
1:B:365:ARG:NH1	1:B:414:LYS:HA	2.26	0.51
1:C:210:ILE:O	1:C:213:LYS:NZ	2.43	0.51
1:G:242:ARG:HD3	1:G:462:TYR:CE2	2.45	0.51
1:B:485:GLN:HA	1:B:504:ARG:NH2	2.26	0.51
1:D:360:LEU:HB3	1:D:432:ILE:HG21	1.91	0.51
1:D:378:LEU:HD12	1:D:379:PRO:HD3	1.91	0.51
2:H:578:LYS:CG	2:H:579:TYR:CD1	2.91	0.51
2:J:58:ALA:HA	2:J:61:LYS:HE2	1.93	0.51
1:B:259:TYR:N	1:B:371:THR:OG1	2.42	0.51
1:B:438:GLN:HA	1:B:441:GLU:OE2	2.10	0.51
1:C:259:TYR:CE2	1:C:261:ILE:HD11	2.36	0.51
1:D:639:LEU:HD12	1:D:639:LEU:O	2.11	0.51
1:F:192:TYR:N	1:F:192:TYR:CD2	2.78	0.51
1:F:626:GLY:HA3	1:F:676:ILE:O	2.10	0.51
2:I:107:ILE:HD11	2:I:146:ASN:HA	1.93	0.51
2:I:110:LYS:HD3	2:I:110:LYS:N	2.25	0.51
1:D:509:ASN:N	1:D:515:GLU:OE1	2.39	0.51
1:D:549:GLU:O	1:D:595:ARG:NH1	2.44	0.51
1:E:415:ASN:C	1:E:416:LEU:HD12	2.36	0.51
2:H:582:LEU:HD12	2:H:583:ILE:CD1	2.41	0.51
2:H:686:HIS:CE1	2:H:690:HIS:CE1	2.99	0.51
2:I:454:LEU:HD12	2:I:455:VAL:N	2.25	0.51
2:J:170:PHE:HB2	2:J:243:TYR:OH	2.10	0.51
1:A:419:ILE:O	1:A:419:ILE:HG13	2.10	0.51
1:A:584:ASN:O	1:A:587:MET:HG3	2.10	0.51
1:B:498:LEU:HB2	1:B:637:LYS:NZ	2.26	0.51
1:C:298:THR:HG23	1:C:603:ILE:HD11	1.92	0.51
1:C:500:LEU:N	1:C:500:LEU:HD22	2.26	0.51
1:D:244:ASP:C	1:D:246:ASN:H	2.19	0.51
1:D:297:ARG:HA	1:D:330:SER:HA	1.93	0.51
1:E:342:GLY:HA2	1:E:344:ARG:NH1	2.25	0.51
1:E:377:VAL:C	1:E:378:LEU:HD12	2.36	0.51
1:G:330:SER:OG	1:G:450:LEU:HB2	2.11	0.51
2:H:257:GLU:HA	2:H:260:LYS:NZ	2.25	0.51
2:H:434:LYS:HG2	2:H:504:GLN:OE1	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:181:ASP:O	1:B:236:PHE:HB2	2.10	0.51
1:B:198:ASN:ND2	1:B:200:ARG:HH22	2.06	0.51
1:B:443:GLU:OE2	1:B:446:LYS:NZ	2.44	0.51
1:C:410:TYR:CD1	1:C:414:LYS:HE3	2.45	0.51
1:D:185:ASP:OD1	1:D:186:SER:N	2.43	0.51
1:D:554:PHE:HE1	1:D:589:ILE:HD12	1.76	0.51
1:G:255:LEU:HD12	1:G:255:LEU:N	2.26	0.51
1:G:600:ARG:HD2	1:G:601:ASN:N	2.25	0.51
2:H:154:ILE:HG23	2:H:155:LEU:HD22	1.93	0.51
2:I:528:GLU:O	2:I:548:LYS:HG2	2.11	0.51
1:A:345:THR:O	1:A:349:THR:HG23	2.11	0.51
1:B:627:LEU:H	1:B:676:ILE:CG2	2.24	0.51
1:C:227:SER:O	1:C:230:SER:N	2.42	0.51
1:C:447:GLN:O	1:C:448:LEU:HD22	2.10	0.51
1:C:628:LEU:HD12	1:C:628:LEU:O	2.11	0.51
1:E:340:LEU:HD23	1:E:343:GLU:HG2	1.92	0.51
1:E:454:GLN:HA	1:E:456:TYR:CZ	2.45	0.51
1:F:468:ARG:HB2	1:F:468:ARG:HH11	1.75	0.51
1:G:350:MET:O	1:G:352:LEU:N	2.42	0.51
2:H:215:GLU:OE2	2:H:219:LYS:HD2	2.11	0.51
1:B:223:PRO:HG2	1:B:224:GLU:OE2	2.10	0.51
1:G:445:THR:O	1:G:447:GLN:HG2	2.10	0.51
2:H:557:THR:HA	2:H:560:GLN:NE2	2.26	0.51
1:A:634:ASP:OD1	1:A:635:ILE:HG12	2.11	0.50
1:B:597:HIS:N	1:B:606:GLY:O	2.45	0.50
1:D:435:ASN:OD1	1:D:438:GLN:OE1	2.29	0.50
1:D:584:ASN:O	1:D:587:MET:HE3	2.11	0.50
1:E:224:GLU:HB2	1:E:517:THR:HG21	1.93	0.50
1:E:439:PHE:O	1:E:443:GLU:HG2	2.11	0.50
1:E:584:ASN:N	1:E:587:MET:HE2	2.23	0.50
1:F:207:ILE:HG23	2:J:108:TYR:HE2	1.75	0.50
1:F:492:ILE:HD12	1:F:501:VAL:O	2.12	0.50
1:G:176:PRO:HB3	1:G:178:ARG:NH1	2.23	0.50
1:G:290:SER:O	1:G:291:LYS:HE2	2.11	0.50
2:H:388:ILE:O	2:H:391:ARG:HG3	2.10	0.50
2:H:571:ASN:ND2	2:H:578:LYS:O	2.44	0.50
2:H:583:ILE:HG22	2:H:583:ILE:O	2.11	0.50
1:A:435:ASN:OD1	1:A:438:GLN:N	2.34	0.50
1:B:385:LEU:HB3	1:B:391:LEU:HD21	1.93	0.50
1:E:597:HIS:N	1:E:606:GLY:O	2.42	0.50
2:I:162:LYS:HD3	2:I:259:LEU:HD22	1.91	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:516:ASN:OD1	2:I:518:LYS:HD3	2.11	0.50
1:A:200:ARG:HH22	1:B:186:SER:HA	1.75	0.50
1:A:238:LYS:CE	1:A:254:PRO:HA	2.41	0.50
1:B:560:GLN:HA	1:B:563:LYS:HZ2	1.76	0.50
1:C:198:ASN:HD21	2:I:139:GLU:CD	2.17	0.50
1:D:210:ILE:HD11	2:I:188:LEU:HA	1.92	0.50
1:E:524:LYS:O	1:E:528:LYS:HG3	2.11	0.50
1:F:459:ILE:HG12	1:F:477:TRP:NE1	2.25	0.50
1:G:365:ARG:HH22	1:G:418:PRO:HD3	1.77	0.50
1:G:592:ARG:HD3	1:G:598:TYR:CE2	2.47	0.50
1:A:410:TYR:CG	1:A:414:LYS:HD3	2.47	0.50
1:B:705:ASN:CG	1:B:722:LYS:HB3	2.35	0.50
1:C:480:VAL:HG13	1:C:481:LEU:N	2.27	0.50
1:D:331:THR:HG23	1:D:447:GLN:NE2	2.20	0.50
1:D:441:GLU:HA	1:D:444:LYS:NZ	2.26	0.50
1:D:540:LEU:HB3	1:D:547:ILE:HB	1.94	0.50
1:E:609:GLU:HG2	1:E:613:LYS:NZ	2.26	0.50
1:E:628:LEU:O	1:E:628:LEU:HD12	2.10	0.50
1:E:638:ILE:HG22	1:E:638:ILE:O	2.11	0.50
1:F:493:PHE:CE2	1:F:495:GLY:HA3	2.46	0.50
1:F:583:LEU:HD12	1:F:587:MET:HE1	1.93	0.50
1:F:597:HIS:N	1:F:606:GLY:O	2.43	0.50
1:G:401:LEU:HA	1:G:403:GLN:NE2	2.26	0.50
2:H:148:TYR:HA	2:H:151:ILE:HG22	1.93	0.50
2:H:502:ARG:CB	2:H:544:ARG:HH12	2.25	0.50
2:H:562:ALA:O	2:H:566:ILE:HG13	2.10	0.50
2:I:137:TYR:HE2	2:I:143:LYS:HE3	1.76	0.50
2:I:247:PHE:CE2	2:I:252:ILE:HD11	2.46	0.50
1:B:493:PHE:CE2	1:B:495:GLY:HA3	2.46	0.50
1:D:636:ARG:HA	1:D:639:LEU:HG	1.93	0.50
1:E:435:ASN:ND2	1:E:438:GLN:HG3	2.27	0.50
1:E:678:PHE:CB	1:E:687:LEU:HD11	2.42	0.50
1:G:592:ARG:NH1	1:G:598:TYR:CG	2.80	0.50
1:G:592:ARG:HH22	1:G:602:ASN:C	2.19	0.50
2:H:250:GLN:O	2:H:253:ASN:ND2	2.44	0.50
2:J:89:THR:HG21	2:J:115:HIS:CA	2.40	0.50
2:J:502:ARG:NH2	2:J:544:ARG:HB3	2.19	0.50
1:C:209:ASN:HA	1:C:212:GLU:OE1	2.10	0.50
1:C:300:THR:O	1:C:324:PHE:HB3	2.12	0.50
1:E:197:LYS:O	1:E:200:ARG:N	2.35	0.50
1:E:326:ASN:ND2	1:E:485:GLN:HG3	2.24	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:118:TYR:CZ	2:H:143:LYS:HD2	2.46	0.50
2:I:469:ASN:HA	2:I:472:LYS:NZ	2.24	0.50
1:C:381:THR:O	1:C:394:ILE:HG22	2.11	0.50
1:C:548:THR:HA	1:C:575:TYR:HE2	1.77	0.50
1:C:548:THR:HA	1:C:575:TYR:CE2	2.47	0.50
1:C:597:HIS:NE2	1:C:608:ASP:OD1	2.38	0.50
1:C:625:GLU:N	1:C:625:GLU:OE1	2.45	0.50
1:D:471:VAL:HG12	1:E:479:GLU:CD	2.37	0.50
2:H:186:GLN:HB2	2:H:190:PHE:HZ	1.74	0.50
2:I:224:TYR:CZ	2:I:230:ARG:NH1	2.80	0.50
2:I:441:MET:SD	2:I:442:ASN:O	2.69	0.50
2:J:278:TYR:CE1	2:J:425:GLN:HG2	2.47	0.50
1:A:435:ASN:CG	1:A:438:GLN:HG2	2.37	0.50
1:A:459:ILE:HG13	1:A:477:TRP:NE1	2.26	0.50
1:B:238:LYS:HE2	1:B:252:ARG:C	2.36	0.50
1:B:263:HIS:CE1	1:B:297:ARG:HG3	2.47	0.50
1:B:578:LEU:HD12	1:B:579:ASP:N	2.27	0.50
1:C:330:SER:OG	1:C:331:THR:N	2.45	0.50
1:C:575:TYR:O	1:C:578:LEU:HD23	2.11	0.50
1:E:291:LYS:NZ	1:E:335:ASP:H	2.04	0.50
1:E:476:ASN:OD1	1:E:479:GLU:HG3	2.12	0.50
1:F:242:ARG:HB3	1:F:462:TYR:CZ	2.47	0.50
1:F:382:SER:HA	1:F:393:THR:HA	1.94	0.50
2:H:459:ASP:OD1	2:H:461:THR:OG1	2.25	0.50
2:H:530:LYS:HE2	2:H:546:ASP:OD2	2.12	0.50
2:I:437:LEU:HD23	2:I:438:TYR:N	2.27	0.50
2:J:239:GLU:OE1	2:J:239:GLU:N	2.44	0.50
1:A:381:THR:O	1:A:394:ILE:HG22	2.12	0.50
1:A:577:VAL:HG22	1:A:580:LYS:HB2	1.93	0.50
1:B:459:ILE:HG12	1:B:477:TRP:CE2	2.46	0.50
1:C:599:ASP:OD1	1:C:600:ARG:N	2.41	0.50
2:H:66:VAL:HG21	2:H:70:VAL:HG22	1.93	0.50
2:H:410:LYS:HB3	2:H:414:ARG:NH2	2.26	0.50
2:H:579:TYR:C	2:H:581:LYS:HZ1	2.20	0.50
2:I:89:THR:CG2	2:I:115:HIS:HB3	2.34	0.50
2:J:197:HIS:HE1	2:J:200:ASP:O	1.95	0.50
2:J:762:THR:HA	2:J:765:PHE:HE1	1.76	0.50
1:A:206:TRP:CH2	1:A:218:LYS:HB2	2.47	0.49
1:B:199:LYS:H	1:B:200:ARG:NH1	2.10	0.49
1:C:360:LEU:HB3	1:C:432:ILE:HG21	1.92	0.49
1:C:470:ARG:HG2	1:C:470:ARG:HH11	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:521:MET:SD	1:C:526:ALA:HB2	2.52	0.49
1:D:187:LEU:HD21	1:D:205:PRO:HG3	1.93	0.49
1:F:269:ILE:HG22	1:F:270:ILE:H	1.76	0.49
1:G:227:SER:O	1:G:230:SER:N	2.44	0.49
1:A:332:VAL:CG1	1:A:448:LEU:HB2	2.42	0.49
1:B:563:LYS:O	1:B:566:LEU:HG	2.13	0.49
1:E:466:ASN:HB2	1:F:226:TRP:CD2	2.46	0.49
2:H:561:GLU:O	2:H:564:LEU:HG	2.12	0.49
2:I:231:ASP:O	2:I:234:GLN:HG3	2.12	0.49
1:D:185:ASP:OD1	1:D:185:ASP:N	2.41	0.49
1:D:542:TYR:CE2	1:D:543:GLN:NE2	2.80	0.49
1:D:633:LYS:HA	1:D:636:ARG:CZ	2.42	0.49
2:H:436:TYR:CE1	2:H:504:GLN:HB2	2.47	0.49
2:H:553:SER:O	2:H:557:THR:HG23	2.12	0.49
2:H:558:LYS:O	2:H:561:GLU:HG3	2.13	0.49
1:C:443:GLU:O	1:C:446:LYS:NZ	2.40	0.49
1:E:438:GLN:HA	1:E:441:GLU:OE1	2.12	0.49
1:F:195:ASP:OD2	1:F:196:VAL:N	2.44	0.49
1:F:410:TYR:CD2	1:F:414:LYS:HE2	2.47	0.49
2:H:257:GLU:O	2:H:260:LYS:HG2	2.12	0.49
2:I:531:ASP:HB3	2:I:546:ASP:OD2	2.12	0.49
2:I:554:LYS:O	2:I:557:THR:OG1	2.30	0.49
2:J:478:SER:C	2:J:590:ARG:HH21	2.21	0.49
1:A:188:GLU:OE2	1:A:223:PRO:HA	2.13	0.49
1:A:535:GLU:OE2	1:A:540:LEU:HD12	2.12	0.49
1:A:662:MET:O	1:A:664:ASN:N	2.46	0.49
1:B:340:LEU:HB2	1:B:343:GLU:HB3	1.93	0.49
1:C:554:PHE:HB3	1:C:558:THR:OG1	2.12	0.49
1:C:609:GLU:OE2	1:C:613:LYS:HE2	2.12	0.49
1:D:198:ASN:OD1	1:D:200:ARG:NH2	2.45	0.49
1:F:298:THR:HG21	1:F:331:THR:CB	2.43	0.49
1:F:442:LEU:HD23	1:F:446:LYS:HZ2	1.78	0.49
1:F:608:ASP:O	1:F:611:VAL:HG22	2.12	0.49
1:G:491:ILE:CD1	1:G:589:ILE:HB	2.42	0.49
2:H:462:LYS:HA	2:H:541:GLU:CD	2.38	0.49
2:I:206:LEU:O	2:I:210:SER:OG	2.20	0.49
2:J:147:VAL:O	2:J:151:ILE:HG12	2.12	0.49
1:A:326:ASN:ND2	1:A:485:GLN:OE1	2.45	0.49
1:A:558:THR:HG22	1:A:587:MET:HA	1.94	0.49
1:B:265:ASP:OD1	1:B:295:THR:OG1	2.30	0.49
1:B:330:SER:OG	1:B:331:THR:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:183:ILE:O	1:C:183:ILE:HG13	2.11	0.49
1:C:533:PHE:HE2	1:C:542:TYR:HB2	1.75	0.49
1:C:546:ASP:N	1:C:549:GLU:OE1	2.45	0.49
1:D:200:ARG:HG3	1:D:200:ARG:NH1	2.26	0.49
1:D:497:ASP:OD2	1:D:499:ASN:HB2	2.11	0.49
1:D:502:GLU:OE2	1:D:502:GLU:HA	2.11	0.49
1:D:628:LEU:HA	1:D:674:THR:O	2.13	0.49
1:F:210:ILE:HA	1:F:213:LYS:NZ	2.27	0.49
1:G:439:PHE:O	1:G:443:GLU:HG2	2.13	0.49
2:H:499:LEU:HG	2:H:543:ILE:CG2	2.42	0.49
2:H:530:LYS:HZ1	2:H:547:ALA:C	2.21	0.49
2:I:44:VAL:O	2:I:44:VAL:HG13	2.13	0.49
2:J:152:GLY:O	2:J:155:LEU:HG	2.13	0.49
2:J:255:SER:O	2:J:258:GLU:HG3	2.12	0.49
2:J:469:ASN:OD1	2:J:470:GLU:N	2.45	0.49
1:C:639:LEU:C	1:C:703:LYS:HZ2	2.20	0.49
1:F:300:THR:O	1:F:324:PHE:HB3	2.13	0.49
1:F:447:GLN:C	1:F:448:LEU:HD22	2.38	0.49
1:G:543:GLN:HG2	1:G:545:LYS:HZ1	1.76	0.49
2:J:557:THR:O	2:J:560:GLN:HG3	2.12	0.49
1:A:593:ASP:OD2	1:A:595:ARG:HB2	2.12	0.49
1:C:522:THR:O	1:C:525:GLU:HG3	2.12	0.49
1:D:297:ARG:NH2	1:D:500:LEU:H	2.11	0.49
1:E:226:TRP:CH2	1:E:234:SER:HB3	2.48	0.49
1:E:609:GLU:HG2	1:E:613:LYS:HZ1	1.77	0.49
1:F:434:MET:SD	1:F:438:GLN:HB2	2.52	0.49
2:I:292:LEU:HD13	2:I:419:ILE:HB	1.94	0.49
2:J:153:LYS:HG2	2:J:157:ARG:HE	1.77	0.49
1:C:267:GLU:H	1:C:267:GLU:CD	2.17	0.49
1:C:633:LYS:HA	1:C:636:ARG:CZ	2.43	0.49
1:D:629:LEU:HB3	1:D:631:ILE:HD11	1.95	0.49
1:D:639:LEU:H	1:D:703:LYS:HZ3	1.61	0.49
1:E:542:TYR:CE2	1:E:543:GLN:NE2	2.81	0.49
1:F:614:GLU:O	1:F:617:ARG:NE	2.46	0.49
2:H:141:THR:O	2:H:145:LEU:HG	2.13	0.49
2:H:525:ILE:HG23	2:H:549:VAL:HG23	1.94	0.49
2:H:607:LYS:HD2	2:H:608:ASN:N	2.28	0.49
1:A:528:LYS:HZ2	1:A:535:GLU:HG2	1.75	0.49
1:C:435:ASN:ND2	1:C:438:GLN:HE22	2.11	0.49
1:C:574:ILE:H	1:C:574:ILE:HD12	1.77	0.49
1:D:224:GLU:OE2	1:D:224:GLU:HA	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:366:TYR:CD2	1:D:378:LEU:HD11	2.47	0.49
1:D:366:TYR:HD2	1:D:378:LEU:HD11	1.78	0.49
1:E:338:LEU:HG	1:E:661:ASP:CB	2.43	0.49
2:H:516:ASN:O	2:H:518:LYS:NZ	2.32	0.49
2:I:271:TRP:NE1	2:I:275:LYS:HE2	2.24	0.49
2:I:561:GLU:O	2:I:564:LEU:HG	2.13	0.49
1:A:200:ARG:HH21	1:B:185:ASP:HB2	1.78	0.48
1:A:353:ASN:HB3	1:A:356:ASP:CG	2.38	0.48
1:B:266:MET:HE1	1:B:332:VAL:HG21	1.94	0.48
1:B:476:ASN:O	1:B:479:GLU:CD	2.56	0.48
1:D:482:PRO:HA	1:D:485:GLN:HG2	1.95	0.48
1:E:178:ARG:HB2	1:E:224:GLU:OE2	2.13	0.48
1:E:240:THR:HG22	1:E:242:ARG:NH1	2.28	0.48
1:E:621:ASN:HB3	1:E:628:LEU:HG	1.95	0.48
1:F:238:LYS:HZ1	1:F:252:ARG:HA	1.78	0.48
1:G:231:ASP:N	1:G:231:ASP:OD1	2.41	0.48
2:I:226:GLU:C	2:I:226:GLU:CD	2.80	0.48
2:I:573:ALA:HB1	2:I:607:LYS:HE3	1.95	0.48
2:J:194:LEU:C	2:J:196:GLU:H	2.21	0.48
1:A:528:LYS:HZ3	1:A:535:GLU:HG2	1.75	0.48
1:B:462:TYR:HE1	1:B:464:PHE:HA	1.76	0.48
1:D:366:TYR:HE2	1:D:378:LEU:HG	1.78	0.48
1:D:385:LEU:HD21	1:D:442:LEU:HD21	1.94	0.48
1:E:271:LEU:HB2	1:E:289:ILE:CG1	2.43	0.48
1:G:647:GLU:HA	1:G:652:LEU:O	2.13	0.48
2:H:54:VAL:O	2:H:58:ALA:N	2.41	0.48
1:A:266:MET:HE3	1:A:362:ALA:CB	2.43	0.48
1:B:350:MET:O	1:B:352:LEU:N	2.42	0.48
1:B:528:LYS:HB2	1:B:528:LYS:HE2	1.57	0.48
1:B:724:ILE:O	1:B:726:ILE:HG12	2.13	0.48
1:C:240:THR:O	1:D:514:LEU:HB2	2.13	0.48
1:C:244:ASP:O	1:C:246:ASN:N	2.47	0.48
1:D:555:ASP:OD2	1:D:556:GLN:N	2.46	0.48
1:F:198:ASN:HB2	1:F:200:ARG:HH12	1.78	0.48
1:F:227:SER:HA	1:F:235:ASP:OD2	2.13	0.48
1:F:600:ARG:HD2	1:F:601:ASN:N	2.28	0.48
1:G:640:SER:HB3	1:G:703:LYS:HD3	1.94	0.48
2:H:410:LYS:O	2:H:413:LYS:HG3	2.12	0.48
2:I:186:GLN:HA	2:I:190:PHE:HD2	1.79	0.48
2:I:495:ASP:OD1	2:I:496:ASN:N	2.46	0.48
2:J:536:LYS:HE3	2:J:539:GLU:HA	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:620:ILE:HG13	1:A:630:ASN:ND2	2.28	0.48
1:B:222:SER:H	1:B:228:THR:CG2	2.27	0.48
1:B:441:GLU:HA	1:B:444:LYS:HZ3	1.77	0.48
1:C:298:THR:CG2	1:C:601:ASN:HB2	2.43	0.48
1:C:449:ARG:C	1:C:450:LEU:HD12	2.38	0.48
1:C:492:ILE:CG2	1:C:500:LEU:HD12	2.43	0.48
1:E:178:ARG:HA	1:E:178:ARG:NE	2.27	0.48
1:G:198:ASN:HB2	1:G:200:ARG:HH22	1.78	0.48
1:G:563:LYS:O	1:G:566:LEU:HG	2.13	0.48
2:H:293:LEU:HA	2:H:296:LEU:HD12	1.94	0.48
2:H:590:ARG:HG2	2:H:590:ARG:HH11	1.78	0.48
2:I:107:ILE:HD13	2:I:145:LEU:HG	1.94	0.48
2:I:274:ILE:HG13	2:I:275:LYS:N	2.28	0.48
1:A:639:LEU:N	1:A:703:LYS:HZ2	2.12	0.48
1:B:207:ILE:HB	1:B:210:ILE:HG22	1.95	0.48
1:B:555:ASP:N	1:B:558:THR:OG1	2.47	0.48
1:F:297:ARG:HH22	1:F:328:ASN:CG	2.21	0.48
1:F:442:LEU:HD23	1:F:446:LYS:NZ	2.27	0.48
2:H:151:ILE:O	2:H:155:LEU:HD23	2.12	0.48
2:H:744:MET:HG3	2:H:745:HIS:CE1	2.48	0.48
1:A:403:GLN:O	1:A:404:ILE:HD13	2.13	0.48
1:A:434:MET:HE1	1:A:439:PHE:HB2	1.94	0.48
1:A:514:LEU:HB2	1:G:240:THR:O	2.14	0.48
1:C:543:GLN:OE1	1:C:543:GLN:N	2.46	0.48
1:C:596:PHE:CD1	1:C:607:ALA:HB2	2.48	0.48
1:C:621:ASN:HB3	1:C:628:LEU:HG	1.96	0.48
1:D:234:SER:N	1:D:237:GLU:OE2	2.44	0.48
1:D:568:GLU:HG2	1:D:569:LEU:CD2	2.41	0.48
1:G:270:ILE:O	1:G:271:LEU:HD22	2.13	0.48
2:H:740:ALA:C	2:H:744:MET:HE3	2.38	0.48
2:I:162:LYS:NZ	2:I:262:GLN:OE1	2.47	0.48
2:I:630:VAL:O	2:I:667:LEU:HA	2.13	0.48
2:I:762:THR:HA	2:I:765:PHE:HE1	1.79	0.48
2:J:211:ASN:O	2:J:214:GLN:HG2	2.13	0.48
1:A:365:ARG:NH2	1:A:418:PRO:HD3	2.28	0.48
1:B:638:ILE:HG22	1:B:638:ILE:O	2.13	0.48
1:C:271:LEU:HB2	1:C:289:ILE:HG23	1.94	0.48
1:C:377:VAL:HG22	1:C:378:LEU:N	2.28	0.48
1:C:626:GLY:HA2	1:C:678:PHE:CE2	2.48	0.48
1:D:466:ASN:HD21	1:D:468:ARG:NH1	2.12	0.48
1:F:515:GLU:O	1:F:518:LYS:HG2	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:300:ILE:HB	2:H:386:TYR:HB3	1.94	0.48
2:I:439:GLU:OE1	2:I:501:TRP:CE3	2.66	0.48
2:I:533:GLN:NE2	2:I:544:ARG:HG3	2.28	0.48
1:C:244:ASP:C	1:C:246:ASN:N	2.71	0.48
1:C:383:LEU:HD12	1:C:384:VAL:H	1.77	0.48
1:D:270:ILE:C	1:D:271:LEU:HD22	2.39	0.48
1:E:244:ASP:C	1:E:246:ASN:N	2.71	0.48
1:E:721:ILE:CG1	1:E:723:LYS:CG	2.87	0.48
1:F:364:ILE:HG12	1:F:421:LEU:HD21	1.95	0.48
1:G:640:SER:OG	1:G:701:VAL:HG13	2.14	0.48
2:H:118:TYR:CD2	2:H:119:VAL:HG13	2.49	0.48
1:B:492:ILE:HG22	1:B:500:LEU:HD12	1.95	0.48
1:B:579:ASP:OD1	1:B:580:LYS:HG2	2.14	0.48
1:C:387:LYS:HD2	1:C:388:ASN:CB	2.42	0.48
1:D:198:ASN:HD21	1:D:200:ARG:HH22	1.62	0.48
1:D:618:GLU:N	1:D:618:GLU:OE1	2.47	0.48
1:E:491:ILE:CD1	1:E:589:ILE:HB	2.44	0.48
1:G:533:PHE:CE2	1:G:542:TYR:HB2	2.49	0.48
2:H:252:ILE:O	2:H:255:SER:OG	2.26	0.48
2:H:491:ARG:HG2	2:H:492:PRO:CD	2.43	0.48
1:B:219:TYR:CD1	1:B:219:TYR:N	2.78	0.48
1:C:721:ILE:HG21	1:C:723:LYS:CE	2.44	0.48
1:E:447:GLN:O	1:E:448:LEU:HD22	2.13	0.48
1:E:558:THR:O	1:E:562:ILE:HG12	2.14	0.48
1:E:700:ALA:CB	1:E:726:ILE:HG13	2.44	0.48
1:F:494:ASN:OD1	1:F:592:ARG:HA	2.13	0.48
1:G:262:VAL:HG11	1:G:379:PRO:HG2	1.96	0.48
2:H:423:LEU:HD22	2:H:512:GLY:HA3	1.95	0.48
2:H:566:ILE:HG12	2:H:600:TYR:CE1	2.48	0.48
2:I:33:GLU:O	2:I:36:LEU:HG	2.13	0.48
1:A:565:GLN:HA	1:A:568:GLU:OE2	2.14	0.47
1:A:640:SER:HA	1:A:703:LYS:HE3	1.96	0.47
1:B:238:LYS:HE3	1:B:251:ALA:O	2.14	0.47
1:B:255:LEU:HD12	1:B:255:LEU:N	2.29	0.47
1:B:558:THR:HG22	1:B:587:MET:HA	1.94	0.47
1:C:203:LEU:HD12	1:C:203:LEU:HA	1.66	0.47
1:D:266:MET:HB3	1:D:295:THR:HG21	1.95	0.47
1:D:447:GLN:C	1:D:448:LEU:HD12	2.39	0.47
1:E:533:PHE:CZ	1:E:542:TYR:HB2	2.49	0.47
2:H:69:ASP:O	2:H:72:GLU:HG2	2.14	0.47
2:H:163:ILE:O	2:H:163:ILE:HG22	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:257:GLU:OE1	2:H:436:TYR:HD2	1.97	0.47
2:I:455:VAL:HA	2:I:463:ILE:HD13	1.95	0.47
1:B:332:VAL:HG12	1:B:448:LEU:HB2	1.96	0.47
1:B:403:GLN:O	1:B:404:ILE:HD13	2.15	0.47
1:C:334:ILE:HG22	1:C:446:LYS:HB3	1.95	0.47
1:C:605:VAL:HG22	1:C:704:GLU:HB3	1.96	0.47
1:D:198:ASN:CG	1:D:199:LYS:H	2.22	0.47
1:D:606:GLY:HA3	1:D:704:GLU:OE1	2.14	0.47
1:E:583:LEU:HA	1:E:587:MET:HE1	1.95	0.47
1:F:492:ILE:HD11	1:F:500:LEU:HB3	1.94	0.47
1:F:563:LYS:O	1:F:566:LEU:HG	2.14	0.47
2:H:81:ILE:HG22	2:H:129:LEU:HD21	1.96	0.47
2:H:88:ILE:C	2:H:90:LYS:H	2.22	0.47
1:A:225:LYS:HD2	1:A:228:THR:HA	1.96	0.47
1:B:496:LYS:HE2	1:B:496:LYS:HA	1.95	0.47
1:B:598:TYR:CD2	1:B:604:ALA:HA	2.49	0.47
1:D:260:PRO:HD3	1:D:477:TRP:CZ3	2.49	0.47
1:D:491:ILE:CD1	1:D:589:ILE:HB	2.45	0.47
2:I:72:GLU:HA	2:I:75:LYS:NZ	2.29	0.47
2:J:256:LEU:O	2:J:259:LEU:HG	2.14	0.47
1:A:523:LEU:HD23	1:A:527:LEU:HD13	1.96	0.47
1:A:599:ASP:CG	1:A:600:ARG:N	2.71	0.47
1:B:502:GLU:OE2	1:B:504:ARG:HG2	2.15	0.47
1:B:549:GLU:HB3	1:B:595:ARG:NH1	2.29	0.47
1:C:360:LEU:HD12	1:C:361:ASN:N	2.28	0.47
1:C:476:ASN:N	1:C:476:ASN:OD1	2.47	0.47
1:D:558:THR:HG21	1:D:588:ASN:H	1.80	0.47
1:D:629:LEU:HD23	1:D:631:ILE:HD11	1.96	0.47
1:E:232:PRO:CD	1:E:233:TYR:CE1	2.88	0.47
1:G:212:GLU:HG2	1:G:213:LYS:HD3	1.96	0.47
2:H:163:ILE:HB	2:H:165:GLN:OE1	2.14	0.47
2:H:469:ASN:OD1	2:H:472:LYS:NZ	2.47	0.47
2:H:699:LEU:HD11	2:H:772:PHE:CD2	2.49	0.47
1:B:462:TYR:CD1	1:B:462:TYR:C	2.93	0.47
1:B:610:SER:HA	1:B:613:LYS:HZ3	1.79	0.47
1:C:456:TYR:N	1:C:456:TYR:CD1	2.82	0.47
1:D:244:ASP:OD1	1:E:483:GLN:NE2	2.46	0.47
1:D:411:TYR:CD2	1:D:411:TYR:C	2.89	0.47
1:E:225:LYS:HD2	1:E:225:LYS:HA	1.74	0.47
1:E:231:ASP:HB2	1:E:232:PRO:CD	2.44	0.47
1:F:504:ARG:O	1:F:505:ILE:HD13	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:560:GLN:OE1	1:G:563:LYS:NZ	2.34	0.47
1:G:629:LEU:O	1:G:674:THR:N	2.47	0.47
1:G:635:ILE:HG23	1:G:636:ARG:HD3	1.95	0.47
2:H:441:MET:CE	2:H:499:LEU:HD22	2.42	0.47
2:H:533:GLN:O	2:H:543:ILE:HD12	2.14	0.47
1:A:702:THR:O	1:A:706:THR:HG23	2.15	0.47
1:E:227:SER:O	1:E:230:SER:N	2.47	0.47
2:H:114:LEU:HD12	2:H:115:HIS:N	2.29	0.47
2:J:83:ILE:HG13	2:J:131:ILE:O	2.15	0.47
1:A:199:LYS:HG3	1:B:189:VAL:HG23	1.96	0.47
1:A:273:LYS:HA	1:A:358:ALA:HA	1.96	0.47
1:A:554:PHE:HB3	1:A:558:THR:OG1	2.13	0.47
1:B:228:THR:HG23	1:B:235:ASP:CG	2.40	0.47
1:B:367:VAL:HG12	1:B:410:TYR:CD1	2.50	0.47
1:B:625:GLU:HA	1:B:678:PHE:HE1	1.78	0.47
1:C:253:HIS:O	1:C:256:VAL:HG22	2.15	0.47
1:C:527:LEU:HB3	1:C:533:PHE:CD1	2.43	0.47
1:D:563:LYS:O	1:D:566:LEU:HG	2.15	0.47
1:D:565:GLN:HA	1:D:568:GLU:OE1	2.14	0.47
1:D:592:ARG:HB3	1:D:598:TYR:HE2	1.79	0.47
1:D:640:SER:OG	1:D:701:VAL:HG13	2.15	0.47
1:E:228:THR:HG23	1:E:235:ASP:CG	2.40	0.47
1:E:264:VAL:HG12	1:E:366:TYR:CE2	2.50	0.47
1:E:533:PHE:CE1	1:E:542:TYR:HB2	2.50	0.47
1:E:545:LYS:N	1:E:545:LYS:HD3	2.30	0.47
2:H:157:ARG:HH11	2:H:214:GLN:HG3	1.76	0.47
2:H:474:ASN:HA	2:H:476:LYS:HZ2	1.80	0.47
2:H:564:LEU:O	2:H:568:GLN:HG3	2.15	0.47
2:H:685:ILE:CG2	2:H:742:ARG:HG2	2.45	0.47
2:I:331:SER:O	2:I:335:LYS:N	2.45	0.47
2:I:469:ASN:HB3	2:I:473:LYS:NZ	2.30	0.47
2:J:67:PRO:O	2:J:70:VAL:HG22	2.14	0.47
1:B:270:ILE:C	1:B:271:LEU:HD22	2.39	0.47
1:C:439:PHE:O	1:C:443:GLU:HG2	2.14	0.47
1:D:249:PRO:HA	1:D:252:ARG:HH11	1.78	0.47
1:E:434:MET:SD	1:E:439:PHE:N	2.88	0.47
1:F:549:GLU:O	1:F:594:LYS:HG2	2.15	0.47
1:G:498:LEU:HB2	1:G:637:LYS:NZ	2.30	0.47
2:H:373:LYS:HA	2:H:376:LEU:HD12	1.97	0.47
2:H:414:ARG:HA	2:H:417:GLN:HE21	1.80	0.47
2:H:514:LEU:HD12	2:H:515:GLU:H	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:724:ASN:O	2:H:725:LEU:HD22	2.15	0.47
2:I:557:THR:O	2:I:560:GLN:HG3	2.15	0.47
2:J:178:LYS:HA	2:J:186:GLN:OE1	2.14	0.47
2:J:188:LEU:HG	2:J:189:LEU:HD22	1.97	0.47
2:J:542:TYR:CB	2:J:544:ARG:HH22	2.27	0.47
1:A:373:PRO:HB2	1:A:375:TYR:CE1	2.46	0.47
1:A:517:THR:HG23	1:G:199:LYS:O	2.15	0.47
1:A:564:ASN:O	1:A:567:ALA:N	2.46	0.47
1:B:269:ILE:HD12	1:B:269:ILE:N	2.30	0.47
1:B:497:ASP:OD1	1:B:633:LYS:NZ	2.37	0.47
1:C:242:ARG:HD3	1:C:462:TYR:CE2	2.50	0.47
1:C:385:LEU:O	1:C:389:GLN:HB2	2.15	0.47
1:F:255:LEU:HD23	1:F:255:LEU:HA	1.52	0.47
1:F:291:LYS:HD3	1:F:291:LYS:C	2.40	0.47
1:F:528:LYS:NZ	1:F:535:GLU:HG2	2.30	0.47
1:G:253:HIS:O	1:G:256:VAL:HG22	2.15	0.47
2:H:81:ILE:HG13	2:H:81:ILE:O	2.15	0.47
2:J:235:LEU:HD23	2:J:236:TYR:CZ	2.50	0.47
2:J:461:THR:HG23	2:J:540:LYS:HA	1.97	0.47
1:A:198:ASN:O	1:A:199:LYS:HD2	2.15	0.47
1:A:360:LEU:O	1:A:432:ILE:HG21	2.14	0.47
1:B:442:LEU:O	1:B:446:LYS:HD2	2.15	0.47
1:C:446:LYS:O	1:C:447:GLN:NE2	2.47	0.47
1:D:614:GLU:O	1:D:617:ARG:HG2	2.15	0.47
1:E:535:GLU:OE1	1:E:540:LEU:HA	2.15	0.47
1:F:203:LEU:HD12	1:F:203:LEU:HA	1.54	0.47
1:F:592:ARG:HH11	1:F:592:ARG:HG3	1.80	0.47
1:F:628:LEU:HA	1:F:674:THR:O	2.15	0.47
1:G:468:ARG:NH2	1:G:470:ARG:HE	2.12	0.47
2:H:722:GLY:HA2	2:H:736:PHE:CE1	2.50	0.47
1:C:188:GLU:HG3	1:C:221:SER:OG	2.15	0.46
1:D:403:GLN:H	1:D:403:GLN:CD	2.23	0.46
1:D:576:THR:C	1:D:578:LEU:H	2.22	0.46
1:F:270:ILE:C	1:F:271:LEU:HD22	2.40	0.46
1:G:234:SER:O	1:G:237:GLU:HG2	2.15	0.46
1:G:626:GLY:HA3	1:G:676:ILE:O	2.15	0.46
2:H:100:ASP:O	2:H:102:LYS:N	2.48	0.46
2:H:163:ILE:HB	2:H:165:GLN:HE22	1.81	0.46
1:B:358:ALA:HB3	1:B:434:MET:HE3	1.97	0.46
1:B:498:LEU:HA	1:B:498:LEU:HD23	1.76	0.46
1:B:628:LEU:O	1:B:628:LEU:HD12	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:297:ARG:NH1	1:C:298:THR:O	2.48	0.46
1:C:592:ARG:CZ	1:C:598:TYR:CD2	2.99	0.46
1:D:245:LYS:HE3	1:D:245:LYS:HB2	1.67	0.46
1:D:442:LEU:O	1:D:446:LYS:HD2	2.14	0.46
1:D:446:LYS:HA	1:D:446:LYS:HE3	1.97	0.46
1:F:198:ASN:CB	1:F:200:ARG:HH12	2.28	0.46
1:G:600:ARG:NH1	1:G:601:ASN:HB3	2.30	0.46
2:H:474:ASN:HA	2:H:476:LYS:NZ	2.31	0.46
2:H:501:TRP:HB3	2:H:503:ILE:HD11	1.98	0.46
2:I:113:LEU:HD23	2:I:115:HIS:HE2	1.80	0.46
1:A:270:ILE:C	1:A:271:LEU:HD22	2.41	0.46
1:A:270:ILE:CG2	1:A:361:ASN:HB3	2.45	0.46
1:E:698:VAL:HB	1:E:727:PHE:HB3	1.97	0.46
1:E:700:ALA:HB3	1:E:726:ILE:HG13	1.96	0.46
1:F:206:TRP:CH2	1:F:218:LYS:HB2	2.49	0.46
1:F:214:LYS:HE2	1:F:214:LYS:HA	1.96	0.46
1:F:354:THR:HA	1:F:436:TYR:CD2	2.50	0.46
1:G:643:ILE:HD11	1:G:701:VAL:HB	1.98	0.46
2:H:83:ILE:HG13	2:H:83:ILE:O	2.16	0.46
2:H:140:ASN:ND2	2:H:143:LYS:HB2	2.30	0.46
2:H:517:GLY:C	2:H:518:LYS:HD3	2.41	0.46
2:H:621:TYR:CE1	2:H:664:ARG:CZ	2.98	0.46
2:I:134:SER:HB2	2:I:137:TYR:CE2	2.50	0.46
2:J:657:GLY:HA3	2:J:667:LEU:O	2.16	0.46
1:C:545:LYS:HD3	1:C:545:LYS:N	2.30	0.46
1:C:640:SER:OG	1:C:701:VAL:HG13	2.15	0.46
1:D:543:GLN:HG2	1:D:545:LYS:NZ	2.31	0.46
1:E:176:PRO:CB	1:E:178:ARG:HH12	2.15	0.46
1:E:543:GLN:HG2	1:E:545:LYS:NZ	2.31	0.46
1:F:258:ALA:HA	1:F:371:THR:OG1	2.15	0.46
1:G:635:ILE:CG2	1:G:636:ARG:HD3	2.45	0.46
2:H:390:GLN:HA	2:H:393:GLN:HE22	1.80	0.46
2:I:517:GLY:C	2:I:518:LYS:HD2	2.41	0.46
2:J:428:GLY:N	2:J:507:PRO:O	2.42	0.46
1:A:507:ALA:C	1:A:518:LYS:HZ3	2.18	0.46
1:B:291:LYS:HZ2	1:B:334:ILE:HB	1.81	0.46
1:B:493:PHE:CZ	1:B:495:GLY:HA3	2.50	0.46
1:C:256:VAL:HG12	1:C:505:ILE:CD1	2.45	0.46
1:C:626:GLY:HA2	1:C:678:PHE:HE2	1.80	0.46
1:D:291:LYS:NZ	1:D:337:SER:O	2.43	0.46
1:D:635:ILE:C	1:D:637:LYS:H	2.24	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:245:LYS:HE2	1:E:245:LYS:HA	1.97	0.46
1:E:269:ILE:HG22	1:E:362:ALA:HB2	1.97	0.46
1:E:527:LEU:HD23	1:E:527:LEU:HA	1.53	0.46
1:F:404:ILE:C	1:F:405:LEU:HD12	2.41	0.46
1:F:568:GLU:HG2	1:F:569:LEU:CD2	2.46	0.46
1:G:244:ASP:C	1:G:246:ASN:N	2.73	0.46
1:G:459:ILE:HG13	1:G:477:TRP:CD1	2.51	0.46
1:G:476:ASN:HB3	1:G:479:GLU:OE2	2.16	0.46
2:H:511:ALA:HB2	2:H:521:LEU:HD13	1.97	0.46
2:H:679:ASN:HD21	2:H:682:GLU:HG3	1.80	0.46
1:A:627:LEU:H	1:A:676:ILE:CG2	2.27	0.46
1:B:291:LYS:NZ	1:B:293:THR:HG22	2.31	0.46
1:B:551:ASP:OD1	1:B:592:ARG:N	2.38	0.46
1:D:291:LYS:HE2	1:D:335:ASP:HB3	1.97	0.46
1:D:403:GLN:O	1:D:404:ILE:HD13	2.16	0.46
1:F:377:VAL:HG12	1:F:378:LEU:N	2.31	0.46
1:G:384:VAL:HG13	1:G:449:ARG:HB2	1.98	0.46
2:H:514:LEU:HD12	2:H:515:GLU:N	2.30	0.46
1:B:449:ARG:O	1:B:450:LEU:HD23	2.15	0.46
1:C:410:TYR:CG	1:C:414:LYS:HE3	2.51	0.46
1:D:271:LEU:HB2	1:D:289:ILE:HB	1.96	0.46
1:D:469:VAL:HG21	1:E:483:GLN:HG3	1.98	0.46
1:D:705:ASN:HD21	1:D:722:LYS:CB	2.28	0.46
1:E:289:ILE:HG13	1:E:289:ILE:O	2.16	0.46
1:F:410:TYR:CE2	1:F:414:LYS:HE2	2.50	0.46
2:H:100:ASP:C	2:H:102:LYS:N	2.74	0.46
2:H:504:GLN:NE2	2:H:505:LEU:HD23	2.31	0.46
2:H:739:GLU:HA	2:H:742:ARG:CZ	2.46	0.46
2:I:140:ASN:ND2	2:I:142:GLU:OE1	2.49	0.46
2:J:91:HIS:HD2	2:J:93:SER:HB2	1.81	0.46
1:A:200:ARG:HH12	1:B:189:VAL:HG11	1.80	0.46
1:B:197:LYS:O	1:B:200:ARG:N	2.46	0.46
1:D:632:ASP:O	1:D:635:ILE:HG22	2.16	0.46
1:D:710:PRO:HB2	1:D:714:GLY:HA2	1.98	0.46
1:E:358:ALA:HB3	1:E:434:MET:CE	2.46	0.46
1:E:521:MET:HE3	1:E:525:GLU:HB2	1.97	0.46
2:H:374:GLU:O	2:H:378:LYS:NZ	2.47	0.46
2:H:615:ILE:O	2:H:619:THR:HG23	2.16	0.46
2:I:168:GLN:HA	2:I:171:LEU:HB3	1.98	0.46
2:I:181:SER:O	2:I:182:ASP:C	2.58	0.46
2:I:468:PHE:HA	2:I:471:PHE:CD1	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:270:ILE:C	1:C:271:LEU:HD22	2.41	0.46
1:D:297:ARG:H	1:D:297:ARG:HG3	1.49	0.46
1:D:386:GLY:HA3	1:D:389:GLN:NE2	2.31	0.46
1:D:493:PHE:O	1:D:500:LEU:HD13	2.16	0.46
1:F:234:SER:O	1:F:237:GLU:HG2	2.16	0.46
2:H:620:ASN:HA	2:H:623:VAL:HG22	1.98	0.46
2:I:107:ILE:HA	2:I:219:LYS:NZ	2.30	0.46
1:A:203:LEU:HG	1:A:204:SER:N	2.30	0.46
1:D:255:LEU:HD23	1:D:255:LEU:HA	1.52	0.46
1:E:197:LYS:O	1:E:199:LYS:N	2.49	0.46
1:E:523:LEU:C	1:E:523:LEU:HD23	2.41	0.46
1:F:381:THR:HG23	1:F:452:THR:HG22	1.99	0.46
1:G:608:ASP:OD1	1:G:609:GLU:N	2.49	0.46
1:G:618:GLU:O	1:G:618:GLU:HG2	2.16	0.46
2:H:188:LEU:O	2:H:188:LEU:HG	2.10	0.46
2:I:564:LEU:O	2:I:568:GLN:N	2.31	0.46
1:A:496:LYS:HE2	1:A:496:LYS:HA	1.98	0.45
1:A:500:LEU:HD23	1:A:500:LEU:HA	1.76	0.45
1:A:605:VAL:HG22	1:A:704:GLU:HB3	1.97	0.45
1:D:298:THR:HG22	1:D:329:SER:C	2.40	0.45
1:D:558:THR:HG22	1:D:587:MET:HA	1.98	0.45
1:D:593:ASP:C	1:D:593:ASP:OD1	2.59	0.45
1:E:334:ILE:HD11	1:E:446:LYS:HE3	1.97	0.45
1:F:244:ASP:OD2	1:F:246:ASN:HB3	2.15	0.45
2:H:160:LEU:HD22	2:H:165:GLN:HG2	1.98	0.45
2:H:502:ARG:CB	2:H:544:ARG:HH22	2.29	0.45
2:I:248:ASN:OD1	2:I:249:GLU:N	2.49	0.45
1:C:216:LEU:HA	1:C:216:LEU:HD23	1.73	0.45
1:D:326:ASN:HD22	1:D:485:GLN:HB2	1.81	0.45
1:D:386:GLY:HA3	1:D:389:GLN:HE22	1.81	0.45
1:D:476:ASN:HB2	1:D:479:GLU:OE2	2.16	0.45
1:E:583:LEU:CD2	1:E:587:MET:HE1	2.46	0.45
1:E:643:ILE:HG21	1:E:723:LYS:HZ1	1.72	0.45
1:F:332:VAL:CG1	1:F:448:LEU:HB2	2.47	0.45
1:G:340:LEU:HB2	1:G:343:GLU:HB3	1.98	0.45
1:G:668:LEU:HA	1:G:674:THR:HA	1.97	0.45
2:H:681:SER:O	2:H:685:ILE:HG12	2.16	0.45
2:J:191:THR:HG22	2:J:194:LEU:HG	1.99	0.45
1:A:523:LEU:HA	1:A:583:LEU:HD11	1.98	0.45
1:A:541:GLN:CD	1:A:544:GLY:H	2.23	0.45
1:B:198:ASN:N	1:B:198:ASN:OD1	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:232:PRO:C	1:C:233:TYR:HD2	2.25	0.45
1:C:263:HIS:NE2	1:C:367:VAL:HB	2.31	0.45
1:D:387:LYS:HE2	1:D:387:LYS:HA	1.98	0.45
1:D:615:ALA:O	1:D:631:ILE:HD12	2.16	0.45
1:E:186:SER:O	1:E:190:GLU:HG2	2.16	0.45
1:F:291:LYS:NZ	1:F:335:ASP:N	2.62	0.45
1:F:535:GLU:HB3	1:F:538:GLY:HA2	1.98	0.45
2:H:533:GLN:OE1	2:H:533:GLN:N	2.49	0.45
2:H:560:GLN:HG2	2:H:561:GLU:N	2.32	0.45
2:H:594:ASN:O	2:H:594:ASN:ND2	2.48	0.45
2:I:563:GLN:O	2:I:566:ILE:HG22	2.16	0.45
1:A:483:GLN:CD	1:A:483:GLN:H	2.23	0.45
1:C:298:THR:HG22	1:C:299:HIS:N	2.31	0.45
1:C:527:LEU:HD12	1:C:533:PHE:HE1	1.81	0.45
1:C:541:GLN:CD	1:C:544:GLY:H	2.24	0.45
1:C:558:THR:HG22	1:C:587:MET:HA	1.97	0.45
1:D:216:LEU:HD12	1:D:216:LEU:N	2.31	0.45
1:F:206:TRP:CD1	1:F:218:LYS:NZ	2.80	0.45
1:F:403:GLN:O	1:F:404:ILE:HD13	2.16	0.45
2:H:113:LEU:HD22	2:H:115:HIS:HE1	1.81	0.45
2:H:122:LYS:HB3	2:H:128:VAL:H	1.81	0.45
2:H:544:ARG:HH11	2:H:544:ARG:HG3	1.80	0.45
2:I:208:GLN:NE2	2:I:209:ASN:OD1	2.49	0.45
2:I:274:ILE:HD12	2:I:488:ILE:HD13	1.99	0.45
1:A:209:ASN:HA	1:A:212:GLU:OE1	2.16	0.45
1:B:491:ILE:CD1	1:B:589:ILE:HB	2.46	0.45
1:E:366:TYR:HE1	1:E:378:LEU:HD23	1.80	0.45
1:G:415:ASN:C	1:G:416:LEU:HD22	2.42	0.45
2:H:578:LYS:HB3	2:H:579:TYR:CD1	2.52	0.45
2:I:62:LEU:HD12	2:I:137:TYR:CD1	2.52	0.45
2:I:107:ILE:HG12	2:I:219:LYS:HZ3	1.82	0.45
2:I:115:HIS:ND1	2:I:116:GLU:N	2.64	0.45
2:I:466:GLY:O	2:I:470:GLU:HG2	2.17	0.45
1:A:203:LEU:HD12	1:A:203:LEU:HA	1.54	0.45
1:A:606:GLY:HA3	1:A:704:GLU:OE1	2.17	0.45
1:B:404:ILE:C	1:B:405:LEU:HD22	2.41	0.45
1:B:640:SER:OG	1:B:701:VAL:HG13	2.17	0.45
1:D:500:LEU:HD13	1:D:500:LEU:HA	1.53	0.45
1:F:272:SER:HB3	1:F:288:THR:HG22	1.98	0.45
1:F:441:GLU:HA	1:F:444:LYS:NZ	2.31	0.45
1:F:479:GLU:OE1	1:F:479:GLU:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:190:PHE:HB3	2:H:216:VAL:HG12	1.98	0.45
2:H:622:LEU:HD23	2:H:622:LEU:HA	1.73	0.45
2:I:150:GLU:OE1	2:I:153:LYS:HD2	2.17	0.45
2:J:155:LEU:HD12	2:J:156:SER:N	2.31	0.45
1:A:291:LYS:HB2	1:A:334:ILE:HD11	1.98	0.45
1:A:330:SER:OG	1:A:331:THR:N	2.49	0.45
1:B:238:LYS:HZ1	1:B:253:HIS:C	2.21	0.45
1:B:263:HIS:ND1	1:B:297:ARG:HG3	2.31	0.45
1:C:195:ASP:O	1:C:195:ASP:OD1	2.34	0.45
1:D:271:LEU:N	1:D:289:ILE:O	2.49	0.45
1:D:384:VAL:O	1:D:449:ARG:HG2	2.16	0.45
1:E:404:ILE:C	1:E:405:LEU:HD22	2.41	0.45
1:E:490:ARG:HH21	1:E:588:ASN:ND2	2.15	0.45
1:F:183:ILE:CD1	1:F:236:PHE:HD1	2.28	0.45
1:F:291:LYS:HZ2	1:F:334:ILE:HG23	1.82	0.45
1:G:376:ASN:OD1	1:G:377:VAL:N	2.48	0.45
2:H:62:LEU:HD11	2:H:137:TYR:CB	2.47	0.45
2:H:375:PHE:HA	2:H:378:LYS:HE2	1.97	0.45
2:H:513:TYR:HD1	2:H:519:LEU:HD22	1.82	0.45
2:H:630:VAL:HG12	2:H:632:THR:HG23	1.98	0.45
2:H:735:GLU:O	2:H:739:GLU:OE1	2.34	0.45
2:I:247:PHE:CZ	2:I:252:ILE:HD11	2.52	0.45
1:B:518:LYS:HB2	1:B:519:PRO:HD2	1.99	0.45
1:B:542:TYR:O	1:B:545:LYS:HE2	2.17	0.45
1:C:294:SER:O	1:C:333:ALA:N	2.34	0.45
1:D:528:LYS:NZ	1:D:534:ASN:HA	2.32	0.45
1:E:335:ASP:OD1	1:E:336:HIS:N	2.50	0.45
1:E:634:ASP:O	1:E:637:LYS:HG2	2.17	0.45
1:G:718:THR:CB	1:G:723:LYS:HZ3	2.28	0.45
2:H:566:ILE:HG12	2:H:600:TYR:CZ	2.52	0.45
1:A:406:ALA:O	1:A:409:ASN:HB2	2.17	0.45
1:A:665:ILE:O	1:A:676:ILE:HD12	2.17	0.45
1:B:192:TYR:C	1:B:192:TYR:CD2	2.95	0.45
1:B:227:SER:O	1:B:230:SER:N	2.50	0.45
1:B:258:ALA:HA	1:B:371:THR:OG1	2.16	0.45
1:C:232:PRO:C	1:C:233:TYR:CD2	2.94	0.45
1:C:331:THR:HG22	1:C:449:ARG:NE	2.31	0.45
1:C:627:LEU:H	1:C:676:ILE:CG2	2.27	0.45
1:E:206:TRP:CH2	1:E:218:LYS:HB2	2.52	0.45
1:E:524:LYS:HG3	1:E:578:LEU:HG	1.98	0.45
1:E:568:GLU:HG2	1:E:569:LEU:CD2	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:434:MET:SD	1:G:438:GLN:HB2	2.56	0.45
2:I:255:SER:O	2:I:259:LEU:HG	2.16	0.45
2:J:485:ILE:HA	2:J:519:LEU:O	2.17	0.45
1:A:662:MET:O	1:A:663:LEU:C	2.59	0.45
1:B:233:TYR:HA	1:B:237:GLU:OE2	2.17	0.45
1:B:269:ILE:CG2	1:B:270:ILE:N	2.80	0.45
1:B:447:GLN:C	1:B:448:LEU:HD22	2.42	0.45
1:B:476:ASN:C	1:B:476:ASN:OD1	2.60	0.45
1:C:176:PRO:HB3	1:C:178:ARG:HH12	1.82	0.45
1:C:197:LYS:O	1:C:199:LYS:N	2.50	0.45
1:D:202:PHE:CD2	1:D:202:PHE:C	2.91	0.45
1:D:363:ASN:HD21	1:D:418:PRO:HG2	1.78	0.45
1:D:624:THR:O	1:D:687:LEU:HD13	2.17	0.45
1:E:299:HIS:O	1:E:602:ASN:HB2	2.17	0.45
1:F:527:LEU:HA	1:F:527:LEU:HD23	1.70	0.45
1:G:365:ARG:NH1	1:G:416:LEU:O	2.37	0.45
1:G:404:ILE:C	1:G:405:LEU:HD12	2.42	0.45
2:H:336:GLU:HA	2:H:339:LYS:HE2	1.99	0.45
2:H:414:ARG:O	2:H:417:GLN:NE2	2.50	0.45
2:H:548:LYS:NZ	2:H:549:VAL:HG12	2.32	0.45
2:I:186:GLN:HA	2:I:190:PHE:CD2	2.53	0.45
2:I:587:VAL:HA	2:I:632:THR:HA	1.99	0.45
1:A:471:VAL:HG13	1:A:471:VAL:O	2.17	0.44
1:B:229:ALA:C	1:B:230:SER:HG	2.14	0.44
1:B:449:ARG:C	1:B:450:LEU:HD23	2.42	0.44
1:B:678:PHE:HZ	1:B:686:PRO:HA	1.82	0.44
1:C:383:LEU:HD12	1:C:384:VAL:N	2.32	0.44
1:C:528:LYS:HE2	1:C:528:LYS:HB2	1.52	0.44
1:D:197:LYS:HZ2	1:D:200:ARG:NH2	2.15	0.44
1:D:198:ASN:C	1:D:199:LYS:HD2	2.42	0.44
1:D:459:ILE:HD11	1:D:477:TRP:N	2.32	0.44
1:E:293:THR:HG22	1:E:334:ILE:HG22	1.99	0.44
1:E:445:THR:O	1:E:447:GLN:OE1	2.35	0.44
1:E:449:ARG:C	1:E:450:LEU:HD22	2.42	0.44
1:F:609:GLU:OE1	1:F:609:GLU:N	2.39	0.44
1:G:542:TYR:CE2	1:G:543:GLN:NE2	2.85	0.44
2:I:120:TYR:CG	2:I:121:ALA:N	2.85	0.44
2:J:581:LYS:C	2:J:583:ILE:H	2.25	0.44
1:A:183:ILE:HD12	1:A:183:ILE:N	2.32	0.44
1:B:197:LYS:O	1:B:199:LYS:N	2.51	0.44
1:B:332:VAL:CG1	1:B:448:LEU:HB2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:331:THR:HG22	1:C:449:ARG:CD	2.46	0.44
1:C:367:VAL:HG22	1:C:410:TYR:CE1	2.52	0.44
1:C:490:ARG:O	1:C:491:ILE:HD13	2.17	0.44
1:C:699:TYR:CD1	1:C:725:LEU:HA	2.52	0.44
1:D:492:ILE:HD12	1:D:492:ILE:HG23	1.80	0.44
1:F:558:THR:O	1:F:562:ILE:HG12	2.16	0.44
2:H:73:MET:O	2:H:77:ILE:HG12	2.17	0.44
2:H:484:MET:N	2:H:484:MET:SD	2.90	0.44
2:I:530:LYS:HB3	2:I:548:LYS:HZ2	1.82	0.44
2:J:117:HIS:NE2	2:J:119:VAL:O	2.50	0.44
2:J:239:GLU:HG2	2:J:240:ALA:N	2.32	0.44
2:J:281:TRP:CH2	2:J:423:LEU:HA	2.52	0.44
1:A:229:ALA:O	1:A:230:SER:HB2	2.18	0.44
1:C:241:GLY:O	1:C:245:LYS:NZ	2.32	0.44
1:C:553:ASN:OD1	1:C:553:ASN:C	2.60	0.44
1:D:378:LEU:HD12	1:D:379:PRO:CD	2.47	0.44
1:D:533:PHE:N	1:D:533:PHE:CD2	2.86	0.44
1:D:591:ILE:O	1:D:591:ILE:HG13	2.17	0.44
1:E:242:ARG:HG2	1:E:462:TYR:CZ	2.52	0.44
1:F:435:ASN:OD1	1:F:438:GLN:HG3	2.17	0.44
1:F:480:VAL:HG12	1:F:484:ILE:CD1	2.45	0.44
1:F:576:THR:C	1:F:578:LEU:H	2.25	0.44
1:G:627:LEU:HB3	1:G:629:LEU:CD2	2.48	0.44
2:H:438:TYR:HE1	2:H:544:ARG:NH2	2.15	0.44
2:H:676:GLU:OE1	2:H:676:GLU:N	2.50	0.44
1:A:470:ARG:HD3	1:A:471:VAL:N	2.31	0.44
1:B:639:LEU:C	1:B:703:LYS:HE3	2.42	0.44
1:B:643:ILE:HG12	1:B:723:LYS:HE2	1.99	0.44
1:C:200:ARG:HH22	1:D:189:VAL:CG1	2.27	0.44
1:C:415:ASN:OD1	1:C:416:LEU:HD23	2.18	0.44
1:D:354:THR:HA	1:D:436:TYR:CD1	2.52	0.44
1:E:335:ASP:OD1	1:E:337:SER:N	2.44	0.44
1:E:525:GLU:OE2	1:E:528:LYS:NZ	2.51	0.44
1:F:291:LYS:HZ2	1:F:335:ASP:H	1.63	0.44
1:F:378:LEU:HD12	1:F:379:PRO:HD3	2.00	0.44
1:G:192:TYR:CD2	1:G:192:TYR:N	2.85	0.44
1:G:259:TYR:CE1	1:G:261:ILE:HD11	2.52	0.44
2:H:224:TYR:CE2	2:H:248:ASN:ND2	2.86	0.44
2:I:281:TRP:CH2	2:I:423:LEU:HA	2.45	0.44
2:I:438:TYR:HD2	2:I:490:GLU:N	2.15	0.44
2:I:615:ILE:HA	2:I:618:VAL:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:243:TYR:O	2:J:247:PHE:HD2	2.01	0.44
1:A:245:LYS:HB3	1:B:486:GLU:OE1	2.18	0.44
1:A:432:ILE:HG23	1:A:432:ILE:O	2.17	0.44
1:A:470:ARG:HA	1:A:470:ARG:HE	1.82	0.44
1:B:490:ARG:HH11	1:B:502:GLU:HG3	1.80	0.44
1:B:678:PHE:CZ	1:B:686:PRO:HA	2.53	0.44
1:C:557:GLN:CD	1:C:557:GLN:H	2.24	0.44
1:D:197:LYS:HD3	1:D:197:LYS:C	2.42	0.44
1:D:245:LYS:HD3	1:D:245:LYS:HA	1.78	0.44
1:D:592:ARG:HB3	1:D:598:TYR:CE2	2.52	0.44
1:D:597:HIS:N	1:D:606:GLY:O	2.51	0.44
1:F:643:ILE:HG21	1:F:723:LYS:HZ3	1.83	0.44
2:H:636:LEU:HD23	2:H:636:LEU:HA	1.85	0.44
2:J:122:LYS:HE3	2:J:128:VAL:HB	1.99	0.44
2:J:136:ASP:HA	2:J:139:GLU:OE1	2.18	0.44
1:A:354:THR:HA	1:A:436:TYR:CD2	2.52	0.44
1:A:699:TYR:CD1	1:A:725:LEU:HA	2.53	0.44
1:B:291:LYS:C	1:B:291:LYS:HD3	2.43	0.44
1:B:491:ILE:HD13	1:B:589:ILE:HB	2.00	0.44
1:B:500:LEU:HA	1:B:500:LEU:HD13	1.68	0.44
1:C:178:ARG:NE	1:C:178:ARG:HA	2.32	0.44
1:D:203:LEU:HD12	1:D:203:LEU:HA	1.64	0.44
1:D:609:GLU:OE1	1:D:609:GLU:N	2.44	0.44
1:D:631:ILE:O	1:D:636:ARG:NH1	2.47	0.44
1:E:244:ASP:OD1	1:F:483:GLN:NE2	2.50	0.44
1:E:300:THR:HG22	1:E:601:ASN:HA	1.99	0.44
1:F:596:PHE:CD1	1:F:607:ALA:HB2	2.53	0.44
2:H:210:SER:HA	2:H:213:VAL:HG12	1.97	0.44
2:H:413:LYS:O	2:H:417:GLN:HG3	2.18	0.44
2:H:686:HIS:CE1	2:H:690:HIS:HE1	2.35	0.44
2:I:129:LEU:HD23	2:I:129:LEU:C	2.43	0.44
2:I:162:LYS:HZ3	2:I:163:ILE:HD11	1.82	0.44
2:I:162:LYS:HG3	2:I:163:ILE:HG12	1.99	0.44
2:I:437:LEU:HG	2:I:488:ILE:HA	2.00	0.44
2:J:115:HIS:NE2	2:J:116:GLU:HG3	2.32	0.44
1:B:203:LEU:HA	1:B:203:LEU:HD13	1.80	0.44
1:B:266:MET:HA	1:B:364:ILE:HA	2.00	0.44
1:B:490:ARG:HD3	1:B:492:ILE:HD11	2.00	0.44
1:C:299:HIS:O	1:C:602:ASN:HB2	2.17	0.44
1:D:700:ALA:O	1:D:724:ILE:HG22	2.18	0.44
1:E:718:THR:O	1:E:721:ILE:HG12	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:338:LEU:HG	1:F:661:ASP:CB	2.48	0.44
1:G:200:ARG:NH1	1:G:200:ARG:HG3	2.33	0.44
2:H:446:LEU:HA	2:H:446:LEU:HD13	1.68	0.44
2:H:475:PHE:C	2:H:476:LYS:HD3	2.42	0.44
2:H:599:ALA:C	2:H:601:LEU:H	2.26	0.44
2:H:679:ASN:OD1	2:H:681:SER:N	2.51	0.44
2:I:36:LEU:HD12	2:I:37:LYS:N	2.32	0.44
2:I:235:LEU:HD12	2:I:235:LEU:HA	1.60	0.44
2:J:206:LEU:O	2:J:210:SER:OG	2.24	0.44
1:A:558:THR:O	1:A:562:ILE:HG23	2.18	0.44
1:A:612:VAL:O	1:A:616:HIS:CD2	2.70	0.44
1:B:377:VAL:HG12	1:B:378:LEU:N	2.33	0.44
1:C:200:ARG:HB3	1:D:178:ARG:HH22	1.82	0.44
1:D:549:GLU:C	1:D:594:LYS:HE3	2.43	0.44
1:E:514:LEU:HD23	1:E:514:LEU:C	2.43	0.44
1:F:253:HIS:CE1	1:F:254:PRO:HD2	2.53	0.44
1:F:550:PHE:CD2	1:F:593:ASP:HA	2.52	0.44
1:G:520:ASP:C	1:G:521:MET:HE2	2.42	0.44
1:G:633:LYS:HD2	1:G:636:ARG:HH21	1.83	0.44
2:H:172:ASP:O	2:H:176:THR:HG23	2.18	0.44
2:H:300:ILE:HD13	2:H:386:TYR:CD2	2.49	0.44
2:H:611:GLN:HG3	2:H:613:ASP:OD1	2.18	0.44
2:I:162:LYS:NZ	2:I:163:ILE:HD11	2.33	0.44
2:I:179:ASN:ND2	2:I:179:ASN:O	2.51	0.44
1:B:295:THR:HG22	1:B:332:VAL:CG2	2.47	0.44
1:B:468:ARG:HG2	1:B:468:ARG:HH11	1.83	0.44
1:B:528:LYS:NZ	1:B:535:GLU:HG2	2.33	0.44
1:B:559:SER:O	1:B:563:LYS:HG3	2.17	0.44
1:D:240:THR:O	1:E:514:LEU:HB2	2.18	0.44
1:D:492:ILE:CG2	1:D:500:LEU:HD12	2.48	0.44
1:E:493:PHE:HD1	1:E:591:ILE:HB	1.80	0.44
1:G:184:PRO:O	1:G:188:GLU:HG3	2.18	0.44
1:G:612:VAL:HG12	1:G:616:HIS:HE1	1.83	0.44
2:H:178:LYS:HD2	2:H:201:PHE:CZ	2.53	0.44
2:H:486:VAL:HG23	2:H:519:LEU:HB2	1.98	0.44
2:H:582:LEU:HD12	2:H:583:ILE:HD12	1.99	0.44
2:H:617:LYS:HE3	2:H:695:TYR:HE2	1.82	0.44
2:I:91:HIS:HB3	2:I:94:LEU:HG	1.99	0.44
1:A:224:GLU:OE1	1:A:224:GLU:N	2.51	0.43
1:A:332:VAL:HG12	1:A:448:LEU:HB2	2.00	0.43
1:A:505:ILE:N	1:A:505:ILE:HD12	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:508:VAL:HG23	1:B:516:THR:HA	2.00	0.43
1:C:353:ASN:HB3	1:C:356:ASP:CG	2.43	0.43
1:C:406:ALA:O	1:C:409:ASN:HB2	2.18	0.43
1:C:455:VAL:HG13	1:C:455:VAL:O	2.18	0.43
1:D:197:LYS:O	1:D:198:ASN:C	2.61	0.43
1:E:270:ILE:C	1:E:271:LEU:HD22	2.42	0.43
1:F:666:SER:OG	1:F:676:ILE:HG12	2.17	0.43
1:G:295:THR:HA	1:G:332:VAL:HA	2.00	0.43
2:H:438:TYR:HA	2:H:501:TRP:O	2.18	0.43
2:H:680:ASP:OD1	2:H:680:ASP:N	2.49	0.43
2:I:243:TYR:CE2	2:I:244:MET:HE3	2.53	0.43
2:I:264:MET:N	2:I:264:MET:SD	2.91	0.43
1:B:196:VAL:HG11	1:C:516:THR:HG21	2.01	0.43
1:B:224:GLU:CD	1:B:224:GLU:N	2.76	0.43
1:B:627:LEU:HB2	1:B:676:ILE:HG22	1.98	0.43
1:C:596:PHE:CE1	1:C:638:ILE:HD13	2.54	0.43
1:D:454:GLN:HA	1:D:456:TYR:CZ	2.53	0.43
1:E:361:ASN:ND2	1:E:422:ASN:HB3	2.33	0.43
1:F:232:PRO:C	1:F:233:TYR:CD1	2.96	0.43
1:F:421:LEU:HA	1:F:421:LEU:HD23	1.63	0.43
2:H:157:ARG:HA	2:H:214:GLN:NE2	2.33	0.43
2:H:442:ASN:HD21	2:H:444:ASN:HB2	1.83	0.43
2:H:565:ASN:O	2:H:568:GLN:NE2	2.50	0.43
2:J:235:LEU:HA	2:J:235:LEU:HD12	1.75	0.43
2:J:554:LYS:O	2:J:557:THR:OG1	2.36	0.43
1:A:198:ASN:OD1	1:A:198:ASN:N	2.48	0.43
1:A:552:PHE:HB3	1:A:554:PHE:HZ	1.82	0.43
1:A:578:LEU:HA	1:A:578:LEU:HD12	1.60	0.43
1:B:391:LEU:HB3	1:B:432:ILE:CD1	2.42	0.43
1:B:609:GLU:OE1	1:B:609:GLU:N	2.46	0.43
1:D:597:HIS:H	1:D:607:ALA:HA	1.83	0.43
1:D:606:GLY:HA3	1:D:704:GLU:CD	2.43	0.43
1:E:291:LYS:C	1:E:291:LYS:HD3	2.42	0.43
1:E:404:ILE:HD11	1:F:478:SER:O	2.19	0.43
1:F:523:LEU:HD23	1:F:523:LEU:C	2.44	0.43
1:F:565:GLN:HA	1:F:568:GLU:OE2	2.18	0.43
1:F:620:ILE:HB	1:F:628:LEU:O	2.18	0.43
1:F:636:ARG:HG3	1:F:637:LYS:HZ3	1.82	0.43
1:G:233:TYR:HB2	1:G:238:LYS:CE	2.48	0.43
1:G:449:ARG:HG3	1:G:449:ARG:HH11	1.84	0.43
2:H:107:ILE:H	2:H:107:ILE:HD12	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:190:PHE:HD1	2:H:194:LEU:HB2	1.82	0.43
2:H:386:TYR:CE1	2:H:412:TYR:CE1	3.06	0.43
2:H:610:ILE:HB	2:H:615:ILE:HD11	2.01	0.43
2:H:744:MET:SD	2:H:766:ILE:HG12	2.58	0.43
2:I:104:ILE:O	2:I:111:ASP:HA	2.19	0.43
2:I:108:TYR:O	2:I:110:LYS:NZ	2.46	0.43
2:I:113:LEU:HD12	2:I:113:LEU:HA	1.59	0.43
2:J:57:GLU:O	2:J:60:GLU:HG3	2.18	0.43
1:B:592:ARG:NE	1:B:598:TYR:CD1	2.86	0.43
1:C:227:SER:O	1:C:228:THR:C	2.61	0.43
1:C:300:THR:HG22	1:C:601:ASN:HA	1.99	0.43
1:D:350:MET:O	1:D:352:LEU:N	2.48	0.43
1:D:368:ASN:HB2	1:D:405:LEU:HD21	2.01	0.43
1:D:610:SER:O	1:D:613:LYS:HG2	2.18	0.43
1:E:200:ARG:HH21	2:J:139:GLU:HB3	1.84	0.43
1:F:528:LYS:HE2	1:F:528:LYS:HB2	1.60	0.43
1:G:643:ILE:HD13	1:G:723:LYS:HG2	2.00	0.43
2:H:77:ILE:HG13	2:H:159:ILE:HD11	1.99	0.43
2:H:84:VAL:HG22	2:H:85:ASP:H	1.82	0.43
2:H:315:GLU:O	2:H:319:LEU:N	2.42	0.43
2:H:407:ASP:N	2:H:407:ASP:OD1	2.50	0.43
2:H:739:GLU:HA	2:H:742:ARG:NH2	2.33	0.43
1:D:587:MET:HE2	1:D:587:MET:HB3	1.82	0.43
1:F:596:PHE:HD1	1:F:607:ALA:HB2	1.83	0.43
1:G:256:VAL:HG23	1:G:256:VAL:O	2.18	0.43
2:H:68:SER:O	2:H:69:ASP:C	2.62	0.43
1:B:226:TRP:CE2	1:B:234:SER:HB2	2.54	0.43
1:B:471:VAL:HG13	1:B:471:VAL:O	2.19	0.43
1:B:505:ILE:HD13	1:B:505:ILE:HA	1.73	0.43
1:B:697:ASN:HB2	1:B:699:TYR:HE1	1.84	0.43
1:C:255:LEU:HA	1:C:255:LEU:HD23	1.66	0.43
1:C:326:ASN:ND2	1:C:485:GLN:OE1	2.51	0.43
1:C:500:LEU:N	1:C:500:LEU:CD2	2.82	0.43
1:D:440:LEU:HD12	1:D:440:LEU:N	2.33	0.43
1:D:598:TYR:CD1	1:D:604:ALA:HA	2.54	0.43
1:E:192:TYR:CD2	1:E:192:TYR:C	2.95	0.43
1:E:200:ARG:NH2	2:J:139:GLU:HB3	2.34	0.43
1:E:377:VAL:HG12	1:E:378:LEU:N	2.34	0.43
1:E:435:ASN:OD1	1:E:435:ASN:C	2.62	0.43
1:E:498:LEU:HA	1:E:498:LEU:HD13	1.81	0.43
1:F:245:LYS:HD3	1:F:245:LYS:HA	1.80	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:244:ASP:O	1:G:246:ASN:N	2.52	0.43
2:I:72:GLU:HG3	2:I:75:LYS:HZ3	1.83	0.43
2:I:134:SER:HB3	2:I:136:ASP:OD1	2.19	0.43
2:I:256:LEU:C	2:I:260:LYS:HZ3	2.27	0.43
2:I:602:ILE:O	2:I:605:GLU:HG2	2.18	0.43
2:J:259:LEU:HD12	2:J:260:LYS:N	2.34	0.43
2:J:718:PHE:HA	2:J:722:GLY:HA3	2.01	0.43
1:A:197:LYS:O	1:A:199:LYS:N	2.52	0.43
1:A:687:LEU:HD12	1:A:687:LEU:O	2.18	0.43
1:B:557:GLN:NE2	1:B:561:ASN:OD1	2.46	0.43
1:C:500:LEU:HA	1:C:500:LEU:HD13	1.53	0.43
1:D:248:SER:HG	1:D:250:GLU:CD	2.26	0.43
1:E:206:TRP:CD1	1:E:218:LYS:NZ	2.83	0.43
1:G:632:ASP:O	1:G:635:ILE:HG22	2.19	0.43
2:H:70:VAL:HA	2:H:73:MET:SD	2.58	0.43
2:I:71:LEU:HD13	2:I:71:LEU:HA	1.83	0.43
2:I:120:TYR:CZ	2:I:121:ALA:O	2.71	0.43
2:I:169:LYS:HZ3	2:I:533:GLN:HB2	1.84	0.43
1:A:494:ASN:OD1	1:A:592:ARG:HA	2.19	0.43
1:A:525:GLU:N	1:A:525:GLU:CD	2.76	0.43
1:A:629:LEU:N	1:A:674:THR:O	2.48	0.43
1:B:189:VAL:O	1:B:220:LYS:NZ	2.21	0.43
1:B:216:LEU:N	1:B:216:LEU:HD12	2.34	0.43
1:B:217:THR:OG1	1:B:219:TYR:HE1	2.00	0.43
1:B:222:SER:H	1:B:228:THR:HG21	1.84	0.43
1:C:256:VAL:HG23	1:C:256:VAL:O	2.19	0.43
1:C:665:ILE:O	1:C:676:ILE:HD12	2.18	0.43
1:D:272:SER:HB3	1:D:288:THR:HG22	2.00	0.43
1:D:345:THR:O	1:D:349:THR:HG23	2.19	0.43
1:E:234:SER:OG	1:E:237:GLU:HG2	2.19	0.43
1:E:259:TYR:CZ	1:E:261:ILE:HD11	2.54	0.43
1:E:535:GLU:OE2	1:E:540:LEU:HD12	2.19	0.43
1:E:551:ASP:HB2	1:E:592:ARG:HG2	2.01	0.43
1:F:199:LYS:HE2	1:G:516:THR:O	2.18	0.43
1:G:523:LEU:HD23	1:G:523:LEU:C	2.44	0.43
2:H:189:LEU:HD23	2:H:219:LYS:HE2	2.01	0.43
2:I:57:GLU:O	2:I:61:LYS:NZ	2.49	0.43
2:I:102:LYS:HA	2:I:114:LEU:HD23	2.00	0.43
1:A:225:LYS:HE3	1:A:228:THR:HA	2.00	0.43
1:A:657:ASN:C	1:A:659:ARG:H	2.26	0.43
1:B:481:LEU:HD23	1:B:481:LEU:HA	1.78	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:590:LEU:HA	1:B:590:LEU:HD12	1.69	0.43
1:C:635:ILE:C	1:C:637:LYS:N	2.77	0.43
1:C:705:ASN:HD21	1:C:722:LYS:CB	2.27	0.43
1:D:269:ILE:HG22	1:D:270:ILE:H	1.81	0.43
1:D:627:LEU:HB3	1:D:629:LEU:CD1	2.49	0.43
1:E:222:SER:HB3	1:E:228:THR:HG22	2.01	0.43
1:E:332:VAL:CG1	1:E:448:LEU:HB2	2.48	0.43
1:G:254:PRO:C	1:G:255:LEU:HD12	2.44	0.43
1:G:266:MET:HE2	1:G:269:ILE:CG2	2.49	0.43
2:H:61:LYS:O	2:H:65:LYS:HD2	2.19	0.43
2:I:167:TYR:CE2	2:I:534:ILE:HG12	2.49	0.43
2:J:165:GLN:N	2:J:166:PRO:HD2	2.33	0.43
1:B:554:PHE:HB3	1:B:558:THR:OG1	2.18	0.43
1:C:361:ASN:HA	1:C:422:ASN:OD1	2.19	0.43
1:C:569:LEU:HD23	1:C:569:LEU:HA	1.90	0.43
1:E:187:LEU:HA	1:E:187:LEU:HD13	1.78	0.43
1:E:200:ARG:N	1:E:200:ARG:HD3	2.34	0.43
1:E:472:ASP:OD1	1:E:473:THR:N	2.51	0.43
1:G:643:ILE:N	1:G:699:TYR:O	2.47	0.43
2:H:224:TYR:CD2	2:H:224:TYR:C	2.96	0.43
2:H:594:ASN:HD22	2:H:594:ASN:C	2.24	0.43
2:H:617:LYS:HE3	2:H:695:TYR:CE2	2.54	0.43
2:H:659:TYR:HE2	2:H:694:ASP:OD2	2.02	0.43
2:H:739:GLU:HG3	2:H:742:ARG:HH22	1.84	0.43
2:I:169:LYS:NZ	2:I:533:GLN:HB2	2.33	0.43
2:I:477:TYR:HE2	2:I:559:ILE:HD11	1.84	0.43
2:I:480:SER:O	2:I:525:ILE:N	2.49	0.43
1:A:527:LEU:HD23	1:A:533:PHE:HE2	1.84	0.42
1:B:338:LEU:HG	1:B:661:ASP:CB	2.48	0.42
1:B:555:ASP:HB3	1:B:558:THR:HG23	2.01	0.42
1:C:498:LEU:HD23	1:C:498:LEU:HA	1.88	0.42
1:D:472:ASP:OD1	1:D:473:THR:N	2.52	0.42
1:E:234:SER:H	1:E:237:GLU:CD	2.15	0.42
1:F:178:ARG:HB2	1:F:224:GLU:OE2	2.19	0.42
1:F:269:ILE:HG13	1:F:362:ALA:HB2	2.01	0.42
1:F:334:ILE:H	1:F:334:ILE:HD12	1.83	0.42
1:F:459:ILE:HG12	1:F:477:TRP:CE2	2.54	0.42
1:F:520:ASP:C	1:F:520:ASP:OD2	2.62	0.42
1:F:543:GLN:OE1	1:F:543:GLN:N	2.52	0.42
2:H:412:TYR:O	2:H:416:ILE:HD12	2.18	0.42
2:H:576:LEU:HG	2:H:577:PRO:HD2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:656:LYS:HD3	2:H:673:LYS:C	2.44	0.42
2:I:252:ILE:HD13	2:I:252:ILE:HA	1.90	0.42
2:I:582:LEU:O	2:I:629:PHE:N	2.45	0.42
2:J:405:ASN:OD1	2:J:405:ASN:N	2.51	0.42
1:A:411:TYR:CD2	1:A:411:TYR:C	2.92	0.42
1:B:387:LYS:HE2	1:B:387:LYS:HA	2.01	0.42
1:B:463:ASN:HB3	1:B:470:ARG:HH21	1.83	0.42
1:B:596:PHE:N	1:B:596:PHE:CD1	2.87	0.42
1:C:366:TYR:HD2	1:C:378:LEU:HD11	1.82	0.42
1:C:404:ILE:C	1:C:405:LEU:HD22	2.44	0.42
1:C:599:ASP:CG	1:C:600:ARG:H	2.27	0.42
1:D:226:TRP:CZ3	1:D:234:SER:HB3	2.54	0.42
1:D:405:LEU:HD12	1:D:405:LEU:HA	1.83	0.42
1:E:364:ILE:CD1	1:E:421:LEU:HD21	2.49	0.42
1:E:381:THR:HG23	1:E:451:ASP:O	2.18	0.42
1:G:300:THR:O	1:G:324:PHE:HB3	2.18	0.42
2:H:384:GLN:OE1	2:H:384:GLN:HA	2.18	0.42
2:H:391:ARG:HH12	2:H:399:ILE:HG22	1.83	0.42
2:H:522:GLN:HG3	2:H:525:ILE:HD11	2.00	0.42
1:A:227:SER:O	1:A:228:THR:C	2.62	0.42
1:B:587:MET:HE2	1:B:587:MET:HB2	1.76	0.42
1:C:237:GLU:OE1	1:C:237:GLU:N	2.47	0.42
1:C:535:GLU:OE2	1:C:540:LEU:HD22	2.19	0.42
1:C:590:LEU:HD23	1:C:590:LEU:C	2.45	0.42
1:G:377:VAL:HG12	1:G:378:LEU:N	2.35	0.42
1:G:471:VAL:HG13	1:G:471:VAL:O	2.18	0.42
1:G:506:ALA:HB1	1:G:518:LYS:NZ	2.30	0.42
1:G:643:ILE:HG12	1:G:723:LYS:NZ	2.34	0.42
2:H:120:TYR:O	2:H:130:VAL:N	2.42	0.42
2:H:521:LEU:HD13	2:H:521:LEU:HA	1.87	0.42
2:H:557:THR:HA	2:H:560:GLN:CD	2.45	0.42
2:H:615:ILE:H	2:H:615:ILE:HD12	1.84	0.42
2:H:699:LEU:HD12	2:H:700:LEU:HD22	2.02	0.42
2:J:61:LYS:O	2:J:64:GLU:HB2	2.19	0.42
1:A:250:GLU:OE1	1:A:250:GLU:N	2.30	0.42
1:A:365:ARG:NH1	1:A:414:LYS:HA	2.35	0.42
1:A:587:MET:HB2	1:A:587:MET:HE3	1.79	0.42
1:B:228:THR:HG23	1:B:235:ASP:OD2	2.19	0.42
1:B:365:ARG:HE	1:B:418:PRO:CB	2.27	0.42
1:C:187:LEU:HA	1:C:187:LEU:HD13	1.79	0.42
1:C:353:ASN:HB3	1:C:356:ASP:OD1	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:383:LEU:HD11	1:C:448:LEU:HB3	2.01	0.42
1:C:629:LEU:HA	1:C:629:LEU:HD12	1.82	0.42
1:D:360:LEU:HA	1:D:360:LEU:HD12	1.73	0.42
1:F:353:ASN:H	1:F:356:ASP:CG	2.27	0.42
2:I:39:ILE:HD12	2:I:39:ILE:H	1.85	0.42
2:I:125:TYR:O	2:I:127:PRO:HD3	2.18	0.42
2:J:527:LEU:HA	2:J:548:LYS:O	2.19	0.42
2:J:664:ARG:HG3	2:J:664:ARG:O	2.19	0.42
1:A:255:LEU:HA	1:A:255:LEU:HD23	1.69	0.42
1:A:633:LYS:HE2	1:A:636:ARG:NH2	2.33	0.42
1:B:535:GLU:OE2	1:B:540:LEU:HD22	2.20	0.42
1:B:549:GLU:HB3	1:B:595:ARG:HH11	1.85	0.42
1:D:389:GLN:O	1:D:389:GLN:HG2	2.19	0.42
1:E:228:THR:HG23	1:E:235:ASP:OD2	2.20	0.42
1:F:438:GLN:HA	1:F:441:GLU:OE1	2.19	0.42
1:F:645:GLU:HA	1:F:654:GLU:O	2.19	0.42
1:G:178:ARG:NE	1:G:178:ARG:HA	2.34	0.42
1:G:199:LYS:H	1:G:200:ARG:HH12	1.66	0.42
1:G:228:THR:N	1:G:235:ASP:OD2	2.38	0.42
1:G:463:ASN:OD1	1:G:465:GLU:OE1	2.38	0.42
1:G:533:PHE:CZ	1:G:542:TYR:HB2	2.54	0.42
1:G:618:GLU:N	1:G:618:GLU:OE2	2.52	0.42
1:G:702:THR:OG1	1:G:704:GLU:OE1	2.32	0.42
2:H:281:TRP:CE2	2:H:285:LEU:HD21	2.54	0.42
2:I:84:VAL:HG22	2:I:85:ASP:H	1.84	0.42
2:I:512:GLY:O	2:I:519:LEU:HA	2.20	0.42
2:I:543:ILE:HG22	2:I:545:ILE:HD11	2.01	0.42
2:I:566:ILE:HG21	2:I:583:ILE:HG21	2.01	0.42
2:J:85:ASP:OD1	2:J:86:GLY:N	2.52	0.42
1:A:224:GLU:OE1	1:A:517:THR:HG21	2.19	0.42
1:A:345:THR:O	1:A:348:GLU:HG3	2.19	0.42
1:B:202:PHE:CD2	1:B:202:PHE:C	2.97	0.42
1:B:253:HIS:CE1	1:B:255:LEU:HD13	2.55	0.42
1:B:484:ILE:HG22	1:B:504:ARG:CZ	2.50	0.42
1:B:524:LYS:HE2	1:B:540:LEU:HD21	2.01	0.42
1:C:270:ILE:HG22	1:C:290:SER:HB3	2.02	0.42
1:C:373:PRO:HB2	1:C:375:TYR:CE2	2.55	0.42
1:C:374:ILE:CG1	1:C:405:LEU:HB2	2.50	0.42
1:C:549:GLU:HA	1:C:594:LYS:CE	2.50	0.42
1:F:245:LYS:HB3	1:G:483:GLN:OE1	2.19	0.42
1:F:259:TYR:HE2	1:F:261:ILE:HD11	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:455:VAL:HG13	1:F:455:VAL:O	2.19	0.42
1:F:648:ASP:C	1:F:650:GLU:N	2.76	0.42
1:G:244:ASP:C	1:G:244:ASP:OD1	2.63	0.42
2:H:118:TYR:HA	2:H:132:GLN:OE1	2.19	0.42
2:H:296:LEU:HD11	2:H:419:ILE:HD12	2.02	0.42
2:H:434:LYS:HD3	2:H:436:TYR:CE1	2.53	0.42
2:I:107:ILE:HG12	2:I:219:LYS:NZ	2.35	0.42
2:I:226:GLU:OE1	2:I:228:GLN:OE1	2.38	0.42
1:A:621:ASN:OD1	1:A:622:SER:N	2.53	0.42
1:A:698:VAL:O	1:A:726:ILE:HB	2.20	0.42
1:B:195:ASP:OD1	1:B:195:ASP:O	2.38	0.42
1:B:455:VAL:O	1:B:455:VAL:HG13	2.20	0.42
1:B:494:ASN:OD1	1:B:592:ARG:HA	2.18	0.42
1:B:500:LEU:N	1:B:500:LEU:HD22	2.35	0.42
1:B:520:ASP:OD1	1:B:521:MET:N	2.52	0.42
1:B:588:ASN:O	1:B:589:ILE:HD13	2.20	0.42
1:B:646:ILE:N	1:B:654:GLU:O	2.43	0.42
1:C:185:ASP:O	1:C:186:SER:C	2.63	0.42
1:C:226:TRP:CD2	1:C:234:SER:HB3	2.55	0.42
1:C:297:ARG:HD2	1:C:298:THR:N	2.34	0.42
1:C:365:ARG:NH2	1:C:413:SER:O	2.53	0.42
1:C:445:THR:HG22	1:C:447:GLN:HB2	2.01	0.42
1:C:530:ALA:C	1:C:531:PHE:CD2	2.98	0.42
1:D:191:GLY:HA2	1:D:219:TYR:O	2.20	0.42
1:E:540:LEU:HB3	1:E:547:ILE:CG2	2.47	0.42
1:E:576:THR:C	1:E:578:LEU:H	2.28	0.42
1:G:187:LEU:HD23	1:G:187:LEU:HA	1.69	0.42
1:G:385:LEU:O	1:G:389:GLN:HB2	2.20	0.42
1:G:416:LEU:HD13	1:G:416:LEU:HA	1.80	0.42
1:G:421:LEU:HD23	1:G:421:LEU:C	2.44	0.42
1:G:643:ILE:HG12	1:G:723:LYS:CD	2.48	0.42
2:H:70:VAL:O	2:H:73:MET:SD	2.78	0.42
2:H:163:ILE:C	2:H:165:GLN:OE1	2.63	0.42
2:H:235:LEU:HD13	2:H:235:LEU:HA	1.65	0.42
2:H:442:ASN:ND2	2:H:444:ASN:HB2	2.34	0.42
2:H:617:LYS:HD3	2:H:773:ILE:HD13	2.01	0.42
2:H:628:ARG:HH11	2:H:628:ARG:HG3	1.84	0.42
2:I:243:TYR:CD2	2:I:244:MET:HE3	2.54	0.42
2:J:226:GLU:CD	2:J:229:HIS:HD1	2.20	0.42
1:A:411:TYR:CD1	1:A:412:PRO:HA	2.54	0.42
1:B:269:ILE:CG2	1:B:270:ILE:H	2.31	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:702:THR:HG1	1:B:704:GLU:CD	2.28	0.42
1:C:226:TRP:CZ3	1:C:234:SER:HB3	2.54	0.42
1:C:266:MET:HE2	1:C:269:ILE:HG22	2.02	0.42
1:C:466:ASN:OD1	1:C:466:ASN:N	2.52	0.42
1:C:639:LEU:N	1:C:703:LYS:NZ	2.68	0.42
1:D:175:VAL:HG12	2:I:228:GLN:HE21	1.85	0.42
1:D:225:LYS:HE2	1:D:225:LYS:HB3	1.85	0.42
1:D:334:ILE:CG2	1:D:446:LYS:HB3	2.49	0.42
1:E:192:TYR:CD1	1:E:192:TYR:N	2.87	0.42
1:F:203:LEU:HG	1:F:204:SER:N	2.33	0.42
1:F:391:LEU:HD13	1:F:391:LEU:HA	1.90	0.42
1:F:583:LEU:HD22	1:F:583:LEU:N	2.34	0.42
1:G:198:ASN:HB2	1:G:200:ARG:NH2	2.34	0.42
1:G:468:ARG:NH1	1:G:470:ARG:HH21	2.18	0.42
2:H:77:ILE:HG13	2:H:159:ILE:CD1	2.50	0.42
2:H:137:TYR:HE1	2:H:143:LYS:HE3	1.85	0.42
2:H:186:GLN:HB2	2:H:190:PHE:CE2	2.53	0.42
2:H:390:GLN:OE1	2:H:390:GLN:N	2.52	0.42
2:H:570:TRP:CZ2	2:H:603:LEU:HB3	2.54	0.42
2:H:725:LEU:HB3	2:H:726:THR:H	1.71	0.42
2:I:41:LYS:HE3	2:I:41:LYS:HB3	1.78	0.42
1:A:358:ALA:HB3	1:A:434:MET:HE3	2.01	0.42
1:A:565:GLN:O	1:A:569:LEU:HD23	2.19	0.42
1:B:649:THR:CB	1:B:691:ASN:HD22	2.31	0.42
1:C:270:ILE:CG1	1:C:361:ASN:HB3	2.50	0.42
1:C:366:TYR:CE2	1:C:378:LEU:HD21	2.54	0.42
1:C:552:PHE:HB3	1:C:554:PHE:HZ	1.82	0.42
1:C:579:ASP:OD1	1:C:580:LYS:HG2	2.20	0.42
1:D:183:ILE:HD12	1:D:183:ILE:N	2.33	0.42
1:D:267:GLU:HG2	1:D:268:ASN:N	2.34	0.42
1:D:297:ARG:CZ	1:D:500:LEU:HD23	2.49	0.42
1:D:366:TYR:HE2	1:D:378:LEU:CG	2.33	0.42
1:D:640:SER:HB3	1:D:703:LYS:HA	2.01	0.42
1:E:229:ALA:O	1:E:230:SER:HB2	2.19	0.42
1:E:365:ARG:HH11	1:E:414:LYS:HD2	1.84	0.42
1:E:603:ILE:O	1:E:605:VAL:HG23	2.20	0.42
1:F:450:LEU:HA	1:F:450:LEU:HD23	1.69	0.42
1:F:482:PRO:O	1:F:486:GLU:HG2	2.20	0.42
1:G:353:ASN:O	1:G:436:TYR:HD2	2.02	0.42
1:G:364:ILE:HD11	1:G:421:LEU:HD12	2.02	0.42
1:G:638:ILE:C	1:G:703:LYS:HZ2	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:475:PHE:CD2	2:H:529:ILE:HG13	2.55	0.42
2:H:475:PHE:CE2	2:H:529:ILE:HG13	2.54	0.42
2:H:578:LYS:CB	2:H:579:TYR:CD1	3.03	0.42
2:H:623:VAL:C	2:H:625:GLY:N	2.77	0.42
2:I:69:ASP:HA	2:I:72:GLU:OE1	2.20	0.42
2:I:150:GLU:HA	2:I:153:LYS:HZ2	1.85	0.42
2:I:630:VAL:N	2:I:666:ILE:O	2.47	0.42
2:J:234:GLN:HA	2:J:241:PHE:HB2	2.01	0.42
1:A:199:LYS:NZ	1:B:516:THR:O	2.53	0.42
1:A:324:PHE:HZ	1:A:588:ASN:HB3	1.85	0.42
1:A:324:PHE:CZ	1:A:588:ASN:HB3	2.55	0.42
1:B:374:ILE:CG1	1:B:405:LEU:HB2	2.50	0.42
1:B:385:LEU:HB3	1:B:391:LEU:CD2	2.50	0.42
1:C:338:LEU:HG	1:C:661:ASP:CB	2.50	0.42
1:D:187:LEU:HA	1:D:187:LEU:HD23	1.53	0.42
1:D:555:ASP:O	1:D:558:THR:OG1	2.27	0.42
1:E:244:ASP:O	1:E:246:ASN:N	2.53	0.42
1:E:592:ARG:NH1	1:E:598:TYR:CG	2.88	0.42
1:F:199:LYS:HD2	1:G:517:THR:HA	2.02	0.42
1:G:579:ASP:OD1	1:G:580:LYS:HG2	2.20	0.42
2:H:97:LEU:HB2	2:H:101:LYS:HE2	2.02	0.42
2:H:437:LEU:HD23	2:H:437:LEU:HA	1.83	0.42
2:I:63:LEU:N	2:I:63:LEU:HD22	2.35	0.42
2:I:490:GLU:O	2:I:491:ARG:CZ	2.68	0.42
2:J:194:LEU:C	2:J:196:GLU:N	2.78	0.42
1:A:382:SER:HA	1:A:393:THR:HA	2.02	0.41
1:A:527:LEU:HD12	1:A:527:LEU:N	2.35	0.41
1:B:468:ARG:CZ	1:B:468:ARG:HB2	2.50	0.41
1:B:593:ASP:C	1:B:593:ASP:OD1	2.63	0.41
1:B:629:LEU:N	1:B:674:THR:O	2.52	0.41
1:B:696:VAL:N	1:B:729:LYS:O	2.36	0.41
1:C:471:VAL:O	1:C:471:VAL:HG13	2.20	0.41
1:C:523:LEU:HD23	1:C:523:LEU:C	2.45	0.41
1:C:527:LEU:HD13	1:C:527:LEU:HA	1.89	0.41
1:E:471:VAL:O	1:E:471:VAL:HG13	2.20	0.41
1:E:624:THR:O	1:E:687:LEU:HB2	2.21	0.41
1:E:722:LYS:HA	1:E:722:LYS:HD2	1.70	0.41
1:F:228:THR:HG23	1:F:235:ASP:OD1	2.20	0.41
1:G:183:ILE:HD11	1:G:236:PHE:HD1	1.84	0.41
2:H:65:LYS:HD2	2:H:65:LYS:H	1.85	0.41
2:H:155:LEU:HD13	2:H:155:LEU:HA	1.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:81:ILE:O	2:I:81:ILE:HG13	2.20	0.41
1:A:382:SER:CB	1:A:393:THR:HG22	2.49	0.41
1:A:497:ASP:OD1	1:A:499:ASN:HB2	2.20	0.41
1:A:543:GLN:O	1:A:545:LYS:NZ	2.50	0.41
1:A:594:LYS:HB2	1:A:594:LYS:HE2	1.78	0.41
1:B:211:HIS:HA	1:B:214:LYS:NZ	2.36	0.41
1:B:435:ASN:OD1	1:B:435:ASN:C	2.63	0.41
1:B:512:ASP:OD1	1:B:513:PRO:HD2	2.21	0.41
1:C:253:HIS:HE1	1:C:255:LEU:HD12	1.85	0.41
1:C:476:ASN:HD21	1:C:479:GLU:HG3	1.85	0.41
1:C:588:ASN:O	1:C:589:ILE:HD13	2.19	0.41
1:D:198:ASN:ND2	1:D:200:ARG:HH22	2.18	0.41
1:E:548:THR:O	1:E:594:LYS:NZ	2.37	0.41
1:E:552:PHE:HB3	1:E:554:PHE:HZ	1.81	0.41
1:E:577:VAL:HG22	1:E:580:LYS:HB2	2.02	0.41
1:G:203:LEU:HD22	1:G:203:LEU:N	2.35	0.41
1:G:643:ILE:HG21	1:G:723:LYS:NZ	2.31	0.41
2:H:391:ARG:HD2	2:H:391:ARG:C	2.45	0.41
2:H:459:ASP:CG	2:H:462:LYS:HZ3	2.28	0.41
2:I:194:LEU:C	2:I:196:GLU:H	2.28	0.41
2:J:247:PHE:O	2:J:252:ILE:HG12	2.20	0.41
2:J:433:ASN:CG	2:J:434:LYS:H	2.28	0.41
1:A:258:ALA:HA	1:A:371:THR:OG1	2.20	0.41
1:A:435:ASN:O	1:A:438:GLN:HB2	2.20	0.41
1:B:200:ARG:N	1:B:200:ARG:HD3	2.35	0.41
1:C:198:ASN:CG	1:C:199:LYS:H	2.28	0.41
1:C:521:MET:SD	1:C:521:MET:C	3.04	0.41
1:C:558:THR:HG22	1:C:587:MET:HG3	2.02	0.41
1:D:181:ASP:O	1:D:183:ILE:HD12	2.19	0.41
1:D:197:LYS:O	1:D:200:ARG:N	2.46	0.41
1:D:241:GLY:O	1:D:243:ILE:N	2.52	0.41
1:F:520:ASP:OD2	1:F:521:MET:N	2.53	0.41
1:F:638:ILE:HG13	1:F:639:LEU:HD22	2.02	0.41
1:F:722:LYS:HZ3	1:F:723:LYS:N	2.18	0.41
1:G:441:GLU:HA	1:G:444:LYS:NZ	2.35	0.41
2:H:171:LEU:O	2:H:174:LEU:HB2	2.19	0.41
2:I:38:GLU:O	2:I:41:LYS:HG2	2.20	0.41
2:I:126:GLU:O	2:I:128:VAL:HG23	2.20	0.41
2:I:202:SER:H	2:I:205:PHE:HD2	1.67	0.41
2:I:474:ASN:HD22	2:I:597:GLU:HB2	1.86	0.41
2:I:501:TRP:CZ3	2:I:590:ARG:NH1	2.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:535:GLU:HB3	1:A:538:GLY:HA2	2.03	0.41
1:A:592:ARG:HH22	1:A:602:ASN:HA	1.85	0.41
1:A:663:LEU:O	1:A:665:ILE:N	2.53	0.41
1:B:225:LYS:NZ	1:B:230:SER:HB3	2.34	0.41
1:B:227:SER:O	1:B:228:THR:C	2.63	0.41
1:B:415:ASN:C	1:B:416:LEU:HD23	2.45	0.41
1:B:641:GLY:C	1:B:701:VAL:HG12	2.45	0.41
1:D:192:TYR:CD2	1:D:192:TYR:C	2.97	0.41
1:D:527:LEU:HD12	1:D:527:LEU:N	2.35	0.41
1:D:590:LEU:CD2	1:D:592:ARG:HG3	2.50	0.41
1:G:481:LEU:HB2	1:G:482:PRO:HD3	2.02	0.41
1:G:555:ASP:O	1:G:558:THR:OG1	2.26	0.41
2:H:97:LEU:HB2	2:H:101:LYS:CE	2.50	0.41
2:H:189:LEU:HD23	2:H:189:LEU:HA	1.71	0.41
2:J:224:TYR:CZ	2:J:230:ARG:NH1	2.89	0.41
1:A:524:LYS:HE2	1:A:540:LEU:HD11	2.03	0.41
1:A:568:GLU:HG2	1:A:569:LEU:CD2	2.50	0.41
1:A:614:GLU:OE2	1:A:617:ARG:NH1	2.44	0.41
1:B:366:TYR:HE1	1:B:378:LEU:CD1	2.23	0.41
1:B:608:ASP:OD1	1:B:609:GLU:N	2.53	0.41
1:C:438:GLN:HA	1:C:441:GLU:OE1	2.21	0.41
1:C:517:THR:HG22	1:C:517:THR:O	2.19	0.41
1:D:374:ILE:C	1:D:375:TYR:HD1	2.28	0.41
1:D:635:ILE:O	1:D:637:LYS:N	2.53	0.41
1:F:271:LEU:HD13	1:F:360:LEU:HA	2.01	0.41
1:F:378:LEU:HD12	1:F:379:PRO:CD	2.50	0.41
1:F:502:GLU:O	1:F:503:ARG:NH1	2.50	0.41
1:F:515:GLU:N	1:F:515:GLU:OE2	2.54	0.41
1:G:364:ILE:O	1:G:419:ILE:HG22	2.20	0.41
1:G:500:LEU:HD23	1:G:500:LEU:HA	1.85	0.41
1:G:631:ILE:HB	1:G:636:ARG:HD2	2.02	0.41
2:H:200:ASP:C	2:H:200:ASP:OD1	2.62	0.41
2:I:52:GLU:O	2:I:52:GLU:HG3	2.20	0.41
2:I:149:TYR:CE1	2:I:219:LYS:HE2	2.55	0.41
2:I:541:GLU:O	2:I:542:TYR:HD1	2.04	0.41
2:I:541:GLU:O	2:I:542:TYR:CD1	2.73	0.41
2:J:243:TYR:CE1	2:J:247:PHE:HE2	2.38	0.41
1:A:438:GLN:HA	1:A:441:GLU:CD	2.46	0.41
1:B:481:LEU:HB3	1:B:485:GLN:OE1	2.20	0.41
1:C:199:LYS:HD2	1:C:199:LYS:HA	1.85	0.41
1:C:403:GLN:C	1:C:404:ILE:HD13	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:596:PHE:HD1	1:C:607:ALA:HB2	1.84	0.41
1:D:377:VAL:HG12	1:D:378:LEU:N	2.35	0.41
1:D:643:ILE:HG21	1:D:723:LYS:HZ2	1.85	0.41
1:E:405:LEU:HD13	1:E:405:LEU:HA	1.64	0.41
1:F:383:LEU:HD13	1:F:450:LEU:HD21	2.02	0.41
1:G:406:ALA:HB3	1:G:409:ASN:OD1	2.20	0.41
1:G:506:ALA:CB	1:G:518:LYS:HZ2	2.26	0.41
2:H:203:VAL:HA	2:H:206:LEU:CD2	2.51	0.41
2:I:602:ILE:HA	2:I:605:GLU:HG2	2.02	0.41
1:A:374:ILE:C	1:A:375:TYR:HD1	2.28	0.41
1:B:220:LYS:O	1:B:255:LEU:HD11	2.21	0.41
1:B:378:LEU:HA	1:B:379:PRO:HD3	1.88	0.41
1:C:198:ASN:OD1	1:C:198:ASN:N	2.52	0.41
1:C:232:PRO:CD	1:C:233:TYR:HD2	2.21	0.41
1:C:238:LYS:HG2	1:C:252:ARG:O	2.19	0.41
1:C:481:LEU:HA	1:C:481:LEU:HD23	1.61	0.41
1:C:692:PRO:O	1:C:732:TYR:HD2	2.04	0.41
1:E:227:SER:O	1:E:228:THR:C	2.62	0.41
1:E:291:LYS:NZ	1:E:292:ASN:O	2.54	0.41
1:E:326:ASN:HD22	1:E:485:GLN:CG	2.26	0.41
1:E:383:LEU:HA	1:E:383:LEU:HD13	1.83	0.41
1:E:480:VAL:O	1:E:481:LEU:C	2.61	0.41
1:F:199:LYS:HD3	1:F:199:LYS:HA	1.63	0.41
1:F:244:ASP:C	1:F:246:ASN:H	2.29	0.41
1:F:554:PHE:HB3	1:F:558:THR:OG1	2.21	0.41
2:H:544:ARG:O	2:H:545:ILE:HD13	2.20	0.41
2:I:224:TYR:CE1	2:I:248:ASN:ND2	2.88	0.41
2:J:503:ILE:CG1	2:J:549:VAL:HG23	2.50	0.41
1:A:198:ASN:CG	1:A:199:LYS:H	2.29	0.41
1:A:592:ARG:NH2	1:A:598:TYR:CG	2.89	0.41
1:D:197:LYS:HB2	2:I:235:LEU:HD21	2.02	0.41
1:D:228:THR:HG23	1:D:235:ASP:CG	2.45	0.41
1:D:367:VAL:HG22	1:D:410:TYR:CE2	2.54	0.41
1:E:188:GLU:OE1	1:E:223:PRO:HA	2.21	0.41
1:E:272:SER:HB3	1:E:288:THR:HG22	2.01	0.41
1:E:556:GLN:O	1:E:559:SER:OG	2.30	0.41
1:G:611:VAL:HA	1:G:614:GLU:OE1	2.20	0.41
2:H:226:GLU:OE2	2:H:228:GLN:HB2	2.21	0.41
2:H:585:PHE:CE1	2:H:596:VAL:HG12	2.56	0.41
2:I:84:VAL:HG22	2:I:85:ASP:N	2.35	0.41
2:I:255:SER:O	2:I:258:GLU:HG3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:408:VAL:HG12	2:J:412:TYR:CE2	2.56	0.41
1:A:406:ALA:HB3	1:A:409:ASN:HD22	1.86	0.41
1:A:416:LEU:HA	1:A:416:LEU:HD13	1.76	0.41
1:A:596:PHE:CD1	1:A:596:PHE:N	2.88	0.41
1:B:384:VAL:HG13	1:B:449:ARG:HB2	2.02	0.41
1:B:469:VAL:HG23	1:B:469:VAL:O	2.20	0.41
1:C:385:LEU:CG	1:C:391:LEU:HD21	2.50	0.41
1:D:244:ASP:C	1:D:246:ASN:N	2.76	0.41
1:D:492:ILE:HG22	1:D:500:LEU:CD1	2.50	0.41
1:D:549:GLU:HB3	1:D:595:ARG:HH11	1.86	0.41
1:D:583:LEU:HA	1:D:583:LEU:HD23	1.65	0.41
1:E:291:LYS:NZ	1:E:335:ASP:N	2.65	0.41
1:E:421:LEU:HA	1:E:421:LEU:HD23	1.56	0.41
1:E:638:ILE:C	1:E:639:LEU:HD22	2.46	0.41
1:F:226:TRP:CE2	1:F:234:SER:HB3	2.55	0.41
1:F:228:THR:HG23	1:F:235:ASP:CG	2.46	0.41
1:G:198:ASN:CB	1:G:200:ARG:HH22	2.33	0.41
1:G:207:ILE:HG22	1:G:209:ASN:OD1	2.21	0.41
1:G:354:THR:HA	1:G:436:TYR:CD2	2.56	0.41
1:G:481:LEU:H	1:G:481:LEU:HD12	1.86	0.41
1:G:595:ARG:HD2	1:G:611:VAL:HG11	2.02	0.41
2:H:234:GLN:HG2	2:H:241:PHE:CG	2.56	0.41
2:H:478:SER:HG	2:H:590:ARG:HA	1.85	0.41
2:I:153:LYS:HE3	2:I:153:LYS:HB3	1.87	0.41
2:J:61:LYS:O	2:J:65:LYS:HD2	2.21	0.41
2:J:81:ILE:HG13	2:J:81:ILE:O	2.21	0.41
2:J:170:PHE:HE1	2:J:217:PHE:HD1	1.66	0.41
1:A:541:GLN:CD	1:A:541:GLN:C	2.88	0.41
1:B:377:VAL:CG1	1:B:378:LEU:N	2.84	0.41
1:B:421:LEU:HA	1:B:421:LEU:HD12	1.70	0.41
1:B:490:ARG:HG3	1:B:502:GLU:OE2	2.20	0.41
1:B:575:TYR:O	1:B:578:LEU:HD23	2.21	0.41
1:B:598:TYR:HA	1:B:605:VAL:HG12	2.03	0.41
1:C:530:ALA:O	1:C:531:PHE:HD2	2.04	0.41
1:C:542:TYR:O	1:C:543:GLN:C	2.64	0.41
1:C:639:LEU:H	1:C:703:LYS:HZ3	1.69	0.41
1:D:727:PHE:CD2	1:D:728:SER:N	2.89	0.41
1:E:435:ASN:CG	1:E:438:GLN:HG3	2.45	0.41
1:F:243:ILE:O	1:F:244:ASP:C	2.63	0.41
1:F:490:ARG:HG3	1:F:502:GLU:OE2	2.21	0.41
1:F:638:ILE:C	1:F:639:LEU:HD22	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:242:ARG:HB3	1:G:462:TYR:CZ	2.56	0.41
1:G:243:ILE:HD12	1:G:243:ILE:HA	1.89	0.41
1:G:294:SER:O	1:G:333:ALA:N	2.42	0.41
1:G:364:ILE:HG22	1:G:365:ARG:N	2.36	0.41
1:G:571:ALA:CB	1:G:577:VAL:HG21	2.51	0.41
1:G:577:VAL:HG12	1:G:577:VAL:O	2.21	0.41
2:H:165:GLN:O	2:H:165:GLN:HG2	2.20	0.41
2:H:246:LYS:HB3	2:H:250:GLN:NE2	2.36	0.41
2:J:83:ILE:HG13	2:J:131:ILE:HB	2.02	0.41
1:A:481:LEU:HB3	1:A:482:PRO:HD3	2.03	0.40
1:A:583:LEU:HD23	1:A:583:LEU:HA	1.83	0.40
1:B:176:PRO:HB3	1:B:178:ARG:HH12	1.85	0.40
1:B:628:LEU:HA	1:B:674:THR:O	2.20	0.40
1:C:190:GLU:C	1:C:220:LYS:HE2	2.46	0.40
1:C:214:LYS:HE2	1:C:214:LYS:HB3	1.85	0.40
1:C:227:SER:OG	1:C:230:SER:HA	2.21	0.40
1:C:244:ASP:OD1	1:C:244:ASP:C	2.64	0.40
1:C:542:TYR:O	1:C:545:LYS:HE2	2.21	0.40
1:D:244:ASP:O	1:D:246:ASN:N	2.54	0.40
1:D:266:MET:SD	1:D:362:ALA:HB1	2.61	0.40
1:D:378:LEU:HD12	1:D:378:LEU:HA	1.78	0.40
1:D:470:ARG:HA	1:E:479:GLU:OE1	2.21	0.40
1:E:269:ILE:HB	1:E:360:LEU:HD11	2.03	0.40
1:F:227:SER:O	1:F:230:SER:N	2.49	0.40
1:F:256:VAL:HG23	1:F:256:VAL:O	2.21	0.40
1:F:342:GLY:HA2	1:F:344:ARG:NH1	2.35	0.40
1:F:503:ARG:HD3	1:F:503:ARG:HA	1.88	0.40
1:G:271:LEU:HB2	1:G:289:ILE:CG2	2.49	0.40
1:G:565:GLN:HA	1:G:568:GLU:OE2	2.21	0.40
1:G:588:ASN:O	1:G:589:ILE:HD13	2.20	0.40
1:G:594:LYS:HB2	1:G:594:LYS:HE3	1.71	0.40
2:H:124:GLY:CA	2:H:127:PRO:HG3	2.50	0.40
2:H:427:ILE:HD13	2:H:505:LEU:HD12	2.01	0.40
2:H:464:ASN:OD1	2:H:466:GLY:N	2.53	0.40
2:I:177:ILE:HD13	2:I:177:ILE:HA	1.83	0.40
2:I:472:LYS:O	2:I:473:LYS:C	2.64	0.40
2:I:537:GLN:NE2	2:I:538:SER:HB3	2.36	0.40
2:J:552:LYS:O	2:J:555:ILE:HG22	2.21	0.40
1:A:482:PRO:O	1:A:486:GLU:HG2	2.21	0.40
1:B:291:LYS:HE3	1:B:335:ASP:O	2.20	0.40
1:B:438:GLN:HA	1:B:441:GLU:CD	2.47	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:592:ARG:NE	1:B:598:TYR:CE1	2.84	0.40
1:B:592:ARG:HE	1:B:598:TYR:HE1	1.60	0.40
1:C:494:ASN:HD21	1:C:593:ASP:H	1.69	0.40
1:C:575:TYR:CD1	1:C:575:TYR:N	2.89	0.40
1:C:641:GLY:O	1:C:701:VAL:HG12	2.21	0.40
1:C:667:SER:N	1:C:675:PHE:O	2.52	0.40
1:D:590:LEU:HD23	1:D:590:LEU:C	2.46	0.40
1:E:233:TYR:HD2	1:E:243:ILE:CD1	2.33	0.40
1:E:273:LYS:C	1:E:359:ARG:HH11	2.28	0.40
1:E:583:LEU:HA	1:E:583:LEU:HD23	1.87	0.40
1:F:251:ALA:HA	1:F:256:VAL:CG2	2.50	0.40
1:F:480:VAL:O	1:F:484:ILE:HD12	2.20	0.40
1:F:648:ASP:C	1:F:650:GLU:H	2.29	0.40
1:G:558:THR:HG22	1:G:587:MET:HA	2.02	0.40
2:H:122:LYS:N	2:H:128:VAL:O	2.49	0.40
2:H:302:PRO:HD3	2:H:385:PRO:HA	2.02	0.40
2:H:480:SER:HA	2:H:590:ARG:NH1	2.35	0.40
2:H:513:TYR:CD1	2:H:519:LEU:HD22	2.56	0.40
2:H:627:GLY:C	2:H:628:ARG:HG3	2.46	0.40
2:H:627:GLY:HA3	2:H:664:ARG:O	2.21	0.40
2:H:722:GLY:HA2	2:H:736:PHE:CZ	2.56	0.40
2:H:752:ARG:O	2:H:755:VAL:HG22	2.21	0.40
2:I:765:PHE:O	2:I:769:GLN:HG2	2.22	0.40
1:A:192:TYR:CD2	1:A:192:TYR:C	2.99	0.40
1:A:237:GLU:HB2	1:A:242:ARG:O	2.20	0.40
1:A:267:GLU:HG2	1:A:268:ASN:N	2.36	0.40
1:A:492:ILE:CD1	1:A:502:GLU:HB2	2.52	0.40
1:B:199:LYS:C	1:B:200:ARG:HD3	2.46	0.40
1:B:238:LYS:NZ	1:B:254:PRO:CA	2.80	0.40
1:B:404:ILE:HD12	1:B:404:ILE:HG23	1.90	0.40
1:C:405:LEU:HD21	1:C:411:TYR:CB	2.51	0.40
1:C:434:MET:O	1:C:434:MET:SD	2.79	0.40
1:C:472:ASP:OD1	1:C:473:THR:N	2.54	0.40
1:C:635:ILE:O	1:C:637:LYS:N	2.54	0.40
1:D:496:LYS:NZ	1:D:497:ASP:OD1	2.54	0.40
1:D:611:VAL:HA	1:D:614:GLU:OE2	2.20	0.40
1:E:441:GLU:HA	1:E:444:LYS:HE3	2.03	0.40
1:E:469:VAL:HG13	1:E:469:VAL:O	2.21	0.40
1:E:506:ALA:HB1	1:E:518:LYS:HZ3	1.86	0.40
1:F:381:THR:CG2	1:F:452:THR:HG22	2.52	0.40
1:G:274:ASN:N	1:G:357:THR:O	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:328:ASN:OD1	1:G:329:SER:N	2.55	0.40
2:H:493:ALA:HB1	2:H:497:GLU:HB2	2.04	0.40
2:H:499:LEU:HG	2:H:543:ILE:HG21	2.03	0.40
2:I:63:LEU:HD13	2:I:63:LEU:HA	1.88	0.40
2:I:266:ALA:O	2:I:269:GLU:HG3	2.22	0.40
2:J:477:TYR:O	2:J:593:SER:OG	2.39	0.40
1:A:549:GLU:N	1:A:549:GLU:OE1	2.54	0.40
1:B:199:LYS:HD2	1:B:199:LYS:HA	1.81	0.40
1:B:472:ASP:OD1	1:B:473:THR:N	2.54	0.40
1:B:608:ASP:OD1	1:B:608:ASP:C	2.64	0.40
1:C:242:ARG:HG3	1:C:242:ARG:NH1	2.36	0.40
1:C:557:GLN:CD	1:C:557:GLN:N	2.80	0.40
1:D:227:SER:O	1:D:227:SER:OG	2.36	0.40
1:D:505:ILE:HA	1:D:505:ILE:HD13	1.83	0.40
1:E:226:TRP:O	1:E:234:SER:HA	2.22	0.40
1:E:326:ASN:HB2	1:E:485:GLN:HE21	1.86	0.40
1:E:524:LYS:HZ2	1:E:579:ASP:N	2.18	0.40
1:F:291:LYS:HZ2	1:F:334:ILE:CG2	2.35	0.40
1:F:297:ARG:NH1	1:F:328:ASN:HB3	2.22	0.40
1:F:366:TYR:HE2	1:F:378:LEU:HG	1.87	0.40
1:G:203:LEU:HD13	1:G:203:LEU:HA	1.79	0.40
2:H:173:VAL:O	2:H:177:ILE:HG12	2.21	0.40
2:H:388:ILE:HG23	2:H:389:ASN:N	2.37	0.40
2:H:530:LYS:HB2	2:H:546:ASP:OD2	2.21	0.40
2:I:264:MET:O	2:I:267:ARG:HG2	2.21	0.40
2:J:237:ALA:CB	2:J:240:ALA:HB3	2.51	0.40
2:J:282:SER:HB3	2:J:513:TYR:OH	2.21	0.40
1:A:238:LYS:HZ3	1:A:254:PRO:HA	1.83	0.40
1:C:238:LYS:HD2	1:C:254:PRO:HA	2.02	0.40
1:C:366:TYR:HE2	1:C:378:LEU:HG	1.86	0.40
1:C:698:VAL:O	1:C:726:ILE:HB	2.21	0.40
1:D:228:THR:HG23	1:D:235:ASP:OD1	2.21	0.40
1:D:386:GLY:O	1:D:449:ARG:NH1	2.55	0.40
1:D:455:VAL:O	1:D:455:VAL:HG13	2.22	0.40
1:E:406:ALA:HB3	1:E:409:ASN:HD22	1.86	0.40
1:E:551:ASP:HB2	1:E:592:ARG:CG	2.51	0.40
1:F:521:MET:O	1:F:583:LEU:HD23	2.20	0.40
1:F:587:MET:HE3	1:F:587:MET:HB2	1.95	0.40
1:F:696:VAL:O	1:F:728:SER:HA	2.22	0.40
1:G:197:LYS:HB3	1:G:198:ASN:H	1.73	0.40
2:H:602:ILE:HD11	2:H:680:ASP:CG	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:716:ASP:OD1	2:H:716:ASP:N	2.54	0.40
2:I:48:VAL:O	2:I:48:VAL:HG13	2.22	0.40
2:I:467:ILE:H	2:I:467:ILE:HD12	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	523/759 (69%)	480 (92%)	39 (8%)	4 (1%)	16	52
1	B	523/759 (69%)	480 (92%)	42 (8%)	1 (0%)	43	77
1	C	523/759 (69%)	478 (91%)	44 (8%)	1 (0%)	43	77
1	D	522/759 (69%)	474 (91%)	45 (9%)	3 (1%)	21	58
1	E	523/759 (69%)	473 (90%)	49 (9%)	1 (0%)	43	77
1	F	523/759 (69%)	471 (90%)	50 (10%)	2 (0%)	30	66
1	G	523/759 (69%)	479 (92%)	42 (8%)	2 (0%)	30	66
2	H	695/809 (86%)	638 (92%)	52 (8%)	5 (1%)	18	54
2	I	700/809 (86%)	649 (93%)	51 (7%)	0	100	100
2	J	649/809 (80%)	604 (93%)	44 (7%)	1 (0%)	43	77
All	All	5704/7740 (74%)	5226 (92%)	458 (8%)	20 (0%)	31	66

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	198	ASN
1	B	198	ASN
1	C	198	ASN
1	D	198	ASN

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Mol	Chain	Res	Type
1	E	198	ASN
2	H	67	PRO
2	H	90	LYS
2	J	582	LEU
1	A	663	LEU
1	F	199	LYS
2	H	101	LYS
1	A	345	THR
1	D	175	VAL
1	G	199	LYS
2	H	640	ALA
1	A	175	VAL
1	F	633	LYS
1	D	633	LYS
1	G	577	VAL
2	H	639	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	410/683 (60%)	410 (100%)	0	100	100
1	B	415/683 (61%)	414 (100%)	1 (0%)	87	85
1	C	415/683 (61%)	414 (100%)	1 (0%)	87	85
1	D	414/683 (61%)	414 (100%)	0	100	100
1	E	415/683 (61%)	414 (100%)	1 (0%)	87	85
1	F	415/683 (61%)	415 (100%)	0	100	100
1	G	415/683 (61%)	415 (100%)	0	100	100
2	H	544/739 (74%)	543 (100%)	1 (0%)	87	85
2	I	338/739 (46%)	338 (100%)	0	100	100
2	J	274/739 (37%)	274 (100%)	0	100	100
All	All	4055/6998 (58%)	4051 (100%)	4 (0%)	87	88

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	233	TYR
1	C	233	TYR
1	E	233	TYR
2	H	579	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (54) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	557	GLN
1	A	564	ASN
1	A	630	ASN
1	B	246	ASN
1	B	376	ASN
1	B	422	ASN
1	B	458	ASN
1	B	485	GLN
1	B	541	GLN
1	B	553	ASN
1	B	557	GLN
1	B	561	ASN
1	B	565	GLN
1	C	246	ASN
1	C	447	GLN
1	C	499	ASN
1	C	539	ASN
1	C	573	ASN
1	C	705	ASN
1	D	422	ASN
1	D	447	GLN
1	D	553	ASN
1	D	561	ASN
1	D	565	GLN
1	D	602	ASN
1	D	705	ASN
1	E	246	ASN
1	E	326	ASN
1	E	361	ASN
1	E	415	ASN
1	E	485	GLN
1	F	553	ASN
1	F	602	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	709	ASN
1	G	263	HIS
1	G	437	ASN
1	G	616	HIS
1	G	709	ASN
2	H	115	HIS
2	H	117	HIS
2	H	140	ASN
2	H	168	GLN
2	H	417	GLN
2	H	489	ASN
2	H	563	GLN
2	H	611	GLN
2	H	638	ASN
2	H	669	HIS
2	H	690	HIS
2	I	179	ASN
2	I	469	ASN
2	I	588	HIS
2	I	594	ASN
2	J	445	ASN

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	E	1
1	A	1
1	F	1
1	B	1
1	G	1
1	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	517:THR	C	518:LYS	N	1.18
1	A	517:THR	C	518:LYS	N	1.17
1	F	517:THR	C	518:LYS	N	1.14
1	B	517:THR	C	518:LYS	N	1.11
1	G	517:THR	C	518:LYS	N	1.10
1	C	517:THR	C	518:LYS	N	1.09

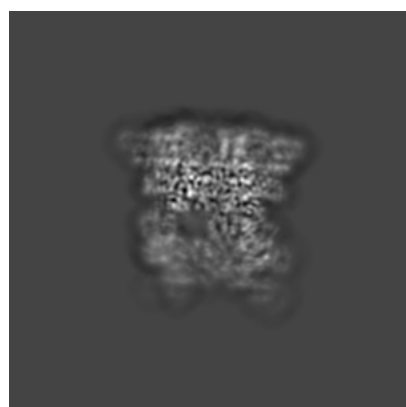
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11524. These allow visual inspection of the internal detail of the map and identification of artifacts.

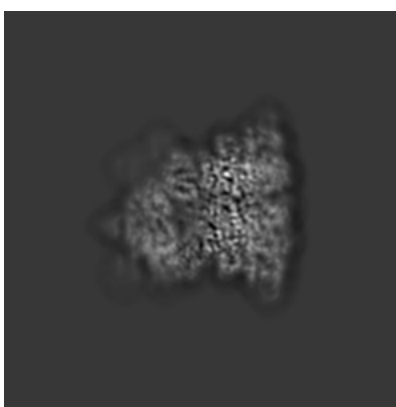
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

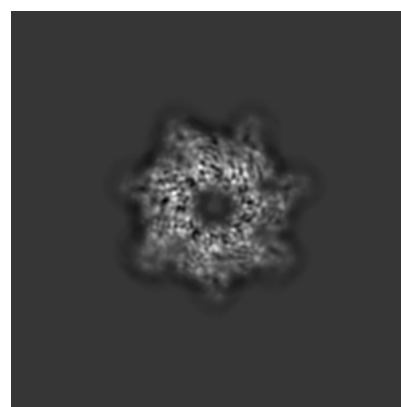
6.1.1 Primary map



X



Y

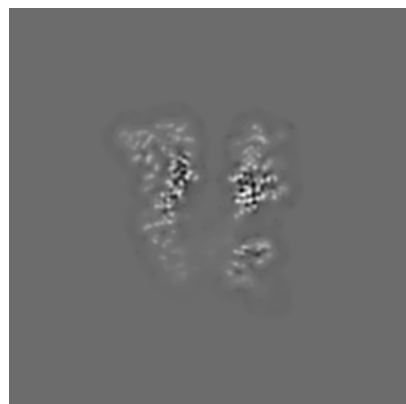


Z

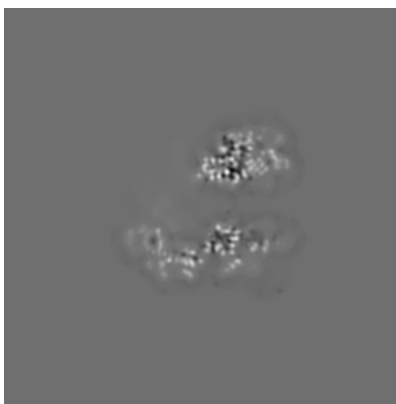
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

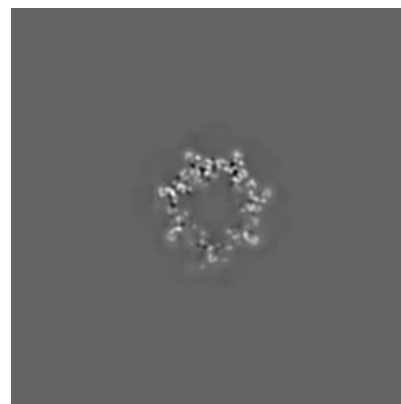
6.2.1 Primary map



X Index: 168



Y Index: 168

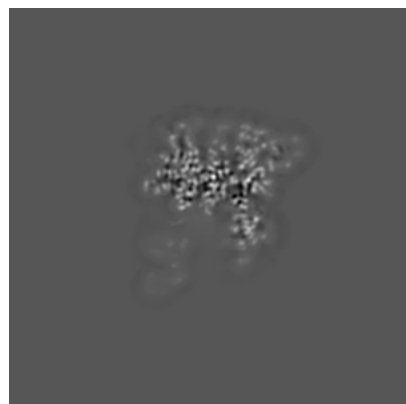


Z Index: 168

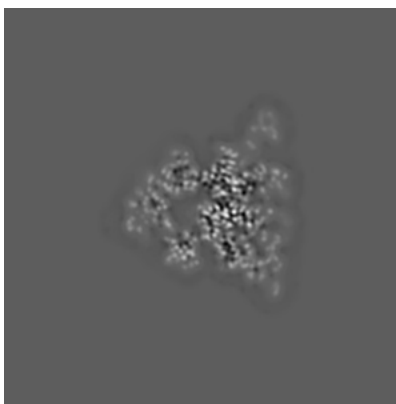
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

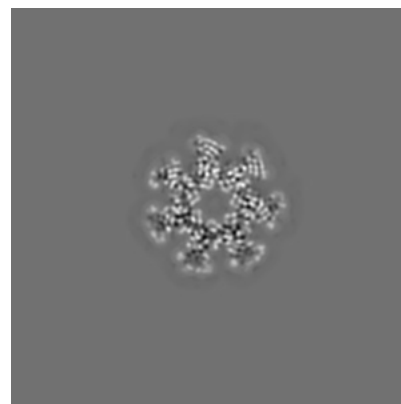
6.3.1 Primary map



X Index: 196



Y Index: 196

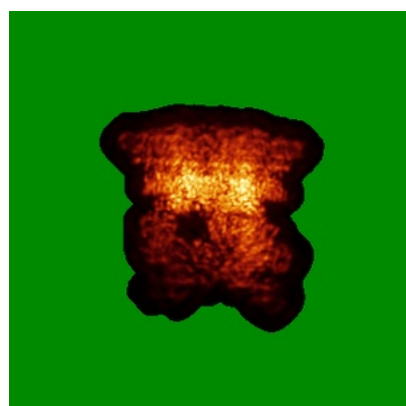


Z Index: 192

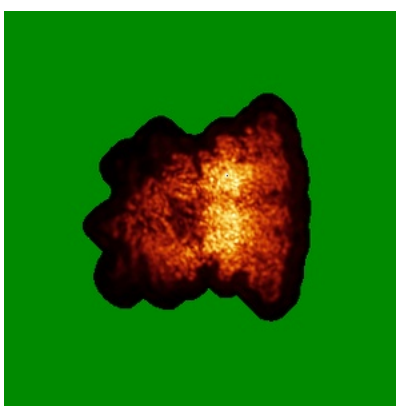
The images above show the largest variance slices of the map in three orthogonal directions.

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

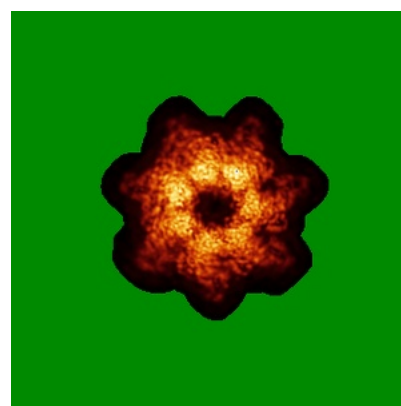
6.4.1 Primary map



X



Y

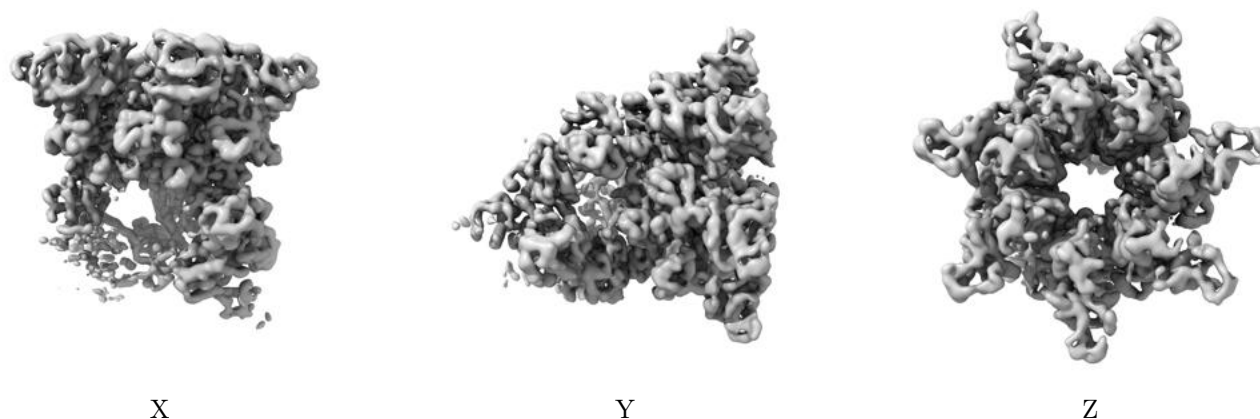


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

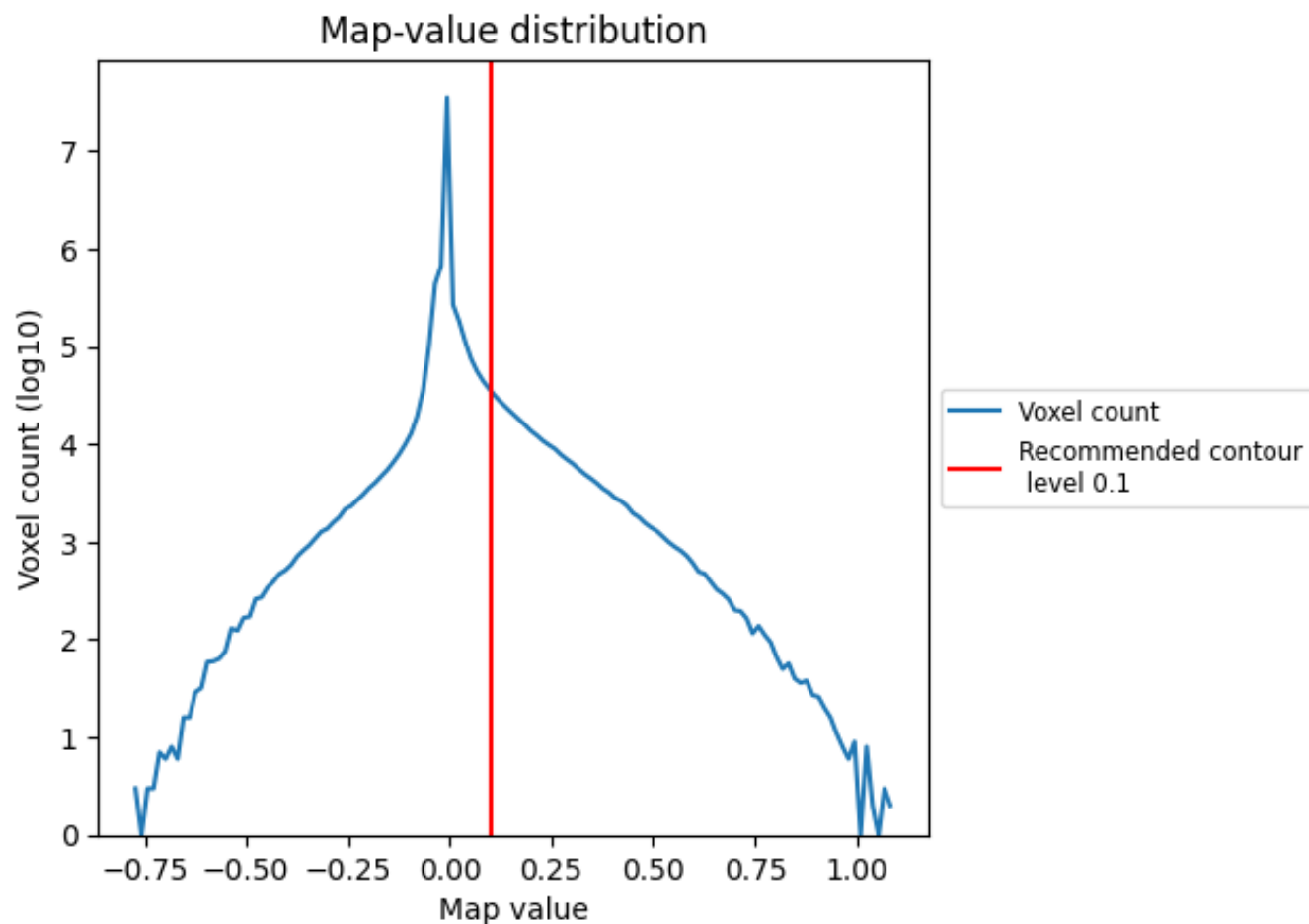
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

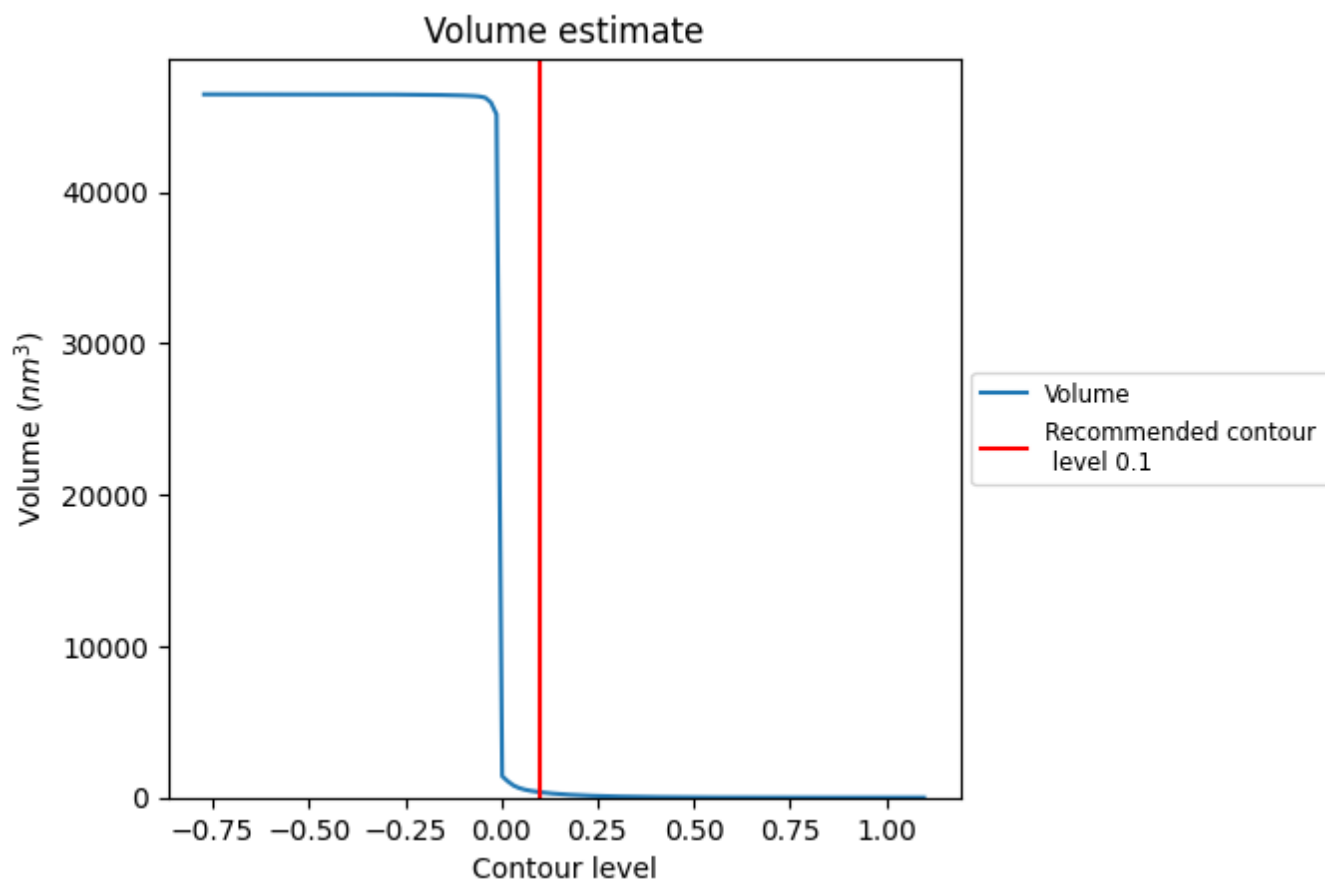
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

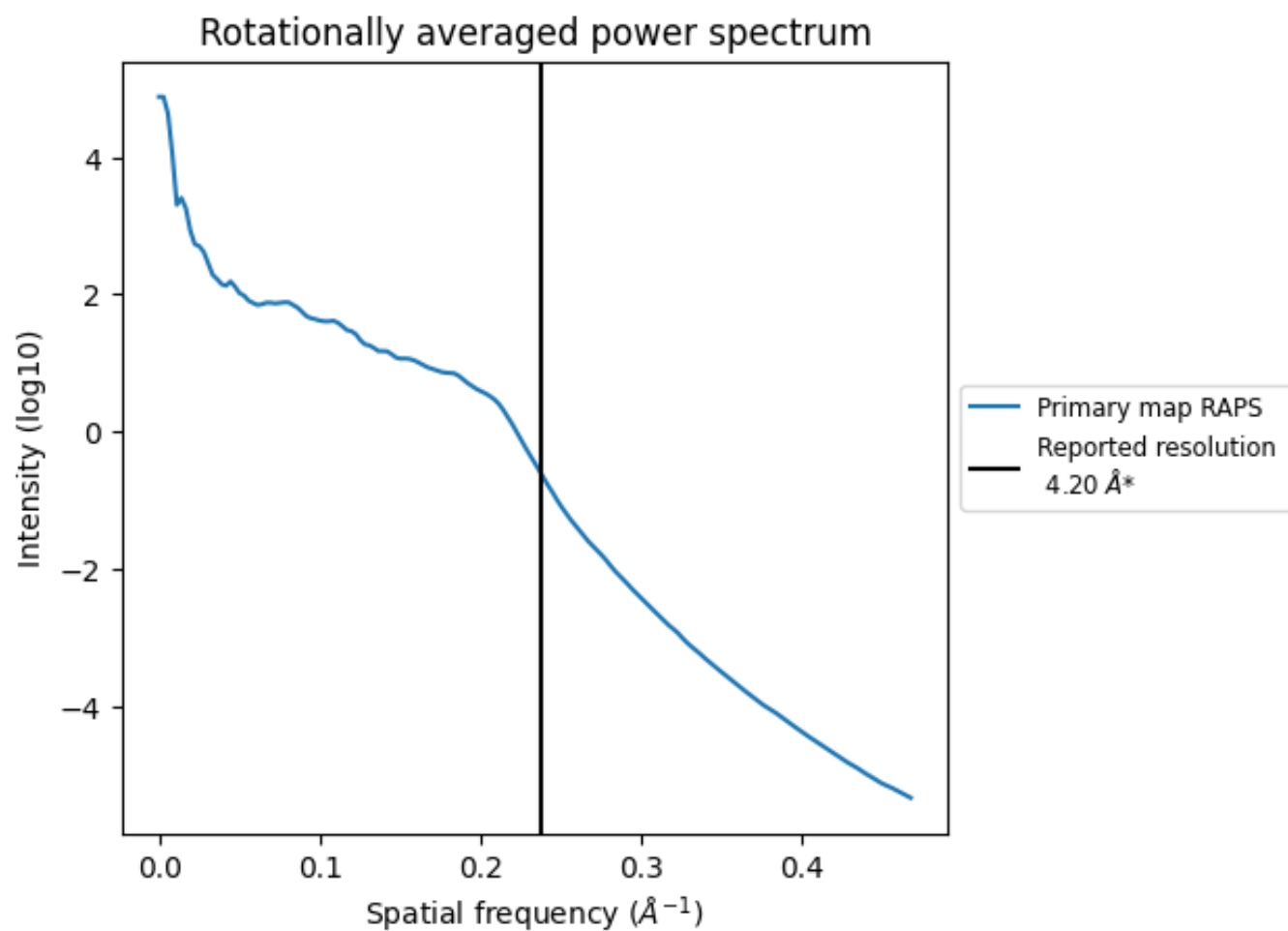
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 357 nm^3 ; this corresponds to an approximate mass of 322 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.238 Å⁻¹

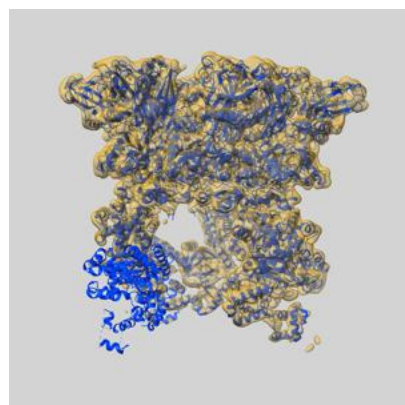
8 Fourier-Shell correlation ⓘ

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

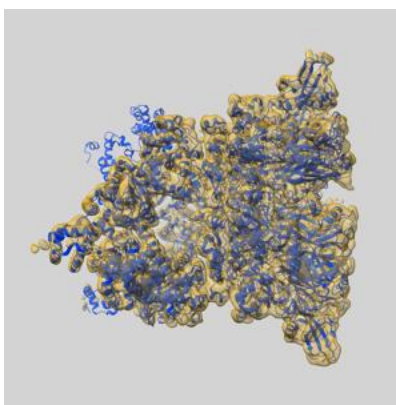
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11524 and PDB model 6ZXL. Per-residue inclusion information can be found in section [3](#) on page [9](#).

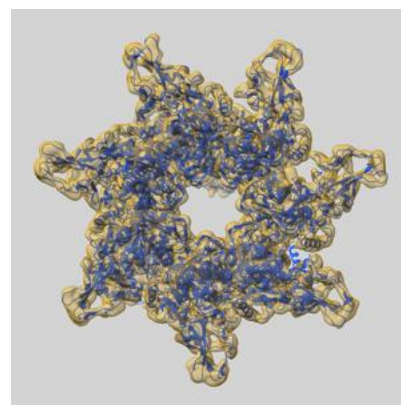
9.1 Map-model overlay [i](#)



X



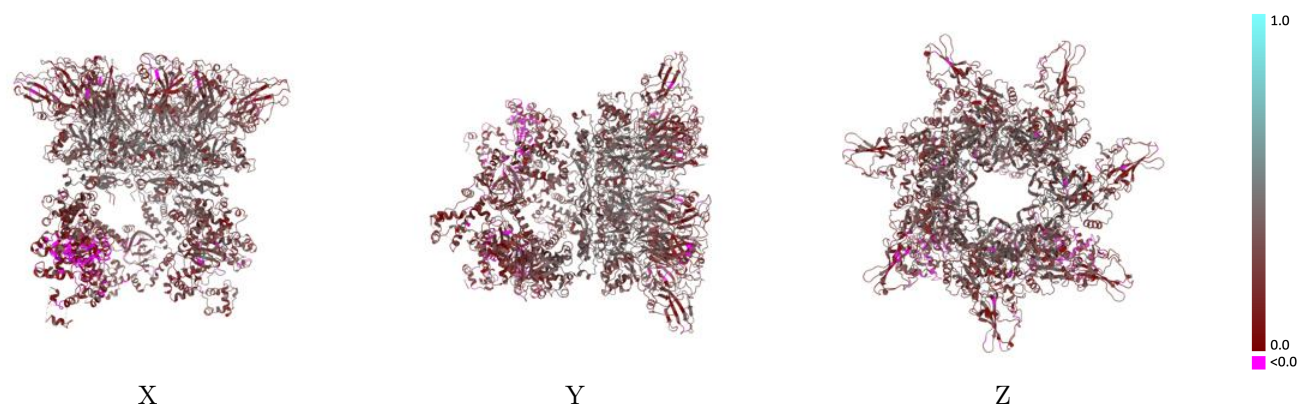
Y



Z

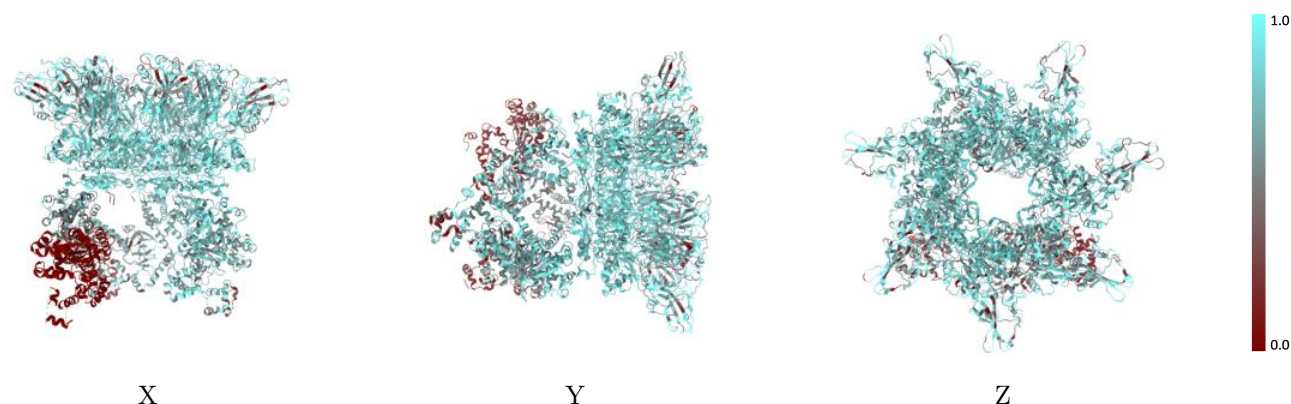
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



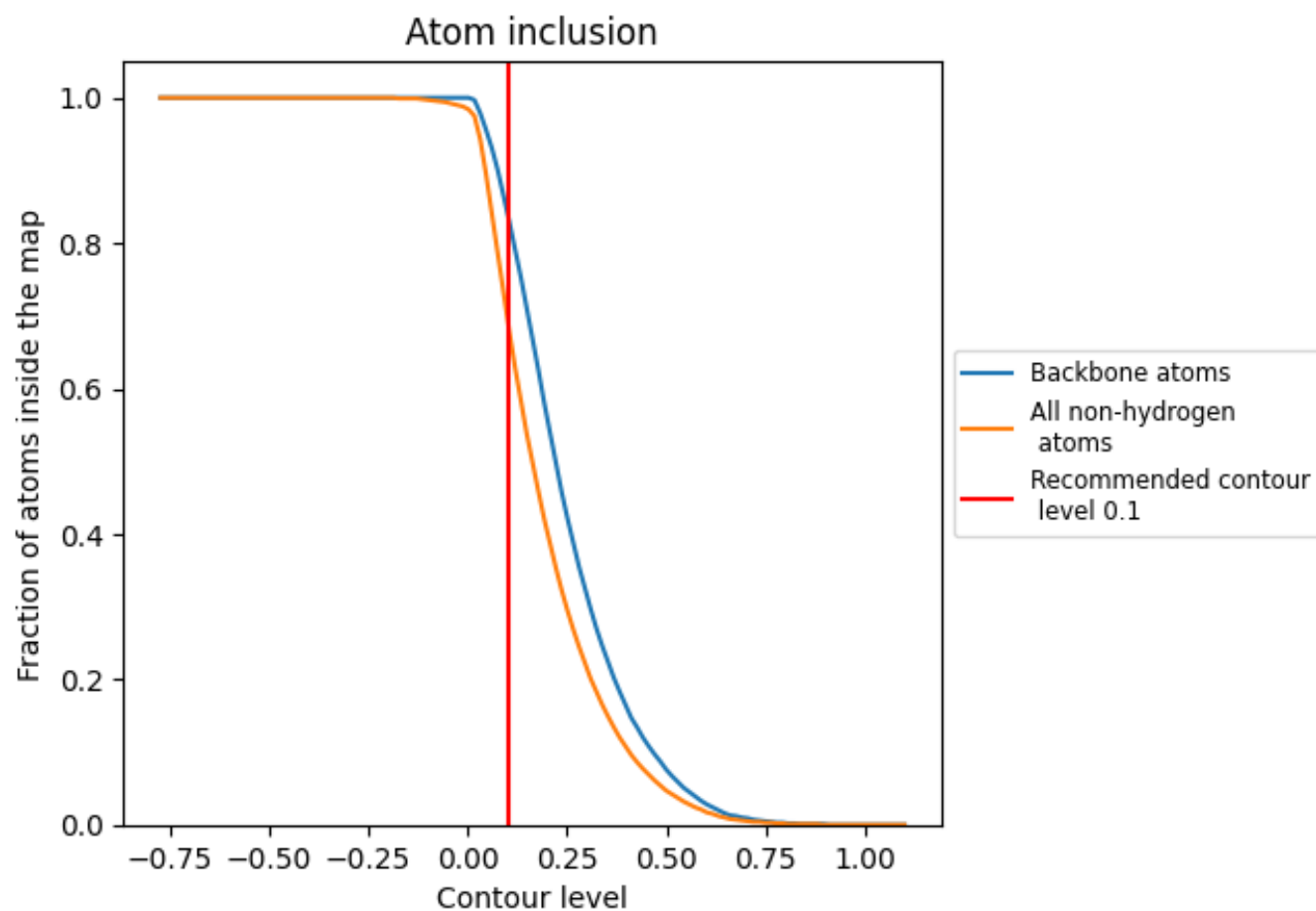
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 70% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6950	0.2870
A	0.7670	0.3190
B	0.7810	0.3230
C	0.7850	0.3270
D	0.7850	0.3280
E	0.7730	0.3160
F	0.7850	0.3240
G	0.7700	0.3130
H	0.7000	0.2540
I	0.5940	0.2320
J	0.2630	0.1620

1.0

0.0

<0.0