



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 02:02 PM UTC

PDB ID : 3J0K / pdb_00003j0k
EMDB ID : EMD-5343
Title : Orientation of RNA polymerase II within the human VP16-Mediator-pol II-TFIIF assembly
Authors : Bernecky, C.; Grob, P.; Ebmeier, C.C.; Nogales, E.; Taatjes, D.J.
Deposited on : 2011-10-04
Resolution : 36.00 Å(reported)
Based on initial model : 1Y1V

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:

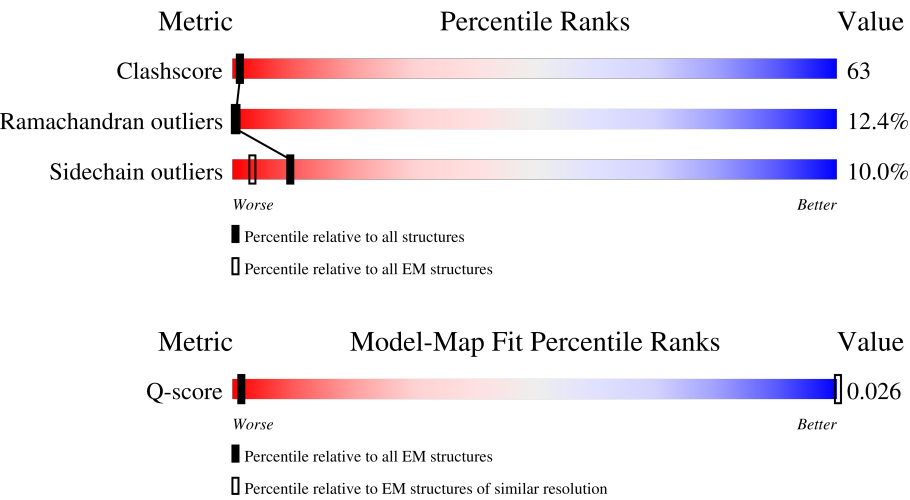
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 36.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	3 (36.00 - 36.44)

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	1455	
2	B	1224	
3	C	268	
4	D	221	

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Mol	Chain	Length	Quality of chain
5	E	215	
6	F	84	
7	G	171	
8	H	146	
9	I	122	
10	J	70	
11	K	120	
12	L	46	

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 31137 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called DNA-directed RNA polymerase II largest subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1426	Total	C	N	O	S	0	0
			11214	7069	1959	2124	62		

- Molecule 2 is a protein called DNA-directed RNA polymerase II 140 kDa polypeptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1112	Total	C	N	O	S	0	0
			8837	5594	1548	1640	55		

- Molecule 3 is a protein called DNA-directed RNA polymerase II 45 kDa polypeptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	266	Total	C	N	O	S	0	0
			2095	1317	348	417	13		

- Molecule 4 is a protein called DNA-directed RNA polymerase II 32 kDa polypeptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	177	Total	C	N	O	S	0	0
			1356	840	241	273	2		

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III 27 kDa polypeptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	214	Total	C	N	O	S	0	0
			1752	1111	309	321	11		

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III 23 kDa polypeptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	84	Total	C	N	O	S	0	0
			679	434	115	127	3		

- Molecule 7 is a protein called DNA-directed RNA polymerase II 19 kDa polypeptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	171	Total	C	N	O	S	0	0
			1340	861	222	249	8		

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III 14.5 kDa polypeptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	133	Total	C	N	O	S	0	0
			1068	673	180	211	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	119	Total	C	N	O	S	0	0
			971	596	179	186	10		

- Molecule 10 is a protein called DNA-directed RNA polymerases I/II/III subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	65	Total	C	N	O	S	0	0
			532	339	93	94	6		

- Molecule 11 is a protein called DNA-directed RNA polymerase II 13.6 kDa polypeptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	114	Total	C	N	O	S	0	0
			919	590	156	171	2		

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III 7.7 kDa polypeptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	46	Total	C	N	O	S	0	0
			364	224	72	64	4		

- Molecule 13 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
13	A	1	Total 1	Mg 1	0

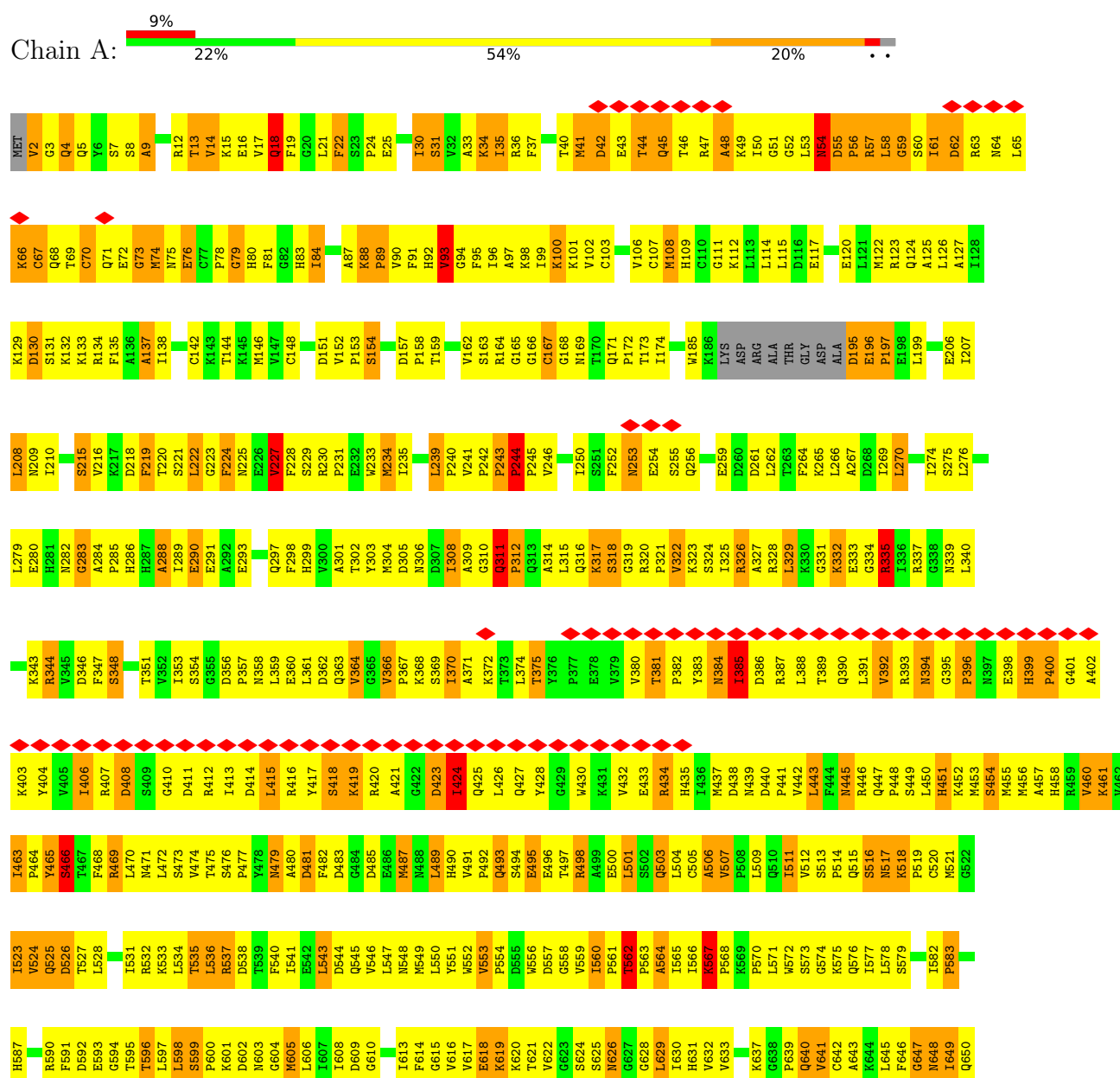
- Molecule 14 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
14	A	3	Total 3	Zn 3	0
14	B	1	Total 1	Zn 1	0
14	C	1	Total 1	Zn 1	0
14	I	2	Total 2	Zn 2	0
14	J	1	Total 1	Zn 1	0
14	L	1	Total 1	Zn 1	0

3 Residue-property plots

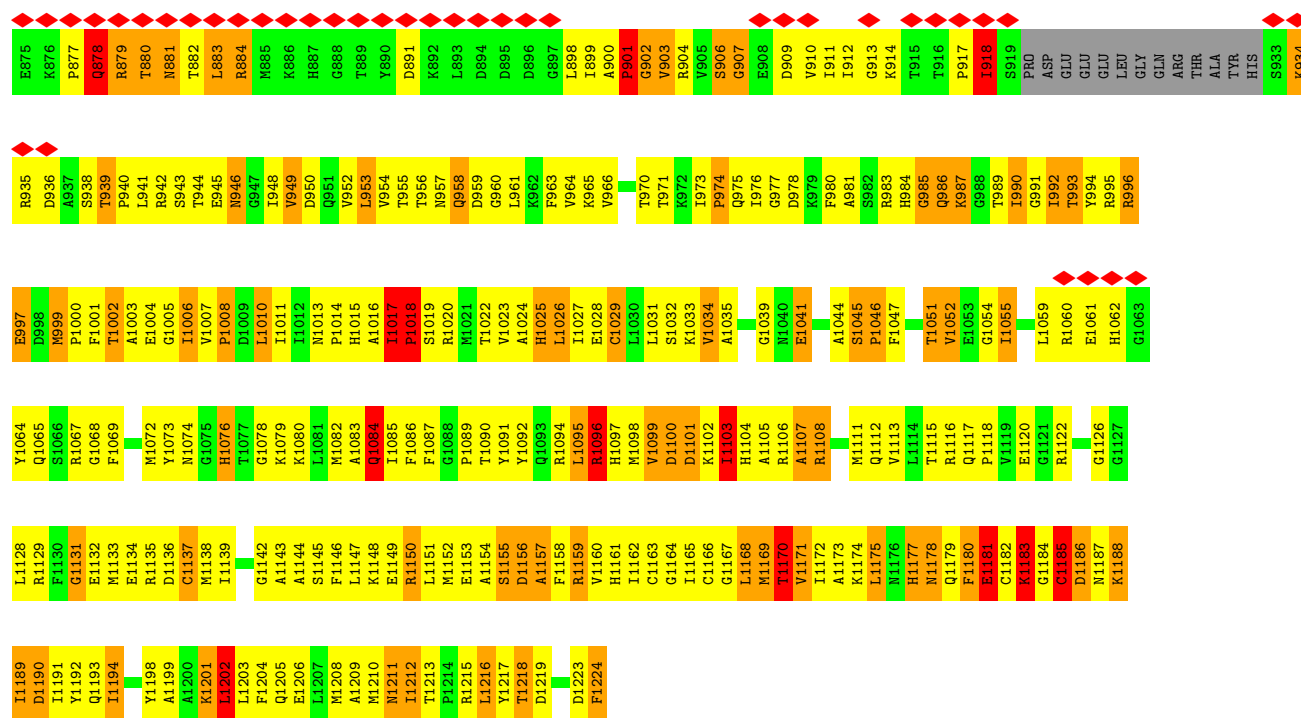
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: DNA-directed RNA polymerase II largest subunit

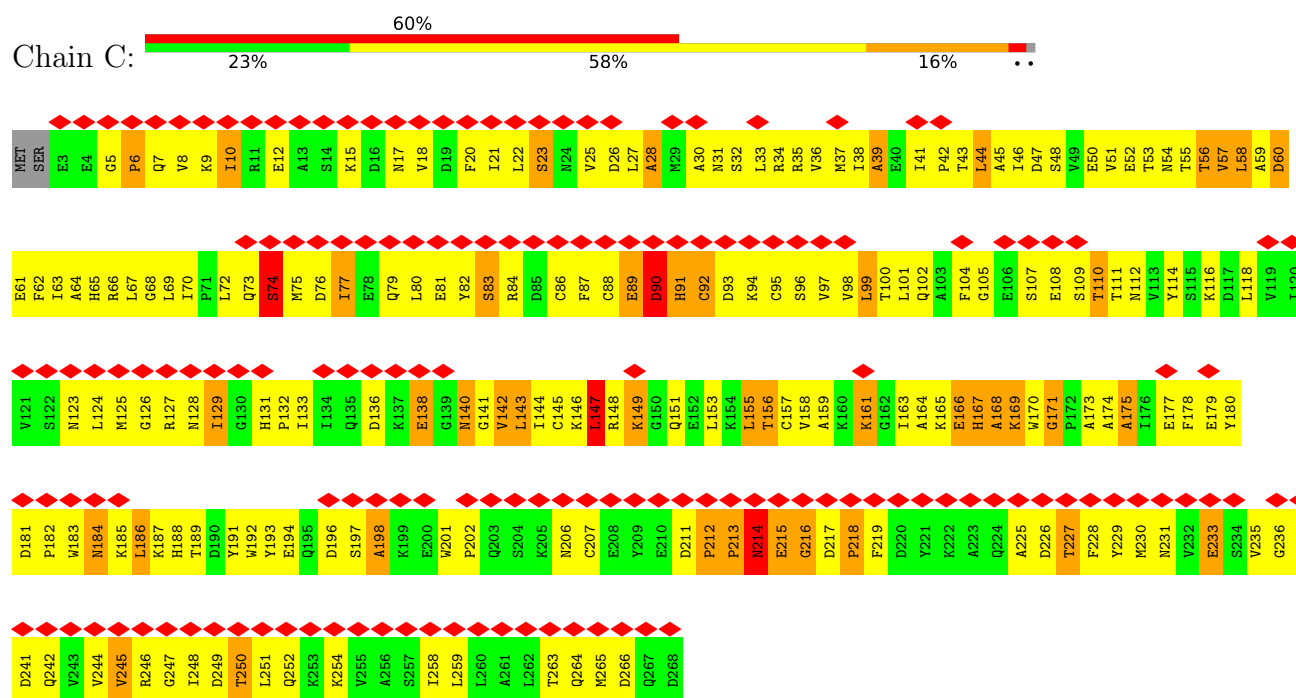




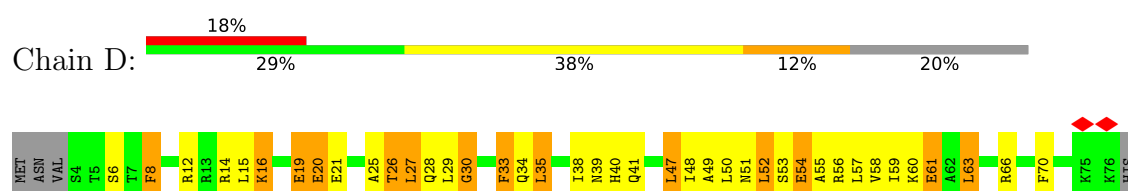
R815	E816	L817	P818	A819	G820	Q821	M822	A823	L824	V825	A826	S827	R828	C829	E830	S831	C832	Y833	N834	M835	E836	D837	S838	M839	L840	N841	N842	F843	L844	S845	L846	D847	R848	G849	R850	F851	R852	S853	L854	F855	F856	R857	S858	T859	M860	D861	Q862	E863	K864	K865	G866	C867	M868	S869	L870	H811	L812	L813	T871	E872	T873	F874																																																																																																																																																																																																																																																																																																																																																																					
A763	S764	T765	T766	L767	L768	P769	D770	H771	N772	Q773	S774	P775	L776	E777	S778	L779	L780	L781	L782	L783	N784	L785	L786	L787	L788	L789	L790	L791	L792	L793	L794	L795	L796	L797	L798	L799	L800	L801	L802	L803	L804	L805	L806	L807	L808	L809	L810	L811	L812	L813	L814	L815	L816	L817	L818	L819	L820	L821																																																																																																																																																																																																																																																																																																																																																																									
L685	L686	L687	L688	L689	L690	L691	L692	L693	L694	L695	L696	L697	L698	L699	L700	L701	L702	L703	L704	L705	L706	L707	L708	L709	L710	L711	L712	L713	L714	L715	L716	L717	L718	L719	L720	L721	L722	L723	L724	L725	L726	L727	L728	L729	L730	L731	L732	L733	L734	L735	L736	L737	L738	L739	L740	L741	L742	L743	L744	L745	L746	L747	L748	L749	L750	L751	L752	L753	L754	L755	L756	L757	L758	L759	L760	L761	L762	L763	L764	L765	L766	L767	L768	L769	L770	L771	L772	L773	L774	L775	L776	L777	L778	L779	L780	L781	L782	L783	L784	L785	L786	L787	L788	L789	L790	L791	L792	L793	L794	L795	L796	L797	L798	L799	L800	L801	L802	L803	L804	L805	L806	L807	L808	L809	L810	L811	L812	L813	L814	L815	L816	L817	L818	L819	L820	L821																																																																																																																																																																																																																																																																																											
K622	E623	L624	K625	L626	T627	T628	D629	A630	C631	R632	V633	V634	R635	L636	L637	S638	L639	L640	E641	D642	D643	E644	S645	L646	L647	H648	K649	L650	L651	L652	L653	L654	L655	L656	L657	L658	L659	L660	L661	L662	A663	T664	E665	L666	Q667	L668	L669	L670	L671	L672	L673	L674	L675	L676	L677	L678	L679	L680	L681	L682	L683	L684	L685	L686	L687	L688	L689	L690	L691	L692	L693	L694	L695	L696	L697	L698	L699	L700	L701	L702	L703	L704	L705	L706	L707	L708	L709	L710	L711	L712	L713	L714	L715	L716	L717	L718	L719	L720	L721	L722	L723	L724	L725	L726	L727	L728	L729	L730	L731	L732	L733	L734	L735	L736	L737	L738	L739	L740	L741	L742	L743	L744	L745	L746	L747	L748	L749	L750	L751	L752	L753	L754	L755	L756	L757	L758	L759	L760	L761	L762	L763	L764	L765	L766	L767	L768	L769	L770	L771	L772	L773	L774	L775	L776	L777	L778	L779	L780	L781	L782	L783	L784	L785	L786	L787	L788	L789	L790	L791	L792	L793	L794	L795	L796	L797	L798	L799	L800	L801	L802	L803	L804	L805	L806	L807	L808	L809	L810	L811	L812	L813	L814	L815	L816	L817	L818	L819	L820	L821																																																																																																																																																																																																																												
G562	N563	E564	P565	L566	E567	D568	Y569	V570	P571	H572	Q573	S574	P575	D576	A577	V578	V579	F580	F581	V582	N583	G584	V585	W586	H587	G588	V589	H590	H591	N592	P593	A594	R595	L596	N597	E598	T599	L600	R601	T602	L603	R604	R605	R606	G607	D608	L609	N610	P611	E612	S613	L614	L615	L616	L617	L618	L619	L620	E621	L622	L623	L624	L625	L626	L627	L628	L629	L630	L631	L632	L633	L634	L635	L636	L637	L638	L639	L640	L641	L642	L643	L644	L645	L646	L647	L648	L649	L650	L651	L652	L653	L654	L655	L656	L657	L658	L659	L660	L661	L662	L663	L664	L665	L666	L667	L668	L669	L670	L671	L672	L673	L674	L675	L676	L677	L678	L679	L680	L681	L682	L683	L684	L685	L686	L687	L688	L689	L690	L691	L692	L693	L694	L695	L696	L697	L698	L699	L700	L701	L702	L703	L704	L705	L706	L707	L708	L709	L710	L711	L712	L713	L714	L715	L716	L717	L718	L719	L720	L721	L722	L723	L724	L725	L726	L727	L728	L729	L730	L731	L732	L733	L734	L735	L736	L737	L738	L739	L740	L741	L742	L743	L744	L745	L746	L747	L748	L749	L750	L751	L752	L753	L754	L755	L756	L757	L758	L759	L760	L761	L762	L763	L764	L765	L766	L767	L768	L769	L770	L771	L772	L773	L774	L775	L776	L777	L778	L779	L780	L781	L782	L783	L784	L785	L786	L787	L788	L789	L790	L791	L792	L793	L794	L795	L796	L797	L798	L799	L800	L801	L802	L803	L804	L805	L806	L807	L808	L809	L810	L811	L812	L813	L814	L815	L816	L817	L818	L819	L820	L821																																																																																																																																																																
Q433	R434	T435	V436	E437	ALA	HIS	ASP	PHE	ASN	MET	LYS	L446	A447	L448	L449	L450	L451	L452	L453	L454	L455	L456	L457	L458	L459	L460	L461	L462	L463	L464	L465	L466	L467	L468	L469	L470	L471	L472	L473	L474	L475	L476	L477	L478	L479	L480	L481	L482	L483	L484	L485	L486	L487	L488	L489	L490	L491	L492	L493	L494	L495	L496	L497	L498	L499	L500	L501	L502	L503	L504	L505	L506	L507	L508	L509	L510	L511	L512	L513	L514	L515	L516	L517	L518	L519	L520	L521	L522	L523	L524	L525	L526	L527	L528	L529	L530	L531	L532	L533	L534	L535	L536	L537	L538	L539	L540	L541	L542	L543	L544	L545	L546	L547	L548	L549	L550	L551	L552	L553	L554	L555	L556	L557	L558	L559	L560	L561	L562	L563	L564	L565	L566	L567	L568	L569	L570	L571	L572	L573	L574	L575	L576	L577	L578	L579	L580	L581	L582	L583	L584	L585	L586	L587	L588	L589	L590	L591	L592	L593	L594	L595	L596	L597	L598	L599	L600	L601	L602	L603	L604	L605	L606	L607	L608	L609	L610	L611	L612	L613	L614	L615	L616	L617	L618	L619	L620	L621	L622	L623	L624	L625	L626	L627	L628	L629	L630	L631	L632	L633	L634	L635	L636	L637	L638	L639	L640	L641	L642	L643	L644	L645	L646	L647	L648	L649	L650	L651	L652	L653	L654	L655	L656	L657	L658	L659	L660	L661	L662	L663	L664	L665	L666	L667	L668	L669	L670	L671	L672	L673	L674	L675	L676	L677	L678	L679	L680	L681	L682	L683	L684	L685	L686	L687	L688	L689	L690	L691	L692	L693	L694	L695	L696	L697	L698	L699	L700	L701	L702	L703	L704	L705	L706	L707	L708	L709	L710	L711	L712	L713	L714	L715	L716	L717	L718	L719	L720	L721	L722	L723	L724	L725	L726	L727	L728	L729	L730	L731	L732	L733	L734	L735	L736	L737	L738	L739	L740	L741	L742	L743	L744	L745	L746	L747	L748	L749	L750	L751	L752	L753	L754	L755	L756	L757	L758	L759	L760	L761	L762	L763	L764	L765	L766	L767	L768	L769	L770	L771	L772	L773	L774	L775	L776	L777	L778	L779	L780	L781	L782	L783	L784	L785	L786	L787	L788	L789	L790	L791	L792	L793	L794	L795	L796	L797	L798	L799	L800	L801	L802	L803	L804	L805	L806	L807	L808	L809	L810	L811	L812	L813	L814	L815	L816	L817	L818	L819	L820	L821																																
E368	G369	F370	E371	S372	R373	K374	A375	F376	F377	L378	G379	V380	M381	L382	N383	R384	L385	L386	L387	C388	L389	D390	D391	R392	K393	D394	Q395	D396	F401	G402	K403	K404	R405	L406	D407	L408	A409	G410	P411	L412	L413	A414	F417	K418	T419	L420	F421	L424	T425	K426	D427	L428	F429	R430	Y431	N432	E368	G369	F370	E371	S372	R373	K374	A375	F376	F377	L378	G379	V380	M381	L382	N383	R384	L385	L386	L387	C388	L389	D390	D391	R392	K393	D394	Q395	D396	F401	G402	K403	K404	R405	L406	D407	L408	A409	G410	P411	L412	L413	A414	F417	K418	T419	L420	F421	L424	T425	K426	D427	L428	F429	R430	Y431	N432	E368	G369	F370	E371	S372	R373	K374	A375	F376	F377	L378	G379	V380	M381	L382	N383	R384	L385	L386	L387	C388	L389	D390	D391	R392	K393	D394	Q395	D396	F401	G402	K403	K404	R405	L406	D407	L408	A409	G410	P411	L412	L413	A414	F417	K418	T419	L420	F421	L424	T425	K426	D427	L428	F429	R430	Y431	N432	E368	G369	F370	E371	S372	R373	K374	A375	F376	F377	L378	G379	V380	M381	L382	N383	R384	L385	L386	L387	C388	L389	D390	D391	R392	K393	D394	Q395	D396	F401	G402	K403	K404	R405	L406	D407	L408	A409	G410	P411	L412	L413	A414	F417	K418	T419	L420	F421	L424	T425	K426	D427	L428	F429	R430	Y431	N432	E368	G369	F370	E371	S372	R373	K374	A375	F376	F377	L378	G379	V380	M381	L382	N383	R384	L385	L386	L387	C388	L389	D390	D391	R392	K393	D394	Q395	D396	F401	G402	K403	K404	R405	L406	D407	L408	A409	G410	P411	L412	L413	A414	F417	K418	T419	L420	F421	L424	T425	K426	D427	L428	F429	R430	Y431	N432	E368	G369	F370	E371	S372	R373	K374	A375	F376	F377	L378	G379	V380	M381	L382	N383	R384	L385	L386	L387	C388	L389	D390	D391	R392	K393	D394	Q395	D396	F401	G402	K403	K404	R405	L406	D407	L408	A409	G410	P411	L412	L413	A414	F417	K418	T419	L420	F421	L424	T425	K426	D427	L428	F429	R430	Y431	N432	E368	G369	F370	E371	S372	R373	K374	A375	F376	F377	L378	G379	V380	M381	L382	N383	R384	L385	L386	L387	C388	L389	D390	D391	R392	K393	D394	Q395	D396	F401	G402	K403	K404	R405	L406	D407	L408	A409	G410	P411	L412	L413	A414	F417	K418	T419	L420	F421	L424	T425	K426	D427	L428	F429	R430	Y431	N432	E368	G369	F370	E371	S372	R373	K374	A375	F376	F377	L378	G379	V380	M381	L382	N383	R384	L385	L386	L387	C388</

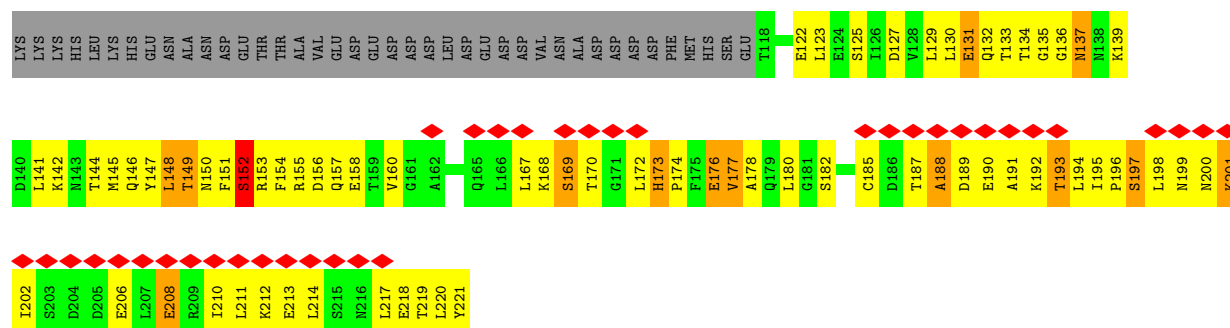


• Molecule 3: DNA-directed RNA polymerase II 45 kDa polypeptide

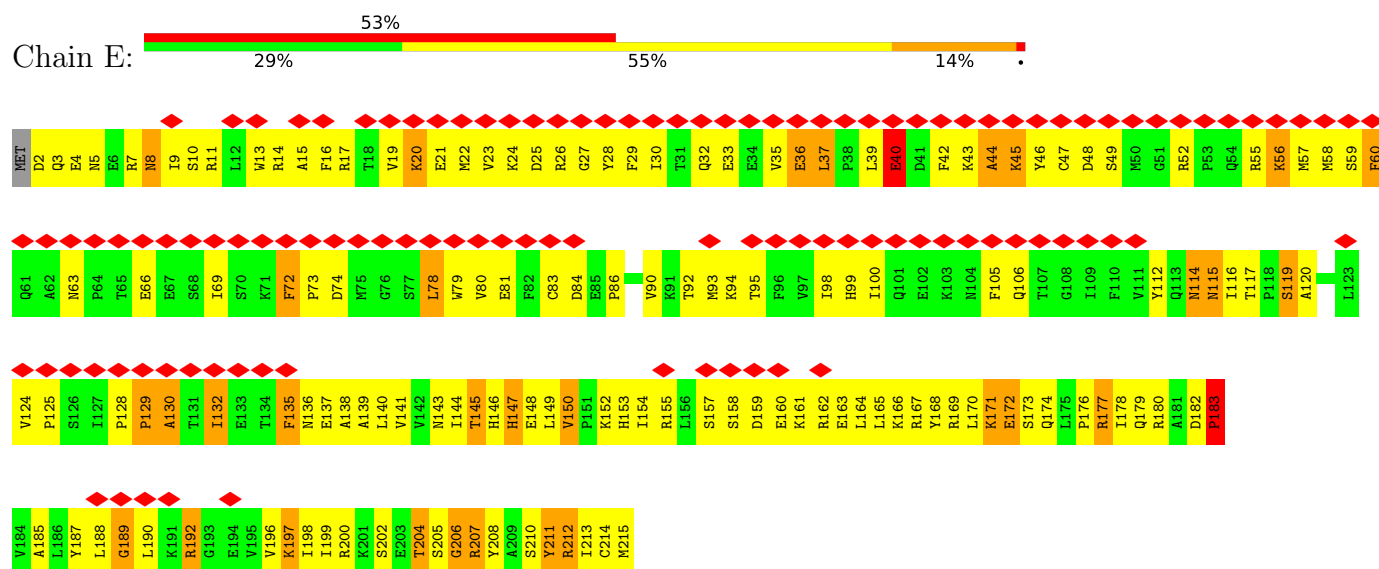


• Molecule 4: DNA-directed RNA polymerase II 32 kDa polypeptide

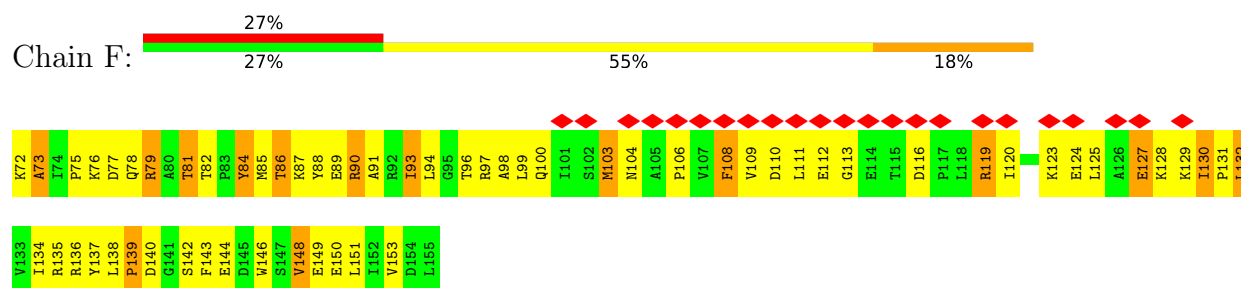




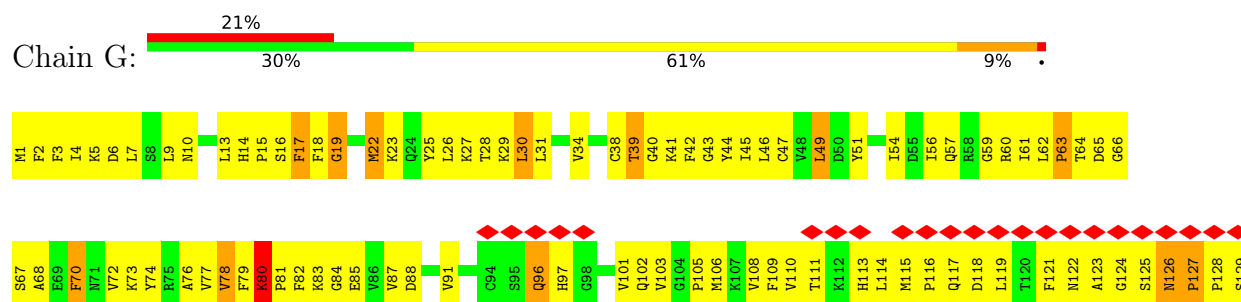
• Molecule 5: DNA-directed RNA polymerases I, II, and III 27 kDa polypeptide

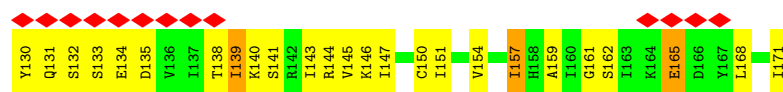


• Molecule 6: DNA-directed RNA polymerases I, II, and III 23 kDa polypeptide

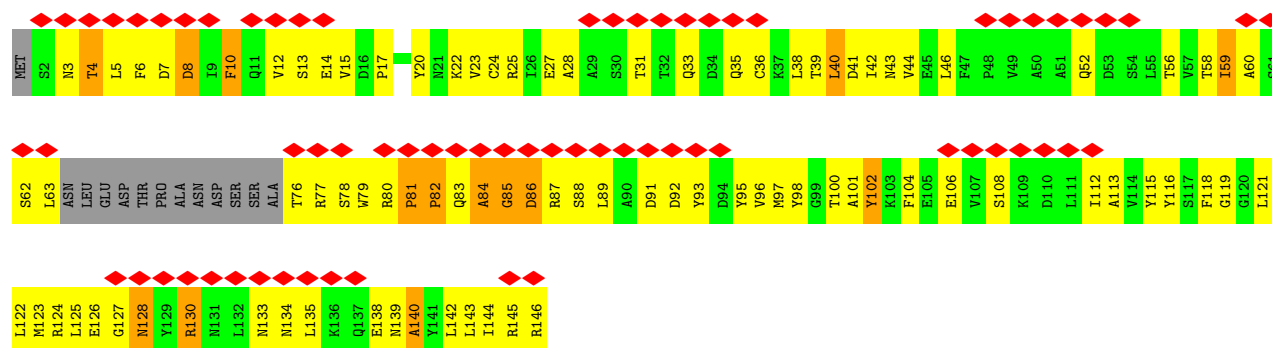


• Molecule 7: DNA-directed RNA polymerase II 19 kDa polypeptide

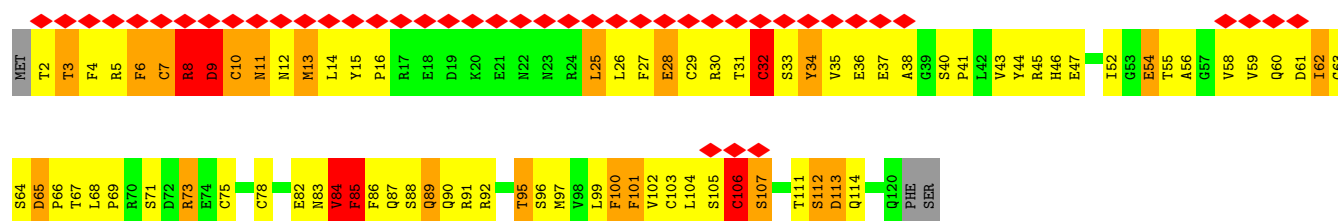




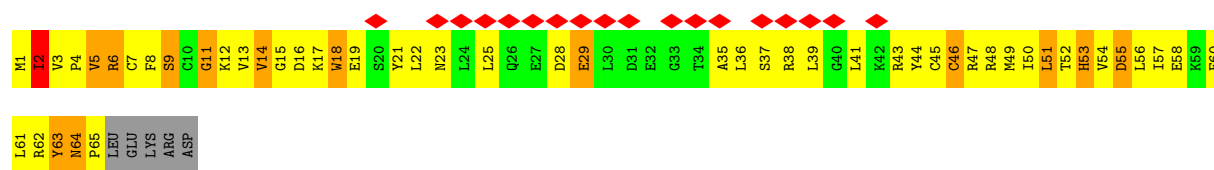
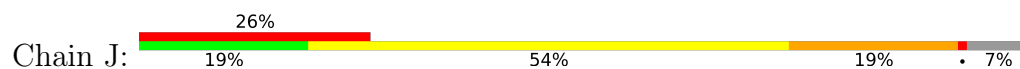
- Molecule 8: DNA-directed RNA polymerases I, II, and III 14.5 kDa polypeptide



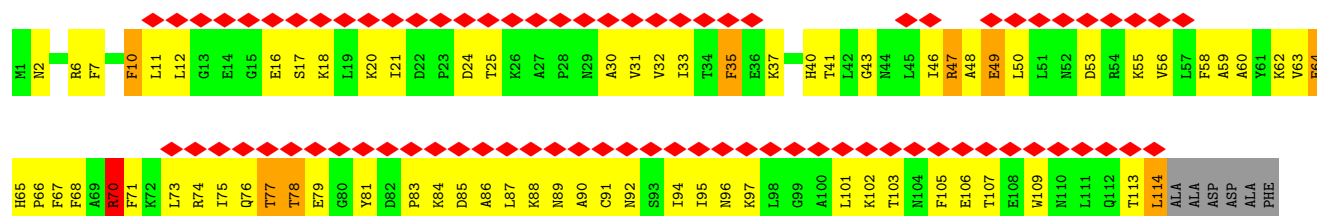
- Molecule 9: DNA-directed RNA polymerase II subunit 9

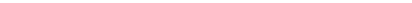


- Molecule 10: DNA-directed RNA polymerases I/II/III subunit 10



- Molecule 11: DNA-directed RNA polymerase II 13.6 kDa polypeptide



- Chain L:  9% 63% 26%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	3146	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	each micrograph	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	15	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	29000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	0.073	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0284	Depositor
Map size ($\text{\AA}$)	690.69, 690.69, 690.69	wwPDB
Map dimensions	161, 161, 161	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing ($\text{\AA}$)	4.29, 4.29, 4.29	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.61	3/11417 (0.0%)	1.16	113/15442 (0.7%)
2	B	0.62	8/9009 (0.1%)	1.15	69/12146 (0.6%)
3	C	0.58	0/2133	1.10	17/2891 (0.6%)
4	D	0.48	0/1365	1.05	15/1837 (0.8%)
5	E	0.54	0/1788	1.03	13/2406 (0.5%)
6	F	0.62	0/691	1.17	5/933 (0.5%)
7	G	0.57	0/1368	1.12	11/1844 (0.6%)
8	H	0.43	0/1086	0.98	5/1470 (0.3%)
9	I	0.52	0/989	1.16	9/1331 (0.7%)
10	J	0.56	0/541	0.99	2/727 (0.3%)
11	K	0.53	0/937	0.96	1/1265 (0.1%)
12	L	0.66	0/366	0.99	1/485 (0.2%)
All	All	0.59	11/31690 (0.0%)	1.13	261/42777 (0.6%)

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	B	0	2

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	467	GLY	C-O	-14.32	1.04	1.23
2	B	510	LYS	CA-C	8.04	1.62	1.52
2	B	510	LYS	N-CA	6.04	1.54	1.46
1	A	195	ASP	CA-C	5.83	1.65	1.52
1	A	195	ASP	N-CA	5.83	1.57	1.46
1	A	196	GLU	N-CA	5.65	1.54	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	509	ALA	CA-CB	-5.50	1.44	1.53
2	B	467	GLY	CA-C	5.49	1.59	1.51
2	B	468	GLU	CB-CG	5.25	1.68	1.52
2	B	469	GLN	N-CA	5.13	1.52	1.46
2	B	510	LYS	CB-CG	5.05	1.67	1.52

All (261) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	510	LYS	CA-C-N	24.71	145.39	119.19
2	B	510	LYS	C-N-CA	24.71	145.39	119.19
2	B	1185	CYS	N-CA-C	-12.66	97.83	113.02
2	B	296	GLU	N-CA-C	-11.29	96.76	112.45
4	D	26	THR	N-CA-C	-11.02	97.71	112.26
1	A	1262	LYS	N-CA-C	-10.04	100.33	111.28
1	A	243	PRO	CA-C-N	10.01	130.69	120.38
1	A	243	PRO	C-N-CA	10.01	130.69	120.38
1	A	344	ARG	N-CA-C	-9.88	95.90	110.52
2	B	512	ARG	N-CA-C	-9.86	100.36	112.38
9	I	28	GLU	N-CA-C	9.20	120.06	107.73
7	G	19	GLY	CA-C-N	9.11	128.84	119.64
7	G	19	GLY	C-N-CA	9.11	128.84	119.64
1	A	195	ASP	N-CA-C	9.03	136.28	111.00
1	A	227	VAL	N-CA-C	9.02	119.20	111.90
7	G	80	LYS	CA-C-N	8.81	129.35	119.92
7	G	80	LYS	C-N-CA	8.81	129.35	119.92
2	B	213	ILE	N-CA-C	8.75	121.18	108.58
1	A	466	SER	N-CA-C	8.70	123.21	113.21
1	A	1310	GLY	N-CA-C	-8.53	96.88	110.18
1	A	567	LYS	CA-C-N	-8.18	109.62	119.84
1	A	567	LYS	C-N-CA	-8.18	109.62	119.84
1	A	366	VAL	CA-C-N	-8.15	111.50	120.14
1	A	366	VAL	C-N-CA	-8.15	111.50	120.14
1	A	866	PHE	N-CA-C	-7.96	103.29	113.16
2	B	1052	VAL	N-CA-C	-7.70	102.94	110.72
2	B	468	GLU	N-CA-C	7.66	127.11	110.80
2	B	510	LYS	CB-CA-C	-7.65	95.10	110.17
2	B	681	TRP	N-CA-C	-7.54	101.18	112.04
2	B	1025	HIS	N-CA-C	-7.53	102.76	110.97
2	B	511	PRO	CB-CA-C	-7.49	101.18	112.11
2	B	832	GLY	N-CA-C	-7.49	103.76	115.67
4	D	188	ALA	N-CA-C	-7.47	103.07	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	208	SER	N-CA-C	7.43	121.01	110.23
2	B	508	LEU	CA-C-N	-7.40	107.41	121.54
2	B	508	LEU	C-N-CA	-7.40	107.41	121.54
1	A	1088	GLY	N-CA-C	-7.33	104.71	115.63
9	I	65	ASP	CA-C-N	7.31	126.95	119.56
9	I	65	ASP	C-N-CA	7.31	126.95	119.56
2	B	805	THR	N-CA-C	7.21	120.37	109.41
1	A	173	THR	N-CA-C	-7.18	100.86	110.55
6	F	130	ILE	CA-C-N	7.13	128.75	119.84
6	F	130	ILE	C-N-CA	7.13	128.75	119.84
2	B	1061	GLU	N-CA-C	-7.13	104.71	113.19
7	G	2	PHE	N-CA-C	-7.05	100.04	110.48
1	A	227	VAL	CB-CA-C	-6.99	104.59	111.30
2	B	475	SER	N-CA-C	6.99	119.54	110.53
8	H	80	ARG	CA-C-N	6.94	127.52	120.38
8	H	80	ARG	C-N-CA	6.94	127.52	120.38
1	A	769	SER	N-CA-C	6.92	119.03	108.52
2	B	112	LEU	N-CA-C	6.90	119.64	110.53
1	A	927	VAL	N-CA-C	-6.90	104.27	111.58
9	I	85	PHE	N-CA-C	6.90	119.87	110.35
10	J	5	VAL	N-CA-C	-6.88	99.80	108.89
1	A	288	ALA	N-CA-C	-6.86	103.31	113.61
3	C	193	TYR	N-CA-C	6.85	117.53	108.07
1	A	22	PHE	N-CA-C	6.83	118.98	109.15
1	A	452	LYS	N-CA-C	-6.81	103.86	111.28
4	D	38	ILE	N-CA-C	6.81	118.39	108.58
1	A	778	GLY	N-CA-C	-6.78	103.68	113.86
2	B	835	GLN	N-CA-C	6.78	119.06	110.24
1	A	398	GLU	N-CA-C	-6.78	100.45	110.48
1	A	827	THR	N-CA-C	-6.77	105.31	113.97
1	A	865	GLN	N-CA-C	-6.75	96.43	110.80
1	A	244	PRO	N-CA-C	6.73	118.91	110.70
6	F	127	GLU	N-CA-C	-6.67	103.08	113.02
1	A	698	GLN	N-CA-C	-6.64	105.22	113.38
4	D	25	ALA	N-CA-C	-6.63	103.51	112.26
1	A	1413	GLY	N-CA-C	-6.61	107.40	114.67
1	A	463	ILE	CA-C-N	6.61	126.56	120.21
1	A	463	ILE	C-N-CA	6.61	126.56	120.21
7	G	140	LYS	N-CA-C	6.59	120.92	113.01
2	B	507	LYS	CA-C-N	-6.56	112.29	122.59
2	B	507	LYS	C-N-CA	-6.56	112.29	122.59
1	A	234	MET	N-CA-C	-6.54	105.30	113.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	G	129	SER	N-CA-C	6.52	117.19	108.38
4	D	54	GLU	N-CA-C	-6.51	104.03	112.23
2	B	363	HIS	N-CA-C	-6.50	102.13	110.19
6	F	132	LEU	N-CA-C	6.47	120.59	110.17
1	A	562	THR	CA-C-N	6.44	126.47	119.90
1	A	562	THR	C-N-CA	6.44	126.47	119.90
5	E	20	LYS	N-CA-C	-6.43	103.89	111.03
9	I	54	GLU	N-CA-C	6.43	119.66	109.81
2	B	35	SER	N-CA-C	-6.43	103.18	111.02
5	E	5	ASN	N-CA-C	-6.41	106.42	114.56
2	B	829	CYS	N-CA-C	-6.37	98.89	109.46
1	A	1339	LEU	N-CA-C	6.37	119.03	111.71
3	C	226	ASP	N-CA-C	-6.36	100.80	110.14
2	B	473	MET	N-CA-C	-6.36	105.49	113.18
1	A	311	GLN	N-CA-C	6.35	123.84	109.81
1	A	999	VAL	N-CA-C	-6.34	106.76	111.90
3	C	93	ASP	N-CA-C	-6.32	104.83	112.54
2	B	1177	HIS	N-CA-C	-6.28	105.56	112.72
1	A	977	LYS	CA-C-N	6.27	126.24	120.03
1	A	977	LYS	C-N-CA	6.27	126.24	120.03
6	F	103	MET	N-CA-C	-6.24	105.53	113.02
2	B	825	VAL	N-CA-C	6.24	118.38	108.89
1	A	984	LYS	N-CA-C	-6.24	104.02	111.69
1	A	1404	GLU	N-CA-C	6.20	120.87	112.88
1	A	432	VAL	CB-CA-C	-6.19	104.98	111.23
1	A	384	ASN	N-CA-C	6.18	121.33	113.55
1	A	293	GLU	N-CA-C	-6.16	104.47	112.23
2	B	511	PRO	CA-N-CD	-6.16	103.38	112.00
1	A	954	TRP	N-CA-C	6.16	118.15	108.55
2	B	1113	VAL	N-CA-C	6.14	116.19	110.42
1	A	1102	LYS	N-CA-C	-6.14	104.28	110.97
3	C	225	ALA	N-CA-C	6.13	120.01	107.69
1	A	196	GLU	CA-C-N	6.11	127.48	119.84
1	A	196	GLU	C-N-CA	6.11	127.48	119.84
8	H	85	GLY	N-CA-C	-6.11	107.62	114.40
9	I	52	ILE	N-CA-C	6.09	116.64	107.75
1	A	222	LEU	N-CA-C	-6.08	102.34	110.55
2	B	918	ILE	N-CA-C	6.08	116.62	108.11
1	A	1405	THR	N-CA-C	6.04	123.67	110.80
3	C	259	LEU	N-CA-C	-6.04	104.70	111.28
5	E	150	VAL	CA-C-N	6.03	127.37	119.84
5	E	150	VAL	C-N-CA	6.03	127.37	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	440	ASP	N-CA-C	-6.02	102.46	109.93
1	A	553	VAL	CA-C-N	6.02	127.36	119.84
1	A	553	VAL	C-N-CA	6.02	127.36	119.84
3	C	23	SER	N-CA-C	5.99	118.58	109.95
1	A	137	ALA	N-CA-C	-5.99	103.92	112.13
1	A	1421	CYS	N-CA-C	-5.98	103.15	111.52
2	B	510	LYS	N-CA-C	5.97	123.01	109.81
1	A	729	ALA	N-CA-C	-5.95	104.86	111.71
5	E	147	HIS	N-CA-C	5.95	118.89	109.96
1	A	229	SER	N-CA-C	5.95	117.14	107.32
2	B	1107	ALA	N-CA-C	-5.92	98.18	110.80
1	A	454	SER	N-CA-C	-5.92	105.89	114.12
1	A	1085	HIS	N-CA-C	-5.92	106.06	113.28
3	C	39	ALA	N-CA-C	5.87	121.22	112.94
4	D	66	ARG	N-CA-C	-5.86	104.25	111.40
5	E	204	THR	N-CA-C	-5.86	104.89	112.68
1	A	535	THR	N-CA-C	5.85	118.54	111.40
5	E	171	LYS	N-CA-C	-5.83	99.74	109.24
1	A	506	ALA	N-CA-C	5.81	118.14	109.25
2	B	606	LYS	N-CA-C	-5.78	106.77	113.88
4	D	157	GLN	N-CA-C	-5.77	106.08	113.01
3	C	211	ASP	CA-C-N	5.76	126.31	120.38
3	C	211	ASP	C-N-CA	5.76	126.31	120.38
1	A	564	ALA	N-CA-C	-5.72	104.95	111.07
1	A	1444	MET	N-CA-C	5.72	117.76	109.07
9	I	25	LEU	N-CA-C	5.71	118.54	109.24
1	A	88	LYS	CA-C-N	5.68	126.94	119.84
1	A	88	LYS	C-N-CA	5.68	126.94	119.84
4	D	173	HIS	CA-C-N	5.68	126.94	119.84
4	D	173	HIS	C-N-CA	5.68	126.94	119.84
1	A	18	GLN	N-CA-C	5.67	118.13	109.62
1	A	239	LEU	N-CA-C	5.67	118.62	108.47
1	A	1071	SER	N-CA-C	5.67	119.30	112.38
2	B	428	ILE	N-CA-C	-5.66	104.01	111.09
1	A	982	THR	N-CA-C	-5.65	101.28	110.20
2	B	1173	ALA	N-CA-C	5.64	117.93	107.99
3	C	155	LEU	N-CA-C	5.64	118.45	109.81
2	B	934	LYS	N-CA-C	5.63	117.11	109.11
1	A	1449	SER	N-CA-C	-5.63	106.41	113.28
12	L	30	ILE	N-CA-C	5.63	116.47	108.42
4	D	195	ILE	CA-C-N	5.62	125.46	119.28
4	D	195	ILE	C-N-CA	5.62	125.46	119.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1072	ILE	N-CA-C	-5.62	106.98	111.81
1	A	511	ILE	N-CA-C	5.61	118.92	111.17
3	C	168	ALA	N-CA-C	5.61	118.11	111.33
1	A	31	SER	N-CA-C	5.59	118.13	110.24
1	A	424	ILE	N-CA-C	5.59	120.98	109.34
1	A	439	ASN	N-CA-C	5.59	120.05	113.23
2	B	297	ILE	N-CA-C	-5.59	105.05	110.42
2	B	427	ASP	N-CA-C	-5.58	107.11	114.31
1	A	1092	LYS	N-CA-C	-5.56	104.03	111.87
4	D	33	PHE	N-CA-C	5.56	118.02	110.06
4	D	169	SER	N-CA-C	-5.56	104.74	112.30
1	A	663	SER	N-CA-C	5.55	115.62	108.34
2	B	1008	PRO	N-CA-C	5.55	119.90	111.19
2	B	1194	ILE	N-CA-C	5.55	116.69	108.65
2	B	510	LYS	CA-C-O	5.54	127.75	120.16
1	A	513	SER	N-CA-C	5.53	116.64	109.72
2	B	66	ASP	N-CA-C	-5.53	106.74	112.93
5	E	152	LYS	N-CA-C	5.53	118.25	109.96
2	B	1101	ASP	N-CA-C	-5.52	106.32	113.16
1	A	1419	ASP	N-CA-C	5.50	117.49	108.52
1	A	950	GLY	N-CA-C	-5.49	108.15	114.69
3	C	92	CYS	CA-CB-SG	-5.48	101.80	114.40
1	A	199	LEU	N-CA-C	5.48	117.16	108.67
2	B	1168	LEU	N-CA-C	5.46	117.56	109.69
1	A	1081	LEU	N-CA-C	5.46	118.30	109.40
8	H	40	LEU	N-CA-C	5.46	117.28	108.32
2	B	1180	PHE	N-CA-C	5.44	119.42	112.12
2	B	846	ILE	N-CA-C	-5.44	105.07	110.62
1	A	1325	THR	N-CA-C	-5.41	107.33	114.04
2	B	854	LEU	N-CA-C	-5.39	102.48	110.46
2	B	833	TYR	N-CA-C	-5.38	106.72	113.72
2	B	580	VAL	N-CA-C	5.38	116.32	108.58
10	J	11	GLY	N-CA-C	5.37	120.07	113.79
1	A	1155	ASP	CA-C-N	5.37	126.55	119.84
1	A	1155	ASP	C-N-CA	5.37	126.55	119.84
2	B	277	LYS	N-CA-C	5.37	117.88	111.71
4	D	176	GLU	N-CA-C	-5.37	104.31	112.04
2	B	857	ARG	N-CA-C	-5.37	101.96	109.69
7	G	127	PRO	CA-C-N	5.36	125.30	119.78
7	G	127	PRO	C-N-CA	5.36	125.30	119.78
2	B	1131	GLY	N-CA-C	5.34	121.45	112.85
1	A	158	PRO	N-CA-C	-5.34	109.13	114.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	978	ASP	N-CA-C	5.34	117.77	110.24
1	A	1343	ALA	N-CA-C	-5.32	105.15	111.69
1	A	797	LYS	N-CA-C	-5.32	106.64	113.02
1	A	756	ILE	CB-CA-C	-5.30	105.09	111.88
2	B	1016	ALA	N-CA-C	-5.30	106.68	112.72
1	A	1021	LEU	N-CA-C	-5.30	105.17	111.69
1	A	1403	GLU	N-CA-C	5.30	122.08	110.80
5	E	200	ARG	N-CA-C	5.30	118.17	110.17
9	I	8	ARG	N-CA-C	-5.29	101.40	109.65
1	A	120	GLU	N-CA-C	5.29	116.73	111.07
1	A	495	GLU	N-CA-C	-5.29	105.10	112.45
2	B	492	LEU	N-CA-C	-5.28	104.57	111.02
5	E	119	SER	N-CA-C	-5.28	105.98	112.90
1	A	1360	GLY	N-CA-C	-5.28	104.91	114.46
5	E	173	SER	N-CA-C	5.27	117.77	111.71
2	B	1181	GLU	N-CA-C	5.26	122.01	110.80
2	B	436	VAL	N-CA-C	-5.26	106.40	112.98
11	K	77	THR	N-CA-C	5.26	116.79	108.96
3	C	12	GLU	N-CA-C	-5.25	103.55	110.43
1	A	537	ARG	N-CA-C	-5.24	105.74	111.82
1	A	706	HIS	N-CA-C	-5.22	105.55	112.34
2	B	949	VAL	N-CA-C	-5.22	102.25	110.09
1	A	174	ILE	N-CA-C	5.22	116.23	108.46
1	A	224	PHE	N-CA-C	5.22	116.22	108.86
1	A	1098	VAL	CB-CA-C	-5.20	108.84	114.35
1	A	230	ARG	N-CA-C	-5.19	103.41	110.36
1	A	1036	ARG	N-CA-C	5.19	121.85	110.80
1	A	1391	ARG	N-CA-C	-5.19	107.62	114.31
2	B	872	GLU	N-CA-C	-5.18	103.76	110.19
7	G	22	MET	N-CA-C	-5.18	105.08	111.40
1	A	479	ASN	N-CA-C	-5.17	104.86	110.91
5	E	177	ARG	N-CA-C	5.16	118.14	110.14
1	A	166	GLY	N-CA-C	5.14	120.49	112.31
3	C	147	LEU	N-CA-C	5.14	116.34	108.52
2	B	1084	GLN	N-CA-C	-5.14	101.60	109.41
7	G	40	GLY	N-CA-C	-5.14	107.42	113.99
1	A	857	ARG	N-CA-C	5.13	117.34	109.95
8	H	4	THR	N-CA-C	-5.13	101.57	109.52
5	E	197	LYS	N-CA-C	5.12	116.92	109.71
1	A	1311	VAL	N-CA-C	5.11	119.97	109.34
2	B	1045	SER	CA-C-N	5.11	126.23	119.84
2	B	1045	SER	C-N-CA	5.11	126.23	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1201	LYS	N-CA-C	-5.11	105.40	110.97
1	A	1032	LEU	N-CA-C	5.09	119.46	112.68
1	A	1368	MET	N-CA-C	-5.08	105.18	111.33
2	B	687	GLU	N-CA-C	-5.08	105.55	112.26
3	C	38	ILE	N-CA-C	5.08	115.36	110.74
1	A	1264	GLU	N-CA-C	-5.07	105.40	112.45
2	B	510	LYS	C-N-CD	-5.07	104.21	125.00
2	B	1120	GLU	N-CA-C	5.07	117.98	110.48
4	D	8	PHE	N-CA-C	5.07	121.60	110.80
2	B	772	ALA	N-CA-C	-5.06	105.89	113.89
1	A	1283	VAL	N-CA-C	5.04	115.44	108.23
9	I	112	SER	N-CA-C	-5.04	105.51	113.02
3	C	90	ASP	N-CA-C	5.04	121.53	110.80
1	A	56	PRO	N-CA-C	-5.03	102.11	112.47
1	A	961	ARG	N-CA-C	-5.03	105.69	111.07
1	A	1316	VAL	N-CA-C	-5.02	106.47	113.00
3	C	92	CYS	N-CA-C	-5.01	102.14	109.81
1	A	683	ILE	N-CA-C	-5.01	106.79	111.45

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	510	LYS	Mainchain
2	B	833	TYR	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	11214	0	11281	1597	0
2	B	8837	0	8871	1269	0
3	C	2095	0	2052	281	0
4	D	1356	0	1319	110	0
5	E	1752	0	1776	204	0
6	F	679	0	701	87	0
7	G	1340	0	1357	169	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	H	1068	0	1040	124	0
9	I	971	0	929	121	0
10	J	532	0	542	118	0
11	K	919	0	929	109	0
12	L	364	0	387	70	0
13	A	1	0	0	0	0
14	A	3	0	0	0	0
14	B	1	0	0	0	0
14	C	1	0	0	0	0
14	I	2	0	0	0	0
14	J	1	0	0	0	0
14	L	1	0	0	0	0
All	All	31137	0	31184	3940	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 63.

All (3940) 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)
3:C:45:ALA:HA	3:C:72:LEU:HD12	1.28	1.13
4:D:40:HIS:HB3	7:G:73:LYS:HZ3	1.10	1.12
7:G:138:THR:HG22	7:G:139:ILE:H	1.11	1.11
1:A:913:LEU:HD12	1:A:914:GLU:H	1.15	1.11
6:F:82:THR:HG22	6:F:84:TYR:H	1.15	1.11
1:A:1017:LEU:HB2	5:E:206:GLY:H	1.11	1.10
1:A:225:ASN:ND2	1:A:228:PHE:H	1.47	1.10
1:A:855:THR:HG21	1:A:857:ARG:HE	1.10	1.10
1:A:899:VAL:HB	1:A:929:LEU:HD11	1.33	1.09
1:A:590:ARG:NH2	1:A:620:LYS:HB3	1.66	1.09
10:J:57:ILE:HA	10:J:60:PHE:HD2	1.14	1.09
1:A:794:PRO:HG2	1:A:795:GLU:OE2	1.49	1.08
1:A:868:TYR:HE1	1:A:1064:VAL:HG11	1.15	1.08
1:A:868:TYR:CE1	1:A:1064:VAL:HG11	1.88	1.07
1:A:1329:THR:H	1:A:1335:ILE:HD11	1.02	1.07
2:B:1095:LEU:H	2:B:1095:LEU:HD12	1.11	1.07
1:A:353:ILE:HG21	1:A:487:MET:HG3	1.31	1.07
7:G:14:HIS:HD2	7:G:16:SER:HB2	1.15	1.06
4:D:40:HIS:HB3	7:G:73:LYS:NZ	1.69	1.05
10:J:64:ASN:HB3	10:J:65:PRO:CD	1.87	1.05
2:B:508:LEU:CB	2:B:510:LYS:H	1.70	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:901:LEU:H	1:A:926:GLN:NE2	1.54	1.04
2:B:112:LEU:HD12	2:B:113:TYR:H	1.18	1.04
1:A:768:GLN:HG2	1:A:816:HIS:HA	1.39	1.03
1:A:779:PHE:HE1	1:A:785:PRO:HD3	1.19	1.03
2:B:1169:MET:HE1	2:B:1201:LYS:HA	1.41	1.03
2:B:839:MET:CG	2:B:1010:LEU:HD11	1.87	1.02
3:C:133:ILE:HD11	3:C:237:SER:HA	1.39	1.02
1:A:834:THR:HG21	1:A:1077:THR:HG23	1.39	1.02
2:B:579:ARG:HB2	2:B:586:TRP:HE1	1.19	1.02
2:B:1159:ARG:HD3	2:B:1193:GLN:HG3	1.42	1.02
7:G:111:THR:HG22	7:G:113:HIS:H	1.19	1.02
2:B:510:LYS:O	2:B:510:LYS:HD2	1.60	1.02
1:A:47:ARG:HH12	1:A:254:GLU:HB3	1.21	1.01
2:B:839:MET:HG3	2:B:1010:LEU:HD11	1.01	1.01
2:B:1065:GLN:HE21	2:B:1067:ARG:N	1.58	1.01
1:A:53:LEU:HD23	1:A:54:ASN:N	1.76	1.01
1:A:63:ARG:HA	1:A:74:MET:SD	2.02	1.00
1:A:896:ARG:HD3	1:A:897:TYR:HE1	1.25	1.00
3:C:33:LEU:HG	3:C:37:MET:HE2	1.43	1.00
2:B:65:GLU:HG3	2:B:66:ASP:H	1.27	0.99
2:B:705:MET:HA	2:B:705:MET:HE3	1.40	0.99
1:A:590:ARG:HH21	1:A:620:LYS:HB3	1.27	0.99
11:K:65:HIS:CD2	11:K:67:PHE:H	1.81	0.98
2:B:589:VAL:HG12	2:B:590:HIS:H	1.24	0.98
1:A:1011:GLN:NE2	1:A:1015:VAL:HG21	1.78	0.98
2:B:273:LEU:HB2	2:B:276:ILE:HD12	1.43	0.98
1:A:490:HIS:HB3	2:B:1150:ARG:NH1	1.79	0.98
1:A:853:ASP:OD1	1:A:855:THR:HB	1.62	0.98
1:A:14:VAL:H	1:A:1432:GLN:HE22	1.05	0.97
10:J:64:ASN:HB3	10:J:65:PRO:HD3	1.45	0.97
2:B:918:ILE:HD12	2:B:935:ARG:HD2	1.42	0.97
3:C:56:THR:HG21	3:C:145:CYS:SG	2.03	0.97
2:B:23:ALA:HB1	2:B:24:PRO:HD2	1.44	0.97
2:B:882:THR:HG22	2:B:884:ARG:H	1.29	0.97
1:A:164:ARG:HG3	1:A:165:GLY:H	1.26	0.97
1:A:886:ILE:HD11	1:A:943:LEU:HB3	1.44	0.96
2:B:211:VAL:O	2:B:480:SER:HA	1.65	0.96
2:B:295:GLY:H	2:B:298:LEU:HD23	1.27	0.96
2:B:863:GLU:OE2	2:B:873:THR:HA	1.64	0.96
1:A:1081:LEU:HD12	1:A:1082:ASN:OD1	1.66	0.96
2:B:583:ASN:HD21	2:B:628:THR:HB	1.29	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1162:ILE:HD11	2:B:1194:ILE:HD13	1.45	0.96
11:K:65:HIS:HD2	11:K:67:PHE:H	1.10	0.96
1:A:399:HIS:HB3	1:A:400:PRO:HD3	1.46	0.96
2:B:287:ARG:HG2	2:B:292:ILE:HA	1.48	0.96
1:A:779:PHE:CE1	1:A:785:PRO:HD3	2.00	0.95
1:A:103:CYS:SG	1:A:108:MET:HE1	2.07	0.95
1:A:913:LEU:HD12	1:A:914:GLU:N	1.81	0.95
2:B:824:ILE:HG12	10:J:48:ARG:HH12	1.31	0.94
1:A:1189:SER:O	1:A:1241:ARG:HD3	1.66	0.94
2:B:999:MET:HG3	2:B:1000:PRO:HD2	1.49	0.94
1:A:1341:ILE:HG23	1:A:1342:GLU:H	1.32	0.93
7:G:1:MET:HG3	7:G:85:GLU:CD	1.93	0.93
10:J:57:ILE:HA	10:J:60:PHE:CD2	2.03	0.93
2:B:1065:GLN:NE2	2:B:1067:ARG:H	1.67	0.93
1:A:337:ARG:CZ	1:A:839:ARG:HH12	1.81	0.93
1:A:1424:VAL:HG22	1:A:1436:ILE:HD11	1.48	0.93
3:C:167:HIS:HD2	3:C:169:LYS:H	1.17	0.93
1:A:49:LYS:NZ	1:A:61:ILE:HG13	1.84	0.93
7:G:14:HIS:CD2	7:G:16:SER:HB2	2.04	0.93
3:C:73:GLN:HE21	3:C:75:MET:H	1.03	0.92
1:A:55:ASP:C	1:A:57:ARG:H	1.73	0.92
1:A:708:MET:HE2	1:A:1089:VAL:HG13	1.52	0.92
1:A:1362:TYR:HD1	1:A:1363:VAL:H	1.18	0.92
7:G:1:MET:HE1	7:G:80:LYS:H	1.33	0.92
1:A:225:ASN:HD22	1:A:228:PHE:H	1.03	0.92
2:B:1002:THR:HG21	2:B:1006:ILE:HD12	1.49	0.92
2:B:1183:LYS:N	2:B:1183:LYS:HE3	1.85	0.92
2:B:846:ILE:HG23	2:B:974:PRO:HG2	1.51	0.92
2:B:563:MET:HE3	2:B:580:VAL:HB	1.51	0.92
5:E:153:HIS:O	5:E:154:ILE:HG13	1.69	0.91
1:A:70:CYS:O	1:A:72:GLU:HG2	1.68	0.91
6:F:76:LYS:O	6:F:79:ARG:HD3	1.70	0.91
3:C:63:ILE:HA	3:C:66:ARG:HG3	1.50	0.91
1:A:666:ILE:HD12	1:A:667:GLY:H	1.35	0.91
9:I:85:PHE:H	9:I:85:PHE:HD2	0.93	0.90
3:C:57:VAL:HG11	10:J:60:PHE:HB3	1.52	0.90
2:B:168:GLY:H	2:B:450:ALA:HB1	1.34	0.90
2:B:839:MET:HG3	2:B:1010:LEU:CD1	1.98	0.90
1:A:1329:THR:HG22	1:A:1331:SER:H	1.36	0.90
1:A:1329:THR:N	1:A:1335:ILE:HD11	1.87	0.90
2:B:549:THR:HG22	2:B:550:ASP:H	1.35	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:40:LEU:HD13	8:H:123:MET:HB2	1.53	0.89
2:B:800:GLN:HB3	10:J:52:THR:HG21	1.54	0.89
4:D:56:ARG:HB2	4:D:148:LEU:HD22	1.52	0.89
1:A:1161:THR:HG22	1:A:1163:ILE:H	1.37	0.89
1:A:1121:GLU:HG2	1:A:1122:PRO:HD2	1.55	0.89
2:B:835:GLN:HA	2:B:1013:ASN:HD22	1.35	0.89
2:B:35:SER:HA	2:B:811:TYR:HE2	1.36	0.88
1:A:351:THR:HG22	2:B:1103:ILE:HA	1.55	0.88
1:A:560:ILE:HG13	8:H:78:SER:HB2	1.51	0.88
1:A:864:ILE:O	1:A:865:GLN:HG3	1.72	0.88
2:B:1095:LEU:HD12	2:B:1095:LEU:N	1.88	0.88
7:G:23:LYS:HG3	7:G:56:ILE:HD11	1.55	0.88
9:I:111:THR:HG22	9:I:112:SER:H	1.37	0.88
1:A:1118:VAL:O	1:A:1305:VAL:HG13	1.71	0.88
10:J:6:ARG:HG2	10:J:13:VAL:HA	1.55	0.88
1:A:490:HIS:HB3	2:B:1150:ARG:HH11	1.36	0.88
1:A:1029:ARG:HH11	1:A:1029:ARG:HG3	1.38	0.88
5:E:197:LYS:HE2	5:E:199:ILE:HD11	1.55	0.88
2:B:254:LEU:HD23	2:B:381:MET:HE1	1.55	0.88
2:B:113:TYR:HB3	2:B:114:PRO:HD2	1.55	0.88
1:A:1100:ARG:HH21	1:A:1351:GLU:HG2	1.39	0.87
1:A:1004:ASN:ND2	5:E:167:ARG:HD2	1.88	0.87
2:B:365:THR:HG23	2:B:367:LEU:HG	1.55	0.87
9:I:29:CYS:SG	9:I:32:CYS:N	2.48	0.87
2:B:313:MET:HE2	2:B:390:LEU:HD21	1.57	0.87
2:B:1007:VAL:HG22	2:B:1008:PRO:HD2	1.56	0.87
2:B:579:ARG:HB2	2:B:586:TRP:NE1	1.90	0.87
2:B:830:TYR:CE2	2:B:1000:PRO:HD3	2.09	0.87
1:A:524:VAL:HG12	1:A:525:GLN:H	1.38	0.87
1:A:1341:ILE:HG23	1:A:1342:GLU:N	1.89	0.87
2:B:39:ARG:NH2	2:B:665:GLU:HG2	1.89	0.87
3:C:213:PRO:O	3:C:214:ASN:HB2	1.74	0.87
2:B:493:SER:HA	2:B:751:VAL:HG21	1.57	0.86
7:G:138:THR:HG22	7:G:139:ILE:N	1.91	0.86
1:A:1313:LEU:HD23	1:A:1338:VAL:HG21	1.57	0.86
1:A:443:LEU:HG	2:B:1146:PHE:HE2	1.38	0.86
1:A:567:LYS:HB3	8:H:96:VAL:H	1.39	0.86
1:A:795:GLU:CD	1:A:795:GLU:H	1.84	0.86
2:B:269:ILE:HD11	2:B:386:LEU:HD21	1.55	0.86
2:B:467:GLY:O	2:B:468:GLU:HB2	1.73	0.86
7:G:13:LEU:HD21	7:G:17:PHE:HB2	1.56	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:43:ARG:HG3	10:J:45:CYS:SG	2.16	0.86
2:B:880:THR:HB	2:B:934:LYS:HD2	1.56	0.86
7:G:1:MET:HG3	7:G:85:GLU:OE2	1.75	0.86
11:K:56:VAL:HA	11:K:77:THR:HG22	1.55	0.86
1:A:537:ARG:HD2	8:H:20:TYR:HE1	1.40	0.86
1:A:963:ILE:HD13	1:A:1049:ILE:HG13	1.58	0.86
1:A:855:THR:HG21	1:A:857:ARG:NE	1.89	0.85
1:A:1362:TYR:CD1	1:A:1363:VAL:N	2.44	0.85
3:C:244:VAL:O	3:C:248:ILE:HG13	1.76	0.85
10:J:14:VAL:CG1	10:J:50:ILE:HD11	2.05	0.85
2:B:955:THR:HG23	12:L:54:ARG:O	1.77	0.85
1:A:466:SER:O	2:B:1103:ILE:HD11	1.75	0.85
2:B:466:TRP:O	2:B:468:GLU:N	2.08	0.85
1:A:896:ARG:HD3	1:A:897:TYR:CE1	2.11	0.85
5:E:117:THR:HG22	5:E:119:SER:H	1.39	0.85
5:E:153:HIS:HB3	5:E:196:VAL:HG11	1.58	0.85
10:J:3:VAL:HG21	10:J:18:TRP:HB2	1.59	0.85
8:H:100:THR:HG23	8:H:138:GLU:HA	1.58	0.85
1:A:49:LYS:HZ3	1:A:61:ILE:HG13	1.42	0.85
1:A:1166:ASP:OD2	1:A:1239:ARG:HD2	1.76	0.85
2:B:510:LYS:HD2	2:B:510:LYS:C	1.98	0.85
1:A:587:HIS:CD2	1:A:969:GLN:HG2	2.11	0.84
5:E:22:MET:HE3	5:E:26:ARG:HE	1.42	0.84
2:B:510:LYS:O	2:B:510:LYS:CD	2.25	0.84
2:B:37:PHE:HE2	2:B:542:MET:HA	1.40	0.84
2:B:510:LYS:HG2	2:B:512:ARG:H	1.43	0.84
1:A:446:ARG:HD2	1:A:480:ALA:HB2	1.58	0.84
1:A:540:PHE:HB3	1:A:571:LEU:HD23	1.59	0.84
1:A:1116:LEU:N	1:A:1308:THR:HG22	1.92	0.84
1:A:1239:ARG:HH22	1:A:1241:ARG:HH22	1.25	0.84
1:A:1291:VAL:HG13	1:A:1292:PRO:HD2	1.59	0.84
2:B:843:GLN:HB2	2:B:993:THR:HB	1.58	0.84
2:B:582:VAL:HG23	2:B:626:ILE:HB	1.57	0.84
2:B:562:GLY:HA3	2:B:590:HIS:CE1	2.12	0.84
2:B:1065:GLN:HE21	2:B:1067:ARG:H	0.86	0.84
8:H:84:ALA:HB1	8:H:87:ARG:HB2	1.57	0.84
1:A:1116:LEU:HD23	1:A:1311:VAL:HG22	1.60	0.84
2:B:217:ARG:HE	2:B:405:ARG:HB2	1.40	0.84
1:A:472:LEU:HD11	2:B:835:GLN:NE2	1.93	0.83
2:B:295:GLY:N	2:B:298:LEU:HD23	1.94	0.83
2:B:653:VAL:HG22	2:B:689:LEU:HB3	1.60	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1107:ALA:O	2:B:1108:ARG:HG2	1.77	0.83
2:B:766:ARG:NH2	2:B:1020:ARG:HG2	1.92	0.83
1:A:901:LEU:H	1:A:926:GLN:HE21	1.22	0.83
5:E:22:MET:HE3	5:E:26:ARG:NE	1.93	0.83
9:I:85:PHE:CD2	9:I:85:PHE:N	2.45	0.83
9:I:111:THR:HG22	9:I:113:ASP:H	1.43	0.83
1:A:743:VAL:O	1:A:747:VAL:HG23	1.79	0.83
2:B:781:PHE:O	2:B:782:LEU:HG	1.78	0.83
1:A:665:GLY:HA2	2:B:1026:LEU:HD21	1.58	0.82
5:E:153:HIS:HB3	5:E:196:VAL:CG1	2.08	0.82
2:B:1095:LEU:H	2:B:1095:LEU:CD1	1.87	0.82
2:B:1020:ARG:HG2	2:B:1020:ARG:HH11	1.44	0.82
10:J:9:SER:OG	10:J:45:CYS:HB2	1.79	0.82
1:A:353:ILE:HD12	1:A:470:LEU:HD21	1.61	0.82
2:B:508:LEU:C	2:B:510:LYS:H	1.81	0.82
2:B:502:ILE:HG22	2:B:502:ILE:O	1.79	0.82
9:I:56:ALA:HB2	9:I:89:GLN:CG	2.10	0.82
1:A:503:GLN:HE21	6:F:90:ARG:HH21	1.25	0.82
1:A:567:LYS:CG	1:A:568:PRO:HD2	2.09	0.82
1:A:1317:MET:O	1:A:1322:ILE:HD11	1.80	0.82
2:B:589:VAL:HG12	2:B:590:HIS:N	1.95	0.82
1:A:649:ILE:O	1:A:653:VAL:HG23	1.80	0.82
6:F:86:THR:OG1	6:F:89:GLU:HG3	1.80	0.81
1:A:1017:LEU:HB2	5:E:206:GLY:N	1.93	0.81
6:F:103:MET:HE2	7:G:66:GLY:H	1.44	0.81
1:A:669:THR:O	1:A:762:SER:HB3	1.81	0.81
1:A:1079:MET:HE3	1:A:1098:VAL:HG22	1.61	0.81
1:A:1116:LEU:H	1:A:1308:THR:HG22	1.41	0.81
2:B:508:LEU:C	2:B:510:LYS:N	2.30	0.81
9:I:6:PHE:HB3	9:I:12:ASN:O	1.80	0.81
1:A:628:GLY:O	1:A:632:VAL:HG23	1.80	0.81
2:B:1169:MET:CE	2:B:1201:LYS:HA	2.11	0.81
7:G:111:THR:HG22	7:G:113:HIS:N	1.95	0.81
2:B:509:ALA:O	2:B:510:LYS:HD2	1.81	0.81
2:B:1099:VAL:HG13	2:B:1100:ASP:H	1.43	0.81
2:B:1007:VAL:CG2	2:B:1008:PRO:HD2	2.10	0.81
3:C:98:VAL:C	3:C:99:LEU:HD23	2.03	0.81
3:C:73:GLN:NE2	3:C:75:MET:H	1.79	0.81
1:A:1372:VAL:O	1:A:1376:THR:HG22	1.81	0.81
2:B:816:GLU:O	2:B:817:LEU:HD23	1.80	0.81
10:J:16:ASP:OD1	10:J:17:LYS:HD2	1.80	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:VAL:HG23	1:A:1432:GLN:NE2	1.95	0.80
1:A:335:ARG:HE	1:A:339:ASN:ND2	1.79	0.80
1:A:49:LYS:HE2	1:A:61:ILE:HD12	1.62	0.80
1:A:399:HIS:O	1:A:401:GLY:N	2.14	0.80
1:A:471:ASN:O	1:A:474:VAL:HG12	1.81	0.80
11:K:65:HIS:HD2	11:K:67:PHE:N	1.79	0.80
2:B:39:ARG:HH21	2:B:665:GLU:HG2	1.46	0.80
2:B:102:VAL:HG23	2:B:112:LEU:HB2	1.63	0.80
2:B:862:GLN:HG2	2:B:963:PHE:HD1	1.45	0.80
1:A:78:PRO:HA	2:B:1201:LYS:NZ	1.96	0.80
3:C:133:ILE:CD1	3:C:237:SER:HA	2.11	0.80
1:A:1094:VAL:HG13	1:A:1113:THR:HG21	1.63	0.80
1:A:1237:ILE:HG22	1:A:1238:ILE:N	1.96	0.80
2:B:359:GLU:O	2:B:362:PRO:HD3	1.82	0.80
2:B:1159:ARG:HB3	2:B:1159:ARG:HH11	1.44	0.80
2:B:1204:PHE:O	2:B:1208:MET:HG3	1.82	0.80
1:A:56:PRO:O	1:A:57:ARG:HG3	1.82	0.80
3:C:212:PRO:HB3	3:C:213:PRO:HD2	1.64	0.80
7:G:18:PHE:HA	7:G:22:MET:HE3	1.63	0.80
9:I:58:VAL:HG22	9:I:62:ILE:HD12	1.63	0.80
1:A:666:ILE:HD12	1:A:667:GLY:N	1.95	0.79
2:B:364:ILE:HG12	2:B:585:VAL:HG13	1.64	0.79
9:I:55:THR:HG23	9:I:100:PHE:HD2	1.48	0.79
11:K:47:ARG:HB3	11:K:47:ARG:HH11	1.47	0.79
2:B:1106:ARG:HG3	2:B:1107:ALA:N	1.96	0.79
1:A:1017:LEU:HB3	5:E:205:SER:HA	1.64	0.79
1:A:1202:MET:HE1	1:A:1212:VAL:HG21	1.63	0.79
1:A:1435:PRO:HA	1:A:1439:GLY:O	1.82	0.79
1:A:1441:PHE:CZ	6:F:89:GLU:HA	2.18	0.79
1:A:164:ARG:HG3	1:A:165:GLY:N	1.98	0.79
1:A:494:SER:O	1:A:498:ARG:HG2	1.83	0.79
1:A:1444:MET:HG2	7:G:60:ARG:HA	1.65	0.79
9:I:58:VAL:HG12	9:I:60:GLN:H	1.47	0.79
12:L:30:ILE:HD11	12:L:59:ALA:HB2	1.64	0.79
1:A:299:HIS:HA	1:A:302:THR:HG22	1.65	0.79
7:G:1:MET:HE1	7:G:80:LYS:N	1.98	0.79
7:G:9:LEU:HD12	7:G:10:ASN:H	1.48	0.79
1:A:537:ARG:HD2	8:H:20:TYR:CE1	2.18	0.78
2:B:510:LYS:HG2	2:B:512:ARG:HG3	1.64	0.78
1:A:608:ILE:HB	1:A:613:ILE:HD11	1.65	0.78
6:F:82:THR:HG22	6:F:84:TYR:N	1.97	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1127:ASP:HB3	1:A:1130:GLN:HB3	1.63	0.78
1:A:825:ILE:HG21	2:B:510:LYS:HE3	1.64	0.78
2:B:593:PRO:HG2	2:B:617:ARG:NH2	1.99	0.78
4:D:35:LEU:H	4:D:35:LEU:HD12	1.48	0.78
5:E:124:VAL:HG13	5:E:132:ILE:HD12	1.64	0.78
1:A:339:ASN:HB3	2:B:1117:GLN:HE22	1.48	0.78
1:A:767:GLN:OE1	1:A:799:PHE:HB2	1.83	0.78
2:B:508:LEU:HB3	2:B:510:LYS:H	1.48	0.78
1:A:225:ASN:HD22	1:A:228:PHE:N	1.80	0.78
2:B:613:VAL:HG13	2:B:627:PHE:O	1.84	0.78
2:B:112:LEU:HD12	2:B:113:TYR:N	1.96	0.78
1:A:1090:ALA:HA	1:A:1093:LYS:HE3	1.66	0.78
1:A:1127:ASP:HB3	1:A:1130:GLN:CB	2.14	0.78
2:B:615:MET:HB3	2:B:626:ILE:HG12	1.66	0.78
2:B:1206:GLU:O	2:B:1209:ALA:HB3	1.83	0.78
1:A:1224:LEU:HD12	1:A:1241:ARG:O	1.84	0.77
2:B:882:THR:HG22	2:B:884:ARG:N	1.99	0.77
1:A:765:VAL:HG23	1:A:802:ASN:O	1.84	0.77
2:B:1165:ILE:HG22	2:B:1166:CYS:N	1.99	0.77
4:D:185:CYS:HA	4:D:190:GLU:OE1	1.84	0.77
2:B:515:HIS:CD2	2:B:517:THR:H	2.03	0.77
8:H:4:THR:HA	8:H:60:ALA:HB2	1.66	0.77
10:J:45:CYS:O	10:J:48:ARG:HG3	1.85	0.77
1:A:908:LEU:HD12	1:A:983:ILE:HD11	1.67	0.77
3:C:167:HIS:CD2	3:C:169:LYS:H	2.02	0.77
3:C:47:ASP:HA	12:L:69:ALA:CB	2.15	0.77
7:G:87:VAL:HB	7:G:103:VAL:HG11	1.67	0.77
11:K:113:THR:O	11:K:114:LEU:HB2	1.84	0.77
1:A:489:LEU:HD12	1:A:490:HIS:N	1.99	0.77
2:B:291:ILE:HD13	2:B:300:HIS:NE2	2.00	0.77
1:A:587:HIS:HD2	1:A:969:GLN:HG2	1.48	0.76
1:A:858:ASN:C	1:A:858:ASN:HD22	1.90	0.76
1:A:590:ARG:HD3	1:A:604:GLY:HA2	1.67	0.76
1:A:826:ASP:O	1:A:830:LYS:HB3	1.85	0.76
2:B:583:ASN:ND2	2:B:628:THR:HB	2.00	0.76
2:B:806:THR:HG22	2:B:808:ALA:H	1.48	0.76
6:F:86:THR:HG23	6:F:89:GLU:CD	2.10	0.76
1:A:563:PRO:HG3	1:A:572:TRP:CZ2	2.21	0.76
2:B:467:GLY:O	2:B:468:GLU:CB	2.29	0.76
2:B:541:LEU:HB2	2:B:747:MET:HE3	1.67	0.76
9:I:26:LEU:HD23	9:I:37:GLU:HA	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:98:THR:O	2:B:126:SER:HB2	1.86	0.76
2:B:1187:ASN:O	2:B:1188:LYS:HB2	1.84	0.76
1:A:107:CYS:H	1:A:114:LEU:HD21	1.51	0.76
1:A:963:ILE:HD11	1:A:1048:ASN:HB2	1.68	0.76
1:A:1406:VAL:HG12	1:A:1410:PHE:CE1	2.21	0.76
1:A:515:GLN:O	1:A:516:SER:HB3	1.85	0.76
2:B:918:ILE:HD12	2:B:935:ARG:CD	2.15	0.76
4:D:170:THR:CG2	4:D:172:LEU:HG	2.16	0.76
5:E:124:VAL:HG13	5:E:132:ILE:HB	1.68	0.76
5:E:154:ILE:H	5:E:196:VAL:HG13	1.49	0.76
1:A:106:VAL:HG13	1:A:112:LYS:O	1.86	0.76
2:B:758:PHE:CE2	2:B:1044:ALA:HA	2.21	0.76
4:D:48:ILE:HG21	7:G:4:ILE:HD12	1.66	0.76
7:G:121:PHE:HB2	7:G:130:TYR:CE2	2.20	0.76
1:A:71:GLN:C	1:A:73:GLY:H	1.91	0.76
2:B:899:ILE:HD11	2:B:911:ILE:HA	1.68	0.76
9:I:62:ILE:O	9:I:62:ILE:HG22	1.84	0.76
10:J:1:MET:HE2	10:J:60:PHE:CE2	2.21	0.76
1:A:95:PHE:CD1	1:A:234:MET:HG2	2.20	0.76
1:A:866:PHE:O	1:A:867:ILE:HD12	1.85	0.76
1:A:1079:MET:HE1	1:A:1101:LEU:HD23	1.68	0.75
2:B:429:PHE:HA	2:B:432:MET:HE3	1.68	0.75
2:B:777:ALA:HA	2:B:1095:LEU:HA	1.68	0.75
1:A:899:VAL:CB	1:A:929:LEU:HD11	2.16	0.75
10:J:7:CYS:SG	10:J:49:MET:HE3	2.27	0.75
10:J:44:TYR:HA	10:J:47:ARG:HB2	1.68	0.75
1:A:754:SER:H	1:A:757:ASN:HD22	1.35	0.75
2:B:745:PRO:O	2:B:748:ILE:HG12	1.86	0.75
9:I:34:TYR:CD2	9:I:35:VAL:N	2.54	0.75
1:A:337:ARG:CZ	1:A:839:ARG:NH1	2.50	0.75
1:A:346:ASP:HB3	2:B:1108:ARG:H	1.50	0.75
2:B:510:LYS:HG2	2:B:512:ARG:CG	2.17	0.75
8:H:59:ILE:HG22	8:H:60:ALA:N	2.01	0.75
2:B:794:ASN:C	2:B:795:ILE:HD12	2.11	0.75
4:D:40:HIS:CB	7:G:73:LYS:HZ3	1.96	0.75
5:E:7:ARG:HG3	5:E:8:ASN:N	2.00	0.75
1:A:1444:MET:HE1	6:F:135:ARG:HB2	1.67	0.75
2:B:508:LEU:CB	2:B:510:LYS:N	2.50	0.75
3:C:73:GLN:HE21	3:C:75:MET:N	1.82	0.75
3:C:90:ASP:O	3:C:91:HIS:CD2	2.39	0.75
8:H:81:PRO:CB	8:H:82:PRO:HD2	2.17	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:PHE:O	1:A:99:ILE:HG13	1.87	0.74
1:A:285:PRO:HG2	1:A:288:ALA:HB3	1.67	0.74
1:A:820:GLY:O	1:A:822:GLU:N	2.20	0.74
1:A:897:TYR:N	1:A:897:TYR:HD1	1.85	0.74
9:I:82:GLU:HB3	9:I:104:LEU:HD12	1.67	0.74
1:A:1027:ALA:HB3	1:A:1030:ARG:HB2	1.68	0.74
3:C:50:GLU:HG2	12:L:64:LEU:HD13	1.69	0.74
1:A:1445:ILE:H	1:A:1445:ILE:HD12	1.53	0.74
3:C:6:PRO:HB3	3:C:25:VAL:HG12	1.69	0.74
7:G:122:ASN:ND2	7:G:125:SER:HB3	2.02	0.74
1:A:567:LYS:HB3	8:H:96:VAL:N	2.01	0.74
1:A:1107:VAL:HG12	1:A:1107:VAL:O	1.87	0.74
2:B:773:MET:C	2:B:775:LYS:H	1.95	0.74
2:B:763:GLN:HG2	2:B:765:PRO:HD2	1.70	0.74
2:B:1084:GLN:N	2:B:1084:GLN:NE2	2.35	0.74
1:A:744:LYS:HG2	1:A:748:MET:HE2	1.68	0.74
7:G:123:ALA:C	7:G:125:SER:H	1.96	0.74
1:A:225:ASN:ND2	1:A:228:PHE:N	2.32	0.74
1:A:1334:ASP:C	1:A:1336:MET:H	1.93	0.74
1:A:830:LYS:HB2	1:A:1081:LEU:HD23	1.67	0.74
2:B:1084:GLN:N	2:B:1084:GLN:HE21	1.84	0.74
2:B:515:HIS:HD2	2:B:517:THR:H	1.35	0.74
1:A:853:ASP:OD1	1:A:855:THR:N	2.21	0.73
2:B:705:MET:HA	2:B:705:MET:CE	2.17	0.73
3:C:104:PHE:HD2	3:C:105:GLY:N	1.86	0.73
9:I:101:PHE:HD1	9:I:101:PHE:H	1.34	0.73
7:G:80:LYS:O	7:G:80:LYS:HG2	1.87	0.73
7:G:43:GLY:HA3	7:G:80:LYS:HB3	1.70	0.73
1:A:903:ASN:HD22	1:A:904:THR:N	1.87	0.73
2:B:508:LEU:HB2	2:B:510:LYS:H	1.52	0.73
4:D:145:MET:O	4:D:149:THR:HB	1.87	0.73
1:A:40:THR:HG21	1:A:259:GLU:OE2	1.88	0.73
1:A:381:THR:HG23	1:A:382:PRO:HD2	1.70	0.73
6:F:111:LEU:HD12	6:F:111:LEU:H	1.54	0.73
6:F:111:LEU:C	6:F:113:GLY:H	1.96	0.73
1:A:901:LEU:HG	1:A:926:GLN:HE21	1.53	0.73
1:A:1170:ILE:HG23	1:A:1174:PHE:CE1	2.22	0.73
1:A:215:SER:HB3	1:A:218:ASP:OD2	1.89	0.73
2:B:1160:VAL:HG12	2:B:1161:HIS:N	2.02	0.73
8:H:36:CYS:HA	8:H:126:GLU:O	1.88	0.73
10:J:41:LEU:HD11	10:J:50:ILE:HG13	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:GLN:HE22	1:A:80:HIS:CD2	2.06	0.73
1:A:288:ALA:HA	1:A:291:GLU:OE2	1.89	0.73
1:A:1239:ARG:HH22	1:A:1241:ARG:NH2	1.85	0.73
2:B:873:THR:O	2:B:914:LYS:HA	1.88	0.73
2:B:1002:THR:CG2	2:B:1006:ILE:HD12	2.19	0.73
5:E:135:PHE:HD2	5:E:140:LEU:HD21	1.52	0.73
1:A:31:SER:HA	1:A:81:PHE:O	1.87	0.73
1:A:289:ILE:C	1:A:291:GLU:H	1.95	0.73
2:B:1142:GLY:HA3	6:F:88:TYR:HE2	1.52	0.73
2:B:1180:PHE:HB3	2:B:1191:ILE:HD12	1.69	0.73
1:A:518:LYS:HB2	1:A:519:PRO:HD2	1.69	0.73
1:A:821:ARG:HB2	1:A:821:ARG:HH11	1.53	0.73
1:A:1444:MET:CE	6:F:135:ARG:HB2	2.18	0.73
3:C:32:SER:O	3:C:36:VAL:HG23	1.89	0.73
4:D:144:THR:O	4:D:148:LEU:HB2	1.89	0.73
2:B:510:LYS:C	2:B:510:LYS:CD	2.61	0.72
7:G:91:VAL:HG23	7:G:141:SER:O	1.88	0.72
9:I:111:THR:HG22	9:I:112:SER:N	2.03	0.72
5:E:213:ILE:HG12	5:E:214:CYS:H	1.54	0.72
1:A:53:LEU:HD23	1:A:54:ASN:H	1.54	0.72
4:D:130:LEU:C	4:D:132:GLN:H	1.97	0.72
1:A:265:LYS:HE2	1:A:322:VAL:CG1	2.19	0.72
1:A:364:VAL:HG12	1:A:458:HIS:HB3	1.71	0.72
7:G:138:THR:CG2	7:G:139:ILE:H	1.95	0.72
9:I:101:PHE:N	9:I:101:PHE:CD1	2.55	0.72
1:A:901:LEU:N	1:A:926:GLN:NE2	2.36	0.72
2:B:53:GLN:HG2	2:B:547:VAL:HG22	1.72	0.72
2:B:637:LEU:O	2:B:690:VAL:HG13	1.90	0.72
1:A:135:PHE:C	1:A:137:ALA:H	1.97	0.72
1:A:741:ASN:HD22	1:A:744:LYS:H	1.35	0.72
1:A:1011:GLN:HE22	1:A:1015:VAL:HG21	1.52	0.72
1:A:1015:VAL:HG12	1:A:1019:CYS:SG	2.30	0.72
2:B:172:ILE:HD13	2:B:178:ASN:CB	2.19	0.72
2:B:801:LYS:O	10:J:52:THR:HG23	1.89	0.72
2:B:976:ILE:HD11	2:B:992:ILE:HA	1.71	0.72
2:B:1031:LEU:HA	2:B:1055:ILE:HD13	1.72	0.72
8:H:44:VAL:O	8:H:44:VAL:HG12	1.89	0.72
1:A:90:VAL:HG12	1:A:91:PHE:N	2.03	0.72
5:E:210:SER:C	5:E:211:TYR:CD1	2.68	0.72
2:B:957:ASN:O	2:B:959:ASP:N	2.22	0.72
2:B:1184:GLY:C	2:B:1186:ASP:H	1.96	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:310:GLY:O	1:A:312:PRO:HD2	1.90	0.72
1:A:335:ARG:NH1	2:B:1206:GLU:OE2	2.22	0.72
1:A:1341:ILE:CG2	1:A:1342:GLU:H	2.03	0.72
1:A:1402:PHE:CE1	1:A:1403:GLU:HG3	2.24	0.72
2:B:604:ARG:NH2	2:B:613:VAL:O	2.23	0.72
2:B:977:GLY:HA3	2:B:1099:VAL:HB	1.70	0.72
2:B:1224:PHE:HE2	5:E:171:LYS:HG3	1.52	0.72
9:I:59:VAL:O	9:I:60:GLN:HB2	1.88	0.72
1:A:648:ASN:O	1:A:652:VAL:HG23	1.88	0.71
1:A:1237:ILE:HG22	1:A:1238:ILE:H	1.55	0.71
2:B:123:THR:O	2:B:125:SER:N	2.22	0.71
3:C:147:LEU:HB2	3:C:151:GLN:HB2	1.69	0.71
7:G:145:VAL:HG12	7:G:146:LYS:N	2.03	0.71
1:A:13:THR:O	2:B:1218:THR:HG22	1.90	0.71
2:B:953:LEU:HD23	2:B:953:LEU:O	1.89	0.71
7:G:115:MET:HB2	7:G:116:PRO:HD2	1.69	0.71
1:A:463:ILE:HB	1:A:464:PRO:HD2	1.72	0.71
2:B:291:ILE:HD13	2:B:300:HIS:CD2	2.25	0.71
2:B:827:ILE:HD12	2:B:1086:PHE:HD2	1.53	0.71
1:A:897:TYR:N	1:A:897:TYR:CD1	2.56	0.71
2:B:114:PRO:HG2	2:B:115:GLN:H	1.54	0.71
2:B:199:MET:HE2	2:B:492:LEU:HD23	1.72	0.71
4:D:54:GLU:O	4:D:58:VAL:HG23	1.89	0.71
1:A:441:PRO:HD2	1:A:498:ARG:NH2	2.06	0.71
1:A:668:ASP:HB3	1:A:743:VAL:HG23	1.71	0.71
2:B:313:MET:HE2	2:B:390:LEU:CD2	2.20	0.71
1:A:256:GLN:HE21	2:B:918:ILE:HD11	1.54	0.71
1:A:1325:THR:O	5:E:148:GLU:HB2	1.90	0.71
2:B:261:ARG:O	2:B:267:ARG:HD3	1.90	0.71
2:B:758:PHE:HE1	2:B:1027:ILE:HG22	1.56	0.71
5:E:16:PHE:CZ	5:E:20:LYS:HE2	2.25	0.71
9:I:56:ALA:HB2	9:I:89:GLN:HG3	1.72	0.71
1:A:351:THR:HB	2:B:1103:ILE:HD12	1.72	0.71
2:B:857:ARG:HG2	2:B:858:SER:H	1.55	0.71
1:A:535:THR:HG21	1:A:616:VAL:HA	1.73	0.71
9:I:34:TYR:CE2	9:I:36:GLU:HB3	2.25	0.71
9:I:71:SER:OG	9:I:83:ASN:HB2	1.90	0.71
1:A:567:LYS:HD2	1:A:568:PRO:HD2	1.73	0.71
1:A:1057:VAL:HG12	1:A:1058:VAL:H	1.53	0.71
8:H:102:TYR:N	8:H:102:TYR:CD2	2.58	0.71
12:L:38:LEU:O	12:L:39:SER:HB3	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:339:ASN:HB3	2:B:1117:GLN:NE2	2.05	0.71
1:A:1279:ILE:HD11	1:A:1316:VAL:HG21	1.72	0.71
1:A:152:VAL:HG13	1:A:153:PRO:HD2	1.72	0.70
1:A:1362:TYR:HD1	1:A:1363:VAL:N	1.85	0.70
1:A:59:GLY:HA2	1:A:67:CYS:SG	2.30	0.70
1:A:1242:VAL:HG12	1:A:1243:VAL:H	1.56	0.70
2:B:496:ARG:HB3	2:B:496:ARG:HH11	1.56	0.70
2:B:510:LYS:HB2	2:B:511:PRO:CD	2.21	0.70
2:B:986:GLN:NE2	2:B:1022:THR:HG21	2.05	0.70
1:A:367:PRO:HB3	1:A:465:TYR:O	1.91	0.70
1:A:666:ILE:HD11	2:B:1067:ARG:O	1.90	0.70
1:A:1261:LYS:HA	1:A:1264:GLU:HB3	1.74	0.70
1:A:1435:PRO:O	1:A:1436:ILE:HG13	1.92	0.70
1:A:711:ARG:CG	9:I:97:MET:HE2	2.22	0.70
1:A:888:GLY:O	1:A:940:ARG:NH2	2.24	0.70
1:A:1428:VAL:HG13	2:B:1151:LEU:HD21	1.71	0.70
5:E:124:VAL:HA	5:E:132:ILE:HD12	1.73	0.70
9:I:56:ALA:HB2	9:I:89:GLN:HG2	1.72	0.70
1:A:825:ILE:C	1:A:827:THR:H	1.96	0.70
1:A:1280:GLU:O	1:A:1281:ARG:O	2.10	0.70
2:B:1166:CYS:O	2:B:1168:LEU:N	2.22	0.70
3:C:39:ALA:HA	3:C:164:ALA:HB3	1.74	0.70
3:C:191:TYR:HD2	3:C:201:TRP:CD1	2.09	0.70
5:E:135:PHE:CD2	5:E:140:LEU:HD21	2.27	0.70
11:K:67:PHE:C	11:K:68:PHE:HD2	1.98	0.70
1:A:265:LYS:N	1:A:265:LYS:HD2	2.06	0.70
1:A:375:THR:OG1	1:A:433:GLU:HB3	1.91	0.70
1:A:852:TYR:CD1	6:F:136:ARG:HB3	2.27	0.70
1:A:1420:ASP:HB3	1:A:1422:ARG:HG3	1.72	0.70
1:A:1443:VAL:O	1:A:1444:MET:HG3	1.91	0.70
1:A:1147:THR:HG22	1:A:1149:ALA:H	1.56	0.70
1:A:370:ILE:HG22	1:A:374:LEU:CD1	2.21	0.70
2:B:510:LYS:CB	2:B:511:PRO:HD2	2.21	0.70
2:B:563:MET:CE	2:B:580:VAL:HB	2.21	0.70
2:B:986:GLN:OE1	2:B:986:GLN:HA	1.92	0.70
8:H:81:PRO:HB2	8:H:82:PRO:HD2	1.74	0.70
1:A:414:ASP:OD1	1:A:416:ARG:HG3	1.91	0.70
1:A:698:GLN:HA	9:I:97:MET:O	1.91	0.70
1:A:1385:THR:O	1:A:1388:GLY:N	2.21	0.70
1:A:1104:ILE:O	1:A:1107:VAL:N	2.23	0.70
1:A:1116:LEU:N	1:A:1308:THR:CG2	2.54	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:282:ILE:HD12	2:B:382:ILE:HD13	1.72	0.70
2:B:705:MET:HE1	2:B:742:GLU:OE1	1.91	0.70
1:A:384:ASN:OD1	1:A:388:LEU:HD12	1.92	0.69
1:A:567:LYS:NZ	8:H:46:LEU:HB2	2.07	0.69
1:A:870:GLU:HG2	5:E:208:TYR:CD2	2.27	0.69
3:C:73:GLN:NE2	3:C:74:SER:H	1.89	0.69
12:L:32:ALA:HB3	12:L:55:ILE:CD1	2.21	0.69
1:A:92:HIS:O	1:A:94:GLY:N	2.25	0.69
1:A:1436:ILE:HD13	2:B:1139:ILE:HG23	1.73	0.69
2:B:857:ARG:HH21	2:B:942:ARG:CZ	2.04	0.69
3:C:238:ILE:CG2	3:C:242:GLN:HB2	2.22	0.69
3:C:263:THR:C	3:C:265:MET:H	1.98	0.69
5:E:202:SER:OG	5:E:204:THR:HG22	1.91	0.69
1:A:55:ASP:CG	1:A:55:ASP:O	2.32	0.69
1:A:1057:VAL:HG12	1:A:1058:VAL:N	2.06	0.69
2:B:281:PRO:HG2	2:B:284:ILE:HG13	1.75	0.69
2:B:510:LYS:HB2	2:B:511:PRO:HD2	1.74	0.69
1:A:370:ILE:HG23	2:B:1105:ALA:HB2	1.72	0.69
1:A:1334:ASP:O	1:A:1336:MET:N	2.25	0.69
5:E:164:LEU:HD13	5:E:211:TYR:CE2	2.28	0.69
1:A:347:PHE:H	2:B:1107:ALA:HA	1.57	0.69
1:A:367:PRO:HG2	1:A:370:ILE:HG13	1.74	0.69
1:A:605:MET:HE1	1:A:617:VAL:HA	1.73	0.69
1:A:1283:VAL:HG12	1:A:1284:MET:H	1.58	0.69
2:B:292:ILE:HD13	2:B:326:ASP:HA	1.73	0.69
3:C:147:LEU:HD12	3:C:151:GLN:O	1.91	0.69
6:F:119:ARG:HH11	6:F:119:ARG:HG3	1.57	0.69
1:A:84:ILE:HD11	1:A:270:LEU:HD13	1.74	0.69
1:A:315:LEU:HD23	1:A:321:PRO:HA	1.73	0.69
1:A:337:ARG:NH2	1:A:839:ARG:HH12	1.90	0.69
1:A:1081:LEU:HD21	1:A:1098:VAL:HG21	1.74	0.69
2:B:642:ASP:HB3	2:B:649:LYS:CD	2.23	0.69
2:B:1023:VAL:O	2:B:1027:ILE:HG13	1.93	0.69
3:C:242:GLN:HA	3:C:245:VAL:HG23	1.73	0.69
5:E:177:ARG:C	5:E:212:ARG:HD3	2.18	0.69
1:A:390:GLN:HE21	1:A:394:ASN:ND2	1.91	0.69
2:B:363:HIS:O	2:B:364:ILE:HB	1.91	0.69
2:B:769:TYR:CE2	2:B:987:LYS:NZ	2.55	0.69
2:B:839:MET:CE	2:B:1010:LEU:HD21	2.23	0.69
2:B:871:THR:HG22	2:B:872:GLU:O	1.93	0.69
2:B:1115:THR:O	2:B:1116:ARG:HB2	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:137:ASN:C	4:D:137:ASN:HD22	2.00	0.69
1:A:407:ARG:HG2	1:A:430:TRP:CZ2	2.27	0.69
1:A:567:LYS:CD	1:A:568:PRO:HD2	2.23	0.69
1:A:903:ASN:HD22	1:A:903:ASN:C	2.00	0.69
1:A:1035:TYR:O	1:A:1037:LEU:N	2.25	0.69
2:B:579:ARG:CB	2:B:586:TRP:HE1	2.00	0.69
1:A:69:THR:O	1:A:71:GLN:N	2.25	0.69
1:A:95:PHE:HD1	1:A:234:MET:HG2	1.57	0.69
2:B:200:GLY:HA2	2:B:202:TYR:CE2	2.27	0.69
2:B:948:ILE:HG22	2:B:949:VAL:O	1.93	0.69
1:A:606:LEU:HG	1:A:613:ILE:HD12	1.74	0.69
2:B:483:LEU:HD11	2:B:491:THR:HG23	1.73	0.69
5:E:2:ASP:O	5:E:3:GLN:HG2	1.92	0.69
7:G:1:MET:HE2	7:G:1:MET:O	1.92	0.69
1:A:608:ILE:HG23	1:A:969:GLN:OE1	1.91	0.68
2:B:37:PHE:CE2	2:B:542:MET:HA	2.27	0.68
2:B:1146:PHE:CD1	2:B:1146:PHE:O	2.47	0.68
1:A:979:SER:OG	1:A:980:ASP:N	2.22	0.68
1:A:996:ASN:C	1:A:998:LEU:HD12	2.18	0.68
2:B:606:LYS:HD2	2:B:608:ASP:OD2	1.92	0.68
2:B:821:GLN:HE22	2:B:851:PHE:H	1.42	0.68
2:B:1102:LYS:O	2:B:1103:ILE:C	2.34	0.68
1:A:49:LYS:NZ	1:A:60:SER:HA	2.08	0.68
1:A:709:THR:HG22	1:A:712:GLU:H	1.59	0.68
1:A:1100:ARG:HH21	1:A:1351:GLU:CG	2.07	0.68
2:B:597:MET:HA	2:B:597:MET:HE3	1.75	0.68
2:B:983:ARG:NH1	2:B:1028:GLU:OE1	2.27	0.68
6:F:97:ARG:NH2	6:F:108:PHE:HE1	1.92	0.68
7:G:96:GLN:HA	7:G:121:PHE:CE2	2.28	0.68
7:G:127:PRO:HG2	7:G:138:THR:HG21	1.74	0.68
10:J:2:ILE:HG12	10:J:57:ILE:HD12	1.74	0.68
1:A:239:LEU:HD12	1:A:240:PRO:HD2	1.74	0.68
1:A:768:GLN:CG	1:A:816:HIS:HA	2.22	0.68
1:A:1079:MET:CE	1:A:1101:LEU:HD23	2.23	0.68
2:B:112:LEU:CD1	2:B:113:TYR:H	2.03	0.68
2:B:294:ASP:C	2:B:296:GLU:H	2.01	0.68
11:K:12:LEU:H	11:K:12:LEU:HD12	1.58	0.68
2:B:282:ILE:CD1	2:B:382:ILE:HD13	2.23	0.68
2:B:546:SER:OG	2:B:631:GLY:N	2.22	0.68
2:B:880:THR:O	2:B:881:ASN:HB2	1.94	0.68
2:B:1159:ARG:HB3	2:B:1159:ARG:NH1	2.09	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:45:ALA:CA	3:C:72:LEU:HD12	2.16	0.68
1:A:1331:SER:OG	1:A:1333:ILE:HG22	1.94	0.68
2:B:172:ILE:HD13	2:B:178:ASN:HB2	1.76	0.68
5:E:143:ASN:HD22	5:E:146:HIS:CE1	2.12	0.68
5:E:207:ARG:HB3	5:E:207:ARG:HH11	1.58	0.68
6:F:85:MET:HE1	6:F:148:VAL:HG12	1.74	0.68
1:A:41:MET:O	1:A:50:ILE:HG13	1.94	0.68
1:A:332:LYS:HG3	1:A:333:GLU:HG2	1.76	0.68
1:A:642:CYS:O	1:A:645:LEU:N	2.27	0.68
1:A:1410:PHE:HA	2:B:1212:ILE:HD11	1.75	0.68
2:B:654:ARG:H	2:B:657:HIS:HD2	1.41	0.68
2:B:831:SER:OG	2:B:840:ILE:HD11	1.93	0.68
1:A:837:ILE:HA	1:A:840:ARG:HD3	1.76	0.68
1:A:853:ASP:OD1	1:A:855:THR:CB	2.40	0.68
1:A:901:LEU:HD22	1:A:919:ILE:CG2	2.24	0.68
1:A:1364:ASN:OD1	1:A:1366:ARG:HD2	1.94	0.68
1:A:1437:GLY:HA3	6:F:88:TYR:CD2	2.30	0.67
2:B:552:MET:HA	2:B:555:ILE:HB	1.75	0.67
1:A:337:ARG:HD3	2:B:1132:GLU:OE1	1.94	0.67
1:A:519:PRO:HG2	1:A:624:SER:O	1.94	0.67
5:E:198:ILE:HD11	5:E:212:ARG:HG3	1.76	0.67
1:A:982:THR:O	1:A:985:ASP:HB2	1.94	0.67
2:B:622:LYS:HE3	9:I:59:VAL:HG22	1.76	0.67
7:G:13:LEU:HD23	7:G:14:HIS:N	2.10	0.67
7:G:73:LYS:HE2	7:G:74:TYR:O	1.95	0.67
8:H:84:ALA:CB	8:H:87:ARG:HB2	2.25	0.67
1:A:1192:LEU:HG	1:A:1193:LEU:N	2.08	0.67
1:A:1342:GLU:CD	5:E:198:ILE:HG21	2.18	0.67
2:B:217:ARG:NE	2:B:405:ARG:HB2	2.10	0.67
3:C:105:GLY:HA3	3:C:149:LYS:O	1.92	0.67
6:F:103:MET:HE1	7:G:65:ASP:HB2	1.76	0.67
7:G:106:MET:HG3	7:G:157:ILE:O	1.93	0.67
1:A:997:LEU:HD13	1:A:1018:PHE:HE2	1.60	0.67
1:A:1325:THR:HG22	1:A:1326:ARG:HG3	1.74	0.67
2:B:37:PHE:CE1	2:B:41:LYS:HG3	2.29	0.67
2:B:204:ILE:C	2:B:205:ILE:HD12	2.19	0.67
2:B:900:ALA:O	2:B:903:VAL:HG23	1.95	0.67
3:C:47:ASP:HA	12:L:69:ALA:HB3	1.77	0.67
1:A:78:PRO:HA	2:B:1201:LYS:HZ1	1.59	0.67
1:A:567:LYS:HD3	8:H:95:TYR:CG	2.30	0.67
1:A:1083:THR:HG21	1:A:1085:HIS:CE1	2.30	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:273:LEU:CB	2:B:276:ILE:HD12	2.21	0.67
2:B:1010:LEU:HD12	2:B:1011:ILE:H	1.60	0.67
3:C:6:PRO:HB3	3:C:25:VAL:CG1	2.24	0.67
1:A:567:LYS:HB2	1:A:568:PRO:CD	2.25	0.67
2:B:95:ILE:HG13	2:B:130:VAL:HG22	1.76	0.67
2:B:97:VAL:HG12	2:B:178:ASN:ND2	2.09	0.67
2:B:378:LEU:HD12	2:B:378:LEU:O	1.94	0.67
1:A:886:ILE:CD1	1:A:943:LEU:HB3	2.22	0.67
1:A:889:SER:HB3	1:A:1297:GLU:HG2	1.75	0.67
1:A:1227:ILE:HG22	1:A:1228:TRP:N	2.09	0.67
2:B:546:SER:OG	2:B:630:ALA:HA	1.95	0.67
1:A:858:ASN:ND2	1:A:860:LEU:H	1.92	0.67
1:A:1447:GLU:OE2	7:G:23:LYS:HB2	1.94	0.67
2:B:899:ILE:CG2	2:B:903:VAL:HG21	2.25	0.67
2:B:1165:ILE:HG22	2:B:1166:CYS:H	1.59	0.67
1:A:75:ASN:O	1:A:76:GLU:HB3	1.95	0.67
1:A:87:ALA:HB3	1:A:276:LEU:HD23	1.77	0.67
1:A:1089:VAL:O	1:A:1089:VAL:HG12	1.94	0.67
2:B:854:LEU:HB3	2:B:856:PHE:HE1	1.60	0.67
3:C:86:CYS:O	3:C:88:CYS:N	2.27	0.67
1:A:34:LYS:HB2	1:A:36:ARG:HH21	1.60	0.66
1:A:829:VAL:HG13	2:B:507:LYS:HG2	1.76	0.66
1:A:1161:THR:OG1	1:A:1170:ILE:HD11	1.95	0.66
2:B:205:ILE:HD12	2:B:205:ILE:N	2.10	0.66
2:B:237:VAL:HG22	2:B:257:LYS:HA	1.78	0.66
2:B:1065:GLN:HB3	2:B:1069:PHE:O	1.95	0.66
10:J:7:CYS:SG	10:J:46:CYS:HA	2.34	0.66
12:L:61:THR:HG21	12:L:63:ARG:HG2	1.78	0.66
1:A:134:ARG:O	1:A:134:ARG:HG2	1.94	0.66
1:A:1121:GLU:CG	1:A:1122:PRO:HD2	2.24	0.66
2:B:240:ILE:HG22	2:B:254:LEU:HB3	1.77	0.66
2:B:411:PRO:O	2:B:414:ALA:HB3	1.95	0.66
12:L:58:LYS:O	12:L:59:ALA:O	2.13	0.66
1:A:55:ASP:N	1:A:56:PRO:HD3	2.11	0.66
1:A:265:LYS:HD2	1:A:265:LYS:H	1.60	0.66
1:A:1291:VAL:HG13	1:A:1292:PRO:CD	2.25	0.66
2:B:594:ALA:HA	2:B:617:ARG:HH12	1.61	0.66
2:B:882:THR:CG2	2:B:884:ARG:HB2	2.25	0.66
2:B:1065:GLN:HB2	3:C:201:TRP:CZ3	2.31	0.66
5:E:55:ARG:C	5:E:57:MET:H	2.04	0.66
1:A:1283:VAL:HG12	1:A:1284:MET:N	2.11	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:594:ALA:HA	2:B:617:ARG:NH1	2.09	0.66
2:B:705:MET:H	2:B:710:LEU:CD1	2.09	0.66
7:G:91:VAL:HB	7:G:139:ILE:O	1.95	0.66
9:I:58:VAL:HG13	9:I:62:ILE:CG1	2.25	0.66
1:A:550:LEU:HD22	1:A:556:TRP:CE2	2.31	0.66
2:B:579:ARG:HD2	2:B:586:TRP:CZ2	2.30	0.66
2:B:616:ILE:HD12	2:B:616:ILE:N	2.11	0.66
2:B:820:GLY:N	2:B:1091:TYR:OH	2.29	0.66
3:C:92:CYS:SG	3:C:94:LYS:HB3	2.36	0.66
3:C:107:SER:C	3:C:109:SER:H	2.04	0.66
3:C:174:ALA:O	3:C:175:ALA:HB2	1.95	0.66
1:A:50:ILE:C	1:A:52:GLY:H	2.03	0.66
1:A:90:VAL:HG13	1:A:297:GLN:OE1	1.96	0.66
1:A:254:GLU:HB2	2:B:935:ARG:HH22	1.60	0.66
1:A:1313:LEU:HD23	1:A:1338:VAL:CG2	2.26	0.66
2:B:322:PHE:HZ	9:I:30:ARG:HB3	1.61	0.66
2:B:862:GLN:HG2	2:B:963:PHE:CD1	2.28	0.66
5:E:182:ASP:O	5:E:185:ALA:N	2.28	0.66
9:I:34:TYR:HE2	9:I:36:GLU:HB3	1.60	0.66
12:L:31:CYS:HB3	12:L:34:CYS:C	2.21	0.66
2:B:1223:ASP:O	2:B:1224:PHE:HB2	1.96	0.66
12:L:60:ARG:HG2	12:L:61:THR:H	1.60	0.66
1:A:538:ASP:OD2	8:H:22:LYS:HB2	1.96	0.66
2:B:773:MET:C	2:B:775:LYS:N	2.49	0.66
2:B:898:LEU:HB2	12:L:58:LYS:NZ	2.10	0.66
2:B:1099:VAL:HG13	2:B:1100:ASP:N	2.10	0.66
3:C:50:GLU:HG2	12:L:64:LEU:CD1	2.25	0.66
1:A:870:GLU:HB2	5:E:204:THR:HG21	1.76	0.66
1:A:1195:LEU:HD11	1:A:1267:MET:HE1	1.78	0.66
1:A:1376:THR:OG1	1:A:1377:THR:N	2.23	0.66
1:A:1445:ILE:HD12	1:A:1445:ILE:N	2.11	0.66
2:B:169:ARG:HB2	2:B:454:THR:HG23	1.75	0.66
2:B:365:THR:HG23	2:B:367:LEU:H	1.62	0.66
2:B:910:VAL:HG12	2:B:911:ILE:N	2.11	0.66
5:E:157:SER:OG	5:E:160:GLU:HG3	1.96	0.66
1:A:133:LYS:C	1:A:135:PHE:H	2.02	0.65
1:A:908:LEU:CD1	1:A:983:ILE:HD11	2.25	0.65
1:A:1118:VAL:HG12	1:A:1327:ILE:HG13	1.77	0.65
2:B:294:ASP:OD2	2:B:294:ASP:N	2.25	0.65
2:B:1159:ARG:NE	2:B:1193:GLN:HE21	1.94	0.65
2:B:1198:TYR:CE1	2:B:1201:LYS:HD2	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:5:GLY:O	3:C:7:GLN:HG3	1.96	0.65
7:G:143:ILE:HG22	7:G:144:ARG:N	2.11	0.65
8:H:41:ASP:O	8:H:42:ILE:HG13	1.97	0.65
12:L:28:LYS:HB2	12:L:39:SER:HB2	1.78	0.65
1:A:550:LEU:HD22	1:A:556:TRP:NE1	2.11	0.65
1:A:556:TRP:C	1:A:558:GLY:H	2.05	0.65
1:A:709:THR:HB	1:A:712:GLU:HB2	1.77	0.65
3:C:73:GLN:HB3	3:C:131:HIS:H	1.60	0.65
3:C:241:ASP:O	3:C:245:VAL:HG23	1.96	0.65
1:A:866:PHE:C	1:A:867:ILE:HD12	2.21	0.65
1:A:886:ILE:HG22	1:A:887:GLY:N	2.11	0.65
2:B:117:ALA:HA	2:B:122:LEU:HD12	1.78	0.65
2:B:797:TYR:C	2:B:798:TYR:HD2	2.04	0.65
2:B:955:THR:HG22	2:B:956:THR:N	2.12	0.65
1:A:63:ARG:HG2	1:A:74:MET:SD	2.36	0.65
1:A:275:SER:O	1:A:279:LEU:HG	1.96	0.65
1:A:591:PHE:HA	1:A:595:THR:HG21	1.77	0.65
1:A:1161:THR:C	1:A:1163:ILE:H	2.04	0.65
4:D:35:LEU:HD12	4:D:35:LEU:N	2.12	0.65
2:B:794:ASN:O	2:B:795:ILE:HD12	1.96	0.65
2:B:802:PRO:HA	2:B:822:ASN:HD21	1.61	0.65
2:B:1156:ASP:O	2:B:1157:ALA:O	2.15	0.65
3:C:43:THR:HG22	3:C:44:LEU:N	2.10	0.65
5:E:157:SER:C	5:E:159:ASP:H	2.04	0.65
9:I:85:PHE:HD2	9:I:85:PHE:N	1.78	0.65
2:B:261:ARG:NH1	2:B:261:ARG:HB3	2.11	0.65
2:B:825:VAL:HG22	2:B:1010:LEU:HB3	1.79	0.65
2:B:1020:ARG:HH11	2:B:1020:ARG:CG	2.09	0.65
5:E:78:LEU:HD23	5:E:79:TRP:N	2.11	0.65
7:G:111:THR:CG2	7:G:113:HIS:H	2.04	0.65
1:A:107:CYS:N	1:A:114:LEU:HD21	2.11	0.65
1:A:264:PHE:O	1:A:267:ALA:HB3	1.96	0.65
1:A:489:LEU:HD12	1:A:489:LEU:C	2.21	0.65
1:A:855:THR:CG2	1:A:857:ARG:HE	1.99	0.65
1:A:1283:VAL:O	1:A:1306:LEU:HA	1.96	0.65
1:A:1329:THR:H	1:A:1335:ILE:CD1	1.95	0.65
2:B:827:ILE:HD12	2:B:1086:PHE:CD2	2.32	0.65
9:I:101:PHE:HD1	9:I:101:PHE:N	1.91	0.65
1:A:67:CYS:O	1:A:70:CYS:HB3	1.97	0.65
1:A:689:LYS:HE2	1:A:721:PHE:CE2	2.32	0.65
1:A:871:ASP:OD1	1:A:1366:ARG:NH2	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:120:ARG:HG2	2:B:955:THR:HG21	1.79	0.65
2:B:227:LYS:HB2	2:B:395:GLN:OE1	1.97	0.65
2:B:322:PHE:CZ	9:I:30:ARG:HB3	2.32	0.65
2:B:687:GLU:O	2:B:689:LEU:HG	1.96	0.65
2:B:750:GLY:O	2:B:751:VAL:C	2.39	0.65
2:B:981:ALA:HB2	2:B:987:LYS:HA	1.78	0.65
2:B:991:GLY:O	2:B:992:ILE:HB	1.95	0.65
8:H:91:ASP:C	8:H:93:TYR:H	2.05	0.65
8:H:123:MET:HE1	8:H:142:LEU:CD1	2.26	0.65
1:A:443:LEU:HG	2:B:1146:PHE:CE2	2.27	0.65
2:B:824:ILE:HG12	10:J:48:ARG:NH1	2.08	0.65
2:B:953:LEU:CD2	2:B:965:LYS:HB2	2.26	0.65
3:C:179:GLU:HG2	3:C:180:TYR:N	2.12	0.65
1:A:115:LEU:O	1:A:122:MET:HE2	1.97	0.64
2:B:856:PHE:CD1	2:B:856:PHE:N	2.64	0.64
3:C:235:VAL:HG13	10:J:13:VAL:HG23	1.79	0.64
1:A:593:GLU:O	1:A:595:THR:N	2.30	0.64
2:B:361:LEU:HD21	2:B:377:PHE:CD2	2.32	0.64
2:B:770:GLN:HG2	2:B:983:ARG:O	1.96	0.64
8:H:89:LEU:HB3	8:H:91:ASP:OD1	1.97	0.64
1:A:407:ARG:HD2	1:A:413:ILE:HD11	1.78	0.64
1:A:855:THR:HG23	1:A:857:ARG:HG3	1.78	0.64
1:A:1423:GLY:O	1:A:1424:VAL:C	2.40	0.64
7:G:34:VAL:HG12	7:G:45:ILE:HG21	1.80	0.64
1:A:243:PRO:O	1:A:246:VAL:HG23	1.98	0.64
1:A:683:ILE:HG21	1:A:801:GLU:HG3	1.80	0.64
1:A:704:ALA:O	1:A:705:LYS:HB2	1.97	0.64
2:B:446:LEU:O	2:B:447:ALA:HB3	1.97	0.64
2:B:508:LEU:HB2	2:B:510:LYS:N	2.10	0.64
2:B:952:VAL:HG12	2:B:953:LEU:N	2.11	0.64
4:D:47:LEU:HD13	4:D:48:ILE:H	1.63	0.64
6:F:97:ARG:HH22	6:F:108:PHE:HE1	1.45	0.64
1:A:820:GLY:C	1:A:822:GLU:H	2.05	0.64
1:A:1409:LEU:O	1:A:1412:ALA:HB3	1.97	0.64
2:B:54:PHE:CE2	2:B:59:LEU:HD13	2.32	0.64
2:B:508:LEU:HB2	2:B:510:LYS:CA	2.28	0.64
2:B:859:TYR:HD1	2:B:859:TYR:H	1.44	0.64
7:G:14:HIS:ND1	7:G:15:PRO:HD2	2.12	0.64
1:A:1148:ILE:O	1:A:1148:ILE:HG22	1.98	0.64
2:B:294:ASP:O	2:B:296:GLU:N	2.30	0.64
7:G:126:ASN:HD22	7:G:127:PRO:HA	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1120:LEU:O	1:A:1323:ASP:HB2	1.98	0.64
2:B:23:ALA:HB1	2:B:24:PRO:CD	2.23	0.64
2:B:37:PHE:HD2	2:B:542:MET:SD	2.21	0.64
2:B:737:THR:HG21	9:I:66:PRO:HA	1.79	0.64
2:B:855:PHE:CD1	2:B:855:PHE:C	2.75	0.64
6:F:86:THR:HG23	6:F:89:GLU:OE1	1.97	0.64
8:H:93:TYR:HB3	8:H:144:ILE:O	1.98	0.64
1:A:25:GLU:H	1:A:25:GLU:CD	2.06	0.64
2:B:54:PHE:HE1	2:B:414:ALA:HA	1.62	0.64
2:B:789:MET:HE2	2:B:965:LYS:O	1.97	0.64
1:A:534:LEU:O	1:A:574:GLY:HA3	1.98	0.64
1:A:1334:ASP:C	1:A:1336:MET:N	2.55	0.64
2:B:705:MET:H	2:B:710:LEU:HD12	1.61	0.64
7:G:6:ASP:O	7:G:7:LEU:HD23	1.98	0.64
1:A:370:ILE:HG22	1:A:374:LEU:HD11	1.80	0.64
1:A:1422:ARG:HH22	2:B:1224:PHE:C	2.06	0.64
1:A:1423:GLY:O	1:A:1426:GLU:N	2.31	0.64
1:A:42:ASP:C	1:A:44:THR:H	2.06	0.63
1:A:47:ARG:NH2	1:A:255:SER:H	1.95	0.63
2:B:35:SER:HA	2:B:811:TYR:CE2	2.26	0.63
2:B:390:LEU:O	2:B:392:ARG:HG3	1.98	0.63
2:B:1060:ARG:HG2	2:B:1060:ARG:HH11	1.61	0.63
3:C:35:ARG:NH1	11:K:41:THR:H	1.96	0.63
9:I:88:SER:C	9:I:90:GLN:H	2.07	0.63
1:A:61:ILE:O	1:A:63:ARG:N	2.32	0.63
1:A:283:GLY:O	1:A:285:PRO:HD3	1.99	0.63
1:A:845:LEU:HB3	1:A:848:ILE:HD12	1.80	0.63
9:I:113:ASP:O	9:I:114:GLN:HG3	1.98	0.63
11:K:47:ARG:HB3	11:K:47:ARG:NH1	2.12	0.63
2:B:315:LYS:N	2:B:316:PRO:HD2	2.11	0.63
2:B:859:TYR:N	2:B:859:TYR:CD1	2.67	0.63
2:B:63:ILE:HA	2:B:421:PHE:CE2	2.33	0.63
2:B:604:ARG:NH2	2:B:614:SER:HA	2.13	0.63
7:G:14:HIS:CE1	7:G:15:PRO:HD2	2.34	0.63
7:G:49:LEU:HD21	7:G:77:VAL:HG23	1.80	0.63
12:L:28:LYS:HB2	12:L:39:SER:CB	2.28	0.63
1:A:305:ASP:CG	1:A:326:ARG:HD2	2.24	0.63
1:A:335:ARG:HE	1:A:339:ASN:HD22	1.45	0.63
1:A:367:PRO:HA	1:A:463:ILE:O	1.99	0.63
2:B:284:ILE:HD13	2:B:333:PHE:HD2	1.64	0.63
2:B:640:VAL:O	2:B:641:GLU:C	2.41	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:2:THR:O	9:I:3:THR:C	2.41	0.63
1:A:17:VAL:HG23	1:A:1421:CYS:SG	2.38	0.63
1:A:256:GLN:NE2	2:B:918:ILE:HD11	2.14	0.63
1:A:637:LYS:HB3	1:A:641:VAL:HG21	1.81	0.63
1:A:1074:GLU:HB3	1:A:1075:PRO:HD3	1.80	0.63
1:A:1098:VAL:N	1:A:1099:PRO:HD2	2.13	0.63
2:B:589:VAL:CG1	2:B:590:HIS:H	2.06	0.63
4:D:211:LEU:HD23	4:D:214:LEU:HD12	1.79	0.63
5:E:78:LEU:HD21	5:E:80:VAL:HG23	1.81	0.63
7:G:80:LYS:HE2	7:G:82:PHE:CZ	2.34	0.63
10:J:5:VAL:HG12	10:J:6:ARG:HG3	1.80	0.63
1:A:546:VAL:HG21	1:A:572:TRP:CE3	2.34	0.63
1:A:845:LEU:HD12	1:A:1069:ALA:HB2	1.80	0.63
1:A:1206:ASP:O	1:A:1274:ARG:NH1	2.31	0.63
2:B:39:ARG:HH21	2:B:665:GLU:CG	2.10	0.63
3:C:34:ARG:HA	3:C:37:MET:HE3	1.79	0.63
3:C:75:MET:HE2	3:C:239:PRO:HD3	1.81	0.63
1:A:858:ASN:C	1:A:858:ASN:ND2	2.53	0.63
1:A:922:ASP:OD1	1:A:924:LYS:N	2.32	0.63
1:A:1019:CYS:O	1:A:1022:LEU:HB3	1.99	0.63
1:A:1213:GLY:HA2	1:A:1216:ILE:HD12	1.81	0.63
1:A:1428:VAL:HG13	2:B:1151:LEU:CD2	2.28	0.63
2:B:526:GLU:OE2	2:B:752:ALA:HB2	1.98	0.63
2:B:542:MET:HE2	2:B:743:ILE:HG13	1.81	0.63
2:B:762:ASN:HD21	2:B:1024:ALA:HB3	1.64	0.63
2:B:1224:PHE:CE2	5:E:171:LYS:HG3	2.33	0.63
5:E:197:LYS:HG2	5:E:197:LYS:O	1.97	0.63
8:H:84:ALA:C	8:H:86:ASP:H	2.06	0.63
3:C:35:ARG:NH1	11:K:41:THR:N	2.47	0.63
5:E:168:TYR:HB3	5:E:170:LEU:HG	1.81	0.63
1:A:244:PRO:HG2	1:A:245:PRO:HD3	1.81	0.62
1:A:1230:GLU:O	1:A:1232:ASN:N	2.32	0.62
2:B:129:PHE:HA	2:B:165:VAL:O	1.99	0.62
2:B:601:ARG:O	2:B:605:ARG:HG3	1.99	0.62
3:C:22:LEU:HD13	3:C:230:MET:HE1	1.81	0.62
6:F:77:ASP:C	6:F:79:ARG:H	2.07	0.62
8:H:42:ILE:HG23	8:H:95:TYR:CE1	2.34	0.62
1:A:265:LYS:HE2	1:A:322:VAL:HG13	1.81	0.62
1:A:849:MET:CE	1:A:1061:GLY:HA2	2.28	0.62
1:A:1081:LEU:HD11	1:A:1098:VAL:HB	1.81	0.62
2:B:1147:LEU:C	2:B:1147:LEU:HD23	2.24	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:691:LEU:O	1:A:694:THR:HB	1.99	0.62
1:A:783:THR:HG21	1:A:815:PHE:CZ	2.33	0.62
1:A:1017:LEU:CB	5:E:205:SER:HA	2.29	0.62
3:C:235:VAL:HG21	10:J:6:ARG:NH2	2.14	0.62
7:G:80:LYS:HE2	7:G:82:PHE:HZ	1.64	0.62
1:A:90:VAL:CG1	1:A:91:PHE:N	2.63	0.62
1:A:265:LYS:O	1:A:266:LEU:C	2.41	0.62
1:A:1072:ILE:O	1:A:1075:PRO:HG2	1.98	0.62
1:A:1080:THR:O	1:A:1081:LEU:HD22	1.98	0.62
2:B:773:MET:O	2:B:776:GLN:N	2.28	0.62
3:C:33:LEU:CG	3:C:37:MET:HE2	2.26	0.62
3:C:147:LEU:HB2	3:C:151:GLN:CB	2.29	0.62
2:B:292:ILE:CD1	2:B:326:ASP:HA	2.30	0.62
5:E:192:ARG:HH11	5:E:192:ARG:HG3	1.64	0.62
7:G:23:LYS:HG3	7:G:56:ILE:CD1	2.28	0.62
7:G:117:GLN:C	7:G:119:LEU:H	2.07	0.62
9:I:87:GLN:O	9:I:89:GLN:OE1	2.18	0.62
1:A:14:VAL:N	1:A:1432:GLN:HE22	1.88	0.62
1:A:21:LEU:HG	1:A:1413:GLY:O	2.00	0.62
1:A:399:HIS:CB	1:A:400:PRO:HD3	2.26	0.62
1:A:818:MET:HG2	2:B:514:LEU:HG	1.81	0.62
2:B:604:ARG:HH22	2:B:614:SER:HA	1.62	0.62
2:B:835:GLN:HA	2:B:1013:ASN:ND2	2.10	0.62
2:B:1099:VAL:HG22	2:B:1103:ILE:HD13	1.80	0.62
3:C:63:ILE:CA	3:C:66:ARG:HG3	2.26	0.62
3:C:143:LEU:HD12	3:C:145:CYS:H	1.64	0.62
1:A:289:ILE:O	1:A:291:GLU:N	2.33	0.62
1:A:590:ARG:HG3	1:A:590:ARG:NH1	2.15	0.62
1:A:998:LEU:HD12	1:A:998:LEU:H	1.65	0.62
2:B:189:LEU:HA	2:B:192:LEU:HD12	1.82	0.62
3:C:143:LEU:HD12	3:C:143:LEU:C	2.25	0.62
7:G:108:VAL:HG22	7:G:159:ALA:HB3	1.81	0.62
1:A:535:THR:HG21	1:A:617:VAL:H	1.63	0.62
1:A:567:LYS:HG3	1:A:568:PRO:HD2	1.80	0.62
1:A:1279:ILE:HD11	1:A:1316:VAL:CG2	2.29	0.62
1:A:1402:PHE:O	1:A:1404:GLU:N	2.32	0.62
2:B:31:TRP:CZ3	2:B:34:ILE:HD12	2.35	0.62
7:G:6:ASP:HB3	7:G:73:LYS:HZ1	1.64	0.62
11:K:91:CYS:O	11:K:94:ILE:HB	1.99	0.62
1:A:93:VAL:HG22	1:A:301:ALA:HA	1.80	0.62
1:A:1206:ASP:O	1:A:1207:LEU:HG	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:510:LYS:CG	2:B:512:ARG:H	2.11	0.62
1:A:1029:ARG:HH11	1:A:1029:ARG:CG	2.09	0.62
2:B:511:PRO:C	2:B:513:GLN:N	2.51	0.62
2:B:780:VAL:HG12	2:B:782:LEU:O	1.99	0.62
2:B:1149:GLU:O	2:B:1151:LEU:N	2.32	0.62
8:H:23:VAL:HG13	8:H:42:ILE:O	2.00	0.62
8:H:102:TYR:N	8:H:102:TYR:HD2	1.96	0.62
1:A:515:GLN:OE1	1:A:1071:SER:HA	1.99	0.61
1:A:886:ILE:HG13	1:A:943:LEU:CD1	2.30	0.61
2:B:510:LYS:HG2	2:B:512:ARG:CB	2.30	0.61
2:B:1084:GLN:HG2	3:C:201:TRP:CZ2	2.34	0.61
11:K:12:LEU:HD21	11:K:18:LYS:HG2	1.80	0.61
1:A:168:GLY:O	1:A:169:ASN:C	2.43	0.61
1:A:605:MET:SD	1:A:621:THR:HG21	2.40	0.61
2:B:236:HIS:CE1	2:B:389:ALA:HA	2.35	0.61
2:B:557:PHE:C	2:B:557:PHE:CD2	2.77	0.61
2:B:999:MET:HA	2:B:999:MET:HE3	1.81	0.61
2:B:1001:PHE:CZ	2:B:1073:TYR:HB2	2.35	0.61
2:B:1182:CYS:C	2:B:1183:LYS:HE3	2.25	0.61
6:F:79:ARG:HG3	6:F:144:GLU:OE1	2.00	0.61
1:A:289:ILE:C	1:A:291:GLU:N	2.58	0.61
1:A:1081:LEU:CD1	1:A:1098:VAL:HB	2.30	0.61
1:A:1164:PRO:HG2	1:A:1165:GLU:HG3	1.82	0.61
1:A:1227:ILE:HG22	1:A:1228:TRP:H	1.64	0.61
1:A:1353:TYR:C	1:A:1353:TYR:CD2	2.77	0.61
2:B:549:THR:HG22	2:B:550:ASP:N	2.12	0.61
4:D:170:THR:HG22	4:D:172:LEU:HG	1.82	0.61
7:G:1:MET:HE3	7:G:80:LYS:O	2.00	0.61
1:A:503:GLN:C	1:A:504:LEU:HD12	2.25	0.61
1:A:708:MET:O	1:A:709:THR:O	2.17	0.61
1:A:963:ILE:HD11	1:A:1048:ASN:CB	2.30	0.61
1:A:963:ILE:CD1	1:A:1049:ILE:HG13	2.30	0.61
2:B:37:PHE:CD1	2:B:41:LYS:HG3	2.35	0.61
2:B:519:TRP:C	2:B:519:TRP:CD1	2.77	0.61
2:B:880:THR:HG21	2:B:934:LYS:HE3	1.82	0.61
2:B:1033:LYS:HD2	2:B:1087:PHE:O	2.00	0.61
2:B:1145:SER:C	2:B:1147:LEU:N	2.55	0.61
2:B:1201:LYS:HE2	2:B:1205:GLN:OE1	2.00	0.61
6:F:97:ARG:NH2	6:F:108:PHE:CE1	2.68	0.61
10:J:3:VAL:HG21	10:J:18:TRP:CB	2.30	0.61
1:A:549:MET:HE1	1:A:656:TRP:HD1	1.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:852:TYR:CE2	1:A:1060:PRO:HB2	2.36	0.61
2:B:129:PHE:HE2	2:B:166:PHE:HD1	1.49	0.61
2:B:824:ILE:CG1	10:J:48:ARG:HH12	2.11	0.61
2:B:1051:THR:HB	2:B:1054:GLY:H	1.64	0.61
2:B:1177:HIS:C	2:B:1179:GLN:H	2.08	0.61
2:B:1183:LYS:N	2:B:1183:LYS:CE	2.62	0.61
3:C:67:LEU:HA	3:C:70:ILE:CD1	2.30	0.61
1:A:90:VAL:HG13	1:A:297:GLN:CD	2.25	0.61
1:A:528:LEU:O	1:A:531:ILE:HG22	2.01	0.61
1:A:1237:ILE:CG2	1:A:1238:ILE:N	2.63	0.61
2:B:292:ILE:HD11	2:B:327:ARG:H	1.64	0.61
4:D:144:THR:HG21	7:G:46:LEU:HD13	1.81	0.61
11:K:67:PHE:C	11:K:68:PHE:CD2	2.78	0.61
1:A:442:VAL:O	1:A:457:ALA:HA	2.00	0.61
2:B:487:THR:HG22	2:B:488:TYR:N	2.15	0.61
2:B:1096:ARG:O	2:B:1097:HIS:HB2	2.00	0.61
4:D:40:HIS:CE1	4:D:41:GLN:HG3	2.35	0.61
7:G:114:LEU:HD23	7:G:161:GLY:O	2.00	0.61
1:A:152:VAL:CG1	1:A:153:PRO:HD2	2.31	0.61
1:A:541:ILE:HD13	1:A:549:MET:HE1	1.83	0.61
1:A:852:TYR:CE1	6:F:136:ARG:HG2	2.36	0.61
1:A:897:TYR:HD2	1:A:936:LEU:HD13	1.65	0.61
2:B:705:MET:N	2:B:710:LEU:HD12	2.16	0.61
2:B:975:GLN:NE2	2:B:1100:ASP:OD2	2.30	0.61
3:C:177:GLU:HB2	3:C:231:ASN:HB3	1.83	0.61
8:H:59:ILE:HG22	8:H:60:ALA:H	1.64	0.61
8:H:81:PRO:CB	8:H:82:PRO:CD	2.77	0.61
1:A:254:GLU:CB	2:B:935:ARG:HH22	2.14	0.61
1:A:694:THR:O	1:A:698:GLN:HG3	1.99	0.61
2:B:533:CYS:C	2:B:535:LEU:H	2.09	0.61
2:B:758:PHE:CE1	2:B:1027:ILE:HG22	2.35	0.61
2:B:1180:PHE:HB3	2:B:1191:ILE:CD1	2.31	0.61
3:C:58:LEU:H	3:C:58:LEU:CD2	2.14	0.61
5:E:35:VAL:C	5:E:37:LEU:H	2.08	0.61
8:H:40:LEU:HD22	8:H:123:MET:HE3	1.82	0.61
1:A:761:MET:HA	1:A:804:TYR:HB2	1.82	0.61
1:A:823:GLY:C	1:A:825:ILE:H	2.08	0.61
1:A:857:ARG:HD3	1:A:861:GLY:O	2.00	0.61
2:B:47:GLN:O	2:B:173:MET:HE1	2.01	0.61
2:B:545:ILE:HG22	2:B:546:SER:O	2.01	0.61
4:D:51:ASN:O	4:D:54:GLU:HB3	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:ARG:O	1:A:138:ILE:HG13	2.01	0.60
1:A:849:MET:HE1	1:A:1061:GLY:HA2	1.83	0.60
1:A:1202:MET:HE1	1:A:1212:VAL:CG2	2.30	0.60
2:B:65:GLU:HG3	2:B:66:ASP:N	2.07	0.60
2:B:69:LEU:HD22	2:B:429:PHE:CE1	2.35	0.60
2:B:604:ARG:NH1	2:B:691:GLU:OE2	2.33	0.60
2:B:952:VAL:HG12	2:B:953:LEU:H	1.65	0.60
5:E:86:PRO:O	5:E:114:ASN:HB2	1.99	0.60
1:A:69:THR:C	1:A:71:GLN:N	2.57	0.60
1:A:332:LYS:H	1:A:337:ARG:HB3	1.66	0.60
1:A:804:TYR:OH	2:B:763:GLN:HA	2.00	0.60
1:A:869:GLY:O	5:E:204:THR:HG21	2.01	0.60
1:A:1001:ARG:O	1:A:1002:GLY:O	2.18	0.60
1:A:1203:ASN:O	1:A:1204:ASP:C	2.44	0.60
2:B:653:VAL:CG2	2:B:689:LEU:HB3	2.30	0.60
2:B:839:MET:HE3	2:B:1010:LEU:HD21	1.81	0.60
2:B:1169:MET:HE1	2:B:1201:LYS:CA	2.26	0.60
3:C:169:LYS:NZ	12:L:69:ALA:HB3	2.16	0.60
4:D:210:ILE:O	4:D:214:LEU:HG	2.01	0.60
1:A:44:THR:O	1:A:45:GLN:HB2	1.99	0.60
1:A:708:MET:HE2	1:A:1089:VAL:CG1	2.28	0.60
2:B:778:MET:CE	2:B:1094:ARG:HD3	2.32	0.60
3:C:212:PRO:CB	3:C:213:PRO:HD2	2.31	0.60
3:C:248:ILE:HD13	11:K:101:LEU:HD22	1.82	0.60
5:E:60:PHE:CE2	5:E:80:VAL:HB	2.36	0.60
10:J:23:ASN:C	10:J:25:LEU:H	2.09	0.60
10:J:57:ILE:HG23	10:J:58:GLU:N	2.16	0.60
10:J:57:ILE:HG23	10:J:58:GLU:H	1.66	0.60
1:A:91:PHE:HD2	1:A:96:ILE:HG12	1.66	0.60
1:A:711:ARG:HA	9:I:97:MET:HE2	1.83	0.60
2:B:310:MET:O	2:B:313:MET:HB2	2.02	0.60
2:B:807:ARG:HB3	2:B:807:ARG:HH11	1.66	0.60
3:C:31:ASN:O	3:C:32:SER:C	2.45	0.60
3:C:90:ASP:O	3:C:90:ASP:CG	2.43	0.60
9:I:106:CYS:O	9:I:107:SER:HB2	1.99	0.60
1:A:412:ARG:NH2	2:B:1108:ARG:NH1	2.47	0.60
1:A:606:LEU:HB2	1:A:614:PHE:CE2	2.37	0.60
1:A:821:ARG:O	1:A:825:ILE:HG13	2.01	0.60
1:A:901:LEU:N	1:A:926:GLN:HE21	1.98	0.60
1:A:902:LEU:O	1:A:903:ASN:HB2	2.01	0.60
1:A:1394:THR:HG23	1:A:1398:MET:HE3	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:113:TYR:HB3	2:B:114:PRO:CD	2.29	0.60
2:B:899:ILE:CD1	2:B:911:ILE:HA	2.30	0.60
7:G:145:VAL:CG1	7:G:146:LYS:N	2.64	0.60
8:H:40:LEU:CD1	8:H:123:MET:HB2	2.27	0.60
9:I:58:VAL:HA	9:I:62:ILE:CD1	2.32	0.60
1:A:144:THR:O	1:A:146:MET:HG3	2.01	0.60
1:A:820:GLY:C	1:A:822:GLU:N	2.60	0.60
1:A:1424:VAL:HG11	2:B:1139:ILE:HD13	1.84	0.60
2:B:216:GLU:HA	2:B:406:LEU:HD23	1.84	0.60
3:C:9:LYS:O	3:C:10:ILE:C	2.44	0.60
8:H:83:GLN:C	8:H:85:GLY:H	2.08	0.60
1:A:47:ARG:HH22	1:A:254:GLU:HA	1.65	0.60
1:A:225:ASN:ND2	1:A:227:VAL:H	1.98	0.60
1:A:469:ARG:HG2	1:A:469:ARG:HH11	1.67	0.60
1:A:714:PHE:CD2	9:I:97:MET:HE1	2.36	0.60
1:A:855:THR:CG2	1:A:857:ARG:HG3	2.32	0.60
2:B:605:ARG:CZ	2:B:639:ILE:HD13	2.31	0.60
3:C:46:ILE:HD13	3:C:157:CYS:SG	2.41	0.60
3:C:142:VAL:H	10:J:16:ASP:HB3	1.66	0.60
8:H:113:ALA:HB2	8:H:126:GLU:HG3	1.84	0.60
1:A:1191:TRP:CD1	1:A:1256:GLU:HB2	2.37	0.60
4:D:19:GLU:O	4:D:21:GLU:N	2.35	0.60
7:G:9:LEU:HD12	7:G:10:ASN:N	2.16	0.60
1:A:49:LYS:HE2	1:A:61:ILE:CD1	2.29	0.60
1:A:407:ARG:HG2	1:A:430:TRP:CH2	2.37	0.60
1:A:629:LEU:O	1:A:633:VAL:HG23	2.01	0.60
2:B:642:ASP:HB3	2:B:649:LYS:HD2	1.84	0.60
2:B:1166:CYS:HB2	2:B:1168:LEU:HD12	1.84	0.60
12:L:31:CYS:HB3	12:L:35:SER:HA	1.84	0.60
1:A:40:THR:HG23	1:A:54:ASN:HD21	1.67	0.60
1:A:391:LEU:O	1:A:394:ASN:N	2.35	0.60
1:A:730:GLY:C	1:A:732:LEU:H	2.09	0.60
1:A:863:VAL:O	1:A:864:ILE:HG12	2.02	0.60
1:A:863:VAL:HG12	1:A:864:ILE:N	2.17	0.60
2:B:701:ILE:HD11	2:B:703:ILE:HD11	1.83	0.60
2:B:841:MET:O	2:B:993:THR:HG22	2.02	0.60
2:B:954:VAL:O	12:L:55:ILE:O	2.20	0.60
5:E:23:VAL:HG13	5:E:78:LEU:HD13	1.84	0.60
5:E:46:TYR:CE2	5:E:58:MET:HA	2.37	0.60
6:F:72:LYS:O	6:F:73:ALA:HB3	2.02	0.60
8:H:56:THR:O	8:H:144:ILE:HA	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:8:ARG:O	9:I:10:CYS:N	2.33	0.60
1:A:69:THR:C	1:A:71:GLN:H	2.10	0.59
1:A:335:ARG:HH11	2:B:1206:GLU:CD	2.10	0.59
1:A:343:LYS:HE2	2:B:1156:ASP:OD2	2.02	0.59
1:A:567:LYS:HB3	8:H:95:TYR:HA	1.83	0.59
1:A:782:ARG:NH2	2:B:699:GLU:O	2.34	0.59
1:A:786:HIS:N	1:A:786:HIS:CD2	2.69	0.59
1:A:1116:LEU:HB3	1:A:1311:VAL:HG22	1.83	0.59
1:A:1164:PRO:HG2	1:A:1165:GLU:H	1.66	0.59
1:A:1265:ASN:C	1:A:1267:MET:H	2.09	0.59
1:A:1397:LEU:HA	1:A:1400:CYS:CB	2.32	0.59
2:B:533:CYS:O	2:B:535:LEU:N	2.34	0.59
2:B:1159:ARG:HE	2:B:1193:GLN:NE2	2.00	0.59
7:G:146:LYS:HB2	7:G:168:LEU:HD11	1.82	0.59
8:H:56:THR:HB	8:H:145:ARG:HG2	1.84	0.59
9:I:55:THR:HG23	9:I:100:PHE:CD2	2.33	0.59
1:A:446:ARG:CD	1:A:480:ALA:HB2	2.31	0.59
1:A:853:ASP:CG	1:A:855:THR:HB	2.26	0.59
1:A:1155:ASP:HB3	1:A:1241:ARG:HH21	1.66	0.59
2:B:1160:VAL:CG1	2:B:1161:HIS:N	2.66	0.59
5:E:198:ILE:CD1	5:E:212:ARG:HH11	2.14	0.59
1:A:475:THR:HG23	1:A:476:SER:N	2.17	0.59
1:A:896:ARG:HB3	1:A:897:TYR:CD1	2.37	0.59
4:D:134:THR:HG22	4:D:135:GLY:N	2.16	0.59
12:L:61:THR:CG2	12:L:63:ARG:HG2	2.31	0.59
1:A:1237:ILE:CG2	1:A:1238:ILE:H	2.15	0.59
2:B:496:ARG:NH1	2:B:539:LEU:HB2	2.16	0.59
2:B:511:PRO:C	2:B:513:GLN:H	2.08	0.59
2:B:847:ASP:C	2:B:849:GLY:H	2.09	0.59
2:B:899:ILE:HG22	2:B:900:ALA:N	2.17	0.59
2:B:1034:VAL:HG12	2:B:1035:ALA:N	2.17	0.59
8:H:42:ILE:HG23	8:H:95:TYR:HE1	1.67	0.59
11:K:50:LEU:HD11	11:K:75:ILE:CD1	2.32	0.59
12:L:32:ALA:HB3	12:L:55:ILE:HD12	1.83	0.59
1:A:567:LYS:HD3	8:H:95:TYR:CD2	2.37	0.59
1:A:687:LYS:O	1:A:690:VAL:HB	2.03	0.59
1:A:870:GLU:HG2	5:E:208:TYR:CG	2.36	0.59
3:C:58:LEU:CD2	3:C:58:LEU:N	2.65	0.59
1:A:55:ASP:C	1:A:57:ARG:N	2.46	0.59
1:A:68:GLN:C	1:A:70:CYS:H	2.09	0.59
1:A:563:PRO:HG3	1:A:572:TRP:CE2	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:605:MET:HE2	1:A:615:GLY:O	2.02	0.59
1:A:1261:LYS:O	1:A:1264:GLU:HB3	2.01	0.59
1:A:1372:VAL:CG1	1:A:1373:ASP:N	2.65	0.59
2:B:521:LEU:HB3	2:B:633:VAL:HG11	1.85	0.59
2:B:815:ARG:HD3	2:B:1041:GLU:OE2	2.03	0.59
4:D:48:ILE:HG21	7:G:4:ILE:HB	1.85	0.59
1:A:500:GLU:OE2	1:A:1438:THR:HG21	2.03	0.59
1:A:848:ILE:HB	1:A:1065:GLY:HA3	1.85	0.59
1:A:1127:ASP:O	1:A:1130:GLN:HB3	2.03	0.59
2:B:879:ARG:O	2:B:880:THR:HB	2.02	0.59
2:B:1169:MET:HE3	2:B:1201:LYS:HG2	1.85	0.59
3:C:239:PRO:O	3:C:240:VAL:C	2.45	0.59
1:A:22:PHE:HB2	2:B:1211:ASN:OD1	2.03	0.59
1:A:321:PRO:O	1:A:322:VAL:HG23	2.03	0.59
1:A:446:ARG:HB2	1:A:487:MET:SD	2.43	0.59
1:A:590:ARG:HH21	1:A:620:LYS:CB	2.08	0.59
1:A:825:ILE:C	1:A:827:THR:N	2.61	0.59
2:B:483:LEU:HD12	2:B:484:ASN:H	1.67	0.59
2:B:992:ILE:HD13	2:B:994:TYR:CE1	2.38	0.59
3:C:17:ASN:OD1	3:C:233:GLU:HG3	2.02	0.59
5:E:164:LEU:HD22	5:E:211:TYR:CD2	2.37	0.59
10:J:14:VAL:HG13	10:J:50:ILE:HD11	1.85	0.59
1:A:1017:LEU:HD23	5:E:204:THR:C	2.27	0.59
1:A:1095:THR:OG1	1:A:1112:LYS:HB2	2.03	0.59
1:A:1125:ALA:C	1:A:1127:ASP:H	2.10	0.59
1:A:1151:GLU:HB3	1:A:1153:TYR:HE1	1.68	0.59
1:A:1342:GLU:CG	5:E:198:ILE:HD13	2.33	0.59
2:B:102:VAL:CG2	2:B:112:LEU:HB2	2.33	0.59
2:B:461:LEU:HD12	2:B:461:LEU:H	1.68	0.59
2:B:1007:VAL:HG22	2:B:1008:PRO:CD	2.32	0.59
4:D:35:LEU:H	4:D:35:LEU:CD1	2.14	0.59
8:H:40:LEU:HD12	8:H:122:LEU:O	2.03	0.59
9:I:6:PHE:HA	9:I:14:LEU:HG	1.85	0.59
1:A:72:GLU:O	1:A:73:GLY:O	2.20	0.59
1:A:697:ALA:HB2	1:A:702:LEU:HD12	1.85	0.59
1:A:1104:ILE:O	1:A:1106:ASN:N	2.35	0.59
2:B:508:LEU:HB2	2:B:510:LYS:HB3	1.83	0.59
2:B:578:THR:HG23	2:B:622:LYS:HA	1.84	0.59
2:B:1106:ARG:HG3	2:B:1107:ALA:H	1.65	0.59
4:D:33:PHE:CE2	7:G:80:LYS:NZ	2.70	0.59
1:A:535:THR:CG2	1:A:616:VAL:HA	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:905:ASP:C	1:A:906:HIS:HD1	2.10	0.58
1:A:963:ILE:HD13	1:A:1049:ILE:CG1	2.32	0.58
1:A:1436:ILE:O	1:A:1437:GLY:C	2.46	0.58
2:B:240:ILE:CG2	2:B:254:LEU:HB3	2.31	0.58
2:B:854:LEU:HB3	2:B:856:PHE:CE1	2.37	0.58
4:D:176:GLU:OE2	4:D:198:LEU:HD23	2.02	0.58
5:E:94:LYS:HE2	5:E:98:ILE:HD11	1.84	0.58
10:J:1:MET:HE2	10:J:60:PHE:CZ	2.38	0.58
1:A:808:LEU:HD21	1:A:816:HIS:HD2	1.68	0.58
1:A:984:LYS:O	1:A:988:LEU:HB2	2.03	0.58
2:B:46:GLN:HG3	2:B:47:GLN:H	1.68	0.58
2:B:603:LEU:HB3	2:B:609:ILE:HD11	1.84	0.58
2:B:785:TYR:HE2	10:J:60:PHE:CE1	2.22	0.58
2:B:798:TYR:CE1	10:J:4:PRO:HB3	2.38	0.58
3:C:35:ARG:HH11	11:K:41:THR:N	2.01	0.58
3:C:59:ALA:O	3:C:62:PHE:HB3	2.03	0.58
1:A:41:MET:O	1:A:42:ASP:C	2.46	0.58
1:A:57:ARG:O	1:A:58:LEU:O	2.21	0.58
1:A:598:LEU:HD22	8:H:25:ARG:NH1	2.18	0.58
1:A:667:GLY:HA3	3:C:192:TRP:CH2	2.38	0.58
1:A:695:LYS:C	1:A:697:ALA:H	2.11	0.58
1:A:1370:LEU:O	1:A:1374:VAL:HG23	2.02	0.58
2:B:240:ILE:HG23	2:B:240:ILE:O	2.02	0.58
2:B:404:LYS:HE2	2:B:404:LYS:HA	1.85	0.58
3:C:174:ALA:O	3:C:175:ALA:CB	2.51	0.58
5:E:114:ASN:O	5:E:115:ASN:HB3	2.03	0.58
10:J:41:LEU:CD1	10:J:50:ILE:HG13	2.31	0.58
1:A:360:GLU:HB2	1:A:363:GLN:HG3	1.84	0.58
1:A:1441:PHE:HZ	6:F:89:GLU:HA	1.67	0.58
2:B:172:ILE:HD13	2:B:178:ASN:HB3	1.86	0.58
2:B:296:GLU:O	2:B:299:GLU:HB2	2.04	0.58
2:B:1032:SER:C	2:B:1034:VAL:H	2.12	0.58
3:C:27:LEU:O	3:C:28:ALA:C	2.46	0.58
1:A:847:ASP:HB2	1:A:859:SER:H	1.68	0.58
1:A:1161:THR:HG22	1:A:1163:ILE:N	2.14	0.58
2:B:562:GLY:HA3	2:B:590:HIS:HE1	1.65	0.58
2:B:782:LEU:HD12	2:B:788:ARG:HH11	1.67	0.58
3:C:66:ARG:NH2	10:J:5:VAL:HG23	2.19	0.58
7:G:1:MET:O	7:G:1:MET:SD	2.61	0.58
8:H:24:CYS:SG	8:H:44:VAL:HG21	2.43	0.58
10:J:8:PHE:HD1	10:J:49:MET:HE1	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:VAL:HG13	1:A:415:LEU:HD11	1.84	0.58
1:A:567:LYS:CB	1:A:568:PRO:CD	2.81	0.58
1:A:868:TYR:CE1	1:A:1064:VAL:CG1	2.77	0.58
1:A:1134:ILE:O	1:A:1138:ILE:HG13	2.02	0.58
1:A:1222:ASN:O	1:A:1223:ASP:HB3	2.04	0.58
2:B:325:GLN:HG2	9:I:31:THR:HG23	1.86	0.58
2:B:973:ILE:HG23	2:B:974:PRO:HD2	1.84	0.58
5:E:157:SER:O	5:E:159:ASP:N	2.37	0.58
5:E:162:ARG:HH11	5:E:162:ARG:HG2	1.69	0.58
9:I:4:PHE:CE1	9:I:13:MET:HE1	2.39	0.58
9:I:58:VAL:HG13	9:I:62:ILE:HG13	1.84	0.58
9:I:61:ASP:C	9:I:63:GLY:H	2.12	0.58
1:A:895:LYS:HG2	1:A:895:LYS:O	2.03	0.58
1:A:1316:VAL:O	1:A:1322:ILE:HD13	2.04	0.58
1:A:1376:THR:O	1:A:1377:THR:C	2.46	0.58
2:B:830:TYR:HE2	2:B:1000:PRO:HD3	1.66	0.58
2:B:840:ILE:HB	2:B:1011:ILE:HB	1.85	0.58
1:A:827:THR:O	1:A:831:THR:HB	2.04	0.58
1:A:834:THR:HG23	1:A:1077:THR:HA	1.85	0.58
1:A:1086:PHE:O	1:A:1087:ALA:C	2.47	0.58
1:A:1090:ALA:CA	1:A:1093:LYS:HE3	2.34	0.58
2:B:903:VAL:HG12	2:B:904:ARG:N	2.17	0.58
3:C:88:CYS:SG	3:C:91:HIS:C	2.87	0.58
3:C:167:HIS:CE1	12:L:70:ARG:HA	2.39	0.58
4:D:33:PHE:CE1	7:G:80:LYS:HE3	2.39	0.58
7:G:119:LEU:HD13	7:G:132:SER:HB2	1.86	0.58
8:H:100:THR:HG22	8:H:101:ALA:N	2.19	0.58
1:A:361:LEU:HG	1:A:507:VAL:HG11	1.85	0.58
1:A:618:GLU:C	1:A:618:GLU:CD	2.71	0.58
1:A:642:CYS:O	1:A:645:LEU:HB3	2.04	0.58
1:A:1289:ARG:NH1	1:A:1326:ARG:NH1	2.52	0.58
2:B:773:MET:O	2:B:775:LYS:N	2.37	0.58
2:B:807:ARG:HB3	2:B:807:ARG:NH1	2.19	0.58
5:E:153:HIS:O	5:E:154:ILE:CG1	2.49	0.58
9:I:59:VAL:O	9:I:59:VAL:HG12	2.04	0.58
10:J:19:GLU:O	10:J:23:ASN:HB2	2.03	0.58
11:K:31:VAL:HG12	11:K:32:VAL:N	2.18	0.58
1:A:532:ARG:HH22	1:A:745:GLN:HG2	1.69	0.58
1:A:785:PRO:HG2	1:A:786:HIS:HD2	1.68	0.58
1:A:1074:GLU:N	1:A:1075:PRO:HD2	2.18	0.58
2:B:205:ILE:O	2:B:206:ASN:C	2.47	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:762:ASN:HD21	2:B:1024:ALA:CB	2.17	0.58
5:E:144:ILE:O	5:E:146:HIS:N	2.36	0.58
8:H:89:LEU:C	8:H:91:ASP:H	2.12	0.58
1:A:798:GLY:HA2	1:A:815:PHE:CD1	2.39	0.57
1:A:1265:ASN:C	1:A:1267:MET:N	2.60	0.57
2:B:620:ARG:NH2	9:I:89:GLN:NE2	2.52	0.57
2:B:911:ILE:HD11	2:B:941:LEU:CD1	2.33	0.57
2:B:911:ILE:HD11	2:B:941:LEU:HD13	1.86	0.57
2:B:1002:THR:O	2:B:1005:GLY:N	2.32	0.57
1:A:115:LEU:HD12	1:A:142:CYS:SG	2.44	0.57
1:A:528:LEU:HD23	1:A:751:SER:HA	1.85	0.57
1:A:730:GLY:C	1:A:732:LEU:N	2.59	0.57
1:A:775:ILE:HG13	1:A:798:GLY:HA3	1.86	0.57
1:A:1116:LEU:HB3	1:A:1311:VAL:CG2	2.33	0.57
2:B:29:ASP:HB3	2:B:658:ILE:CD1	2.35	0.57
2:B:527:THR:OG1	2:B:528:PRO:HD2	2.03	0.57
2:B:551:PRO:C	2:B:553:PRO:HD2	2.29	0.57
3:C:124:LEU:O	3:C:127:ARG:HG2	2.04	0.57
3:C:163:ILE:O	3:C:166:GLU:N	2.36	0.57
5:E:78:LEU:HD23	5:E:78:LEU:C	2.30	0.57
5:E:198:ILE:CD1	5:E:212:ARG:HG3	2.34	0.57
7:G:123:ALA:C	7:G:125:SER:N	2.63	0.57
9:I:101:PHE:O	9:I:102:VAL:HG23	2.03	0.57
11:K:47:ARG:HD3	11:K:59:ALA:O	2.04	0.57
1:A:35:ILE:HD12	1:A:241:VAL:HG21	1.86	0.57
1:A:516:SER:O	1:A:517:ASN:C	2.47	0.57
1:A:808:LEU:HD12	1:A:808:LEU:N	2.20	0.57
1:A:1161:THR:C	1:A:1163:ILE:N	2.61	0.57
2:B:918:ILE:CD1	2:B:935:ARG:HD2	2.27	0.57
2:B:1159:ARG:HE	2:B:1193:GLN:HE21	1.50	0.57
4:D:47:LEU:HD11	7:G:3:PHE:CD2	2.39	0.57
12:L:62:LYS:H	12:L:62:LYS:HD2	1.70	0.57
1:A:14:VAL:H	1:A:1432:GLN:NE2	1.89	0.57
1:A:711:ARG:HG3	9:I:97:MET:HE2	1.86	0.57
1:A:1164:PRO:O	1:A:1166:ASP:N	2.36	0.57
2:B:286:PHE:HE2	2:B:375:ALA:HB1	1.70	0.57
2:B:1186:ASP:OD1	2:B:1186:ASP:O	2.22	0.57
7:G:117:GLN:O	7:G:119:LEU:N	2.37	0.57
1:A:115:LEU:HB2	1:A:122:MET:HE2	1.86	0.57
1:A:864:ILE:O	1:A:865:GLN:CG	2.50	0.57
1:A:1130:GLN:HA	1:A:1133:LEU:HD12	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:278:GLN:HG2	2:B:279:ASP:H	1.69	0.57
2:B:558:LEU:O	2:B:560:GLU:N	2.37	0.57
2:B:635:ARG:NH2	2:B:742:GLU:OE2	2.29	0.57
2:B:694:ASP:O	2:B:698:GLU:HB2	2.05	0.57
2:B:708:GLU:O	2:B:710:LEU:N	2.37	0.57
2:B:953:LEU:HD21	2:B:965:LYS:HB2	1.87	0.57
2:B:1065:GLN:HG3	2:B:1068:GLY:H	1.69	0.57
8:H:126:GLU:C	8:H:130:ARG:HH22	2.11	0.57
9:I:111:THR:CG2	9:I:112:SER:H	2.13	0.57
1:A:316:GLN:O	1:A:317:LYS:C	2.47	0.57
1:A:666:ILE:H	2:B:1026:LEU:HD22	1.70	0.57
1:A:1030:ARG:HG3	1:A:1034:GLU:OE2	2.03	0.57
2:B:235:SER:HB3	2:B:258:LEU:HG	1.86	0.57
2:B:325:GLN:HG2	9:I:31:THR:CG2	2.34	0.57
3:C:82:TYR:CE1	3:C:161:LYS:HD3	2.39	0.57
3:C:196:ASP:OD1	3:C:198:ALA:HB3	2.05	0.57
3:C:263:THR:C	3:C:265:MET:N	2.63	0.57
4:D:196:PRO:C	4:D:198:LEU:H	2.11	0.57
10:J:8:PHE:CD1	10:J:49:MET:SD	2.98	0.57
1:A:49:LYS:HZ1	1:A:61:ILE:HG13	1.70	0.57
1:A:845:LEU:O	1:A:1065:GLY:HA3	2.05	0.57
1:A:903:ASN:ND2	1:A:905:ASP:H	2.02	0.57
2:B:522:VAL:HG12	2:B:523:CYS:N	2.19	0.57
2:B:766:ARG:NH2	2:B:1020:ARG:CG	2.67	0.57
12:L:36:SER:O	12:L:37:LYS:C	2.48	0.57
1:A:42:ASP:HB3	1:A:45:GLN:H	1.70	0.57
1:A:560:ILE:HD12	8:H:79:TRP:O	2.05	0.57
1:A:996:ASN:O	1:A:998:LEU:HD12	2.04	0.57
1:A:1044:TRP:O	1:A:1047:SER:N	2.38	0.57
1:A:1299:VAL:HG12	1:A:1300:LYS:N	2.19	0.57
2:B:168:GLY:HA2	2:B:454:THR:OG1	2.05	0.57
2:B:558:LEU:C	2:B:560:GLU:H	2.12	0.57
5:E:13:TRP:O	5:E:16:PHE:HB3	2.03	0.57
5:E:48:ASP:CG	5:E:49:SER:H	2.11	0.57
1:A:672:ASP:HB2	1:A:736:ASN:OD1	2.05	0.57
1:A:1446:ASP:HB3	1:A:1449:SER:OG	2.04	0.57
2:B:57:TYR:CD1	2:B:57:TYR:N	2.72	0.57
2:B:360:PHE:O	2:B:361:LEU:C	2.47	0.57
3:C:82:TYR:O	3:C:84:ARG:N	2.38	0.57
3:C:114:TYR:HB3	3:C:140:ASN:O	2.04	0.57
4:D:51:ASN:ND2	4:D:54:GLU:OE2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:56:ARG:HA	4:D:148:LEU:HD13	1.86	0.57
9:I:64:SER:O	9:I:66:PRO:HD3	2.05	0.57
1:A:18:GLN:HG3	1:A:228:PHE:CE1	2.40	0.57
1:A:382:PRO:HD3	1:A:428:TYR:CE2	2.40	0.57
1:A:705:LYS:C	1:A:707:GLY:N	2.62	0.57
2:B:575:PRO:C	2:B:577:ALA:H	2.13	0.57
2:B:1168:LEU:HD22	2:B:1208:MET:HE3	1.86	0.57
3:C:27:LEU:HD12	3:C:228:PHE:HE2	1.70	0.57
5:E:84:ASP:O	5:E:86:PRO:HD3	2.05	0.57
7:G:13:LEU:HD23	7:G:14:HIS:H	1.70	0.57
1:A:399:HIS:HB3	1:A:400:PRO:CD	2.26	0.56
1:A:688:LYS:C	1:A:690:VAL:N	2.61	0.56
1:A:1341:ILE:HD12	1:A:1379:GLY:O	2.05	0.56
1:A:1453:TYR:CZ	6:F:129:LYS:HA	2.40	0.56
2:B:541:LEU:HD12	2:B:747:MET:HE1	1.86	0.56
2:B:1147:LEU:O	2:B:1148:LYS:C	2.45	0.56
3:C:133:ILE:CD1	3:C:237:SER:CA	2.82	0.56
3:C:181:ASP:OD1	3:C:186:LEU:HD13	2.05	0.56
3:C:242:GLN:O	3:C:246:ARG:N	2.37	0.56
5:E:204:THR:CG2	5:E:205:SER:N	2.67	0.56
6:F:75:PRO:O	6:F:77:ASP:O	2.23	0.56
8:H:84:ALA:C	8:H:86:ASP:N	2.60	0.56
1:A:899:VAL:CG2	1:A:908:LEU:HD21	2.35	0.56
1:A:1063:MET:CG	1:A:1436:ILE:HG23	2.35	0.56
1:A:1074:GLU:HB3	1:A:1075:PRO:CD	2.34	0.56
1:A:1208:THR:O	1:A:1209:MET:C	2.48	0.56
2:B:394:ASP:OD1	9:I:91:ARG:HB3	2.04	0.56
2:B:1132:GLU:O	2:B:1135:ARG:HB3	2.04	0.56
5:E:22:MET:HE3	5:E:26:ARG:CZ	2.35	0.56
6:F:111:LEU:HD12	6:F:111:LEU:N	2.18	0.56
7:G:80:LYS:CE	7:G:82:PHE:HZ	2.17	0.56
10:J:1:MET:HE2	10:J:60:PHE:HE2	1.66	0.56
12:L:43:THR:HG22	12:L:43:THR:O	2.04	0.56
1:A:98:LYS:O	1:A:102:VAL:HG23	2.05	0.56
1:A:306:ASN:ND2	1:A:322:VAL:HB	2.21	0.56
1:A:547:LEU:HD22	11:K:58:PHE:CD1	2.40	0.56
1:A:668:ASP:CB	1:A:743:VAL:HG23	2.36	0.56
1:A:688:LYS:C	1:A:690:VAL:H	2.12	0.56
2:B:247:GLY:H	2:B:418:LYS:HZ3	1.53	0.56
2:B:570:VAL:HG23	2:B:573:GLN:HB3	1.85	0.56
2:B:1000:PRO:O	2:B:1007:VAL:HG23	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1085:ILE:HG22	2:B:1086:PHE:N	2.19	0.56
2:B:1156:ASP:HB3	2:B:1198:TYR:H	1.70	0.56
7:G:109:PHE:CD1	7:G:110:VAL:N	2.71	0.56
9:I:58:VAL:HA	9:I:62:ILE:HD11	1.87	0.56
1:A:42:ASP:C	1:A:44:THR:N	2.64	0.56
1:A:47:ARG:NH1	1:A:254:GLU:HB3	2.06	0.56
1:A:78:PRO:CB	2:B:1201:LYS:HE3	2.36	0.56
1:A:403:LYS:O	1:A:404:TYR:CG	2.58	0.56
1:A:730:GLY:O	1:A:732:LEU:N	2.38	0.56
1:A:896:ARG:HB3	1:A:897:TYR:HD1	1.70	0.56
1:A:986:ILE:HD11	1:A:1032:LEU:HD11	1.87	0.56
1:A:1080:THR:HG22	1:A:1081:LEU:N	2.20	0.56
3:C:104:PHE:CD2	3:C:105:GLY:N	2.71	0.56
1:A:34:LYS:CB	1:A:36:ARG:HH21	2.18	0.56
1:A:50:ILE:C	1:A:52:GLY:N	2.62	0.56
1:A:92:HIS:O	1:A:93:VAL:C	2.48	0.56
1:A:306:ASN:HB2	1:A:324:SER:HB3	1.87	0.56
1:A:861:GLY:HA3	5:E:174:GLN:NE2	2.21	0.56
1:A:928:LEU:O	1:A:930:ASP:N	2.39	0.56
2:B:192:LEU:O	2:B:193:LYS:HB2	2.04	0.56
2:B:582:VAL:HA	2:B:626:ILE:O	2.06	0.56
2:B:1017:ILE:HG22	2:B:1018:PRO:N	2.21	0.56
2:B:1149:GLU:O	2:B:1150:ARG:C	2.47	0.56
2:B:1172:ILE:HG22	2:B:1172:ILE:O	2.05	0.56
3:C:69:LEU:H	3:C:69:LEU:HD12	1.69	0.56
5:E:176:PRO:O	5:E:212:ARG:HA	2.06	0.56
10:J:21:TYR:HA	10:J:39:LEU:HD11	1.87	0.56
1:A:84:ILE:HG23	1:A:239:LEU:HB3	1.86	0.56
1:A:353:ILE:HG21	1:A:487:MET:CG	2.21	0.56
1:A:874:ASP:CA	1:A:1058:VAL:HG23	2.36	0.56
2:B:798:TYR:HE1	10:J:4:PRO:HB3	1.71	0.56
2:B:860:MET:HB2	2:B:965:LYS:HG2	1.87	0.56
2:B:996:ARG:NH2	3:C:175:ALA:HA	2.20	0.56
2:B:999:MET:HB3	2:B:1007:VAL:HG21	1.88	0.56
5:E:19:VAL:O	5:E:23:VAL:HG23	2.06	0.56
11:K:53:ASP:HB3	11:K:56:VAL:HG23	1.86	0.56
1:A:92:HIS:O	1:A:95:PHE:N	2.37	0.56
1:A:130:ASP:O	1:A:132:LYS:N	2.39	0.56
1:A:965:GLN:O	1:A:968:GLN:HB2	2.06	0.56
1:A:1335:ILE:HG22	1:A:1335:ILE:O	2.05	0.56
1:A:1373:ASP:O	1:A:1376:THR:HG23	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:242:SER:OG	2:B:252:SER:O	2.23	0.56
2:B:377:PHE:O	2:B:380:TYR:N	2.39	0.56
2:B:498:THR:O	2:B:536:VAL:HG13	2.05	0.56
3:C:58:LEU:H	3:C:58:LEU:HD23	1.71	0.56
3:C:101:LEU:HD13	3:C:118:LEU:HD23	1.88	0.56
6:F:84:TYR:N	6:F:84:TYR:CD1	2.73	0.56
8:H:7:ASP:O	8:H:8:ASP:HB2	2.06	0.56
12:L:49:LYS:O	12:L:50:ASP:HB2	2.05	0.56
1:A:936:LEU:HD23	1:A:936:LEU:N	2.21	0.56
1:A:1349:TYR:C	1:A:1349:TYR:CD2	2.83	0.56
2:B:569:TYR:CE1	2:B:589:VAL:HG21	2.41	0.56
2:B:603:LEU:HB3	2:B:609:ILE:CD1	2.35	0.56
10:J:1:MET:H2	10:J:56:LEU:N	2.02	0.56
1:A:567:LYS:CB	8:H:95:TYR:HA	2.36	0.56
1:A:597:LEU:HD12	1:A:597:LEU:N	2.21	0.56
1:A:1081:LEU:HD21	1:A:1098:VAL:CG2	2.35	0.56
2:B:31:TRP:CE3	2:B:34:ILE:HD12	2.41	0.56
2:B:60:GLN:O	2:B:63:ILE:HG22	2.06	0.56
2:B:644:GLU:C	2:B:646:LEU:H	2.13	0.56
2:B:1202:LEU:O	2:B:1203:LEU:C	2.49	0.56
3:C:89:GLU:O	3:C:90:ASP:HB3	2.05	0.56
8:H:62:SER:O	8:H:63:LEU:C	2.48	0.56
10:J:13:VAL:HG12	10:J:14:VAL:N	2.21	0.56
1:A:71:GLN:O	1:A:73:GLY:N	2.39	0.56
1:A:133:LYS:C	1:A:135:PHE:N	2.60	0.56
1:A:472:LEU:CD1	2:B:835:GLN:CD	2.79	0.56
1:A:491:VAL:HG12	1:A:492:PRO:O	2.04	0.56
1:A:1051:ALA:O	1:A:1053:PHE:N	2.39	0.56
1:A:1134:ILE:O	1:A:1135:ARG:C	2.49	0.56
1:A:1364:ASN:O	1:A:1365:TYR:C	2.49	0.56
1:A:1421:CYS:HA	1:A:1426:GLU:HB3	1.86	0.56
2:B:44:VAL:O	2:B:45:SER:C	2.49	0.56
2:B:209:GLU:CD	2:B:485:ARG:HE	2.14	0.56
2:B:555:ILE:HG22	2:B:556:THR:N	2.21	0.56
2:B:593:PRO:HG2	2:B:617:ARG:CZ	2.35	0.56
2:B:945:GLU:O	2:B:946:ASN:HB3	2.07	0.56
2:B:1098:MET:HE3	2:B:1101:ASP:OD2	2.05	0.56
5:E:47:CYS:HA	5:E:52:ARG:O	2.06	0.56
1:A:390:GLN:HE21	1:A:394:ASN:HD21	1.53	0.55
1:A:469:ARG:NH2	2:B:991:GLY:O	2.37	0.55
1:A:492:PRO:O	1:A:493:GLN:NE2	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:25:ILE:HG23	2:B:29:ASP:HB3	1.88	0.55
2:B:528:PRO:HG2	2:B:533:CYS:HA	1.87	0.55
5:E:55:ARG:C	5:E:57:MET:N	2.63	0.55
6:F:77:ASP:C	6:F:79:ARG:N	2.61	0.55
1:A:1015:VAL:HG12	1:A:1019:CYS:HG	1.69	0.55
1:A:1313:LEU:O	1:A:1315:GLU:N	2.39	0.55
2:B:521:LEU:HB3	2:B:633:VAL:CG1	2.36	0.55
2:B:784:ASN:O	2:B:788:ARG:HG3	2.06	0.55
2:B:839:MET:HE2	2:B:1010:LEU:HD21	1.88	0.55
2:B:857:ARG:HH21	2:B:942:ARG:NH1	2.04	0.55
5:E:161:LYS:C	5:E:163:GLU:H	2.14	0.55
5:E:161:LYS:C	5:E:163:GLU:N	2.61	0.55
5:E:178:ILE:HG22	5:E:213:ILE:O	2.06	0.55
5:E:211:TYR:CD1	5:E:211:TYR:N	2.74	0.55
7:G:15:PRO:HA	7:G:18:PHE:CD1	2.40	0.55
7:G:114:LEU:HG	7:G:162:SER:CB	2.36	0.55
8:H:123:MET:HE1	8:H:142:LEU:HD13	1.88	0.55
9:I:90:GLN:NE2	9:I:92:ARG:HD2	2.21	0.55
10:J:64:ASN:HB3	10:J:65:PRO:HD2	1.84	0.55
12:L:30:ILE:O	12:L:56:LEU:HA	2.06	0.55
1:A:495:GLU:O	1:A:498:ARG:HG3	2.04	0.55
1:A:648:ASN:O	1:A:649:ILE:C	2.47	0.55
1:A:685:GLU:HG3	1:A:686:ALA:N	2.20	0.55
1:A:715:GLU:O	1:A:717:ASN:N	2.39	0.55
1:A:785:PRO:HG2	1:A:786:HIS:CD2	2.42	0.55
2:B:1189:ILE:HG22	2:B:1190:ASP:N	2.22	0.55
3:C:183:TRP:O	3:C:185:LYS:HG3	2.06	0.55
8:H:5:LEU:HB2	8:H:60:ALA:H	1.71	0.55
11:K:21:ILE:HG23	11:K:31:VAL:HG11	1.88	0.55
12:L:31:CYS:HB3	12:L:35:SER:N	2.21	0.55
1:A:414:ASP:OD1	1:A:416:ARG:CG	2.54	0.55
1:A:666:ILE:CD1	1:A:667:GLY:N	2.66	0.55
1:A:818:MET:HA	2:B:514:LEU:HB3	1.87	0.55
1:A:1230:GLU:C	1:A:1232:ASN:H	2.14	0.55
1:A:1438:THR:HB	2:B:1144:ALA:CB	2.36	0.55
1:A:1443:VAL:C	1:A:1444:MET:HG3	2.30	0.55
2:B:37:PHE:CD2	2:B:542:MET:SD	2.99	0.55
2:B:681:TRP:C	2:B:683:SER:H	2.15	0.55
2:B:744:HIS:CG	2:B:745:PRO:HD2	2.41	0.55
3:C:236:GLY:C	3:C:238:ILE:H	2.13	0.55
4:D:27:LEU:HD11	4:D:197:SER:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:GLN:HG3	1:A:228:PHE:HE1	1.72	0.55
1:A:679:ILE:O	1:A:683:ILE:HG13	2.07	0.55
1:A:741:ASN:HD21	1:A:743:VAL:HB	1.72	0.55
2:B:502:ILE:O	2:B:502:ILE:CG2	2.52	0.55
2:B:877:PRO:C	2:B:878:GLN:HG3	2.31	0.55
3:C:70:ILE:HD13	3:C:144:ILE:HD11	1.88	0.55
3:C:82:TYR:CD1	3:C:161:LYS:HD3	2.41	0.55
3:C:123:ASN:ND2	3:C:125:MET:SD	2.79	0.55
3:C:250:THR:O	3:C:254:LYS:HG3	2.07	0.55
6:F:93:ILE:O	6:F:94:LEU:C	2.49	0.55
6:F:103:MET:HE2	7:G:66:GLY:N	2.18	0.55
10:J:57:ILE:O	10:J:60:PHE:N	2.39	0.55
1:A:382:PRO:HD3	1:A:428:TYR:CD2	2.42	0.55
1:A:993:LEU:HD22	1:A:1046:LEU:HD22	1.88	0.55
1:A:1140:HIS:HB2	1:A:1276:VAL:O	2.06	0.55
1:A:1323:ASP:C	1:A:1325:THR:H	2.14	0.55
1:A:1394:THR:O	1:A:1399:ARG:NE	2.38	0.55
2:B:293:PRO:C	2:B:294:ASP:O	2.47	0.55
2:B:658:ILE:O	2:B:661:LEU:HB2	2.07	0.55
2:B:970:THR:HG22	2:B:971:THR:N	2.22	0.55
3:C:90:ASP:O	3:C:91:HIS:CG	2.60	0.55
4:D:39:ASN:ND2	4:D:41:GLN:HB2	2.21	0.55
4:D:52:LEU:C	4:D:54:GLU:H	2.14	0.55
5:E:56:LYS:HE3	5:E:84:ASP:HB2	1.87	0.55
11:K:58:PHE:HB3	11:K:76:GLN:HE21	1.72	0.55
1:A:453:MET:HE3	1:A:520:CYS:SG	2.47	0.55
1:A:604:GLY:O	1:A:605:MET:HB2	2.07	0.55
1:A:1005:GLU:O	1:A:1006:ILE:C	2.49	0.55
1:A:1102:LYS:HG2	1:A:1106:ASN:ND2	2.22	0.55
1:A:1127:ASP:HB3	1:A:1130:GLN:HB2	1.88	0.55
1:A:1397:LEU:O	1:A:1400:CYS:HB3	2.06	0.55
2:B:1131:GLY:O	2:B:1132:GLU:C	2.50	0.55
2:B:1145:SER:C	2:B:1147:LEU:H	2.14	0.55
3:C:18:VAL:HG12	3:C:20:PHE:HD2	1.70	0.55
7:G:18:PHE:HZ	7:G:68:ALA:HB2	1.71	0.55
7:G:146:LYS:NZ	7:G:165:GLU:OE2	2.38	0.55
8:H:127:GLY:HA3	8:H:130:ARG:NH2	2.22	0.55
2:B:431:TYR:CE2	2:B:447:ALA:HB2	2.42	0.55
3:C:166:GLU:O	3:C:167:HIS:HB2	2.07	0.55
8:H:14:GLU:HG2	8:H:15:VAL:N	2.22	0.55
9:I:84:VAL:O	9:I:84:VAL:HG22	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:21:TYR:C	10:J:23:ASN:H	2.15	0.55
1:A:15:LYS:HG3	2:B:1218:THR:O	2.06	0.55
1:A:49:LYS:HZ1	1:A:61:ILE:N	2.04	0.55
1:A:49:LYS:HZ2	1:A:60:SER:HA	1.71	0.55
1:A:298:PHE:CZ	1:A:314:ALA:HB2	2.42	0.55
1:A:311:GLN:O	1:A:312:PRO:C	2.49	0.55
1:A:356:ASP:HB3	1:A:359:LEU:HG	1.88	0.55
1:A:848:ILE:HB	1:A:1065:GLY:CA	2.37	0.55
1:A:877:HIS:CD2	1:A:1056:SER:HA	2.42	0.55
1:A:1334:ASP:O	1:A:1337:GLU:N	2.40	0.55
2:B:363:HIS:CD2	2:B:364:ILE:HG13	2.42	0.55
2:B:459:TYR:C	2:B:459:TYR:CD2	2.85	0.55
2:B:546:SER:HG	2:B:631:GLY:H	1.53	0.55
2:B:597:MET:SD	2:B:624:LEU:HD11	2.47	0.55
6:F:100:GLN:O	6:F:103:MET:HB2	2.07	0.55
7:G:88:ASP:HA	7:G:144:ARG:HA	1.88	0.55
10:J:64:ASN:CB	10:J:65:PRO:CD	2.74	0.55
1:A:391:LEU:O	1:A:392:VAL:C	2.49	0.55
1:A:808:LEU:CD1	1:A:808:LEU:H	2.19	0.55
1:A:1116:LEU:CD2	1:A:1311:VAL:HG22	2.36	0.55
1:A:1344:GLY:O	1:A:1345:ARG:C	2.50	0.55
2:B:363:HIS:CD2	2:B:585:VAL:HG22	2.42	0.55
2:B:526:GLU:CD	2:B:752:ALA:HB2	2.33	0.55
2:B:546:SER:HG	2:B:630:ALA:HA	1.72	0.55
2:B:711:GLU:H	2:B:712:PRO:HD2	1.72	0.55
2:B:806:THR:HG22	2:B:808:ALA:N	2.22	0.55
2:B:873:THR:HG22	2:B:874:PHE:N	2.22	0.55
2:B:1065:GLN:HG2	2:B:1069:PHE:HB2	1.88	0.55
2:B:1095:LEU:N	2:B:1095:LEU:CD1	2.59	0.55
5:E:42:PHE:O	5:E:43:LYS:C	2.50	0.55
9:I:62:ILE:O	9:I:62:ILE:CG2	2.55	0.55
11:K:65:HIS:CD2	11:K:66:PRO:CD	2.90	0.55
1:A:4:GLN:O	1:A:5:GLN:HB2	2.06	0.54
1:A:919:ILE:O	1:A:921:GLY:N	2.40	0.54
1:A:1127:ASP:O	1:A:1128:GLN:C	2.51	0.54
2:B:217:ARG:HE	2:B:405:ARG:CB	2.15	0.54
2:B:327:ARG:O	2:B:331:LEU:HD13	2.06	0.54
8:H:95:TYR:HE2	8:H:97:MET:HG2	1.72	0.54
8:H:130:ARG:HA	8:H:133:ASN:HB2	1.89	0.54
12:L:30:ILE:HG22	12:L:31:CYS:N	2.20	0.54
1:A:75:ASN:O	1:A:76:GLU:CB	2.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:308:ILE:HG22	1:A:309:ALA:H	1.73	0.54
1:A:774:ARG:O	1:A:775:ILE:C	2.49	0.54
1:A:775:ILE:CG1	1:A:798:GLY:HA3	2.37	0.54
1:A:1029:ARG:CG	1:A:1029:ARG:NH1	2.70	0.54
2:B:377:PHE:O	2:B:378:LEU:C	2.50	0.54
2:B:642:ASP:O	2:B:644:GLU:N	2.30	0.54
4:D:14:ARG:O	4:D:16:LYS:N	2.41	0.54
4:D:51:ASN:O	4:D:52:LEU:C	2.48	0.54
5:E:124:VAL:CA	5:E:132:ILE:HD12	2.37	0.54
5:E:144:ILE:HG13	5:E:145:THR:H	1.71	0.54
1:A:381:THR:HG23	1:A:382:PRO:CD	2.36	0.54
1:A:470:LEU:CD2	1:A:487:MET:HE3	2.35	0.54
1:A:897:TYR:HB3	1:A:936:LEU:HD12	1.89	0.54
1:A:982:THR:HG22	1:A:984:LYS:H	1.72	0.54
2:B:382:ILE:O	2:B:385:LEU:HB3	2.08	0.54
2:B:693:ILE:HD11	2:B:740:HIS:CD2	2.43	0.54
2:B:763:GLN:C	2:B:765:PRO:HD2	2.32	0.54
2:B:1032:SER:C	2:B:1034:VAL:N	2.64	0.54
2:B:1135:ARG:O	2:B:1139:ILE:HG13	2.06	0.54
8:H:143:LEU:C	8:H:144:ILE:HG13	2.32	0.54
9:I:25:LEU:HB3	9:I:38:ALA:HB2	1.89	0.54
9:I:88:SER:O	9:I:90:GLN:N	2.41	0.54
1:A:849:MET:HE3	1:A:1061:GLY:O	2.07	0.54
1:A:1155:ASP:OD2	1:A:1161:THR:HG23	2.07	0.54
1:A:1305:VAL:CG1	1:A:1306:LEU:N	2.71	0.54
2:B:378:LEU:O	2:B:382:ILE:HG13	2.07	0.54
3:C:67:LEU:HD23	3:C:70:ILE:HD11	1.89	0.54
5:E:25:ASP:C	5:E:27:GLY:N	2.63	0.54
5:E:90:VAL:HA	5:E:120:ALA:HB2	1.89	0.54
7:G:81:PRO:HG3	7:G:106:MET:SD	2.47	0.54
9:I:34:TYR:HD2	9:I:35:VAL:N	2.06	0.54
11:K:47:ARG:HH11	11:K:48:ALA:N	2.06	0.54
1:A:265:LYS:HE2	1:A:322:VAL:HG11	1.88	0.54
1:A:384:ASN:O	1:A:385:ILE:C	2.49	0.54
1:A:896:ARG:O	1:A:1029:ARG:HB3	2.07	0.54
1:A:939:ASP:O	1:A:940:ARG:C	2.50	0.54
1:A:1017:LEU:HD12	1:A:1017:LEU:O	2.07	0.54
2:B:901:PRO:O	2:B:903:VAL:N	2.41	0.54
5:E:124:VAL:HG13	5:E:132:ILE:CD1	2.36	0.54
9:I:7:CYS:SG	9:I:8:ARG:O	2.66	0.54
12:L:47:ARG:HH11	12:L:47:ARG:HG3	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:PRO:HB3	2:B:1201:LYS:HE3	1.88	0.54
1:A:468:PHE:CE2	1:A:489:LEU:HD23	2.43	0.54
1:A:663:SER:OG	2:B:1085:ILE:HG23	2.06	0.54
1:A:867:ILE:CG2	1:A:872:GLY:N	2.71	0.54
1:A:1313:LEU:CD1	1:A:1327:ILE:HD13	2.38	0.54
1:A:1396:ALA:O	1:A:1398:MET:N	2.41	0.54
2:B:637:LEU:HD12	2:B:693:ILE:HD12	1.88	0.54
2:B:1187:ASN:O	2:B:1188:LYS:CB	2.56	0.54
3:C:46:ILE:HG13	3:C:72:LEU:HD11	1.88	0.54
3:C:92:CYS:H	3:C:95:CYS:HG	1.56	0.54
11:K:83:PRO:O	11:K:86:ALA:N	2.41	0.54
1:A:72:GLU:HB3	1:A:76:GLU:HG3	1.88	0.54
1:A:476:SER:OG	1:A:477:PRO:HD3	2.08	0.54
1:A:523:ILE:HG22	1:A:528:LEU:HB2	1.88	0.54
1:A:903:ASN:C	1:A:903:ASN:ND2	2.65	0.54
1:A:1410:PHE:C	1:A:1412:ALA:H	2.15	0.54
2:B:118:ARG:HH11	2:B:204:ILE:HD11	1.72	0.54
2:B:168:GLY:HA2	2:B:454:THR:HG1	1.73	0.54
2:B:203:PHE:HB3	2:B:205:ILE:CD1	2.37	0.54
2:B:210:LYS:HA	2:B:481:GLN:O	2.07	0.54
2:B:356:LEU:HA	2:B:360:PHE:HB2	1.90	0.54
2:B:861:ASP:OD1	2:B:862:GLN:N	2.41	0.54
2:B:1219:ASP:OD1	2:B:1219:ASP:O	2.25	0.54
6:F:111:LEU:C	6:F:113:GLY:N	2.62	0.54
10:J:3:VAL:HG21	10:J:18:TRP:CG	2.43	0.54
11:K:31:VAL:CG1	11:K:32:VAL:N	2.70	0.54
1:A:71:GLN:C	1:A:73:GLY:N	2.60	0.54
1:A:335:ARG:NH1	2:B:1206:GLU:CD	2.65	0.54
1:A:470:LEU:CD2	1:A:487:MET:CE	2.86	0.54
1:A:1329:THR:HG22	1:A:1331:SER:N	2.15	0.54
2:B:611:PRO:HB3	2:B:685:LEU:HD11	1.89	0.54
2:B:635:ARG:HB2	2:B:636:PRO:CD	2.36	0.54
3:C:39:ALA:CA	3:C:164:ALA:HB3	2.37	0.54
7:G:14:HIS:HD2	7:G:16:SER:CB	2.03	0.54
8:H:142:LEU:C	8:H:143:LEU:HD12	2.33	0.54
9:I:55:THR:CG2	9:I:100:PHE:HD2	2.17	0.54
1:A:35:ILE:HA	1:A:52:GLY:O	2.07	0.54
1:A:534:LEU:HD13	1:A:656:TRP:CG	2.43	0.54
1:A:626:ASN:O	1:A:631:HIS:HB2	2.07	0.54
1:A:1173:HIS:CD2	1:A:1227:ILE:HG23	2.43	0.54
1:A:1396:ALA:O	1:A:1399:ARG:N	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:54:PHE:HA	2:B:58:THR:HB	1.88	0.54
2:B:94:LYS:HG2	2:B:95:ILE:N	2.22	0.54
2:B:168:GLY:N	2:B:450:ALA:HB1	2.14	0.54
2:B:230:ALA:N	2:B:231:PRO:HD2	2.23	0.54
2:B:488:TYR:CE2	2:B:813:LYS:HB2	2.42	0.54
4:D:213:GLU:O	4:D:217:LEU:HG	2.07	0.54
7:G:1:MET:O	7:G:1:MET:CE	2.54	0.54
8:H:33:GLN:C	8:H:35:GLN:H	2.16	0.54
1:A:339:ASN:CB	2:B:1117:GLN:HE22	2.19	0.54
1:A:703:THR:O	1:A:705:LYS:HG2	2.07	0.54
1:A:708:MET:SD	1:A:1091:SER:OG	2.66	0.54
1:A:886:ILE:HG13	1:A:943:LEU:HD12	1.90	0.54
1:A:1038:THR:O	1:A:1039:LYS:C	2.49	0.54
1:A:1063:MET:CE	1:A:1436:ILE:HG12	2.38	0.54
2:B:54:PHE:CE1	2:B:414:ALA:HA	2.43	0.54
5:E:163:GLU:O	5:E:164:LEU:C	2.51	0.54
7:G:6:ASP:C	7:G:7:LEU:HD23	2.33	0.54
8:H:116:TYR:HB2	8:H:123:MET:HB3	1.90	0.54
9:I:105:SER:O	9:I:106:CYS:HB3	2.06	0.54
1:A:303:TYR:CE1	1:A:325:ILE:HD11	2.43	0.53
1:A:472:LEU:CD1	2:B:835:GLN:NE2	2.69	0.53
2:B:46:GLN:CG	2:B:47:GLN:H	2.22	0.53
2:B:100:PRO:HD2	2:B:180:TYR:CE1	2.42	0.53
2:B:125:SER:HA	2:B:171:PRO:HA	1.89	0.53
2:B:265:SER:O	2:B:266:ALA:HB3	2.07	0.53
2:B:879:ARG:O	2:B:934:LYS:HD2	2.08	0.53
2:B:1115:THR:HG22	2:B:1117:GLN:HG3	1.90	0.53
2:B:1165:ILE:CG2	2:B:1185:CYS:HB3	2.38	0.53
4:D:60:LYS:O	4:D:61:GLU:C	2.51	0.53
5:E:60:PHE:HE2	5:E:80:VAL:HB	1.73	0.53
8:H:102:TYR:HD2	8:H:102:TYR:H	1.51	0.53
9:I:103:CYS:HB3	9:I:106:CYS:SG	2.48	0.53
1:A:135:PHE:C	1:A:137:ALA:N	2.60	0.53
1:A:348:SER:HB2	2:B:1128:LEU:HB2	1.90	0.53
1:A:381:THR:HG22	1:A:383:TYR:H	1.73	0.53
1:A:590:ARG:HG3	1:A:590:ARG:HH11	1.72	0.53
1:A:1406:VAL:CG1	1:A:1410:PHE:CE1	2.90	0.53
1:A:1420:ASP:O	1:A:1421:CYS:HB2	2.07	0.53
2:B:203:PHE:HB3	2:B:205:ILE:HD11	1.91	0.53
2:B:225:VAL:HA	2:B:237:VAL:O	2.08	0.53
2:B:857:ARG:HG2	2:B:858:SER:N	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1165:ILE:CG2	2:B:1166:CYS:N	2.70	0.53
2:B:1182:CYS:O	2:B:1182:CYS:SG	2.66	0.53
3:C:143:LEU:HD12	3:C:145:CYS:N	2.22	0.53
5:E:90:VAL:O	5:E:90:VAL:HG22	2.07	0.53
5:E:124:VAL:CG1	5:E:132:ILE:HD12	2.37	0.53
1:A:84:ILE:HG22	1:A:239:LEU:O	2.08	0.53
2:B:31:TRP:O	2:B:34:ILE:N	2.42	0.53
2:B:806:THR:O	2:B:807:ARG:C	2.50	0.53
2:B:1010:LEU:HD12	2:B:1011:ILE:N	2.22	0.53
3:C:97:VAL:HG12	3:C:98:VAL:N	2.23	0.53
3:C:183:TRP:O	3:C:185:LYS:N	2.41	0.53
5:E:7:ARG:C	5:E:9:ILE:N	2.65	0.53
5:E:55:ARG:O	5:E:57:MET:N	2.41	0.53
5:E:213:ILE:HG12	5:E:214:CYS:N	2.21	0.53
8:H:58:THR:HG22	8:H:59:ILE:H	1.73	0.53
9:I:43:VAL:O	9:I:43:VAL:HG12	2.09	0.53
1:A:567:LYS:CB	1:A:568:PRO:HD2	2.38	0.53
1:A:786:HIS:HE1	2:B:519:TRP:CZ2	2.25	0.53
1:A:996:ASN:HA	1:A:998:LEU:CD1	2.38	0.53
1:A:1036:ARG:HG2	1:A:1036:ARG:HH11	1.74	0.53
2:B:205:ILE:N	2:B:205:ILE:CD1	2.72	0.53
2:B:487:THR:HG22	2:B:488:TYR:H	1.73	0.53
2:B:498:THR:HB	2:B:537:LYS:O	2.08	0.53
2:B:542:MET:HG2	2:B:747:MET:HB3	1.89	0.53
2:B:619:ILE:C	2:B:621:GLU:H	2.17	0.53
2:B:817:LEU:O	2:B:818:PRO:O	2.26	0.53
2:B:1163:CYS:SG	2:B:1165:ILE:HB	2.48	0.53
3:C:9:LYS:O	3:C:10:ILE:O	2.26	0.53
3:C:168:ALA:C	3:C:170:TRP:N	2.67	0.53
4:D:123:LEU:HD23	4:D:149:THR:HG21	1.90	0.53
6:F:84:TYR:N	6:F:84:TYR:HD1	2.06	0.53
9:I:55:THR:HG1	9:I:100:PHE:HD2	1.51	0.53
1:A:556:TRP:C	1:A:558:GLY:N	2.65	0.53
1:A:823:GLY:O	1:A:825:ILE:N	2.42	0.53
1:A:855:THR:HG23	1:A:856:THR:N	2.23	0.53
1:A:1305:VAL:HG12	1:A:1306:LEU:N	2.22	0.53
1:A:1454:MET:O	1:A:1454:MET:HG3	2.08	0.53
2:B:57:TYR:N	2:B:57:TYR:HD1	2.06	0.53
2:B:214:ALA:HB3	2:B:498:THR:HA	1.90	0.53
2:B:273:LEU:HD21	2:B:360:PHE:CE1	2.44	0.53
2:B:371:GLU:CD	2:B:371:GLU:H	2.17	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:865:LYS:NZ	2:B:869:SER:HA	2.22	0.53
4:D:49:ALA:HB1	4:D:178:ALA:HB2	1.91	0.53
7:G:25:TYR:O	7:G:28:THR:HB	2.09	0.53
7:G:78:VAL:HG12	7:G:79:PHE:H	1.74	0.53
9:I:106:CYS:SG	9:I:107:SER:N	2.82	0.53
1:A:437:MET:O	1:A:438:ASP:C	2.50	0.53
1:A:726:ARG:O	1:A:727:ASP:C	2.50	0.53
1:A:867:ILE:HG22	1:A:871:ASP:N	2.24	0.53
1:A:1123:GLY:O	1:A:1125:ALA:N	2.41	0.53
1:A:1385:THR:O	1:A:1387:HIS:N	2.42	0.53
1:A:1397:LEU:HA	1:A:1400:CYS:HB3	1.90	0.53
2:B:179:CYS:SG	2:B:181:LEU:HB2	2.48	0.53
2:B:1001:PHE:CE1	2:B:1073:TYR:HB2	2.43	0.53
3:C:35:ARG:HH11	11:K:41:THR:CA	2.22	0.53
1:A:129:LYS:O	1:A:130:ASP:HB2	2.08	0.53
1:A:423:ASP:OD1	1:A:424:ILE:N	2.42	0.53
1:A:1021:LEU:O	1:A:1025:ARG:HG2	2.08	0.53
1:A:1310:GLY:O	1:A:1311:VAL:HG23	2.08	0.53
2:B:380:TYR:OH	2:B:623:GLU:OE2	2.21	0.53
2:B:898:LEU:HB2	12:L:58:LYS:HZ2	1.72	0.53
2:B:1045:SER:O	2:B:1046:PRO:O	2.27	0.53
3:C:63:ILE:O	3:C:64:ALA:C	2.50	0.53
7:G:128:PRO:O	7:G:138:THR:HG23	2.09	0.53
1:A:455:MET:HE3	2:B:1134:GLU:HG3	1.91	0.53
1:A:901:LEU:HD22	1:A:919:ILE:HG21	1.91	0.53
1:A:997:LEU:HD13	1:A:1018:PHE:CE2	2.42	0.53
1:A:1011:GLN:O	1:A:1015:VAL:HG23	2.09	0.53
1:A:1072:ILE:C	1:A:1075:PRO:HD2	2.33	0.53
2:B:69:LEU:HD22	2:B:429:PHE:HE1	1.74	0.53
2:B:167:ILE:HG22	2:B:453:ILE:HD12	1.91	0.53
2:B:458:LYS:O	2:B:459:TYR:C	2.50	0.53
2:B:955:THR:CG2	2:B:956:THR:N	2.71	0.53
3:C:99:LEU:HD23	3:C:99:LEU:N	2.23	0.53
3:C:99:LEU:HD12	3:C:118:LEU:HD13	1.91	0.53
3:C:174:ALA:HB2	3:C:235:VAL:HG22	1.90	0.53
5:E:39:LEU:O	5:E:42:PHE:HB3	2.08	0.53
6:F:116:ASP:O	6:F:120:ILE:HG13	2.09	0.53
1:A:41:MET:HB3	1:A:48:ALA:O	2.08	0.53
1:A:711:ARG:HG2	9:I:97:MET:HE2	1.90	0.53
1:A:853:ASP:OD1	1:A:853:ASP:C	2.51	0.53
1:A:1073:GLY:HA2	1:A:1076:ALA:HB3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1299:VAL:HG12	1:A:1300:LYS:H	1.74	0.53
2:B:334:ILE:HG22	2:B:334:ILE:O	2.09	0.53
2:B:347:LYS:HG3	2:B:348:ARG:H	1.74	0.53
2:B:763:GLN:HG2	2:B:765:PRO:CD	2.39	0.53
2:B:856:PHE:N	2:B:856:PHE:HD1	2.06	0.53
2:B:1201:LYS:HE2	2:B:1205:GLN:CD	2.33	0.53
3:C:112:ASN:HB3	3:C:114:TYR:CE1	2.44	0.53
4:D:129:LEU:O	4:D:132:GLN:HB2	2.08	0.53
5:E:7:ARG:O	5:E:9:ILE:N	2.42	0.53
10:J:57:ILE:O	10:J:60:PHE:HB2	2.09	0.53
11:K:46:ILE:O	11:K:50:LEU:HB2	2.07	0.53
1:A:720:ARG:O	1:A:724:GLU:HB2	2.09	0.53
1:A:1329:THR:O	1:A:1330:ASN:C	2.50	0.53
1:A:1343:ALA:O	1:A:1346:ALA:HB3	2.09	0.53
2:B:257:LYS:O	2:B:385:LEU:HD21	2.08	0.53
2:B:984:HIS:NE2	2:B:1025:HIS:HA	2.24	0.53
1:A:78:PRO:O	1:A:79:GLY:O	2.25	0.52
1:A:122:MET:O	1:A:123:ARG:C	2.51	0.52
1:A:151:ASP:OD1	1:A:163:SER:HB3	2.09	0.52
1:A:356:ASP:C	1:A:358:ASN:H	2.16	0.52
1:A:817:ALA:O	1:A:818:MET:C	2.51	0.52
1:A:1097:GLY:O	1:A:1100:ARG:HB3	2.09	0.52
1:A:1101:LEU:HB2	1:A:1355:VAL:HG11	1.91	0.52
2:B:189:LEU:O	2:B:192:LEU:N	2.31	0.52
2:B:247:GLY:C	2:B:249:ARG:H	2.16	0.52
2:B:827:ILE:CD1	2:B:1086:PHE:HD2	2.21	0.52
1:A:53:LEU:HD23	1:A:54:ASN:HB3	1.91	0.52
1:A:472:LEU:HD13	2:B:835:GLN:CD	2.33	0.52
1:A:511:ILE:O	1:A:519:PRO:HA	2.08	0.52
1:A:583:PRO:O	1:A:610:GLY:HA3	2.10	0.52
1:A:779:PHE:O	1:A:780:VAL:C	2.52	0.52
1:A:853:ASP:O	1:A:854:ASN:HB2	2.09	0.52
2:B:102:VAL:HG22	2:B:112:LEU:HD22	1.92	0.52
2:B:118:ARG:HH22	2:B:194:GLU:CD	2.18	0.52
2:B:376:PHE:CE2	2:B:569:TYR:HD2	2.28	0.52
3:C:31:ASN:O	3:C:34:ARG:N	2.43	0.52
3:C:44:LEU:HD23	3:C:72:LEU:HB2	1.90	0.52
4:D:130:LEU:C	4:D:132:GLN:N	2.61	0.52
5:E:154:ILE:O	5:E:196:VAL:HA	2.09	0.52
8:H:139:ASN:O	8:H:140:ALA:HB2	2.08	0.52
11:K:58:PHE:HE2	11:K:74:ARG:HE	1.54	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:LEU:HD22	1:A:303:TYR:HE1	1.73	0.52
1:A:412:ARG:NH2	2:B:1108:ARG:HH12	2.06	0.52
1:A:877:HIS:C	1:A:878:ILE:HG13	2.33	0.52
2:B:39:ARG:HG2	2:B:39:ARG:HH11	1.73	0.52
2:B:224:GLN:O	2:B:238:ALA:HA	2.08	0.52
2:B:601:ARG:HG2	2:B:615:MET:HE1	1.92	0.52
4:D:47:LEU:HD11	7:G:3:PHE:HD2	1.72	0.52
8:H:24:CYS:HB2	8:H:44:VAL:HG21	1.89	0.52
8:H:128:ASN:CG	8:H:128:ASN:O	2.52	0.52
11:K:68:PHE:CD2	11:K:68:PHE:N	2.77	0.52
1:A:725:ALA:O	1:A:729:ALA:N	2.42	0.52
1:A:808:LEU:HD21	1:A:816:HIS:CD2	2.44	0.52
1:A:823:GLY:C	1:A:825:ILE:N	2.66	0.52
1:A:898:ARG:HD3	1:A:933:TYR:CD1	2.44	0.52
1:A:1114:PRO:O	1:A:1311:VAL:CG2	2.58	0.52
2:B:94:LYS:HG2	2:B:95:ILE:H	1.73	0.52
2:B:225:VAL:HG22	2:B:396:ASP:OD2	2.10	0.52
2:B:298:LEU:N	2:B:298:LEU:CD2	2.72	0.52
2:B:373:ARG:HA	2:B:566:LEU:HD23	1.91	0.52
2:B:413:LEU:O	2:B:414:ALA:C	2.52	0.52
3:C:44:LEU:HB2	3:C:77:ILE:HD11	1.92	0.52
3:C:144:ILE:O	3:C:145:CYS:HB2	2.08	0.52
7:G:18:PHE:CZ	7:G:68:ALA:HB2	2.44	0.52
7:G:109:PHE:CG	7:G:110:VAL:N	2.78	0.52
8:H:89:LEU:C	8:H:91:ASP:N	2.68	0.52
11:K:87:LEU:HD12	11:K:87:LEU:O	2.09	0.52
1:A:751:SER:O	1:A:752:LYS:HG2	2.09	0.52
1:A:785:PRO:HG2	2:B:703:ILE:HD12	1.91	0.52
1:A:1148:ILE:O	1:A:1149:ALA:HB2	2.09	0.52
1:A:1213:GLY:O	1:A:1216:ILE:N	2.42	0.52
2:B:210:LYS:HD2	2:B:481:GLN:O	2.09	0.52
2:B:857:ARG:NH2	2:B:942:ARG:NH1	2.57	0.52
3:C:51:VAL:HG22	3:C:155:LEU:CD2	2.39	0.52
3:C:61:GLU:HA	3:C:64:ALA:HB3	1.91	0.52
3:C:168:ALA:C	3:C:170:TRP:H	2.17	0.52
4:D:51:ASN:C	4:D:52:LEU:O	2.52	0.52
10:J:48:ARG:HE	10:J:49:MET:HE2	1.74	0.52
10:J:61:LEU:C	10:J:63:TYR:H	2.16	0.52
11:K:31:VAL:O	11:K:74:ARG:HA	2.10	0.52
1:A:477:PRO:CG	1:A:521:MET:HG2	2.39	0.52
1:A:795:GLU:CD	1:A:795:GLU:N	2.59	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:986:ILE:CD1	1:A:1032:LEU:HD11	2.40	0.52
1:A:1339:LEU:HD13	5:E:147:HIS:CD2	2.45	0.52
1:A:1377:THR:O	1:A:1379:GLY:N	2.42	0.52
2:B:314:LEU:O	2:B:315:LYS:C	2.53	0.52
2:B:488:TYR:HE2	2:B:813:LYS:HB2	1.75	0.52
2:B:522:VAL:CG1	2:B:523:CYS:N	2.71	0.52
2:B:681:TRP:C	2:B:683:SER:N	2.66	0.52
2:B:758:PHE:CE2	2:B:1044:ALA:CA	2.92	0.52
2:B:806:THR:N	2:B:809:MET:HE3	2.25	0.52
2:B:1099:VAL:O	2:B:1102:LYS:N	2.36	0.52
3:C:227:THR:C	3:C:228:PHE:CD1	2.87	0.52
7:G:6:ASP:HB3	7:G:73:LYS:NZ	2.25	0.52
8:H:6:PHE:O	8:H:58:THR:HA	2.09	0.52
1:A:372:LYS:HA	1:A:435:HIS:ND1	2.24	0.52
1:A:808:LEU:HD12	1:A:808:LEU:H	1.74	0.52
1:A:1088:GLY:O	1:A:1089:VAL:HG23	2.09	0.52
1:A:1372:VAL:HG12	1:A:1373:ASP:N	2.25	0.52
2:B:223:VAL:CG1	2:B:381:MET:HG2	2.40	0.52
2:B:431:TYR:CZ	2:B:447:ALA:HB2	2.44	0.52
2:B:640:VAL:HG23	2:B:740:HIS:HA	1.92	0.52
2:B:1020:ARG:HG2	2:B:1020:ARG:NH1	2.20	0.52
2:B:1191:ILE:C	2:B:1192:TYR:CD1	2.88	0.52
4:D:185:CYS:HB3	4:D:211:LEU:CD1	2.39	0.52
12:L:25:ALA:O	12:L:26:THR:HB	2.10	0.52
1:A:24:PRO:HG2	1:A:25:GLU:CD	2.35	0.52
1:A:106:VAL:HA	1:A:114:LEU:HD21	1.91	0.52
1:A:474:VAL:HG22	1:A:474:VAL:O	2.10	0.52
1:A:794:PRO:C	1:A:796:SER:H	2.18	0.52
1:A:894:GLU:C	1:A:896:ARG:H	2.18	0.52
2:B:583:ASN:HD21	2:B:628:THR:CB	2.13	0.52
2:B:781:PHE:CD1	2:B:781:PHE:C	2.88	0.52
3:C:215:GLU:O	3:C:217:ASP:N	2.43	0.52
4:D:47:LEU:HD13	4:D:48:ILE:N	2.25	0.52
7:G:143:ILE:CG2	7:G:144:ARG:N	2.73	0.52
10:J:7:CYS:CA	10:J:49:MET:HE3	2.40	0.52
10:J:23:ASN:C	10:J:25:LEU:N	2.68	0.52
11:K:49:GLU:OE2	11:K:97:LYS:HE3	2.09	0.52
11:K:53:ASP:HB3	11:K:56:VAL:CG2	2.39	0.52
11:K:65:HIS:CD2	11:K:65:HIS:C	2.87	0.52
1:A:964:ILE:O	1:A:968:GLN:HG2	2.09	0.52
1:A:996:ASN:HA	1:A:998:LEU:HD12	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1079:MET:HE1	1:A:1101:LEU:CD2	2.38	0.52
1:A:1272:THR:C	1:A:1273:LEU:HD12	2.34	0.52
2:B:197:PHE:HZ	2:B:816:GLU:HG2	1.74	0.52
2:B:212:LEU:HD21	2:B:466:TRP:HH2	1.74	0.52
2:B:726:ALA:HB1	2:B:1051:THR:HG21	1.91	0.52
2:B:781:PHE:O	2:B:782:LEU:CG	2.54	0.52
2:B:870:ILE:CG2	2:B:917:PRO:HG2	2.40	0.52
2:B:906:SER:O	2:B:941:LEU:HD23	2.10	0.52
2:B:1065:GLN:NE2	2:B:1067:ARG:HG2	2.25	0.52
4:D:198:LEU:O	4:D:200:ASN:N	2.42	0.52
5:E:92:THR:O	5:E:95:THR:HB	2.10	0.52
8:H:143:LEU:HD12	8:H:143:LEU:N	2.25	0.52
9:I:54:GLU:O	9:I:100:PHE:CE2	2.63	0.52
1:A:321:PRO:O	1:A:322:VAL:CB	2.58	0.52
1:A:324:SER:O	1:A:325:ILE:C	2.52	0.52
1:A:514:PRO:O	1:A:875:ALA:HB1	2.09	0.52
1:A:1157:ASP:C	1:A:1159:ARG:H	2.18	0.52
1:A:1280:GLU:O	1:A:1281:ARG:C	2.52	0.52
2:B:298:LEU:N	2:B:298:LEU:HD22	2.24	0.52
2:B:401:PHE:HD2	2:B:521:LEU:HD12	1.75	0.52
2:B:508:LEU:O	2:B:510:LYS:N	2.42	0.52
2:B:708:GLU:HG3	2:B:709:ASP:H	1.75	0.52
2:B:1082:MET:O	3:C:189:THR:HG23	2.10	0.52
2:B:1166:CYS:O	2:B:1166:CYS:SG	2.68	0.52
3:C:58:LEU:N	3:C:58:LEU:HD22	2.25	0.52
5:E:147:HIS:CD2	5:E:149:LEU:H	2.27	0.52
9:I:99:LEU:C	9:I:100:PHE:HD1	2.18	0.52
2:B:798:TYR:CD1	10:J:4:PRO:HG3	2.45	0.51
2:B:800:GLN:CB	10:J:52:THR:HG21	2.33	0.51
2:B:1034:VAL:HG23	2:B:1059:LEU:CD1	2.40	0.51
3:C:80:LEU:CD1	3:C:95:CYS:HA	2.40	0.51
12:L:28:LYS:HB2	12:L:39:SER:HA	1.91	0.51
1:A:35:ILE:HG22	1:A:35:ILE:O	2.11	0.51
1:A:78:PRO:HA	2:B:1201:LYS:HZ2	1.73	0.51
1:A:317:LYS:O	1:A:318:SER:CB	2.57	0.51
1:A:549:MET:O	1:A:550:LEU:C	2.53	0.51
2:B:323:VAL:O	2:B:323:VAL:HG12	2.09	0.51
2:B:457:LEU:O	2:B:461:LEU:HD12	2.10	0.51
2:B:1084:GLN:HE21	2:B:1084:GLN:H	1.55	0.51
5:E:124:VAL:HB	5:E:125:PRO:HD3	1.92	0.51
9:I:68:LEU:HB3	9:I:84:VAL:HG23	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:65:HIS:CD2	11:K:66:PRO:HD2	2.46	0.51
1:A:50:ILE:O	1:A:52:GLY:N	2.39	0.51
1:A:543:LEU:O	1:A:544:ASP:C	2.52	0.51
1:A:647:GLY:O	1:A:648:ASN:C	2.54	0.51
1:A:668:ASP:CG	1:A:742:ASN:HD22	2.19	0.51
1:A:858:ASN:HD21	1:A:860:LEU:HB2	1.76	0.51
1:A:1051:ALA:C	1:A:1053:PHE:N	2.67	0.51
2:B:57:TYR:O	2:B:59:LEU:N	2.42	0.51
2:B:429:PHE:HA	2:B:432:MET:CE	2.40	0.51
2:B:546:SER:HA	2:B:612:GLU:OE2	2.11	0.51
2:B:843:GLN:O	2:B:846:ILE:HB	2.11	0.51
2:B:865:LYS:HE2	2:B:871:THR:OG1	2.10	0.51
2:B:936:ASP:OD1	2:B:938:SER:N	2.42	0.51
3:C:43:THR:CG2	3:C:44:LEU:N	2.74	0.51
5:E:100:ILE:CG2	5:E:105:PHE:HB2	2.40	0.51
1:A:55:ASP:N	1:A:56:PRO:CD	2.73	0.51
1:A:100:LYS:O	1:A:101:LYS:C	2.54	0.51
1:A:392:VAL:HG21	1:A:426:LEU:HD11	1.91	0.51
1:A:877:HIS:O	1:A:878:ILE:HG12	2.10	0.51
1:A:1313:LEU:O	1:A:1314:SER:C	2.52	0.51
2:B:38:PHE:CD1	2:B:811:TYR:CD2	2.98	0.51
2:B:49:ASP:HA	2:B:52:ASN:HD22	1.75	0.51
2:B:242:SER:HB2	2:B:362:PRO:HG2	1.93	0.51
2:B:424:LEU:HD22	2:B:453:ILE:HD11	1.92	0.51
2:B:508:LEU:HB2	2:B:510:LYS:CB	2.40	0.51
2:B:1182:CYS:O	2:B:1183:LYS:C	2.53	0.51
3:C:107:SER:C	3:C:109:SER:N	2.69	0.51
5:E:25:ASP:C	5:E:27:GLY:H	2.17	0.51
8:H:17:PRO:HB3	8:H:24:CYS:SG	2.49	0.51
8:H:59:ILE:O	8:H:60:ALA:HB3	2.10	0.51
9:I:58:VAL:HG12	9:I:60:GLN:N	2.20	0.51
9:I:100:PHE:HD1	9:I:100:PHE:N	2.07	0.51
12:L:38:LEU:HG	12:L:39:SER:N	2.26	0.51
1:A:18:GLN:HB3	2:B:1215:ARG:HG3	1.92	0.51
1:A:445:ASN:ND2	1:A:455:MET:HE3	2.26	0.51
1:A:547:LEU:HD22	11:K:58:PHE:CE1	2.46	0.51
1:A:675:THR:O	1:A:679:ILE:HG13	2.11	0.51
1:A:798:GLY:HA2	1:A:815:PHE:HD1	1.75	0.51
1:A:852:TYR:CD2	1:A:1060:PRO:HB2	2.45	0.51
1:A:866:PHE:CD2	5:E:168:TYR:CE1	2.98	0.51
2:B:401:PHE:HB2	2:B:517:THR:OG1	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:758:PHE:CE1	2:B:1027:ILE:CG2	2.94	0.51
2:B:1177:HIS:O	2:B:1179:GLN:N	2.44	0.51
3:C:60:ASP:OD2	12:L:60:ARG:NH2	2.44	0.51
5:E:124:VAL:HG13	5:E:132:ILE:CB	2.39	0.51
7:G:49:LEU:N	7:G:49:LEU:HD23	2.25	0.51
1:A:34:LYS:HG2	1:A:36:ARG:NH2	2.26	0.51
1:A:172:PRO:HB3	1:A:185:TRP:CE2	2.46	0.51
1:A:406:ILE:HG22	1:A:411:ASP:O	2.11	0.51
1:A:416:ARG:O	1:A:417:TYR:HD2	1.94	0.51
1:A:1122:PRO:O	1:A:1123:GLY:C	2.54	0.51
1:A:1451:VAL:C	1:A:1453:TYR:H	2.19	0.51
2:B:97:VAL:HG12	2:B:178:ASN:HD21	1.74	0.51
2:B:210:LYS:HE2	2:B:462:ALA:O	2.11	0.51
2:B:446:LEU:N	2:B:446:LEU:HD23	2.26	0.51
2:B:546:SER:HA	2:B:612:GLU:CD	2.35	0.51
2:B:562:GLY:HA3	2:B:590:HIS:ND1	2.25	0.51
2:B:996:ARG:HH22	3:C:175:ALA:HA	1.75	0.51
10:J:5:VAL:O	10:J:6:ARG:O	2.28	0.51
1:A:898:ARG:HB2	1:A:933:TYR:HE1	1.75	0.51
1:A:1336:MET:HE2	1:A:1381:LEU:HG	1.92	0.51
2:B:510:LYS:HG2	2:B:512:ARG:N	2.19	0.51
2:B:809:MET:O	2:B:812:LEU:N	2.37	0.51
2:B:879:ARG:O	2:B:880:THR:CB	2.58	0.51
5:E:10:SER:O	5:E:13:TRP:HB3	2.10	0.51
5:E:144:ILE:C	5:E:146:HIS:H	2.19	0.51
5:E:212:ARG:HG3	5:E:212:ARG:HH11	1.75	0.51
9:I:100:PHE:N	9:I:100:PHE:CD1	2.78	0.51
11:K:67:PHE:O	11:K:68:PHE:HD2	1.93	0.51
1:A:525:GLN:HB3	2:B:1015:HIS:HD2	1.75	0.51
1:A:744:LYS:HE2	1:A:748:MET:HE2	1.92	0.51
1:A:768:GLN:HG2	1:A:816:HIS:CA	2.27	0.51
1:A:785:PRO:CG	2:B:703:ILE:HD12	2.40	0.51
1:A:902:LEU:HG	1:A:926:GLN:HG3	1.93	0.51
1:A:928:LEU:O	1:A:929:LEU:C	2.53	0.51
1:A:1030:ARG:CG	1:A:1034:GLU:OE2	2.59	0.51
1:A:1261:LYS:CA	1:A:1264:GLU:HB3	2.38	0.51
1:A:1424:VAL:CG2	1:A:1436:ILE:HD11	2.32	0.51
2:B:51:PHE:O	2:B:52:ASN:C	2.53	0.51
2:B:62:ILE:HG23	2:B:418:LYS:HG2	1.92	0.51
2:B:261:ARG:HB3	2:B:261:ARG:HH11	1.76	0.51
2:B:310:MET:HE1	2:B:383:ASN:OD1	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:570:VAL:HG21	2:B:573:GLN:CD	2.36	0.51
2:B:766:ARG:HH21	2:B:1020:ARG:HG2	1.70	0.51
2:B:980:PHE:CE2	2:B:1094:ARG:HG3	2.46	0.51
3:C:53:THR:O	3:C:153:LEU:HA	2.10	0.51
4:D:26:THR:O	4:D:28:GLN:HG3	2.11	0.51
5:E:79:TRP:HE1	5:E:81:GLU:HB2	1.76	0.51
7:G:1:MET:HE3	7:G:80:LYS:C	2.36	0.51
8:H:40:LEU:HG	8:H:41:ASP:O	2.11	0.51
10:J:55:ASP:OD2	10:J:58:GLU:HG2	2.10	0.51
11:K:50:LEU:HD11	11:K:75:ILE:HD13	1.92	0.51
11:K:78:THR:O	11:K:79:GLU:C	2.53	0.51
1:A:841:LEU:O	1:A:845:LEU:HG	2.10	0.51
1:A:856:THR:HB	1:A:865:GLN:HB2	1.93	0.51
1:A:864:ILE:O	1:A:864:ILE:HG22	2.10	0.51
2:B:91:SER:OG	2:B:133:LYS:HB2	2.11	0.51
2:B:1111:MET:O	2:B:1112:GLN:C	2.54	0.51
3:C:31:ASN:O	3:C:34:ARG:HB3	2.10	0.51
4:D:134:THR:HG22	4:D:136:GLY:H	1.76	0.51
5:E:192:ARG:HG3	5:E:192:ARG:NH1	2.26	0.51
12:L:52:GLY:O	12:L:53:HIS:C	2.54	0.51
1:A:7:SER:O	1:A:8:SER:C	2.54	0.51
1:A:863:VAL:HG12	1:A:865:GLN:H	1.76	0.51
1:A:871:ASP:O	1:A:873:MET:HE2	2.11	0.51
1:A:898:ARG:HD3	1:A:933:TYR:CE1	2.45	0.51
1:A:989:GLY:O	1:A:992:ASP:N	2.44	0.51
1:A:1148:ILE:O	1:A:1148:ILE:CG2	2.59	0.51
2:B:390:LEU:O	2:B:391:ASP:C	2.54	0.51
2:B:525:ALA:O	2:B:768:THR:HG23	2.11	0.51
2:B:770:GLN:CD	2:B:983:ARG:HA	2.36	0.51
2:B:899:ILE:HG22	2:B:900:ALA:H	1.75	0.51
2:B:1102:LYS:O	2:B:1103:ILE:O	2.29	0.51
3:C:133:ILE:HD11	3:C:237:SER:CA	2.24	0.51
3:C:235:VAL:HG13	10:J:13:VAL:CG2	2.40	0.51
4:D:40:HIS:CB	7:G:73:LYS:NZ	2.58	0.51
7:G:123:ALA:O	7:G:125:SER:N	2.43	0.51
9:I:95:THR:HG22	9:I:96:SER:N	2.25	0.51
1:A:63:ARG:CA	1:A:74:MET:SD	2.89	0.50
1:A:709:THR:CG2	1:A:712:GLU:H	2.23	0.50
1:A:770:VAL:O	1:A:771:GLU:HB2	2.11	0.50
1:A:877:HIS:CG	1:A:1056:SER:HA	2.46	0.50
1:A:1104:ILE:O	1:A:1105:LEU:C	2.53	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1330:ASN:C	1:A:1330:ASN:OD1	2.52	0.50
2:B:782:LEU:CD1	2:B:788:ARG:HH11	2.23	0.50
2:B:843:GLN:O	2:B:846:ILE:N	2.44	0.50
2:B:882:THR:HB	2:B:934:LYS:O	2.11	0.50
1:A:695:LYS:C	1:A:697:ALA:N	2.69	0.50
1:A:871:ASP:CG	1:A:1366:ARG:HH22	2.19	0.50
1:A:1011:GLN:NE2	1:A:1015:VAL:CG2	2.65	0.50
1:A:1067:LEU:O	1:A:1068:ALA:C	2.54	0.50
1:A:1161:THR:O	1:A:1163:ILE:N	2.45	0.50
1:A:1242:VAL:HG12	1:A:1243:VAL:N	2.25	0.50
1:A:1398:MET:HB2	1:A:1426:GLU:OE2	2.11	0.50
1:A:1398:MET:O	1:A:1401:SER:OG	2.22	0.50
2:B:218:SER:O	2:B:219:ALA:O	2.29	0.50
2:B:254:LEU:HD23	2:B:381:MET:CE	2.36	0.50
2:B:806:THR:C	2:B:808:ALA:N	2.68	0.50
2:B:851:PHE:CD2	2:B:1094:ARG:HB2	2.46	0.50
2:B:994:TYR:HB2	2:B:999:MET:HE1	1.92	0.50
2:B:1029:CYS:SG	2:B:1086:PHE:CE2	3.05	0.50
3:C:104:PHE:HD2	3:C:105:GLY:H	1.56	0.50
5:E:164:LEU:CD2	5:E:211:TYR:CD2	2.95	0.50
7:G:30:LEU:O	7:G:34:VAL:HG23	2.12	0.50
10:J:46:CYS:O	10:J:49:MET:N	2.44	0.50
1:A:254:GLU:HB2	2:B:935:ARG:NH2	2.25	0.50
1:A:335:ARG:HA	1:A:339:ASN:ND2	2.26	0.50
1:A:519:PRO:HG3	1:A:625:SER:O	2.12	0.50
1:A:1167:GLU:O	1:A:1169:ILE:N	2.44	0.50
1:A:1169:ILE:O	1:A:1170:ILE:C	2.54	0.50
1:A:1193:LEU:C	1:A:1193:LEU:HD12	2.35	0.50
1:A:1308:THR:HG23	1:A:1309:ASP:N	2.26	0.50
2:B:758:PHE:HE2	2:B:1044:ALA:HA	1.73	0.50
2:B:901:PRO:O	2:B:902:GLY:C	2.53	0.50
2:B:1149:GLU:C	2:B:1151:LEU:N	2.67	0.50
2:B:1178:ASN:O	2:B:1179:GLN:C	2.55	0.50
3:C:35:ARG:HD3	11:K:41:THR:HA	1.93	0.50
3:C:170:TRP:O	3:C:171:GLY:C	2.54	0.50
4:D:147:TYR:CZ	7:G:103:VAL:HG13	2.47	0.50
5:E:93:MET:C	5:E:95:THR:N	2.68	0.50
9:I:27:PHE:O	9:I:28:GLU:HB3	2.11	0.50
10:J:52:THR:O	10:J:53:HIS:O	2.30	0.50
12:L:30:ILE:HG22	12:L:31:CYS:O	2.10	0.50
1:A:90:VAL:CG1	1:A:91:PHE:H	2.23	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:326:ARG:HG2	1:A:327:ALA:N	2.24	0.50
1:A:335:ARG:NE	1:A:339:ASN:HD22	2.10	0.50
1:A:340:LEU:HD13	1:A:1429:ILE:HG23	1.93	0.50
1:A:351:THR:HG21	2:B:1103:ILE:HG13	1.91	0.50
1:A:556:TRP:O	1:A:558:GLY:N	2.44	0.50
1:A:814:PHE:C	1:A:814:PHE:CD2	2.88	0.50
1:A:1283:VAL:CG1	1:A:1284:MET:H	2.24	0.50
1:A:1444:MET:O	6:F:132:LEU:HA	2.10	0.50
2:B:20:ASP:C	2:B:22:SER:H	2.19	0.50
2:B:23:ALA:CB	2:B:24:PRO:HD2	2.31	0.50
2:B:911:ILE:HG22	2:B:912:ILE:HG13	1.93	0.50
2:B:984:HIS:CD2	2:B:1025:HIS:HB2	2.47	0.50
2:B:1059:LEU:HD23	2:B:1065:GLN:O	2.12	0.50
3:C:31:ASN:OD1	3:C:34:ARG:HD3	2.10	0.50
3:C:84:ARG:NH2	11:K:11:LEU:HD21	2.27	0.50
3:C:167:HIS:HD2	3:C:169:LYS:N	1.97	0.50
5:E:7:ARG:C	5:E:9:ILE:H	2.19	0.50
5:E:157:SER:C	5:E:159:ASP:N	2.68	0.50
11:K:65:HIS:CD2	11:K:67:PHE:N	2.60	0.50
1:A:93:VAL:CG2	1:A:301:ALA:HA	2.40	0.50
1:A:125:ALA:C	1:A:127:ALA:H	2.20	0.50
1:A:1041:ALA:O	1:A:1044:TRP:HB3	2.12	0.50
1:A:1102:LYS:C	1:A:1106:ASN:HD22	2.18	0.50
1:A:1341:ILE:O	1:A:1344:GLY:N	2.45	0.50
1:A:1354:ASN:O	1:A:1355:VAL:C	2.54	0.50
1:A:1444:MET:HG2	7:G:60:ARG:CA	2.40	0.50
2:B:510:LYS:O	2:B:513:GLN:HB2	2.11	0.50
3:C:163:ILE:O	3:C:164:ALA:C	2.54	0.50
4:D:196:PRO:C	4:D:198:LEU:N	2.67	0.50
7:G:17:PHE:N	7:G:17:PHE:CD2	2.76	0.50
7:G:70:PHE:N	7:G:70:PHE:CD1	2.79	0.50
7:G:96:GLN:HG3	7:G:97:HIS:HD2	1.76	0.50
10:J:1:MET:HA	10:J:57:ILE:H	1.76	0.50
10:J:21:TYR:O	10:J:23:ASN:N	2.44	0.50
12:L:49:LYS:O	12:L:50:ASP:CB	2.59	0.50
1:A:115:LEU:HB2	1:A:122:MET:CE	2.40	0.50
1:A:590:ARG:O	1:A:591:PHE:HB2	2.12	0.50
1:A:811:GLN:O	1:A:812:GLU:C	2.55	0.50
1:A:992:ASP:O	1:A:995:GLU:HB2	2.11	0.50
1:A:1277:GLU:O	1:A:1278:ASN:HB2	2.11	0.50
2:B:59:LEU:HD12	2:B:417:PHE:CE2	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:303:TYR:CD2	2:B:303:TYR:N	2.80	0.50
3:C:51:VAL:HG22	3:C:155:LEU:HD21	1.93	0.50
3:C:69:LEU:HD12	3:C:69:LEU:N	2.27	0.50
3:C:88:CYS:SG	3:C:88:CYS:O	2.70	0.50
3:C:168:ALA:O	3:C:170:TRP:N	2.44	0.50
5:E:16:PHE:O	5:E:17:ARG:C	2.54	0.50
6:F:103:MET:O	6:F:104:ASN:HB2	2.11	0.50
6:F:127:GLU:O	6:F:129:LYS:HG3	2.12	0.50
1:A:42:ASP:CG	1:A:45:GLN:HA	2.37	0.50
1:A:496:GLU:OE1	7:G:64:THR:HA	2.11	0.50
1:A:541:ILE:HD12	1:A:577:ILE:HD11	1.93	0.50
1:A:553:VAL:HG22	1:A:652:VAL:HG22	1.92	0.50
1:A:719:VAL:O	1:A:721:PHE:N	2.45	0.50
1:A:1125:ALA:O	1:A:1127:ASP:N	2.45	0.50
1:A:1213:GLY:HA2	1:A:1216:ILE:CD1	2.42	0.50
2:B:54:PHE:O	2:B:59:LEU:HB2	2.12	0.50
2:B:212:LEU:HD21	2:B:466:TRP:CH2	2.47	0.50
2:B:496:ARG:HH12	2:B:539:LEU:HB2	1.75	0.50
2:B:1106:ARG:CG	2:B:1107:ALA:N	2.69	0.50
2:B:1162:ILE:HG22	2:B:1163:CYS:N	2.25	0.50
5:E:168:TYR:CB	5:E:170:LEU:HG	2.40	0.50
8:H:59:ILE:CG2	8:H:60:ALA:N	2.73	0.50
8:H:89:LEU:O	8:H:91:ASP:N	2.39	0.50
8:H:93:TYR:CD1	8:H:93:TYR:N	2.80	0.50
11:K:35:PHE:N	11:K:35:PHE:CD1	2.79	0.50
1:A:602:ASP:OD2	1:A:616:VAL:HG23	2.11	0.50
1:A:791:ASP:C	1:A:791:ASP:OD1	2.55	0.50
1:A:1369:ALA:O	1:A:1372:VAL:HG12	2.11	0.50
2:B:97:VAL:CG1	2:B:178:ASN:ND2	2.74	0.50
2:B:526:GLU:HG2	2:B:538:ASN:HD22	1.77	0.50
2:B:999:MET:HA	2:B:999:MET:CE	2.42	0.50
7:G:25:TYR:HE2	7:G:29:LYS:HD2	1.77	0.50
7:G:91:VAL:HA	7:G:101:VAL:HA	1.94	0.50
1:A:231:PRO:HA	1:A:234:MET:HE2	1.94	0.50
1:A:456:MET:HE3	1:A:507:VAL:HG22	1.93	0.50
1:A:470:LEU:HD11	1:A:482:PHE:CZ	2.46	0.50
1:A:575:LYS:O	1:A:579:SER:OG	2.30	0.50
1:A:899:VAL:HG22	1:A:908:LEU:HD21	1.93	0.50
2:B:48:LEU:O	2:B:51:PHE:N	2.44	0.50
2:B:197:PHE:CZ	2:B:816:GLU:HG2	2.46	0.50
2:B:376:PHE:HB3	2:B:586:TRP:CZ3	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:428:ILE:HG22	2:B:432:MET:HE2	1.94	0.50
3:C:136:ASP:OD1	3:C:138:GLU:N	2.45	0.50
3:C:143:LEU:HD21	3:C:146:LYS:HE2	1.94	0.50
3:C:164:ALA:O	3:C:167:HIS:N	2.43	0.50
5:E:23:VAL:O	5:E:28:TYR:HB2	2.12	0.50
5:E:144:ILE:HG13	5:E:145:THR:N	2.26	0.50
8:H:25:ARG:HA	8:H:41:ASP:HA	1.93	0.50
9:I:34:TYR:CD2	9:I:34:TYR:C	2.90	0.50
1:A:167:CYS:O	1:A:167:CYS:SG	2.69	0.49
1:A:265:LYS:NZ	1:A:322:VAL:HG22	2.26	0.49
1:A:642:CYS:O	1:A:643:ALA:C	2.55	0.49
1:A:1114:PRO:O	1:A:1311:VAL:HG21	2.11	0.49
1:A:1161:THR:HG22	1:A:1163:ILE:HG13	1.94	0.49
1:A:1213:GLY:O	1:A:1214:GLU:C	2.54	0.49
1:A:1261:LYS:C	1:A:1264:GLU:H	2.20	0.49
1:A:1325:THR:CG2	1:A:1326:ARG:HG3	2.41	0.49
2:B:117:ALA:HA	2:B:122:LEU:HB2	1.94	0.49
5:E:72:PHE:N	5:E:72:PHE:CD1	2.80	0.49
8:H:27:GLU:HA	8:H:38:LEU:O	2.12	0.49
9:I:58:VAL:HG13	9:I:62:ILE:HD12	1.94	0.49
10:J:60:PHE:O	10:J:63:TYR:HD1	1.94	0.49
12:L:28:LYS:HB2	12:L:39:SER:CA	2.42	0.49
1:A:14:VAL:HG23	1:A:1432:GLN:HE22	1.75	0.49
1:A:22:PHE:CE1	2:B:1213:THR:HG22	2.47	0.49
1:A:24:PRO:HG2	1:A:25:GLU:OE2	2.11	0.49
1:A:601:LYS:HB2	1:A:603:ASN:ND2	2.27	0.49
1:A:717:ASN:O	1:A:721:PHE:CD1	2.66	0.49
1:A:937:VAL:C	1:A:939:ASP:N	2.68	0.49
1:A:997:LEU:HB3	1:A:1053:PHE:CE2	2.47	0.49
1:A:1019:CYS:O	1:A:1022:LEU:N	2.45	0.49
1:A:1191:TRP:HD1	1:A:1256:GLU:HB2	1.76	0.49
1:A:1364:ASN:HD22	1:A:1365:TYR:N	2.10	0.49
2:B:217:ARG:HD2	2:B:217:ARG:C	2.37	0.49
2:B:247:GLY:H	2:B:418:LYS:NZ	2.10	0.49
2:B:269:ILE:HG22	2:B:282:ILE:HG23	1.94	0.49
2:B:351:TYR:CE1	2:B:355:ILE:HD11	2.47	0.49
2:B:497:ARG:NH2	2:B:775:LYS:NZ	2.60	0.49
2:B:806:THR:HG22	2:B:808:ALA:HB3	1.94	0.49
3:C:186:LEU:N	3:C:186:LEU:CD1	2.75	0.49
11:K:84:LYS:O	11:K:87:LEU:HB3	2.12	0.49
1:A:208:LEU:HG	1:A:235:ILE:HG21	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:809:THR:OG1	1:A:812:GLU:HG3	2.12	0.49
1:A:877:HIS:O	1:A:878:ILE:CG1	2.61	0.49
1:A:1048:ASN:HD22	1:A:1048:ASN:N	2.10	0.49
1:A:1290:LYS:O	1:A:1291:VAL:HG23	2.11	0.49
2:B:903:VAL:CG1	2:B:904:ARG:N	2.76	0.49
2:B:958:GLN:C	2:B:960:GLY:H	2.19	0.49
2:B:976:ILE:O	2:B:990:ILE:HB	2.12	0.49
5:E:46:TYR:CD2	5:E:58:MET:HG2	2.48	0.49
6:F:72:LYS:HB2	6:F:142:SER:HB3	1.94	0.49
1:A:587:HIS:HD2	1:A:969:GLN:CG	2.19	0.49
1:A:1385:THR:HG22	1:A:1386:ARG:N	2.26	0.49
2:B:215:GLN:OE1	2:B:215:GLN:HA	2.12	0.49
2:B:1074:ASN:O	2:B:1078:GLY:N	2.44	0.49
2:B:1184:GLY:C	2:B:1186:ASP:N	2.66	0.49
4:D:53:SER:O	4:D:57:LEU:HG	2.12	0.49
5:E:7:ARG:HG3	5:E:8:ASN:H	1.73	0.49
5:E:171:LYS:O	5:E:172:GLU:C	2.55	0.49
12:L:31:CYS:HB3	12:L:35:SER:CA	2.42	0.49
1:A:148:CYS:O	1:A:168:GLY:HA2	2.12	0.49
1:A:907:THR:CG2	1:A:908:LEU:N	2.75	0.49
1:A:921:GLY:O	1:A:922:ASP:C	2.55	0.49
1:A:1053:PHE:O	1:A:1056:SER:N	2.44	0.49
1:A:1090:ALA:O	1:A:1091:SER:OG	2.28	0.49
1:A:1342:GLU:HG3	5:E:198:ILE:HG21	1.95	0.49
2:B:115:GLN:HG2	2:B:193:LYS:HB2	1.95	0.49
2:B:508:LEU:CA	2:B:510:LYS:H	2.24	0.49
2:B:615:MET:C	2:B:616:ILE:HD12	2.36	0.49
2:B:760:ASP:O	2:B:761:HIS:CD2	2.66	0.49
3:C:239:PRO:HB2	3:C:241:ASP:OD1	2.12	0.49
4:D:53:SER:HB3	4:D:152:SER:CB	2.42	0.49
5:E:153:HIS:C	5:E:154:ILE:HG13	2.34	0.49
11:K:32:VAL:HG22	11:K:74:ARG:HG3	1.95	0.49
1:A:564:ALA:HB2	1:A:576:GLN:OE1	2.12	0.49
1:A:715:GLU:C	1:A:717:ASN:N	2.71	0.49
1:A:1118:VAL:HG23	1:A:1306:LEU:HB2	1.95	0.49
1:A:1199:ARG:HG3	1:A:1236:LEU:HD11	1.93	0.49
2:B:594:ALA:CA	2:B:617:ARG:HH12	2.25	0.49
2:B:622:LYS:CE	9:I:59:VAL:HG22	2.41	0.49
2:B:760:ASP:OD1	2:B:1046:PRO:HA	2.12	0.49
2:B:845:SER:HB3	10:J:8:PHE:O	2.13	0.49
7:G:114:LEU:HG	7:G:162:SER:HB3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:472:LEU:HD13	2:B:835:GLN:OE1	2.13	0.49
1:A:838:GLN:O	1:A:842:VAL:HG23	2.13	0.49
1:A:852:TYR:CE1	6:F:136:ARG:HB3	2.48	0.49
1:A:898:ARG:HB2	1:A:933:TYR:CE1	2.47	0.49
1:A:1129:GLU:C	1:A:1131:ALA:N	2.67	0.49
2:B:112:LEU:CD1	2:B:113:TYR:N	2.71	0.49
2:B:175:ARG:HG2	2:B:175:ARG:HH11	1.77	0.49
2:B:509:ALA:C	2:B:510:LYS:HD2	2.36	0.49
2:B:563:MET:HA	2:B:589:VAL:O	2.13	0.49
2:B:642:ASP:C	2:B:644:GLU:H	2.19	0.49
3:C:86:CYS:SG	3:C:95:CYS:HB3	2.52	0.49
4:D:127:ASP:O	4:D:131:GLU:HG3	2.13	0.49
4:D:134:THR:CG2	4:D:135:GLY:N	2.75	0.49
10:J:37:SER:OG	10:J:47:ARG:NH2	2.46	0.49
11:K:106:GLU:O	11:K:107:THR:C	2.56	0.49
1:A:348:SER:HB2	2:B:1128:LEU:HD12	1.93	0.49
1:A:387:ARG:O	1:A:390:GLN:HB3	2.13	0.49
1:A:1090:ALA:O	1:A:1091:SER:CB	2.60	0.49
2:B:361:LEU:N	2:B:362:PRO:CD	2.75	0.49
7:G:15:PRO:O	7:G:18:PHE:HB2	2.11	0.49
7:G:101:VAL:CG1	7:G:102:GLN:N	2.76	0.49
9:I:58:VAL:CG2	9:I:62:ILE:HD12	2.40	0.49
9:I:111:THR:HG22	9:I:113:ASP:N	2.19	0.49
10:J:21:TYR:C	10:J:23:ASN:N	2.70	0.49
12:L:30:ILE:CG2	12:L:31:CYS:N	2.75	0.49
1:A:3:GLY:O	1:A:4:GLN:O	2.31	0.49
1:A:42:ASP:O	1:A:44:THR:N	2.38	0.49
1:A:929:LEU:HD23	1:A:983:ILE:HG21	1.95	0.49
1:A:1059:HIS:O	1:A:1061:GLY:N	2.46	0.49
1:A:1308:THR:O	1:A:1309:ASP:HB2	2.12	0.49
2:B:25:ILE:HG23	2:B:29:ASP:CB	2.42	0.49
2:B:811:TYR:N	2:B:811:TYR:CD1	2.80	0.49
3:C:80:LEU:HD22	3:C:129:ILE:HD13	1.94	0.49
5:E:32:GLN:HG3	5:E:36:GLU:OE2	2.12	0.49
1:A:14:VAL:CG2	1:A:1430:LEU:HD13	2.42	0.49
1:A:37:PHE:N	1:A:37:PHE:CD1	2.81	0.49
1:A:370:ILE:HG23	2:B:1105:ALA:CB	2.41	0.49
1:A:525:GLN:O	1:A:526:ASP:C	2.56	0.49
1:A:925:LEU:C	1:A:927:VAL:H	2.20	0.49
1:A:1097:GLY:C	1:A:1099:PRO:HD2	2.37	0.49
1:A:1372:VAL:HG12	1:A:1373:ASP:H	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:457:LEU:O	2:B:461:LEU:CD1	2.61	0.49
2:B:976:ILE:CD1	2:B:992:ILE:HA	2.41	0.49
2:B:1106:ARG:HD3	2:B:1126:GLY:O	2.12	0.49
3:C:8:VAL:HG12	3:C:9:LYS:N	2.28	0.49
7:G:88:ASP:HB3	7:G:144:ARG:HB2	1.95	0.49
8:H:58:THR:HB	8:H:143:LEU:HD13	1.94	0.49
9:I:88:SER:C	9:I:90:GLN:N	2.70	0.49
1:A:315:LEU:HD22	1:A:319:GLY:O	2.13	0.48
1:A:481:ASP:O	1:A:485:ASP:HB2	2.13	0.48
1:A:863:VAL:HG12	1:A:864:ILE:H	1.77	0.48
1:A:874:ASP:N	1:A:1058:VAL:HG23	2.27	0.48
1:A:877:HIS:C	1:A:878:ILE:CG1	2.86	0.48
1:A:1102:LYS:O	1:A:1106:ASN:ND2	2.46	0.48
1:A:1226:VAL:C	1:A:1227:ILE:HG13	2.37	0.48
1:A:1285:MET:HG3	1:A:1307:GLU:OE2	2.12	0.48
2:B:234:ILE:HD12	2:B:234:ILE:N	2.28	0.48
2:B:360:PHE:C	2:B:360:PHE:CD2	2.91	0.48
2:B:378:LEU:HD12	2:B:378:LEU:C	2.35	0.48
2:B:446:LEU:O	2:B:447:ALA:CB	2.61	0.48
2:B:846:ILE:HG23	2:B:974:PRO:CG	2.36	0.48
2:B:910:VAL:CG1	2:B:911:ILE:N	2.76	0.48
3:C:79:GLN:O	3:C:127:ARG:NH1	2.46	0.48
3:C:111:THR:O	3:C:147:LEU:HD23	2.12	0.48
4:D:144:THR:OG1	7:G:105:PRO:HD3	2.12	0.48
5:E:3:GLN:HG3	5:E:4:GLU:N	2.27	0.48
8:H:82:PRO:O	8:H:83:GLN:HB2	2.13	0.48
8:H:83:GLN:O	8:H:85:GLY:N	2.45	0.48
1:A:12:ARG:CZ	2:B:1192:TYR:HE2	2.25	0.48
1:A:418:SER:O	1:A:421:ALA:N	2.46	0.48
1:A:433:GLU:OE2	2:B:1108:ARG:NH1	2.45	0.48
1:A:567:LYS:HZ1	8:H:46:LEU:HB2	1.79	0.48
1:A:809:THR:H	1:A:812:GLU:HB2	1.78	0.48
1:A:946:VAL:HG12	1:A:947:PHE:N	2.28	0.48
2:B:37:PHE:HE2	2:B:542:MET:CA	2.17	0.48
2:B:67:SER:O	2:B:68:THR:C	2.56	0.48
2:B:189:LEU:HD13	2:B:196:PRO:HA	1.94	0.48
2:B:314:LEU:O	2:B:317:CYS:HB3	2.12	0.48
2:B:619:ILE:O	2:B:621:GLU:N	2.47	0.48
7:G:62:LEU:HB3	7:G:63:PRO:HD2	1.96	0.48
9:I:113:ASP:O	9:I:114:GLN:CG	2.61	0.48
11:K:21:ILE:HG23	11:K:31:VAL:CG1	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:65:HIS:CD2	11:K:66:PRO:N	2.81	0.48
1:A:42:ASP:OD1	1:A:45:GLN:HA	2.14	0.48
1:A:384:ASN:CG	1:A:388:LEU:HD12	2.38	0.48
1:A:501:LEU:HD11	2:B:1146:PHE:CD2	2.48	0.48
1:A:1116:LEU:C	1:A:1116:LEU:HD12	2.38	0.48
1:A:1210:GLY:O	1:A:1211:GLN:C	2.56	0.48
2:B:102:VAL:CG2	2:B:112:LEU:HD22	2.43	0.48
2:B:196:PRO:HG2	2:B:197:PHE:H	1.77	0.48
2:B:221:ASN:OD1	2:B:242:SER:HA	2.14	0.48
2:B:498:THR:HG22	2:B:537:LYS:H	1.78	0.48
2:B:583:ASN:OD1	2:B:628:THR:N	2.47	0.48
2:B:757:PRO:O	2:B:758:PHE:HB2	2.13	0.48
2:B:821:GLN:HE22	2:B:851:PHE:N	2.09	0.48
2:B:1165:ILE:HG22	2:B:1185:CYS:HB3	1.94	0.48
3:C:143:LEU:HD21	3:C:146:LYS:CE	2.44	0.48
4:D:173:HIS:O	4:D:177:VAL:HG23	2.13	0.48
5:E:205:SER:O	5:E:206:GLY:C	2.55	0.48
9:I:13:MET:HG3	9:I:14:LEU:N	2.27	0.48
11:K:81:TYR:OH	11:K:86:ALA:HA	2.13	0.48
1:A:645:LEU:O	1:A:646:PHE:C	2.54	0.48
1:A:780:VAL:O	1:A:780:VAL:HG12	2.14	0.48
1:A:1051:ALA:O	1:A:1054:LEU:N	2.47	0.48
2:B:199:MET:HE2	2:B:492:LEU:CD2	2.42	0.48
2:B:482:VAL:O	2:B:483:LEU:C	2.57	0.48
2:B:525:ALA:O	2:B:527:THR:HG22	2.13	0.48
2:B:810:GLU:HG3	2:B:815:ARG:HH22	1.79	0.48
2:B:1020:ARG:CG	2:B:1020:ARG:NH1	2.68	0.48
2:B:1034:VAL:HG23	2:B:1059:LEU:HD12	1.95	0.48
3:C:42:PRO:HA	3:C:163:ILE:CG2	2.44	0.48
4:D:190:GLU:O	4:D:194:LEU:HG	2.14	0.48
6:F:124:GLU:HB3	6:F:130:ILE:HG12	1.95	0.48
7:G:1:MET:CE	7:G:80:LYS:C	2.85	0.48
8:H:10:PHE:N	8:H:10:PHE:CD1	2.81	0.48
11:K:58:PHE:HB3	11:K:76:GLN:HB3	1.96	0.48
1:A:228:PHE:N	1:A:228:PHE:CD2	2.81	0.48
1:A:873:MET:HG2	1:A:957:PRO:HG3	1.96	0.48
2:B:186:GLU:O	2:B:187:SER:C	2.55	0.48
2:B:365:THR:CG2	2:B:367:LEU:HG	2.38	0.48
2:B:393:LYS:HA	2:B:393:LYS:HE3	1.96	0.48
2:B:693:ILE:HD11	2:B:740:HIS:NE2	2.27	0.48
2:B:806:THR:CG2	2:B:808:ALA:HB3	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:109:SER:O	3:C:110:THR:O	2.32	0.48
4:D:220:LEU:O	4:D:221:TYR:HD1	1.97	0.48
5:E:44:ALA:O	5:E:45:LYS:HB2	2.13	0.48
5:E:129:PRO:O	5:E:130:ALA:C	2.57	0.48
6:F:103:MET:CE	7:G:65:ASP:HB2	2.44	0.48
6:F:109:VAL:HG12	6:F:110:ASP:N	2.29	0.48
12:L:39:SER:O	12:L:40:LEU:HG	2.14	0.48
1:A:618:GLU:O	1:A:621:THR:N	2.46	0.48
1:A:869:GLY:O	1:A:870:GLU:HB2	2.12	0.48
1:A:936:LEU:HD23	1:A:936:LEU:H	1.78	0.48
1:A:1198:ASP:O	1:A:1202:MET:HG2	2.13	0.48
1:A:1438:THR:HB	2:B:1144:ALA:HB3	1.96	0.48
2:B:509:ALA:O	2:B:510:LYS:O	2.32	0.48
2:B:681:TRP:O	2:B:683:SER:N	2.46	0.48
2:B:797:TYR:HB3	2:B:798:TYR:CD2	2.49	0.48
6:F:143:PHE:C	6:F:143:PHE:CD1	2.90	0.48
8:H:84:ALA:HB2	8:H:87:ARG:HD2	1.96	0.48
8:H:123:MET:HE1	8:H:142:LEU:HD11	1.96	0.48
9:I:5:ARG:O	9:I:14:LEU:HD12	2.14	0.48
10:J:3:VAL:HG12	10:J:4:PRO:N	2.28	0.48
11:K:113:THR:O	11:K:114:LEU:CB	2.58	0.48
1:A:64:ASN:O	1:A:65:LEU:C	2.56	0.48
1:A:88:LYS:HE3	1:A:280:GLU:OE2	2.13	0.48
1:A:419:LYS:HG3	1:A:420:ARG:N	2.28	0.48
1:A:524:VAL:HG12	1:A:525:GLN:N	2.19	0.48
1:A:626:ASN:O	1:A:628:GLY:N	2.42	0.48
1:A:755:PHE:HA	1:A:758:ILE:HG13	1.94	0.48
1:A:852:TYR:CD2	1:A:1060:PRO:CB	2.97	0.48
1:A:1216:ILE:O	1:A:1219:THR:HB	2.14	0.48
2:B:578:THR:HA	2:B:622:LYS:HB3	1.94	0.48
2:B:839:MET:N	2:B:989:THR:O	2.44	0.48
2:B:992:ILE:HD11	11:K:66:PRO:HB2	1.96	0.48
2:B:1135:ARG:NH2	2:B:1136:ASP:OD1	2.38	0.48
3:C:27:LEU:O	3:C:30:ALA:N	2.47	0.48
4:D:56:ARG:NH2	4:D:155:ARG:HA	2.28	0.48
4:D:185:CYS:HB3	4:D:211:LEU:HD13	1.95	0.48
6:F:99:LEU:O	6:F:103:MET:HG2	2.13	0.48
8:H:81:PRO:HB3	8:H:82:PRO:HD2	1.92	0.48
1:A:14:VAL:HG21	1:A:1430:LEU:HD13	1.96	0.48
1:A:56:PRO:O	1:A:57:ARG:CG	2.57	0.48
1:A:889:SER:C	1:A:891:ALA:N	2.72	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1090:ALA:CB	1:A:1093:LYS:HE3	2.43	0.48
1:A:1121:GLU:O	1:A:1122:PRO:C	2.57	0.48
1:A:1293:SER:OG	1:A:1295:THR:CG2	2.62	0.48
1:A:1394:THR:CG2	1:A:1398:MET:HE3	2.43	0.48
2:B:273:LEU:HD21	2:B:360:PHE:CD1	2.48	0.48
2:B:363:HIS:NE2	2:B:364:ILE:HG13	2.28	0.48
2:B:617:ARG:NE	2:B:619:ILE:HG12	2.28	0.48
2:B:654:ARG:H	2:B:657:HIS:CD2	2.28	0.48
2:B:850:LEU:HD12	2:B:851:PHE:H	1.77	0.48
2:B:1022:THR:HG23	2:B:1022:THR:O	2.12	0.48
2:B:1208:MET:HA	2:B:1212:ILE:O	2.13	0.48
5:E:17:ARG:O	5:E:20:LYS:HB2	2.13	0.48
5:E:136:ASN:OD1	5:E:137:GLU:N	2.46	0.48
6:F:72:LYS:O	6:F:73:ALA:CB	2.61	0.48
1:A:81:PHE:CE2	1:A:242:PRO:HA	2.48	0.48
1:A:261:ASP:O	1:A:264:PHE:HB2	2.13	0.48
1:A:646:PHE:O	1:A:647:GLY:C	2.55	0.48
1:A:706:HIS:C	1:A:708:MET:H	2.22	0.48
1:A:814:PHE:CD1	2:B:519:TRP:HE3	2.31	0.48
1:A:1104:ILE:C	1:A:1106:ASN:N	2.71	0.48
1:A:1193:LEU:HD12	1:A:1194:ARG:N	2.29	0.48
1:A:1265:ASN:O	1:A:1267:MET:N	2.47	0.48
2:B:579:ARG:HG2	2:B:579:ARG:HH11	1.79	0.48
2:B:689:LEU:O	2:B:690:VAL:HG23	2.14	0.48
2:B:753:ALA:O	2:B:756:ILE:N	2.46	0.48
2:B:992:ILE:CG2	2:B:994:TYR:HE1	2.26	0.48
2:B:992:ILE:HG21	2:B:994:TYR:HE1	1.79	0.48
4:D:189:ASP:O	4:D:193:THR:HB	2.14	0.48
4:D:208:GLU:O	4:D:212:LYS:HG3	2.13	0.48
9:I:58:VAL:HG13	9:I:62:ILE:CD1	2.44	0.48
1:A:98:LYS:O	1:A:99:ILE:C	2.56	0.48
1:A:154:SER:HB3	1:A:162:VAL:HG21	1.95	0.48
1:A:351:THR:HB	2:B:1103:ILE:CD1	2.43	0.48
1:A:416:ARG:C	1:A:417:TYR:CD2	2.92	0.48
1:A:503:GLN:O	1:A:504:LEU:HD12	2.13	0.48
2:B:114:PRO:O	2:B:115:GLN:C	2.57	0.48
2:B:591:ARG:O	2:B:592:ASN:C	2.57	0.48
2:B:843:GLN:O	2:B:844:SER:C	2.56	0.48
3:C:67:LEU:HD11	3:C:155:LEU:CD1	2.44	0.48
5:E:167:ARG:O	5:E:168:TYR:HD2	1.97	0.48
1:A:22:PHE:CD1	2:B:1213:THR:HG22	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:525:GLN:HB3	2:B:1015:HIS:CD2	2.48	0.47
1:A:996:ASN:C	1:A:998:LEU:H	2.22	0.47
1:A:1051:ALA:O	1:A:1052:GLN:C	2.57	0.47
1:A:1263:ILE:O	1:A:1263:ILE:HG22	2.14	0.47
1:A:1388:GLY:O	1:A:1391:ARG:HG2	2.14	0.47
2:B:212:LEU:HD23	2:B:212:LEU:HA	1.73	0.47
2:B:283:VAL:O	2:B:284:ILE:C	2.57	0.47
2:B:298:LEU:CD2	2:B:298:LEU:H	2.27	0.47
2:B:486:TYR:CG	2:B:1096:ARG:NH2	2.82	0.47
2:B:545:ILE:C	2:B:634:TYR:HE2	2.22	0.47
2:B:579:ARG:HA	2:B:589:VAL:HG13	1.96	0.47
2:B:847:ASP:C	2:B:849:GLY:N	2.72	0.47
3:C:173:ALA:O	3:C:174:ALA:HB3	2.13	0.47
3:C:213:PRO:O	3:C:214:ASN:CB	2.55	0.47
5:E:16:PHE:CE2	5:E:20:LYS:HE2	2.48	0.47
5:E:147:HIS:O	5:E:148:GLU:C	2.57	0.47
5:E:204:THR:HG23	5:E:205:SER:N	2.28	0.47
9:I:69:PRO:O	9:I:84:VAL:HA	2.14	0.47
10:J:36:LEU:HB2	10:J:47:ARG:NH1	2.28	0.47
1:A:117:GLU:H	1:A:117:GLU:CD	2.23	0.47
1:A:157:ASP:C	1:A:159:THR:H	2.22	0.47
1:A:321:PRO:O	1:A:322:VAL:HB	2.13	0.47
1:A:329:LEU:N	1:A:329:LEU:HD23	2.28	0.47
1:A:393:ARG:O	1:A:395:GLY:N	2.47	0.47
1:A:525:GLN:CD	2:B:836:GLU:HG2	2.39	0.47
1:A:821:ARG:HA	1:A:824:LEU:HD12	1.95	0.47
1:A:1064:VAL:O	1:A:1065:GLY:C	2.55	0.47
1:A:1209:MET:O	1:A:1210:GLY:C	2.55	0.47
2:B:259:TYR:HB2	2:B:268:THR:HG23	1.95	0.47
2:B:371:GLU:CD	2:B:371:GLU:N	2.70	0.47
2:B:872:GLU:CD	2:B:914:LYS:HE2	2.39	0.47
2:B:880:THR:HB	2:B:934:LYS:CD	2.36	0.47
3:C:112:ASN:CB	3:C:114:TYR:CE1	2.98	0.47
5:E:202:SER:HB3	5:E:205:SER:O	2.15	0.47
6:F:132:LEU:O	6:F:148:VAL:HG22	2.14	0.47
12:L:54:ARG:HG3	12:L:54:ARG:NH1	2.29	0.47
1:A:254:GLU:O	2:B:935:ARG:NH1	2.45	0.47
1:A:759:ALA:O	1:A:761:MET:N	2.47	0.47
1:A:1006:ILE:HD11	5:E:163:GLU:CG	2.44	0.47
1:A:1116:LEU:HA	1:A:1329:THR:HA	1.96	0.47
1:A:1311:VAL:HG11	1:A:1329:THR:HG21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:764:SER:N	2:B:765:PRO:HD2	2.29	0.47
2:B:831:SER:HB2	2:B:833:TYR:HD1	1.79	0.47
2:B:1002:THR:HG22	2:B:1006:ILE:O	2.14	0.47
4:D:29:LEU:HD23	4:D:29:LEU:N	2.30	0.47
7:G:126:ASN:HA	7:G:127:PRO:C	2.37	0.47
9:I:26:LEU:CD2	9:I:37:GLU:HA	2.41	0.47
11:K:63:VAL:HG23	11:K:63:VAL:O	2.15	0.47
12:L:48:CYS:O	12:L:50:ASP:N	2.47	0.47
1:A:53:LEU:HD23	1:A:54:ASN:CB	2.45	0.47
1:A:696:GLU:O	1:A:696:GLU:HG2	2.15	0.47
1:A:962:ARG:O	1:A:964:ILE:N	2.47	0.47
2:B:202:TYR:CE1	2:B:209:GLU:HG2	2.50	0.47
2:B:1017:ILE:HG22	2:B:1018:PRO:CD	2.44	0.47
2:B:1060:ARG:HG2	2:B:1060:ARG:NH1	2.26	0.47
3:C:206:ASN:OD1	3:C:229:TYR:CD2	2.67	0.47
4:D:51:ASN:O	4:D:52:LEU:O	2.33	0.47
5:E:207:ARG:HB3	5:E:207:ARG:NH1	2.28	0.47
6:F:77:ASP:O	6:F:79:ARG:N	2.47	0.47
6:F:93:ILE:HD11	6:F:134:ILE:HD11	1.96	0.47
6:F:111:LEU:O	6:F:113:GLY:N	2.47	0.47
7:G:117:GLN:C	7:G:119:LEU:N	2.71	0.47
10:J:7:CYS:HA	10:J:49:MET:HE3	1.95	0.47
1:A:370:ILE:O	1:A:371:ALA:C	2.57	0.47
1:A:650:GLN:O	1:A:654:ASN:HB2	2.14	0.47
1:A:1263:ILE:O	1:A:1267:MET:HG3	2.15	0.47
2:B:702:LEU:C	2:B:703:ILE:HG13	2.39	0.47
2:B:882:THR:O	2:B:883:LEU:CB	2.63	0.47
2:B:999:MET:HB3	2:B:1007:VAL:CG2	2.44	0.47
2:B:1155:SER:OG	2:B:1156:ASP:N	2.47	0.47
3:C:114:TYR:N	3:C:114:TYR:CD1	2.83	0.47
5:E:144:ILE:C	5:E:146:HIS:N	2.72	0.47
6:F:128:LYS:HD3	6:F:149:GLU:O	2.15	0.47
10:J:18:TRP:HA	10:J:18:TRP:CE3	2.49	0.47
10:J:48:ARG:HE	10:J:49:MET:CE	2.28	0.47
11:K:88:LYS:O	11:K:89:ASN:C	2.56	0.47
11:K:105:PHE:O	11:K:106:GLU:C	2.57	0.47
12:L:62:LYS:O	12:L:63:ARG:C	2.58	0.47
1:A:253:ASN:OD1	2:B:884:ARG:HD2	2.14	0.47
1:A:541:ILE:HD13	1:A:549:MET:CE	2.45	0.47
1:A:566:ILE:O	1:A:567:LYS:C	2.57	0.47
1:A:567:LYS:HE3	8:H:46:LEU:HD12	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:647:GLY:O	1:A:650:GLN:HB2	2.14	0.47
1:A:873:MET:C	1:A:1058:VAL:HG23	2.40	0.47
1:A:901:LEU:HB2	1:A:926:GLN:HG2	1.95	0.47
1:A:1125:ALA:C	1:A:1127:ASP:N	2.72	0.47
1:A:1437:GLY:CA	6:F:88:TYR:CD2	2.97	0.47
2:B:38:PHE:HD1	2:B:811:TYR:CD2	2.31	0.47
2:B:95:ILE:CG1	2:B:130:VAL:HG22	2.44	0.47
2:B:510:LYS:HD3	2:B:513:GLN:H	1.80	0.47
2:B:597:MET:C	2:B:599:THR:H	2.22	0.47
2:B:658:ILE:HG22	2:B:659:ALA:N	2.28	0.47
2:B:1090:THR:O	2:B:1091:TYR:C	2.57	0.47
2:B:1210:MET:O	2:B:1212:ILE:N	2.47	0.47
3:C:116:LYS:HD3	3:C:140:ASN:HB3	1.95	0.47
5:E:90:VAL:HG23	5:E:120:ALA:HA	1.97	0.47
6:F:124:GLU:O	6:F:130:ILE:HG13	2.14	0.47
7:G:81:PRO:HA	7:G:85:GLU:OE1	2.15	0.47
1:A:8:SER:O	1:A:9:ALA:C	2.57	0.47
1:A:49:LYS:HZ1	1:A:60:SER:C	2.23	0.47
1:A:95:PHE:HD1	1:A:234:MET:CG	2.25	0.47
1:A:266:LEU:O	1:A:267:ALA:C	2.58	0.47
1:A:317:LYS:O	1:A:318:SER:HB3	2.14	0.47
1:A:356:ASP:HB2	1:A:469:ARG:HG2	1.96	0.47
1:A:368:LYS:O	1:A:369:SER:C	2.58	0.47
1:A:375:THR:HA	1:A:434:ARG:O	2.14	0.47
1:A:447:GLN:HB3	1:A:448:PRO:HA	1.97	0.47
1:A:451:HIS:O	2:B:1137:CYS:SG	2.73	0.47
1:A:590:ARG:HD3	1:A:604:GLY:CA	2.41	0.47
1:A:705:LYS:C	1:A:707:GLY:H	2.22	0.47
1:A:1111:MET:H	1:A:1111:MET:HG2	1.57	0.47
1:A:1162:VAL:O	1:A:1162:VAL:HG12	2.15	0.47
1:A:1329:THR:C	1:A:1331:SER:N	2.71	0.47
1:A:1335:ILE:O	1:A:1335:ILE:CG2	2.63	0.47
2:B:166:PHE:C	2:B:167:ILE:HG13	2.39	0.47
2:B:371:GLU:N	2:B:371:GLU:OE1	2.48	0.47
2:B:465:ASN:HD22	2:B:465:ASN:N	2.12	0.47
2:B:508:LEU:O	2:B:509:ALA:C	2.51	0.47
2:B:642:ASP:HA	2:B:649:LYS:HA	1.95	0.47
2:B:745:PRO:O	2:B:748:ILE:CG1	2.61	0.47
2:B:825:VAL:CG1	2:B:826:ALA:N	2.77	0.47
2:B:847:ASP:OD2	11:K:6:ARG:NH2	2.48	0.47
2:B:850:LEU:HD12	2:B:851:PHE:N	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:863:GLU:O	2:B:961:LEU:HD22	2.15	0.47
2:B:1017:ILE:O	2:B:1018:PRO:C	2.58	0.47
3:C:47:ASP:O	3:C:48:SER:HB2	2.13	0.47
3:C:86:CYS:C	3:C:88:CYS:N	2.72	0.47
3:C:191:TYR:CD2	3:C:201:TRP:CD1	2.97	0.47
3:C:263:THR:O	3:C:265:MET:N	2.47	0.47
5:E:7:ARG:CG	5:E:8:ASN:N	2.76	0.47
5:E:33:GLU:C	5:E:35:VAL:N	2.72	0.47
5:E:117:THR:C	5:E:119:SER:H	2.21	0.47
7:G:145:VAL:CG1	7:G:146:LYS:H	2.27	0.47
8:H:31:THR:O	8:H:31:THR:HG22	2.15	0.47
8:H:39:THR:HB	8:H:124:ARG:HB3	1.97	0.47
10:J:14:VAL:O	10:J:16:ASP:N	2.48	0.47
10:J:57:ILE:CA	10:J:60:PHE:CD2	2.90	0.47
1:A:231:PRO:C	1:A:233:TRP:N	2.72	0.47
1:A:343:LYS:NZ	2:B:1151:LEU:O	2.43	0.47
1:A:556:TRP:NE1	1:A:559:VAL:H	2.13	0.47
1:A:859:SER:OG	1:A:1398:MET:HE1	2.13	0.47
1:A:893:PHE:CD2	1:A:893:PHE:C	2.92	0.47
1:A:1080:THR:C	1:A:1081:LEU:HD22	2.40	0.47
1:A:1081:LEU:HD21	1:A:1098:VAL:CB	2.44	0.47
1:A:1227:ILE:O	1:A:1228:TRP:HB3	2.14	0.47
1:A:1282:VAL:C	1:A:1283:VAL:CG2	2.87	0.47
1:A:1311:VAL:HG21	1:A:1329:THR:HG23	1.96	0.47
1:A:1437:GLY:O	1:A:1438:THR:C	2.56	0.47
2:B:170:LEU:O	2:B:170:LEU:HG	2.14	0.47
2:B:644:GLU:C	2:B:646:LEU:N	2.71	0.47
2:B:899:ILE:HG23	2:B:903:VAL:HG21	1.95	0.47
3:C:228:PHE:CD1	3:C:228:PHE:N	2.83	0.47
6:F:119:ARG:HH11	6:F:119:ARG:CG	2.25	0.47
6:F:132:LEU:HD22	7:G:61:ILE:HD11	1.97	0.47
7:G:56:ILE:O	7:G:57:GLN:HB2	2.15	0.47
9:I:11:ASN:O	9:I:12:ASN:ND2	2.48	0.47
1:A:76:GLU:CG	1:A:76:GLU:O	2.63	0.47
1:A:125:ALA:O	1:A:127:ALA:N	2.48	0.47
1:A:381:THR:HG21	1:A:383:TYR:CD1	2.50	0.47
1:A:385:ILE:HG22	1:A:386:ASP:N	2.29	0.47
1:A:500:GLU:O	1:A:504:LEU:HB2	2.15	0.47
1:A:606:LEU:CB	1:A:614:PHE:CE2	2.97	0.47
1:A:626:ASN:O	1:A:631:HIS:CB	2.63	0.47
1:A:863:VAL:O	1:A:864:ILE:CG1	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:983:ILE:O	1:A:983:ILE:HG22	2.15	0.47
1:A:1057:VAL:CG1	1:A:1058:VAL:N	2.76	0.47
1:A:1293:SER:OG	1:A:1294:PRO:HD2	2.14	0.47
1:A:1377:THR:O	1:A:1378:GLN:C	2.57	0.47
2:B:223:VAL:HG11	2:B:381:MET:HG2	1.96	0.47
2:B:293:PRO:O	2:B:294:ASP:O	2.33	0.47
2:B:577:ALA:HB1	2:B:589:VAL:HG11	1.96	0.47
2:B:834:ASN:HA	2:B:838:SER:O	2.15	0.47
2:B:865:LYS:HZ3	2:B:869:SER:HA	1.79	0.47
2:B:942:ARG:O	2:B:944:THR:N	2.48	0.47
2:B:956:THR:CG2	2:B:960:GLY:HA2	2.45	0.47
2:B:1159:ARG:CD	2:B:1193:GLN:HE21	2.26	0.47
3:C:118:LEU:HB2	3:C:132:PRO:HG2	1.97	0.47
5:E:198:ILE:CD1	5:E:212:ARG:NH1	2.78	0.47
10:J:52:THR:O	10:J:53:HIS:C	2.57	0.47
11:K:40:HIS:O	11:K:41:THR:C	2.58	0.47
1:A:222:LEU:O	1:A:224:PHE:N	2.48	0.47
1:A:408:ASP:C	1:A:410:GLY:H	2.23	0.47
1:A:711:ARG:HA	9:I:97:MET:CE	2.44	0.47
1:A:714:PHE:CB	9:I:97:MET:HE1	2.45	0.47
1:A:809:THR:HG23	1:A:812:GLU:OE1	2.15	0.47
1:A:919:ILE:O	1:A:920:LEU:C	2.57	0.47
1:A:937:VAL:O	1:A:938:LYS:C	2.58	0.47
2:B:45:SER:O	2:B:46:GLN:C	2.58	0.47
2:B:752:ALA:HB1	2:B:771:SER:HB3	1.96	0.47
2:B:785:TYR:HA	2:B:788:ARG:HG3	1.97	0.47
2:B:871:THR:HG22	2:B:872:GLU:N	2.31	0.47
2:B:1204:PHE:CE1	2:B:1216:LEU:HD11	2.50	0.47
4:D:130:LEU:O	4:D:132:GLN:N	2.48	0.47
8:H:106:GLU:HG2	8:H:112:ILE:HG12	1.96	0.47
9:I:99:LEU:HB2	9:I:101:PHE:CE1	2.50	0.47
11:K:12:LEU:HD23	11:K:16:GLU:O	2.14	0.47
11:K:83:PRO:O	11:K:86:ALA:HB3	2.15	0.47
1:A:164:ARG:CG	1:A:165:GLY:H	2.01	0.46
1:A:535:THR:O	1:A:536:LEU:O	2.34	0.46
1:A:548:ASN:HA	11:K:60:ALA:HB1	1.97	0.46
1:A:551:TYR:CE2	11:K:62:LYS:HE2	2.50	0.46
1:A:789:LYS:HE3	9:I:67:THR:HB	1.97	0.46
1:A:866:PHE:HD2	5:E:168:TYR:CE1	2.33	0.46
1:A:897:TYR:HB3	1:A:936:LEU:CD1	2.45	0.46
1:A:944:ARG:NE	1:A:1298:TYR:HE1	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1129:GLU:HG3	1:A:1132:LYS:HE3	1.97	0.46
1:A:1335:ILE:HG23	1:A:1339:LEU:HD12	1.96	0.46
2:B:69:LEU:HD13	2:B:429:PHE:HD1	1.80	0.46
2:B:544:CYS:O	2:B:545:ILE:HG13	2.15	0.46
2:B:1079:LYS:HE3	3:C:188:HIS:CE1	2.51	0.46
2:B:1150:ARG:HA	2:B:1150:ARG:HE	1.80	0.46
5:E:135:PHE:HB3	5:E:140:LEU:HD11	1.98	0.46
7:G:39:THR:C	7:G:41:LYS:N	2.70	0.46
1:A:80:HIS:O	1:A:243:PRO:HB3	2.16	0.46
1:A:541:ILE:HG22	1:A:546:VAL:HG23	1.97	0.46
1:A:560:ILE:CG1	8:H:78:SER:HB2	2.36	0.46
1:A:784:LEU:C	1:A:786:HIS:H	2.23	0.46
1:A:907:THR:HG22	1:A:908:LEU:N	2.30	0.46
1:A:1057:VAL:CG1	1:A:1058:VAL:H	2.26	0.46
1:A:1282:VAL:O	1:A:1283:VAL:HG22	2.14	0.46
2:B:34:ILE:O	2:B:35:SER:C	2.58	0.46
2:B:285:ILE:O	2:B:288:ALA:HB3	2.15	0.46
2:B:798:TYR:CD2	2:B:798:TYR:N	2.83	0.46
2:B:906:SER:O	2:B:907:GLY:O	2.33	0.46
2:B:1106:ARG:HD3	2:B:1126:GLY:C	2.39	0.46
2:B:1202:LEU:HD22	2:B:1206:GLU:CD	2.39	0.46
3:C:197:SER:O	3:C:198:ALA:C	2.58	0.46
5:E:143:ASN:OD1	5:E:187:TYR:CE1	2.68	0.46
11:K:101:LEU:O	11:K:102:LYS:C	2.58	0.46
12:L:27:LEU:HD13	12:L:37:LYS:HE2	1.96	0.46
1:A:63:ARG:HA	1:A:74:MET:CE	2.45	0.46
1:A:285:PRO:CG	1:A:288:ALA:HB3	2.40	0.46
1:A:353:ILE:HG23	1:A:485:ASP:O	2.16	0.46
1:A:590:ARG:HH11	1:A:590:ARG:CG	2.29	0.46
1:A:928:LEU:C	1:A:930:ASP:N	2.70	0.46
1:A:1220:PHE:CE2	1:A:1263:ILE:HG23	2.50	0.46
2:B:281:PRO:O	2:B:283:VAL:N	2.48	0.46
2:B:386:LEU:C	2:B:388:CYS:N	2.73	0.46
2:B:540:SER:HA	2:B:749:LEU:O	2.14	0.46
2:B:743:ILE:H	2:B:743:ILE:HG12	1.51	0.46
2:B:1103:ILE:O	2:B:1122:ARG:NH1	2.48	0.46
4:D:154:PHE:HB2	4:D:160:VAL:HG22	1.97	0.46
11:K:70:ARG:O	11:K:70:ARG:HG3	2.16	0.46
1:A:70:CYS:HA	2:B:1174:LYS:HG2	1.98	0.46
1:A:231:PRO:C	1:A:233:TRP:H	2.23	0.46
1:A:715:GLU:O	1:A:718:VAL:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:928:LEU:O	1:A:931:GLU:N	2.47	0.46
1:A:1007:ILE:C	1:A:1009:ASN:N	2.71	0.46
1:A:1080:THR:HG22	1:A:1081:LEU:H	1.81	0.46
1:A:1083:THR:O	1:A:1084:PHE:O	2.34	0.46
1:A:1327:ILE:HG22	5:E:147:HIS:CE1	2.51	0.46
2:B:58:THR:O	2:B:62:ILE:HG13	2.15	0.46
2:B:549:THR:CG2	2:B:550:ASP:H	2.17	0.46
3:C:22:LEU:HD13	3:C:230:MET:CE	2.44	0.46
3:C:95:CYS:O	3:C:96:SER:HB3	2.15	0.46
3:C:187:LYS:C	3:C:189:THR:H	2.24	0.46
5:E:24:LYS:HG3	5:E:25:ASP:N	2.31	0.46
5:E:165:LEU:O	5:E:166:LYS:C	2.58	0.46
6:F:90:ARG:CG	6:F:91:ALA:N	2.78	0.46
8:H:76:THR:O	8:H:76:THR:HG22	2.15	0.46
8:H:143:LEU:O	8:H:144:ILE:HG13	2.16	0.46
12:L:28:LYS:HG3	12:L:39:SER:OG	2.15	0.46
12:L:66:GLN:C	12:L:67:PHE:CD1	2.94	0.46
1:A:33:ALA:O	1:A:83:HIS:HD2	1.99	0.46
1:A:43:GLU:O	1:A:44:THR:HB	2.15	0.46
1:A:254:GLU:H	2:B:935:ARG:HH12	1.63	0.46
1:A:414:ASP:O	1:A:416:ARG:N	2.48	0.46
1:A:598:LEU:O	1:A:599:SER:C	2.58	0.46
1:A:777:PHE:CE2	1:A:782:ARG:HA	2.51	0.46
1:A:867:ILE:CG2	1:A:872:GLY:H	2.29	0.46
1:A:915:SER:O	1:A:919:ILE:HG13	2.16	0.46
1:A:962:ARG:O	1:A:963:ILE:C	2.58	0.46
1:A:1081:LEU:CD1	1:A:1099:PRO:HD3	2.45	0.46
1:A:1119:TYR:CD2	1:A:1305:VAL:HG21	2.51	0.46
1:A:1435:PRO:C	1:A:1436:ILE:HG13	2.40	0.46
2:B:189:LEU:O	2:B:192:LEU:HB2	2.15	0.46
2:B:615:MET:HA	2:B:625:LYS:O	2.16	0.46
2:B:1023:VAL:HG12	2:B:1027:ILE:HG13	1.97	0.46
2:B:1033:LYS:HB2	2:B:1089:PRO:HD2	1.97	0.46
2:B:1098:MET:O	2:B:1099:VAL:C	2.59	0.46
2:B:1164:GLY:HA3	2:B:1190:ASP:OD2	2.16	0.46
4:D:141:LEU:O	4:D:144:THR:HB	2.16	0.46
4:D:146:GLN:O	4:D:147:TYR:C	2.58	0.46
4:D:170:THR:HG21	4:D:172:LEU:HG	1.94	0.46
5:E:90:VAL:HB	5:E:119:SER:HB2	1.98	0.46
6:F:97:ARG:O	6:F:98:ALA:C	2.58	0.46
9:I:2:THR:O	9:I:2:THR:HG22	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:73:ARG:HD2	9:I:101:PHE:CE2	2.50	0.46
9:I:83:ASN:HA	9:I:102:VAL:O	2.16	0.46
1:A:18:GLN:CB	2:B:1215:ARG:HB2	2.45	0.46
1:A:298:PHE:HZ	1:A:314:ALA:HB2	1.81	0.46
1:A:535:THR:HG23	1:A:575:LYS:HG2	1.96	0.46
1:A:707:GLY:O	1:A:708:MET:O	2.34	0.46
1:A:809:THR:O	1:A:810:PRO:C	2.58	0.46
1:A:1081:LEU:CD2	1:A:1098:VAL:HG21	2.45	0.46
2:B:593:PRO:O	2:B:594:ALA:C	2.59	0.46
2:B:760:ASP:O	2:B:761:HIS:CG	2.69	0.46
2:B:789:MET:CE	2:B:965:LYS:HB3	2.46	0.46
3:C:15:LYS:O	3:C:240:VAL:HG22	2.16	0.46
3:C:164:ALA:O	3:C:165:LYS:C	2.58	0.46
6:F:135:ARG:HD3	6:F:143:PHE:CD2	2.51	0.46
8:H:100:THR:HG22	8:H:101:ALA:H	1.79	0.46
10:J:8:PHE:CE1	10:J:49:MET:SD	3.08	0.46
11:K:55:LYS:HB3	11:K:81:TYR:HD1	1.80	0.46
11:K:88:LYS:O	11:K:91:CYS:N	2.49	0.46
12:L:30:ILE:O	12:L:56:LEU:HD23	2.15	0.46
1:A:18:GLN:C	1:A:18:GLN:OE1	2.59	0.46
1:A:130:ASP:C	1:A:132:LYS:H	2.24	0.46
1:A:321:PRO:O	1:A:322:VAL:CG2	2.63	0.46
1:A:399:HIS:O	1:A:400:PRO:C	2.54	0.46
1:A:543:LEU:HD11	1:A:547:LEU:HD11	1.96	0.46
1:A:608:ILE:O	1:A:609:ASP:C	2.58	0.46
1:A:809:THR:HB	1:A:810:PRO:HD2	1.97	0.46
1:A:1063:MET:HE2	1:A:1436:ILE:HG12	1.96	0.46
1:A:1063:MET:SD	1:A:1436:ILE:HG12	2.56	0.46
1:A:1115:SER:OG	1:A:1116:LEU:N	2.49	0.46
1:A:1342:GLU:CG	5:E:198:ILE:HG21	2.45	0.46
2:B:385:LEU:HD12	2:B:385:LEU:O	2.15	0.46
2:B:520:GLY:H	2:B:748:ILE:HG22	1.81	0.46
2:B:526:GLU:CD	2:B:752:ALA:CB	2.89	0.46
2:B:800:GLN:HB3	10:J:52:THR:CG2	2.35	0.46
2:B:834:ASN:O	2:B:838:SER:O	2.34	0.46
3:C:147:LEU:HD23	3:C:147:LEU:N	2.31	0.46
3:C:249:ASP:O	3:C:250:THR:C	2.58	0.46
4:D:40:HIS:CE1	4:D:41:GLN:HE21	2.34	0.46
4:D:137:ASN:C	4:D:137:ASN:ND2	2.70	0.46
5:E:39:LEU:O	5:E:40:GLU:C	2.59	0.46
5:E:197:LYS:O	5:E:199:ILE:HG13	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:15:TYR:O	9:I:28:GLU:HG2	2.16	0.46
10:J:48:ARG:HD2	10:J:48:ARG:C	2.41	0.46
11:K:10:PHE:N	11:K:10:PHE:CD2	2.84	0.46
1:A:302:THR:HA	1:A:305:ASP:O	2.14	0.46
1:A:933:TYR:C	1:A:935:GLN:N	2.72	0.46
1:A:993:LEU:HD11	1:A:997:LEU:HD21	1.96	0.46
1:A:1100:ARG:NH2	1:A:1351:GLU:HG2	2.19	0.46
1:A:1210:GLY:O	1:A:1214:GLU:HB2	2.16	0.46
2:B:95:ILE:HG13	2:B:130:VAL:CG2	2.44	0.46
2:B:564:GLU:O	2:B:565:PRO:C	2.58	0.46
2:B:613:VAL:HG22	2:B:628:THR:HA	1.98	0.46
2:B:700:SER:C	2:B:701:ILE:CG2	2.89	0.46
2:B:1060:ARG:C	2:B:1062:HIS:H	2.22	0.46
3:C:80:LEU:O	3:C:80:LEU:HG	2.16	0.46
4:D:59:ILE:O	4:D:60:LYS:C	2.58	0.46
7:G:22:MET:O	7:G:23:LYS:C	2.59	0.46
1:A:344:ARG:HA	2:B:1129:ARG:HA	1.98	0.46
1:A:353:ILE:HG13	1:A:482:PHE:CD2	2.51	0.46
1:A:566:ILE:O	1:A:567:LYS:O	2.34	0.46
1:A:814:PHE:O	1:A:817:ALA:HB3	2.15	0.46
1:A:942:PHE:C	1:A:942:PHE:CD2	2.94	0.46
1:A:1116:LEU:HB2	1:A:1329:THR:OG1	2.16	0.46
2:B:687:GLU:O	2:B:688:GLY:C	2.59	0.46
2:B:816:GLU:O	2:B:817:LEU:CD2	2.59	0.46
3:C:183:TRP:O	3:C:184:ASN:C	2.58	0.46
3:C:215:GLU:O	3:C:216:GLY:C	2.59	0.46
3:C:242:GLN:HA	3:C:245:VAL:CG2	2.45	0.46
6:F:123:LYS:C	6:F:125:LEU:N	2.73	0.46
6:F:150:GLU:O	6:F:151:LEU:C	2.59	0.46
7:G:14:HIS:CD2	7:G:16:SER:H	2.34	0.46
12:L:58:LYS:O	12:L:58:LYS:HG2	2.15	0.46
1:A:100:LYS:O	1:A:103:CYS:N	2.49	0.46
1:A:618:GLU:O	1:A:619:LYS:C	2.59	0.46
1:A:897:TYR:HD2	1:A:936:LEU:CD1	2.28	0.46
1:A:1173:HIS:CG	1:A:1227:ILE:HG23	2.51	0.46
2:B:38:PHE:O	2:B:39:ARG:C	2.59	0.46
2:B:172:ILE:CG2	2:B:173:MET:N	2.79	0.46
2:B:401:PHE:C	2:B:403:LYS:H	2.24	0.46
2:B:551:PRO:HG2	2:B:552:MET:H	1.81	0.46
2:B:984:HIS:CD2	2:B:1025:HIS:HA	2.51	0.46
2:B:990:ILE:HG22	2:B:992:ILE:H	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:56:THR:HG21	3:C:145:CYS:HG	1.77	0.46
3:C:214:ASN:HB3	3:C:217:ASP:OD2	2.16	0.46
3:C:236:GLY:C	3:C:238:ILE:N	2.73	0.46
6:F:87:LYS:HG3	6:F:88:TYR:CD1	2.51	0.46
10:J:3:VAL:CG2	10:J:18:TRP:CG	2.99	0.46
10:J:61:LEU:O	10:J:63:TYR:N	2.48	0.46
1:A:707:GLY:C	1:A:708:MET:HG3	2.41	0.45
1:A:821:ARG:O	1:A:821:ARG:HG3	2.12	0.45
1:A:933:TYR:C	1:A:935:GLN:H	2.24	0.45
1:A:937:VAL:HG12	1:A:938:LYS:N	2.30	0.45
1:A:1167:GLU:O	1:A:1168:GLU:C	2.58	0.45
1:A:1402:PHE:CD1	1:A:1403:GLU:HG3	2.50	0.45
2:B:952:VAL:CG1	2:B:953:LEU:N	2.79	0.45
2:B:964:VAL:HG12	2:B:965:LYS:N	2.32	0.45
2:B:1177:HIS:C	2:B:1179:GLN:N	2.73	0.45
2:B:1183:LYS:CE	2:B:1183:LYS:H	2.27	0.45
3:C:66:ARG:HH21	10:J:5:VAL:HG23	1.80	0.45
3:C:75:MET:HE2	3:C:239:PRO:CD	2.46	0.45
4:D:167:LEU:C	4:D:169:SER:H	2.24	0.45
5:E:117:THR:C	5:E:119:SER:N	2.73	0.45
6:F:138:LEU:O	6:F:139:PRO:C	2.59	0.45
1:A:108:MET:O	1:A:109:HIS:HB2	2.16	0.45
1:A:834:THR:CG2	1:A:1077:THR:HA	2.46	0.45
1:A:920:LEU:C	1:A:920:LEU:CD2	2.89	0.45
1:A:1329:THR:O	1:A:1331:SER:N	2.49	0.45
1:A:1330:ASN:OD1	1:A:1331:SER:N	2.49	0.45
2:B:284:ILE:HG12	2:B:324:ILE:HD12	1.98	0.45
2:B:543:SER:C	2:B:544:CYS:SG	2.99	0.45
2:B:558:LEU:C	2:B:560:GLU:N	2.70	0.45
2:B:758:PHE:C	2:B:760:ASP:N	2.72	0.45
2:B:838:SER:HA	2:B:989:THR:O	2.16	0.45
2:B:994:TYR:HB2	2:B:999:MET:CE	2.46	0.45
2:B:995:ARG:O	2:B:996:ARG:C	2.59	0.45
2:B:1115:THR:HG22	2:B:1117:GLN:CG	2.46	0.45
3:C:251:LEU:O	3:C:254:LYS:N	2.49	0.45
6:F:75:PRO:C	6:F:77:ASP:N	2.74	0.45
7:G:27:LYS:O	7:G:31:LEU:HG	2.16	0.45
8:H:24:CYS:CB	8:H:44:VAL:HG21	2.46	0.45
8:H:98:TYR:HE1	8:H:139:ASN:HA	1.80	0.45
1:A:808:LEU:N	1:A:808:LEU:CD1	2.78	0.45
1:A:1016:THR:O	1:A:1018:PHE:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:43:LEU:HD11	2:B:811:TYR:O	2.15	0.45
2:B:281:PRO:HG2	2:B:284:ILE:CG1	2.44	0.45
2:B:466:TRP:O	2:B:467:GLY:C	2.58	0.45
2:B:785:TYR:CE2	10:J:60:PHE:CE1	3.04	0.45
2:B:975:GLN:HG2	2:B:976:ILE:N	2.32	0.45
3:C:46:ILE:HD13	3:C:157:CYS:CB	2.46	0.45
3:C:181:ASP:CG	3:C:186:LEU:HD13	2.42	0.45
4:D:48:ILE:CG2	7:G:4:ILE:HB	2.46	0.45
5:E:124:VAL:CG1	5:E:132:ILE:HB	2.43	0.45
7:G:132:SER:HB3	7:G:135:ASP:HB2	1.97	0.45
8:H:95:TYR:HE2	8:H:97:MET:CG	2.29	0.45
10:J:61:LEU:C	10:J:63:TYR:N	2.75	0.45
12:L:59:ALA:O	12:L:60:ARG:O	2.34	0.45
1:A:70:CYS:O	1:A:71:GLN:C	2.58	0.45
1:A:563:PRO:HB2	1:A:565:ILE:O	2.16	0.45
1:A:688:LYS:O	1:A:690:VAL:N	2.50	0.45
1:A:814:PHE:CD1	2:B:519:TRP:CE3	3.05	0.45
1:A:1170:ILE:HG23	1:A:1174:PHE:HE1	1.78	0.45
2:B:394:ASP:OD2	9:I:91:ARG:HD2	2.17	0.45
2:B:899:ILE:HG22	2:B:903:VAL:HG21	1.95	0.45
4:D:176:GLU:O	4:D:180:LEU:HB2	2.17	0.45
10:J:36:LEU:HB2	10:J:47:ARG:HH12	1.81	0.45
11:K:47:ARG:HH11	11:K:47:ARG:CB	2.22	0.45
1:A:209:ASN:O	1:A:210:ILE:C	2.58	0.45
1:A:506:ALA:O	1:A:507:VAL:C	2.60	0.45
1:A:550:LEU:HD11	1:A:561:PRO:HD2	1.98	0.45
1:A:703:THR:O	1:A:704:ALA:C	2.59	0.45
1:A:760:GLN:O	1:A:804:TYR:CD1	2.70	0.45
1:A:1191:TRP:HB3	1:A:1260:LEU:HD23	1.97	0.45
1:A:1343:ALA:HB2	5:E:150:VAL:HG22	1.99	0.45
1:A:1359:ASP:HB2	1:A:1361:SER:OG	2.16	0.45
2:B:287:ARG:NH1	2:B:324:ILE:O	2.50	0.45
2:B:386:LEU:O	2:B:388:CYS:N	2.50	0.45
2:B:510:LYS:HD3	2:B:513:GLN:N	2.31	0.45
2:B:555:ILE:HD11	2:B:587:HIS:NE2	2.32	0.45
2:B:638:PHE:HD2	2:B:690:VAL:HG22	1.82	0.45
2:B:806:THR:HG22	2:B:808:ALA:CB	2.46	0.45
2:B:882:THR:O	2:B:883:LEU:HB2	2.17	0.45
2:B:1069:PHE:HA	2:B:1085:ILE:O	2.17	0.45
2:B:1198:TYR:O	2:B:1199:ALA:C	2.59	0.45
3:C:21:ILE:O	3:C:21:ILE:HG22	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:52:GLU:HA	12:L:64:LEU:HD22	1.99	0.45
4:D:51:ASN:OD1	4:D:52:LEU:O	2.34	0.45
4:D:156:ASP:C	4:D:158:GLU:N	2.74	0.45
7:G:51:TYR:C	7:G:51:TYR:CD2	2.94	0.45
8:H:23:VAL:HG22	8:H:43:ASN:HA	1.99	0.45
10:J:1:MET:HE3	10:J:56:LEU:HD12	1.99	0.45
12:L:60:ARG:HG2	12:L:61:THR:N	2.27	0.45
1:A:19:PHE:O	1:A:1416:ALA:HA	2.17	0.45
1:A:44:THR:O	1:A:44:THR:HG22	2.16	0.45
1:A:524:VAL:CG1	1:A:525:GLN:H	2.16	0.45
1:A:849:MET:O	1:A:851:HIS:HD2	1.99	0.45
1:A:881:GLN:NE2	1:A:958:VAL:O	2.42	0.45
1:A:922:ASP:OD1	1:A:922:ASP:C	2.60	0.45
1:A:1001:ARG:O	1:A:1002:GLY:C	2.59	0.45
2:B:63:ILE:HD12	2:B:421:PHE:CE2	2.51	0.45
2:B:229:ALA:HB1	2:B:231:PRO:HD2	1.98	0.45
2:B:710:LEU:O	2:B:711:GLU:HG2	2.17	0.45
2:B:855:PHE:CD1	2:B:856:PHE:N	2.85	0.45
3:C:43:THR:HG22	3:C:44:LEU:H	1.81	0.45
5:E:177:ARG:O	5:E:212:ARG:HD3	2.15	0.45
11:K:7:PHE:HA	11:K:10:PHE:CE2	2.51	0.45
1:A:544:ASP:CG	1:A:545:GLN:N	2.74	0.45
1:A:1385:THR:CG2	1:A:1386:ARG:N	2.79	0.45
1:A:1397:LEU:HA	1:A:1400:CYS:HB2	1.99	0.45
1:A:1406:VAL:HG12	1:A:1410:PHE:CD1	2.52	0.45
2:B:280:ILE:HG23	2:B:281:PRO:HD2	1.99	0.45
2:B:295:GLY:H	2:B:298:LEU:CD2	2.13	0.45
2:B:550:ASP:OD1	2:B:551:PRO:HD2	2.17	0.45
2:B:753:ALA:HA	2:B:756:ILE:HG13	1.99	0.45
2:B:758:PHE:O	2:B:760:ASP:N	2.49	0.45
2:B:992:ILE:HD13	2:B:994:TYR:HE1	1.81	0.45
2:B:1064:TYR:O	2:B:1065:GLN:C	2.59	0.45
3:C:22:LEU:CD2	3:C:25:VAL:HG21	2.47	0.45
4:D:53:SER:HB3	4:D:153:ARG:H	1.81	0.45
4:D:122:GLU:HA	4:D:125:SER:OG	2.17	0.45
8:H:91:ASP:C	8:H:93:TYR:N	2.70	0.45
12:L:40:LEU:HD22	12:L:44:ASP:CB	2.47	0.45
1:A:12:ARG:NE	2:B:1192:TYR:HE2	2.15	0.45
1:A:130:ASP:C	1:A:132:LYS:N	2.75	0.45
1:A:512:VAL:HG11	1:A:876:ALA:O	2.16	0.45
1:A:847:ASP:N	1:A:847:ASP:OD1	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1227:ILE:CG2	1:A:1228:TRP:N	2.78	0.45
1:A:1293:SER:OG	1:A:1295:THR:HG23	2.17	0.45
2:B:202:TYR:CD2	2:B:202:TYR:N	2.84	0.45
2:B:255:GLN:O	2:B:271:ALA:HB1	2.17	0.45
2:B:274:PRO:O	2:B:275:TYR:HB2	2.16	0.45
2:B:372:SER:O	2:B:376:PHE:HD1	2.00	0.45
2:B:385:LEU:HD12	2:B:385:LEU:C	2.42	0.45
2:B:763:GLN:O	2:B:764:SER:C	2.59	0.45
2:B:851:PHE:O	2:B:974:PRO:HD3	2.17	0.45
2:B:1181:GLU:OE1	2:B:1183:LYS:HG3	2.17	0.45
2:B:1182:CYS:C	2:B:1183:LYS:O	2.60	0.45
8:H:12:VAL:HA	8:H:28:ALA:HB2	1.99	0.45
1:A:78:PRO:O	1:A:78:PRO:HG2	2.17	0.45
1:A:556:TRP:CE2	1:A:558:GLY:HA2	2.51	0.45
1:A:803:SER:C	1:A:805:LEU:N	2.75	0.45
1:A:901:LEU:CG	1:A:926:GLN:HE21	2.28	0.45
1:A:1018:PHE:O	1:A:1019:CYS:C	2.59	0.45
1:A:1143:LEU:HD12	1:A:1146:VAL:HG23	1.99	0.45
1:A:1347:ALA:O	1:A:1348:LEU:C	2.60	0.45
2:B:281:PRO:O	2:B:282:ILE:C	2.60	0.45
2:B:281:PRO:C	2:B:283:VAL:N	2.75	0.45
2:B:293:PRO:HG2	2:B:296:GLU:OE1	2.16	0.45
2:B:489:SER:OG	2:B:490:SER:N	2.49	0.45
2:B:578:THR:HG23	2:B:622:LYS:CA	2.47	0.45
2:B:981:ALA:CB	2:B:987:LYS:HA	2.46	0.45
3:C:35:ARG:NH1	11:K:41:THR:OG1	2.50	0.45
3:C:50:GLU:HB3	3:C:156:THR:HB	1.98	0.45
3:C:178:PHE:O	3:C:179:GLU:HB2	2.16	0.45
5:E:93:MET:O	5:E:94:LYS:C	2.59	0.45
5:E:117:THR:O	5:E:120:ALA:N	2.45	0.45
5:E:135:PHE:CB	5:E:140:LEU:HD11	2.47	0.45
5:E:138:ALA:HA	5:E:141:VAL:CG2	2.47	0.45
11:K:90:ALA:O	11:K:94:ILE:HG13	2.17	0.45
12:L:38:LEU:O	12:L:39:SER:CB	2.58	0.45
1:A:78:PRO:O	1:A:79:GLY:C	2.58	0.45
1:A:393:ARG:C	1:A:395:GLY:N	2.75	0.45
1:A:840:ARG:O	1:A:841:LEU:C	2.59	0.45
1:A:920:LEU:C	1:A:920:LEU:HD23	2.42	0.45
1:A:1170:ILE:O	1:A:1174:PHE:HD1	1.99	0.45
2:B:233:PRO:HG2	2:B:234:ILE:CD1	2.47	0.45
2:B:374:LYS:O	2:B:375:ALA:C	2.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:604:ARG:C	2:B:606:LYS:H	2.24	0.45
2:B:766:ARG:HH22	2:B:1020:ARG:HG2	1.79	0.45
2:B:936:ASP:CG	2:B:938:SER:H	2.23	0.45
2:B:1026:LEU:HD23	2:B:1086:PHE:CE2	2.52	0.45
3:C:62:PHE:O	3:C:65:HIS:HB3	2.17	0.45
3:C:247:GLY:C	3:C:249:ASP:N	2.72	0.45
8:H:44:VAL:O	8:H:44:VAL:CG1	2.61	0.45
10:J:7:CYS:SG	10:J:49:MET:CE	3.01	0.45
10:J:11:GLY:O	10:J:12:LYS:C	2.60	0.45
11:K:55:LYS:HB3	11:K:81:TYR:CD1	2.52	0.45
1:A:2:VAL:HG21	2:B:1157:ALA:C	2.42	0.44
1:A:381:THR:O	1:A:384:ASN:N	2.45	0.44
1:A:470:LEU:HD11	1:A:482:PHE:CE2	2.52	0.44
1:A:648:ASN:OD1	1:A:648:ASN:N	2.50	0.44
1:A:673:GLY:O	1:A:676:MET:HB2	2.16	0.44
1:A:1230:GLU:C	1:A:1232:ASN:N	2.71	0.44
2:B:878:GLN:O	2:B:879:ARG:C	2.58	0.44
3:C:44:LEU:HG	3:C:159:ALA:HB1	1.99	0.44
3:C:46:ILE:HD13	3:C:157:CYS:HB3	1.99	0.44
3:C:80:LEU:HD11	3:C:95:CYS:CA	2.47	0.44
3:C:88:CYS:SG	3:C:91:HIS:N	2.90	0.44
3:C:158:VAL:O	3:C:158:VAL:HG12	2.17	0.44
3:C:242:GLN:CA	3:C:245:VAL:HG23	2.43	0.44
4:D:147:TYR:CE1	7:G:103:VAL:HG13	2.52	0.44
6:F:86:THR:O	6:F:89:GLU:HB2	2.18	0.44
9:I:15:TYR:N	9:I:15:TYR:CD1	2.85	0.44
9:I:55:THR:HG22	9:I:56:ALA:N	2.32	0.44
10:J:1:MET:N	10:J:56:LEU:N	2.65	0.44
11:K:71:PHE:CD1	11:K:71:PHE:C	2.94	0.44
1:A:30:ILE:HD11	2:B:1168:LEU:HD13	1.99	0.44
1:A:52:GLY:O	1:A:56:PRO:HG2	2.17	0.44
1:A:68:GLN:NE2	1:A:80:HIS:CD2	2.79	0.44
1:A:73:GLY:O	1:A:74:MET:C	2.59	0.44
1:A:388:LEU:O	1:A:389:THR:C	2.61	0.44
1:A:563:PRO:HB3	1:A:571:LEU:O	2.17	0.44
1:A:567:LYS:HB2	1:A:568:PRO:HD2	1.99	0.44
1:A:697:ALA:HB2	1:A:702:LEU:CD1	2.46	0.44
1:A:896:ARG:NH2	1:A:1030:ARG:NH2	2.66	0.44
1:A:1115:SER:O	1:A:1329:THR:HG23	2.17	0.44
1:A:1392:SER:C	1:A:1394:THR:H	2.25	0.44
2:B:97:VAL:CG1	2:B:178:ASN:HD21	2.28	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:460:ALA:HB1	2:B:466:TRP:CE3	2.52	0.44
2:B:800:GLN:HB2	2:B:821:GLN:HA	1.99	0.44
4:D:156:ASP:C	4:D:158:GLU:H	2.25	0.44
8:H:97:MET:HE3	8:H:118:PHE:CD1	2.52	0.44
10:J:1:MET:H2	10:J:55:ASP:C	2.26	0.44
11:K:33:ILE:HB	11:K:35:PHE:HE1	1.81	0.44
1:A:51:GLY:HA2	1:A:56:PRO:HA	1.99	0.44
1:A:470:LEU:HD23	1:A:487:MET:HE3	1.98	0.44
1:A:472:LEU:HD11	2:B:835:GLN:CD	2.41	0.44
1:A:783:THR:HG21	1:A:815:PHE:CE2	2.53	0.44
1:A:890:ASP:H	1:A:1296:GLY:HA3	1.83	0.44
1:A:1007:ILE:C	1:A:1009:ASN:H	2.25	0.44
1:A:1040:GLN:O	1:A:1041:ALA:C	2.60	0.44
1:A:1129:GLU:O	1:A:1130:GLN:C	2.60	0.44
1:A:1341:ILE:CG2	1:A:1342:GLU:N	2.60	0.44
2:B:215:GLN:OE1	2:B:499:ASN:HB3	2.18	0.44
2:B:373:ARG:HG3	2:B:566:LEU:HD23	2.00	0.44
2:B:533:CYS:C	2:B:535:LEU:N	2.72	0.44
2:B:683:SER:O	2:B:687:GLU:HB2	2.16	0.44
2:B:780:VAL:HG21	10:J:56:LEU:HD11	1.99	0.44
3:C:73:GLN:HE21	3:C:74:SER:H	1.60	0.44
5:E:137:GLU:C	5:E:139:ALA:N	2.75	0.44
5:E:179:GLN:O	5:E:180:ARG:C	2.60	0.44
7:G:82:PHE:O	7:G:84:GLY:N	2.50	0.44
8:H:95:TYR:CE2	8:H:97:MET:CG	3.00	0.44
1:A:483:ASP:HB2	2:B:987:LYS:HG3	1.99	0.44
1:A:849:MET:HE3	1:A:1061:GLY:HA2	1.99	0.44
1:A:1313:LEU:HD12	1:A:1327:ILE:HD13	1.99	0.44
1:A:1427:ASN:O	1:A:1430:LEU:N	2.43	0.44
2:B:518:HIS:O	2:B:519:TRP:C	2.60	0.44
2:B:542:MET:CG	2:B:747:MET:HB3	2.48	0.44
2:B:806:THR:H	2:B:809:MET:HE3	1.81	0.44
2:B:828:ALA:HB2	2:B:1085:ILE:HG21	2.00	0.44
2:B:1085:ILE:CG2	2:B:1086:PHE:N	2.80	0.44
2:B:1102:LYS:C	2:B:1103:ILE:O	2.58	0.44
2:B:1150:ARG:HA	2:B:1150:ARG:NE	2.33	0.44
2:B:1182:CYS:O	2:B:1183:LYS:O	2.36	0.44
3:C:62:PHE:C	3:C:62:PHE:CD2	2.95	0.44
3:C:183:TRP:CZ2	3:C:207:CYS:HB3	2.52	0.44
5:E:42:PHE:CZ	5:E:58:MET:HE3	2.52	0.44
1:A:43:GLU:HB2	1:A:46:THR:HB	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:901:LEU:HD22	1:A:919:ILE:HG22	1.99	0.44
1:A:1206:ASP:HB2	1:A:1274:ARG:HH22	1.83	0.44
1:A:1242:VAL:O	1:A:1243:VAL:HB	2.17	0.44
2:B:48:LEU:O	2:B:49:ASP:C	2.60	0.44
2:B:381:MET:O	2:B:382:ILE:C	2.61	0.44
2:B:604:ARG:O	2:B:606:LYS:N	2.50	0.44
2:B:995:ARG:HB3	2:B:997:GLU:OE2	2.16	0.44
5:E:117:THR:HG22	5:E:119:SER:N	2.20	0.44
5:E:177:ARG:HD3	5:E:215:MET:HG3	1.99	0.44
9:I:32:CYS:HB2	9:I:33:SER:H	1.39	0.44
11:K:21:ILE:HG12	11:K:33:ILE:HG12	1.99	0.44
1:A:79:GLY:C	1:A:243:PRO:HG3	2.42	0.44
1:A:299:HIS:C	1:A:301:ALA:N	2.73	0.44
1:A:783:THR:O	1:A:784:LEU:HD23	2.16	0.44
1:A:848:ILE:O	1:A:1065:GLY:N	2.39	0.44
1:A:962:ARG:O	1:A:965:GLN:N	2.51	0.44
1:A:1101:LEU:O	1:A:1101:LEU:HD12	2.17	0.44
1:A:1121:GLU:O	1:A:1122:PRO:O	2.35	0.44
1:A:1343:ALA:O	1:A:1344:GLY:C	2.60	0.44
2:B:824:ILE:CD1	10:J:48:ARG:NH1	2.80	0.44
2:B:910:VAL:HG12	2:B:911:ILE:H	1.79	0.44
3:C:26:ASP:O	3:C:27:LEU:C	2.58	0.44
7:G:16:SER:C	7:G:18:PHE:H	2.26	0.44
7:G:80:LYS:O	7:G:80:LYS:CG	2.62	0.44
7:G:96:GLN:HA	7:G:121:PHE:CD2	2.52	0.44
1:A:55:ASP:O	1:A:57:ARG:N	2.51	0.44
1:A:668:ASP:HA	1:A:741:ASN:OD1	2.17	0.44
1:A:727:ASP:O	1:A:731:ARG:HG3	2.18	0.44
1:A:833:GLU:O	1:A:834:THR:C	2.61	0.44
1:A:935:GLN:C	1:A:937:VAL:N	2.71	0.44
1:A:1092:LYS:HD2	1:A:1092:LYS:HA	1.82	0.44
1:A:1131:ALA:O	1:A:1132:LYS:C	2.58	0.44
2:B:59:LEU:CD1	2:B:417:PHE:CE2	3.01	0.44
2:B:598:GLU:O	2:B:598:GLU:HG2	2.17	0.44
2:B:789:MET:HE2	2:B:965:LYS:HB3	1.99	0.44
2:B:806:THR:O	2:B:808:ALA:N	2.51	0.44
2:B:1084:GLN:OE1	3:C:191:TYR:HA	2.17	0.44
2:B:1107:ALA:O	2:B:1108:ARG:O	2.36	0.44
3:C:67:LEU:O	3:C:68:GLY:C	2.60	0.44
3:C:91:HIS:HB2	3:C:96:SER:OG	2.18	0.44
5:E:128:PRO:HA	5:E:129:PRO:C	2.42	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:119:LEU:HD12	7:G:131:GLN:O	2.18	0.44
1:A:384:ASN:O	1:A:386:ASP:N	2.50	0.44
1:A:570:PRO:C	1:A:571:LEU:HD12	2.43	0.44
1:A:666:ILE:N	2:B:1026:LEU:HD22	2.33	0.44
1:A:789:LYS:HD2	9:I:67:THR:OG1	2.17	0.44
1:A:814:PHE:CE1	2:B:519:TRP:HA	2.52	0.44
1:A:910:PRO:C	1:A:912:LEU:H	2.26	0.44
1:A:1115:SER:HA	1:A:1308:THR:HG23	1.99	0.44
2:B:401:PHE:C	2:B:403:LYS:N	2.76	0.44
2:B:405:ARG:HD2	2:B:631:GLY:C	2.43	0.44
2:B:558:LEU:O	2:B:561:TRP:N	2.49	0.44
2:B:634:TYR:CE1	2:B:692:TYR:CD1	3.06	0.44
2:B:680:THR:HB	2:B:681:TRP:H	1.58	0.44
2:B:874:PHE:HA	2:B:913:GLY:O	2.17	0.44
2:B:1031:LEU:HD13	2:B:1055:ILE:HD11	2.00	0.44
3:C:94:LYS:HB2	3:C:94:LYS:HE3	1.67	0.44
4:D:33:PHE:CZ	7:G:80:LYS:NZ	2.84	0.44
5:E:92:THR:O	5:E:92:THR:HG22	2.18	0.44
8:H:38:LEU:HD12	8:H:39:THR:H	1.82	0.44
8:H:38:LEU:HD12	8:H:124:ARG:O	2.18	0.44
1:A:76:GLU:HG3	1:A:76:GLU:O	2.18	0.44
1:A:269:ILE:HG12	1:A:299:HIS:HB3	1.99	0.44
1:A:396:PRO:HB3	1:A:402:ALA:O	2.18	0.44
1:A:477:PRO:HG2	1:A:521:MET:HG2	1.99	0.44
1:A:573:SER:CB	8:H:119:GLY:O	2.65	0.44
1:A:719:VAL:C	1:A:721:PHE:N	2.76	0.44
1:A:1081:LEU:O	1:A:1082:ASN:C	2.61	0.44
1:A:1101:LEU:HD11	1:A:1105:LEU:HD11	2.00	0.44
1:A:1220:PHE:O	1:A:1221:LYS:HB2	2.18	0.44
1:A:1342:GLU:HG2	5:E:198:ILE:HD13	1.99	0.44
1:A:1348:LEU:O	1:A:1349:TYR:C	2.60	0.44
2:B:129:PHE:CD2	2:B:166:PHE:HA	2.53	0.44
2:B:911:ILE:HG23	2:B:966:VAL:HG11	2.00	0.44
3:C:144:ILE:O	3:C:145:CYS:CB	2.66	0.44
5:E:185:ALA:O	5:E:190:LEU:HG	2.18	0.44
10:J:54:VAL:HG12	10:J:56:LEU:HD23	2.00	0.44
11:K:87:LEU:HD12	11:K:87:LEU:C	2.42	0.44
1:A:489:LEU:C	1:A:489:LEU:CD1	2.91	0.43
1:A:536:LEU:H	1:A:536:LEU:HG	1.51	0.43
1:A:567:LYS:HD3	8:H:95:TYR:HA	1.99	0.43
1:A:815:PHE:O	1:A:816:HIS:C	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:925:LEU:C	1:A:927:VAL:N	2.76	0.43
1:A:1099:PRO:O	1:A:1102:LYS:HB3	2.17	0.43
1:A:1170:ILE:O	1:A:1171:GLN:C	2.61	0.43
1:A:1242:VAL:CG1	1:A:1243:VAL:H	2.23	0.43
1:A:1312:ASN:O	1:A:1316:VAL:HG23	2.18	0.43
1:A:1451:VAL:C	1:A:1453:TYR:N	2.76	0.43
2:B:287:ARG:NH2	2:B:325:GLN:HE22	2.16	0.43
2:B:540:SER:HB3	2:B:747:MET:O	2.18	0.43
2:B:616:ILE:N	2:B:625:LYS:O	2.37	0.43
2:B:695:ALA:O	2:B:698:GLU:HB3	2.18	0.43
5:E:22:MET:HE3	5:E:26:ARG:NH2	2.32	0.43
5:E:29:PHE:O	5:E:30:ILE:HG13	2.18	0.43
5:E:80:VAL:HG12	5:E:81:GLU:N	2.33	0.43
5:E:98:ILE:O	5:E:99:HIS:C	2.61	0.43
7:G:1:MET:CE	7:G:80:LYS:H	2.18	0.43
7:G:44:TYR:HE1	7:G:157:ILE:HB	1.83	0.43
10:J:46:CYS:O	10:J:47:ARG:C	2.60	0.43
12:L:60:ARG:CG	12:L:61:THR:H	2.29	0.43
1:A:577:ILE:O	1:A:578:LEU:C	2.61	0.43
1:A:967:ALA:N	1:A:1044:TRP:HZ3	2.16	0.43
2:B:293:PRO:O	2:B:296:GLU:HB3	2.17	0.43
2:B:486:TYR:CD1	2:B:1096:ARG:NH2	2.86	0.43
2:B:510:LYS:O	2:B:510:LYS:HD3	2.13	0.43
2:B:642:ASP:HB3	2:B:649:LYS:CG	2.47	0.43
2:B:661:LEU:C	2:B:663:ALA:N	2.75	0.43
2:B:912:ILE:HD11	2:B:966:VAL:HG23	1.99	0.43
2:B:1076:HIS:ND1	2:B:1076:HIS:N	2.66	0.43
3:C:77:ILE:HG23	3:C:161:LYS:HE3	2.00	0.43
3:C:86:CYS:C	3:C:88:CYS:H	2.26	0.43
3:C:237:SER:O	3:C:238:ILE:HG13	2.18	0.43
4:D:47:LEU:CD1	4:D:48:ILE:N	2.81	0.43
7:G:66:GLY:O	7:G:67:SER:C	2.60	0.43
11:K:17:SER:O	11:K:18:LYS:C	2.61	0.43
1:A:608:ILE:CB	1:A:613:ILE:HD11	2.44	0.43
1:A:744:LYS:HG2	1:A:748:MET:CE	2.41	0.43
1:A:899:VAL:HB	1:A:929:LEU:CD1	2.25	0.43
1:A:989:GLY:C	1:A:991:LYS:N	2.69	0.43
1:A:1111:MET:HE1	1:A:1331:SER:HA	2.00	0.43
1:A:1384:VAL:O	1:A:1384:VAL:HG12	2.19	0.43
2:B:39:ARG:HG2	2:B:39:ARG:NH1	2.33	0.43
2:B:214:ALA:HA	2:B:408:LEU:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:230:ALA:N	2:B:231:PRO:CD	2.81	0.43
2:B:294:ASP:C	2:B:296:GLU:N	2.68	0.43
2:B:778:MET:HE1	2:B:853:SER:HB3	2.00	0.43
2:B:787:VAL:O	2:B:787:VAL:HG12	2.19	0.43
2:B:866:TYR:O	2:B:867:GLY:C	2.61	0.43
2:B:901:PRO:HB2	12:L:60:ARG:HA	2.00	0.43
2:B:999:MET:HE3	2:B:999:MET:CA	2.48	0.43
2:B:1073:TYR:CE2	2:B:1080:LYS:HG2	2.53	0.43
3:C:242:GLN:HB3	3:C:246:ARG:HG3	1.99	0.43
4:D:48:ILE:HG21	7:G:4:ILE:CD1	2.40	0.43
5:E:188:LEU:O	5:E:189:GLY:C	2.62	0.43
6:F:86:THR:O	6:F:89:GLU:N	2.51	0.43
7:G:1:MET:CE	7:G:80:LYS:O	2.66	0.43
7:G:47:CYS:O	7:G:76:ALA:HB1	2.18	0.43
9:I:111:THR:HG21	9:I:113:ASP:HB2	2.00	0.43
12:L:32:ALA:CB	12:L:55:ILE:HD12	2.48	0.43
1:A:231:PRO:O	1:A:233:TRP:N	2.52	0.43
1:A:347:PHE:N	2:B:1107:ALA:HA	2.26	0.43
1:A:353:ILE:HD13	1:A:487:MET:HG3	2.00	0.43
1:A:458:HIS:CE1	1:A:507:VAL:HG21	2.53	0.43
1:A:582:ILE:O	1:A:583:PRO:O	2.36	0.43
1:A:718:VAL:O	1:A:721:PHE:HB2	2.18	0.43
1:A:773:LYS:O	1:A:774:ARG:C	2.60	0.43
1:A:1081:LEU:HD13	1:A:1081:LEU:HA	1.84	0.43
1:A:1236:LEU:C	1:A:1237:ILE:HG13	2.43	0.43
1:A:1313:LEU:HD11	1:A:1327:ILE:HD13	1.99	0.43
2:B:465:ASN:N	2:B:465:ASN:ND2	2.65	0.43
2:B:597:MET:C	2:B:599:THR:N	2.77	0.43
2:B:781:PHE:HD1	2:B:782:LEU:HG	1.83	0.43
2:B:830:TYR:CD2	2:B:1000:PRO:HD3	2.53	0.43
3:C:44:LEU:HD23	3:C:72:LEU:CB	2.48	0.43
5:E:21:GLU:O	5:E:24:LYS:HG2	2.19	0.43
6:F:88:TYR:CD1	6:F:88:TYR:N	2.85	0.43
6:F:89:GLU:O	6:F:90:ARG:C	2.62	0.43
6:F:135:ARG:HG2	6:F:137:TYR:CE1	2.52	0.43
7:G:1:MET:SD	7:G:79:PHE:CD1	3.12	0.43
7:G:26:LEU:O	7:G:27:LYS:C	2.61	0.43
8:H:97:MET:SD	8:H:121:LEU:HD12	2.59	0.43
9:I:71:SER:O	9:I:83:ASN:ND2	2.51	0.43
11:K:7:PHE:O	11:K:11:LEU:HB2	2.18	0.43
11:K:35:PHE:N	11:K:35:PHE:HD1	2.15	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:53:ASP:OD1	11:K:55:LYS:HB2	2.17	0.43
11:K:91:CYS:O	11:K:92:ASN:C	2.60	0.43
12:L:47:ARG:NH2	12:L:54:ARG:HE	2.16	0.43
1:A:47:ARG:CZ	1:A:255:SER:H	2.31	0.43
1:A:426:LEU:O	1:A:427:GLN:HG2	2.19	0.43
1:A:492:PRO:C	1:A:493:GLN:HE21	2.25	0.43
1:A:496:GLU:OE1	7:G:63:PRO:O	2.37	0.43
1:A:544:ASP:CG	1:A:545:GLN:H	2.25	0.43
1:A:576:GLN:O	1:A:579:SER:HB2	2.18	0.43
1:A:886:ILE:HG13	1:A:943:LEU:HD13	2.00	0.43
1:A:1000:LEU:HD23	1:A:1000:LEU:HA	1.64	0.43
1:A:1189:SER:OG	1:A:1190:PRO:HD2	2.18	0.43
1:A:1208:THR:O	1:A:1211:GLN:N	2.52	0.43
1:A:1396:ALA:O	1:A:1397:LEU:C	2.61	0.43
2:B:20:ASP:O	2:B:22:SER:N	2.48	0.43
2:B:27:ALA:O	2:B:28:GLU:C	2.60	0.43
2:B:235:SER:OG	2:B:236:HIS:CD2	2.72	0.43
2:B:236:HIS:O	2:B:237:VAL:HG23	2.19	0.43
2:B:324:ILE:CG2	2:B:325:GLN:N	2.81	0.43
2:B:789:MET:CE	2:B:965:LYS:O	2.65	0.43
2:B:1002:THR:O	2:B:1003:ALA:C	2.59	0.43
2:B:1145:SER:O	2:B:1147:LEU:N	2.51	0.43
3:C:127:ARG:O	3:C:128:ASN:C	2.60	0.43
8:H:81:PRO:HB3	8:H:82:PRO:CD	2.49	0.43
10:J:25:LEU:O	10:J:29:GLU:HA	2.19	0.43
10:J:28:ASP:O	10:J:29:GLU:C	2.61	0.43
10:J:45:CYS:SG	10:J:46:CYS:N	2.91	0.43
11:K:30:ALA:HA	11:K:75:ILE:O	2.18	0.43
11:K:32:VAL:HA	11:K:73:LEU:O	2.19	0.43
1:A:65:LEU:O	1:A:66:LYS:C	2.60	0.43
1:A:108:MET:SD	1:A:210:ILE:HD13	2.59	0.43
1:A:465:TYR:N	11:K:2:ASN:HB3	2.32	0.43
1:A:483:ASP:HB2	2:B:987:LYS:CG	2.48	0.43
1:A:845:LEU:HD22	1:A:1374:VAL:HG21	2.00	0.43
1:A:1013:ASP:C	1:A:1015:VAL:H	2.26	0.43
1:A:1282:VAL:HG22	1:A:1308:THR:HA	2.01	0.43
1:A:1319:VAL:O	1:A:1322:ILE:HG12	2.19	0.43
2:B:377:PHE:C	2:B:379:GLY:N	2.71	0.43
2:B:798:TYR:HD2	2:B:798:TYR:N	2.16	0.43
2:B:975:GLN:HG2	2:B:976:ILE:H	1.82	0.43
2:B:977:GLY:CA	2:B:1099:VAL:HB	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1132:GLU:O	2:B:1135:ARG:N	2.52	0.43
2:B:1162:ILE:HG22	2:B:1163:CYS:O	2.19	0.43
3:C:73:GLN:NE2	3:C:75:MET:N	2.54	0.43
5:E:33:GLU:C	5:E:35:VAL:H	2.25	0.43
8:H:145:ARG:O	8:H:146:ARG:HB2	2.18	0.43
1:A:43:GLU:O	1:A:44:THR:CB	2.66	0.43
1:A:135:PHE:CE1	1:A:222:LEU:HD22	2.53	0.43
1:A:243:PRO:CB	1:A:244:PRO:HD2	2.46	0.43
1:A:393:ARG:C	1:A:395:GLY:H	2.25	0.43
1:A:814:PHE:HE1	2:B:519:TRP:HA	1.83	0.43
1:A:1239:ARG:NH1	1:A:1239:ARG:HB3	2.33	0.43
2:B:189:LEU:O	2:B:190:TYR:C	2.62	0.43
2:B:282:ILE:HD13	2:B:382:ILE:HD13	2.01	0.43
2:B:597:MET:O	2:B:599:THR:N	2.52	0.43
2:B:1076:HIS:CD2	11:K:40:HIS:NE2	2.86	0.43
2:B:1160:VAL:CG1	2:B:1161:HIS:H	2.30	0.43
3:C:44:LEU:HG	3:C:45:ALA:N	2.34	0.43
3:C:76:ASP:HB2	3:C:128:ASN:O	2.18	0.43
3:C:245:VAL:C	3:C:247:GLY:N	2.73	0.43
4:D:146:GLN:O	4:D:150:ASN:N	2.51	0.43
5:E:11:ARG:C	5:E:13:TRP:N	2.74	0.43
5:E:25:ASP:O	5:E:27:GLY:N	2.52	0.43
5:E:140:LEU:H	5:E:140:LEU:HG	1.63	0.43
7:G:14:HIS:CG	7:G:15:PRO:HD2	2.53	0.43
1:A:264:PHE:O	1:A:265:LYS:C	2.60	0.43
1:A:475:THR:CG2	1:A:476:SER:N	2.81	0.43
1:A:841:LEU:HD13	1:A:1072:ILE:HB	2.00	0.43
1:A:929:LEU:O	1:A:929:LEU:HD13	2.19	0.43
1:A:971:PHE:CE2	1:A:1040:GLN:HG2	2.53	0.43
1:A:1006:ILE:HD11	5:E:163:GLU:HG3	2.00	0.43
1:A:1044:TRP:O	1:A:1045:VAL:C	2.62	0.43
2:B:390:LEU:O	2:B:392:ARG:N	2.51	0.43
2:B:745:PRO:O	2:B:746:SER:C	2.62	0.43
2:B:821:GLN:NE2	2:B:851:PHE:H	2.14	0.43
2:B:939:THR:HA	2:B:940:PRO:HD2	1.92	0.43
2:B:1065:GLN:HG3	2:B:1067:ARG:H	1.83	0.43
3:C:69:LEU:H	3:C:69:LEU:CD1	2.32	0.43
5:E:154:ILE:HG22	5:E:155:ARG:O	2.19	0.43
5:E:198:ILE:HD11	5:E:212:ARG:HH11	1.84	0.43
8:H:83:GLN:C	8:H:85:GLY:N	2.74	0.43
8:H:95:TYR:HB3	8:H:144:ILE:HB	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:73:ARG:HH12	9:I:112:SER:HB2	1.83	0.43
1:A:244:PRO:CG	1:A:245:PRO:HD3	2.47	0.43
1:A:419:LYS:HG3	1:A:420:ARG:H	1.84	0.43
1:A:443:LEU:HD23	1:A:443:LEU:HA	1.72	0.43
1:A:449:SER:O	2:B:1133:MET:HB3	2.18	0.43
1:A:464:PRO:HG2	1:A:465:TYR:HD1	1.84	0.43
1:A:722:LEU:O	1:A:725:ALA:HB3	2.19	0.43
1:A:955:PRO:O	1:A:955:PRO:HG2	2.18	0.43
1:A:1021:LEU:O	1:A:1024:SER:HB3	2.19	0.43
1:A:1151:GLU:HB3	1:A:1153:TYR:CE1	2.50	0.43
1:A:1205:LYS:O	1:A:1206:ASP:C	2.61	0.43
1:A:1261:LYS:C	1:A:1264:GLU:HB3	2.44	0.43
2:B:176:SER:O	2:B:182:SER:HB3	2.19	0.43
2:B:949:VAL:HG12	2:B:950:ASP:N	2.34	0.43
2:B:987:LYS:O	2:B:987:LYS:HG2	2.18	0.43
2:B:1017:ILE:HD13	2:B:1017:ILE:HA	1.82	0.43
4:D:19:GLU:O	4:D:20:GLU:C	2.61	0.43
10:J:56:LEU:O	10:J:57:ILE:C	2.59	0.43
12:L:63:ARG:O	12:L:63:ARG:HG3	2.19	0.43
1:A:49:LYS:HZ1	1:A:60:SER:CA	2.32	0.43
1:A:353:ILE:HG13	1:A:482:PHE:HD2	1.83	0.43
1:A:353:ILE:CD1	1:A:487:MET:HE2	2.48	0.43
1:A:626:ASN:C	1:A:631:HIS:HD2	2.27	0.43
1:A:703:THR:HB	1:A:705:LYS:HE2	2.01	0.43
1:A:715:GLU:C	1:A:717:ASN:H	2.27	0.43
1:A:751:SER:OG	2:B:1015:HIS:CE1	2.72	0.43
1:A:784:LEU:HD11	1:A:815:PHE:CE2	2.54	0.43
1:A:794:PRO:C	1:A:796:SER:N	2.77	0.43
1:A:803:SER:C	1:A:805:LEU:H	2.26	0.43
1:A:858:ASN:O	1:A:860:LEU:N	2.52	0.43
1:A:1116:LEU:O	1:A:1308:THR:HG22	2.19	0.43
1:A:1164:PRO:O	1:A:1167:GLU:HG3	2.19	0.43
1:A:1169:ILE:HD11	1:A:1229:SER:HB3	2.01	0.43
1:A:1284:MET:HE3	1:A:1304:TRP:CZ3	2.54	0.43
1:A:1444:MET:HG2	7:G:59:GLY:O	2.19	0.43
2:B:485:ARG:HH11	2:B:485:ARG:HG3	1.83	0.43
2:B:543:SER:O	2:B:544:CYS:SG	2.75	0.43
2:B:758:PHE:HB2	2:B:1024:ALA:HB1	2.00	0.43
2:B:758:PHE:C	2:B:760:ASP:H	2.26	0.43
2:B:1170:THR:HB	2:B:1171:VAL:H	1.68	0.43
3:C:41:ILE:HD11	3:C:247:GLY:CA	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:82:TYR:O	3:C:83:SER:C	2.62	0.43
4:D:63:LEU:HD13	4:D:133:THR:OG1	2.19	0.43
8:H:27:GLU:HG2	8:H:39:THR:HG23	2.00	0.43
12:L:40:LEU:HD22	12:L:44:ASP:CG	2.44	0.43
12:L:50:ASP:O	12:L:52:GLY:N	2.52	0.43
1:A:79:GLY:HA3	1:A:243:PRO:CG	2.49	0.42
1:A:679:ILE:O	1:A:680:THR:C	2.62	0.42
1:A:738:LYS:HZ2	3:C:194:GLU:HA	1.83	0.42
1:A:784:LEU:C	1:A:786:HIS:N	2.76	0.42
1:A:962:ARG:C	1:A:964:ILE:N	2.76	0.42
1:A:1283:VAL:CG1	1:A:1284:MET:N	2.78	0.42
2:B:616:ILE:N	2:B:616:ILE:CD1	2.81	0.42
3:C:175:ALA:HB3	10:J:43:ARG:NH2	2.33	0.42
4:D:188:ALA:O	4:D:189:ASP:C	2.62	0.42
5:E:182:ASP:O	5:E:185:ALA:HB3	2.19	0.42
6:F:138:LEU:O	6:F:140:ASP:N	2.52	0.42
8:H:38:LEU:HD13	8:H:125:LEU:HD13	2.00	0.42
9:I:61:ASP:C	9:I:63:GLY:N	2.77	0.42
11:K:62:LYS:HG3	11:K:62:LYS:O	2.19	0.42
1:A:2:VAL:HG21	2:B:1158:PHE:N	2.34	0.42
1:A:68:GLN:C	1:A:70:CYS:N	2.76	0.42
1:A:185:TRP:O	1:A:197:PRO:HA	2.18	0.42
1:A:224:PHE:CD2	1:A:231:PRO:HG3	2.54	0.42
1:A:261:ASP:O	1:A:264:PHE:N	2.51	0.42
1:A:343:LYS:HE2	2:B:1156:ASP:HB2	2.01	0.42
1:A:545:GLN:O	1:A:546:VAL:C	2.61	0.42
1:A:1017:LEU:HD23	5:E:204:THR:O	2.18	0.42
1:A:1067:LEU:O	1:A:1067:LEU:HD12	2.20	0.42
1:A:1072:ILE:O	1:A:1075:PRO:CG	2.66	0.42
1:A:1272:THR:HG22	1:A:1273:LEU:N	2.34	0.42
2:B:63:ILE:O	2:B:67:SER:HB3	2.19	0.42
2:B:547:VAL:H	2:B:612:GLU:CD	2.27	0.42
2:B:1085:ILE:N	2:B:1085:ILE:HD12	2.34	0.42
4:D:26:THR:O	4:D:28:GLN:N	2.52	0.42
6:F:100:GLN:HG2	7:G:66:GLY:HA3	2.01	0.42
7:G:115:MET:HB2	7:G:116:PRO:CD	2.44	0.42
8:H:118:PHE:O	8:H:119:GLY:C	2.60	0.42
9:I:55:THR:HG22	9:I:56:ALA:H	1.84	0.42
1:A:274:ILE:C	1:A:276:LEU:N	2.77	0.42
1:A:366:VAL:O	1:A:463:ILE:HG12	2.19	0.42
1:A:533:LYS:HE3	1:A:745:GLN:NE2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:600:PRO:HA	8:H:25:ARG:NH2	2.34	0.42
1:A:693:VAL:O	1:A:693:VAL:HG12	2.18	0.42
1:A:786:HIS:CE1	2:B:519:TRP:CZ2	3.05	0.42
1:A:862:ASN:HA	5:E:174:GLN:O	2.19	0.42
1:A:1152:ILE:HG13	9:I:44:TYR:HD2	1.83	0.42
1:A:1304:TRP:C	1:A:1305:VAL:HG23	2.44	0.42
2:B:591:ARG:O	2:B:593:PRO:HD3	2.19	0.42
2:B:744:HIS:HD2	2:B:746:SER:CB	2.32	0.42
2:B:1003:ALA:HA	3:C:178:PHE:O	2.19	0.42
2:B:1135:ARG:O	2:B:1136:ASP:C	2.61	0.42
3:C:80:LEU:HD11	3:C:96:SER:N	2.33	0.42
5:E:124:VAL:HG13	5:E:132:ILE:CG1	2.50	0.42
9:I:65:ASP:HA	9:I:66:PRO:HD2	1.88	0.42
10:J:1:MET:H2	10:J:55:ASP:HA	1.83	0.42
12:L:32:ALA:CB	12:L:55:ILE:HG13	2.49	0.42
1:A:7:SER:HB2	2:B:1175:LEU:CD2	2.50	0.42
1:A:78:PRO:C	1:A:79:GLY:O	2.62	0.42
1:A:252:PHE:HB2	1:A:256:GLN:HB3	2.01	0.42
1:A:472:LEU:C	1:A:474:VAL:H	2.28	0.42
1:A:532:ARG:HD3	1:A:749:ALA:HB2	2.00	0.42
1:A:716:ASP:OD1	1:A:716:ASP:O	2.37	0.42
1:A:896:ARG:CD	1:A:897:TYR:CE1	2.93	0.42
1:A:1013:ASP:C	1:A:1015:VAL:N	2.76	0.42
1:A:1450:LEU:HD11	6:F:108:PHE:CZ	2.54	0.42
2:B:62:ILE:HG23	2:B:418:LYS:CG	2.49	0.42
2:B:174:LEU:HD11	2:B:204:ILE:CD1	2.49	0.42
2:B:292:ILE:N	2:B:293:PRO:HD2	2.34	0.42
2:B:315:LYS:HE2	9:I:4:PHE:CD2	2.55	0.42
2:B:324:ILE:HG22	2:B:325:GLN:N	2.34	0.42
2:B:431:TYR:CD2	2:B:447:ALA:HB2	2.54	0.42
2:B:496:ARG:HB3	2:B:496:ARG:NH1	2.29	0.42
2:B:515:HIS:CD2	2:B:517:THR:HG23	2.54	0.42
2:B:575:PRO:HG2	2:B:576:ASP:H	1.84	0.42
2:B:805:THR:HA	2:B:809:MET:HE1	2.01	0.42
3:C:41:ILE:HA	3:C:42:PRO:HD3	1.84	0.42
3:C:63:ILE:O	3:C:67:LEU:HG	2.19	0.42
3:C:248:ILE:HG13	3:C:248:ILE:H	1.65	0.42
3:C:258:ILE:HD12	3:C:258:ILE:N	2.35	0.42
7:G:7:LEU:O	7:G:73:LYS:HD2	2.19	0.42
7:G:126:ASN:HD22	7:G:126:ASN:HA	1.64	0.42
11:K:35:PHE:HD1	11:K:35:PHE:H	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:65:HIS:CD2	11:K:67:PHE:HB2	2.54	0.42
11:K:81:TYR:C	11:K:81:TYR:CD2	2.97	0.42
1:A:254:GLU:N	2:B:935:ARG:HH22	2.17	0.42
1:A:304:MET:O	1:A:326:ARG:HB3	2.19	0.42
1:A:324:SER:O	1:A:327:ALA:HB3	2.19	0.42
1:A:675:THR:O	1:A:675:THR:HG22	2.19	0.42
1:A:894:GLU:C	1:A:896:ARG:N	2.78	0.42
1:A:1129:GLU:O	1:A:1131:ALA:N	2.52	0.42
1:A:1143:LEU:HD23	1:A:1267:MET:O	2.19	0.42
1:A:1453:TYR:CE2	6:F:129:LYS:HA	2.54	0.42
2:B:700:SER:O	2:B:701:ILE:HG22	2.20	0.42
5:E:135:PHE:N	5:E:135:PHE:CD1	2.88	0.42
5:E:182:ASP:O	5:E:183:PRO:C	2.63	0.42
6:F:86:THR:HG1	6:F:89:GLU:HG3	1.83	0.42
11:K:47:ARG:C	11:K:47:ARG:HD2	2.44	0.42
1:A:25:GLU:CD	1:A:25:GLU:N	2.75	0.42
1:A:325:ILE:O	1:A:328:ARG:HB2	2.20	0.42
1:A:380:VAL:HG11	1:A:427:GLN:C	2.45	0.42
1:A:453:MET:HE3	1:A:520:CYS:CB	2.50	0.42
1:A:476:SER:O	1:A:477:PRO:C	2.60	0.42
1:A:567:LYS:HB3	8:H:95:TYR:CA	2.48	0.42
1:A:1074:GLU:N	1:A:1075:PRO:CD	2.82	0.42
1:A:1213:GLY:O	1:A:1215:ARG:N	2.53	0.42
1:A:1213:GLY:C	1:A:1215:ARG:N	2.78	0.42
1:A:1373:ASP:HA	1:A:1376:THR:CG2	2.49	0.42
2:B:350:GLN:O	2:B:351:TYR:C	2.61	0.42
2:B:395:GLN:HG2	2:B:396:ASP:H	1.83	0.42
2:B:785:TYR:C	2:B:787:VAL:H	2.28	0.42
2:B:835:GLN:HE21	2:B:835:GLN:HB2	1.57	0.42
2:B:1073:TYR:CD1	2:B:1073:TYR:N	2.87	0.42
3:C:80:LEU:HD12	3:C:95:CYS:HA	2.01	0.42
3:C:251:LEU:O	3:C:252:GLN:C	2.62	0.42
6:F:88:TYR:H	6:F:88:TYR:HD1	1.67	0.42
10:J:21:TYR:HB2	10:J:39:LEU:HD13	2.02	0.42
11:K:95:ILE:O	11:K:96:ASN:C	2.63	0.42
12:L:54:ARG:HG3	12:L:54:ARG:HH11	1.85	0.42
1:A:24:PRO:HG2	1:A:25:GLU:OE1	2.20	0.42
1:A:68:GLN:O	1:A:70:CYS:N	2.43	0.42
1:A:253:ASN:HB2	2:B:935:ARG:NH1	2.34	0.42
1:A:362:ASP:OD2	1:A:362:ASP:N	2.48	0.42
1:A:469:ARG:HH11	1:A:469:ARG:CG	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:472:LEU:O	1:A:475:THR:HG22	2.19	0.42
1:A:475:THR:O	1:A:479:ASN:N	2.53	0.42
1:A:526:ASP:OD2	2:B:829:CYS:HB3	2.20	0.42
1:A:821:ARG:HH11	1:A:821:ARG:CB	2.25	0.42
1:A:830:LYS:HB2	1:A:1081:LEU:CD2	2.43	0.42
1:A:1315:GLU:C	1:A:1317:MET:N	2.74	0.42
1:A:1362:TYR:C	1:A:1363:VAL:HG23	2.44	0.42
2:B:129:PHE:CE2	2:B:166:PHE:HD1	2.34	0.42
2:B:222:ILE:O	2:B:240:ILE:HA	2.19	0.42
2:B:227:LYS:H	2:B:395:GLN:CD	2.27	0.42
2:B:599:THR:O	2:B:603:LEU:HB2	2.20	0.42
2:B:615:MET:HA	2:B:626:ILE:HA	2.01	0.42
2:B:984:HIS:O	2:B:985:GLY:C	2.62	0.42
3:C:91:HIS:CD2	3:C:91:HIS:O	2.72	0.42
3:C:169:LYS:NZ	12:L:69:ALA:CB	2.81	0.42
3:C:241:ASP:O	3:C:244:VAL:HB	2.19	0.42
4:D:33:PHE:CE1	7:G:80:LYS:CE	3.02	0.42
4:D:149:THR:O	4:D:149:THR:HG23	2.20	0.42
10:J:13:VAL:C	10:J:14:VAL:HG23	2.45	0.42
1:A:7:SER:HB2	2:B:1175:LEU:HD22	2.02	0.42
1:A:324:SER:O	1:A:327:ALA:N	2.53	0.42
1:A:695:LYS:O	1:A:697:ALA:N	2.53	0.42
1:A:874:ASP:HA	1:A:1058:VAL:HG23	2.01	0.42
1:A:1001:ARG:HG2	1:A:1001:ARG:HH11	1.83	0.42
1:A:1016:THR:O	1:A:1017:LEU:C	2.62	0.42
1:A:1050:GLU:O	1:A:1050:GLU:HG3	2.18	0.42
1:A:1308:THR:OG1	1:A:1309:ASP:N	2.53	0.42
2:B:259:TYR:N	2:B:259:TYR:CD1	2.88	0.42
2:B:409:ALA:O	2:B:410:GLY:C	2.62	0.42
2:B:730:ARG:O	2:B:731:VAL:O	2.38	0.42
2:B:956:THR:HG22	2:B:960:GLY:HA2	2.02	0.42
2:B:981:ALA:C	2:B:1092:TYR:CD2	2.98	0.42
2:B:1017:ILE:HG22	2:B:1018:PRO:HD3	2.01	0.42
2:B:1073:TYR:HE2	3:C:180:TYR:CE2	2.37	0.42
3:C:62:PHE:C	3:C:62:PHE:HD2	2.27	0.42
3:C:97:VAL:HG12	3:C:98:VAL:H	1.84	0.42
6:F:94:LEU:HD23	6:F:94:LEU:HA	1.64	0.42
6:F:119:ARG:CG	6:F:119:ARG:NH1	2.81	0.42
7:G:39:THR:C	7:G:41:LYS:H	2.28	0.42
7:G:150:CYS:C	7:G:151:ILE:HG13	2.45	0.42
9:I:13:MET:HA	9:I:13:MET:HE3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:55:LYS:HB2	11:K:81:TYR:HE1	1.84	0.42
12:L:31:CYS:SG	12:L:34:CYS:N	2.93	0.42
1:A:282:ASN:O	1:A:284:ALA:N	2.53	0.42
1:A:506:ALA:O	1:A:509:LEU:N	2.51	0.42
1:A:526:ASP:HB3	1:A:657:LEU:HD23	2.01	0.42
1:A:550:LEU:HD22	1:A:556:TRP:CD1	2.55	0.42
1:A:672:ASP:O	1:A:673:GLY:C	2.62	0.42
1:A:738:LYS:HZ2	3:C:194:GLU:CA	2.33	0.42
1:A:757:ASN:O	1:A:761:MET:HG3	2.20	0.42
1:A:960:ILE:O	1:A:960:ILE:HG22	2.20	0.42
1:A:971:PHE:CD1	1:A:971:PHE:N	2.88	0.42
1:A:1271:ILE:O	1:A:1271:ILE:CG2	2.65	0.42
1:A:1300:LYS:H	1:A:1300:LYS:HG3	1.47	0.42
1:A:1348:LEU:HG	1:A:1372:VAL:CG2	2.50	0.42
2:B:114:PRO:HG2	2:B:115:GLN:N	2.29	0.42
2:B:172:ILE:HG22	2:B:173:MET:N	2.35	0.42
2:B:603:LEU:HD13	2:B:608:ASP:HB2	2.00	0.42
2:B:635:ARG:HG3	2:B:635:ARG:NH1	2.35	0.42
2:B:642:ASP:HB3	2:B:649:LYS:CE	2.49	0.42
2:B:644:GLU:O	2:B:646:LEU:N	2.53	0.42
2:B:995:ARG:O	2:B:997:GLU:N	2.52	0.42
2:B:1169:MET:CE	2:B:1201:LYS:CA	2.89	0.42
2:B:1201:LYS:HE2	2:B:1205:GLN:NE2	2.35	0.42
3:C:181:ASP:N	3:C:182:PRO:CD	2.83	0.42
4:D:47:LEU:CD1	7:G:3:PHE:HD2	2.33	0.42
11:K:24:ASP:CG	11:K:74:ARG:NH1	2.77	0.42
1:A:35:ILE:HD12	1:A:241:VAL:CG2	2.50	0.42
1:A:95:PHE:CD1	1:A:234:MET:CG	2.96	0.42
1:A:417:TYR:O	1:A:418:SER:C	2.62	0.42
1:A:460:VAL:CG1	1:A:461:LYS:N	2.79	0.42
1:A:552:TRP:O	1:A:554:PRO:HD3	2.20	0.42
1:A:556:TRP:CD2	1:A:558:GLY:HA2	2.55	0.42
1:A:567:LYS:CE	8:H:46:LEU:HB2	2.50	0.42
1:A:606:LEU:HB3	1:A:614:PHE:CD2	2.55	0.42
1:A:653:VAL:O	1:A:654:ASN:C	2.63	0.42
1:A:1348:LEU:HG	1:A:1372:VAL:HG23	2.01	0.42
1:A:1381:LEU:HD23	1:A:1381:LEU:HA	1.82	0.42
2:B:373:ARG:CG	2:B:566:LEU:HD23	2.50	0.42
2:B:376:PHE:HE2	2:B:569:TYR:HD2	1.65	0.42
2:B:487:THR:CG2	2:B:488:TYR:N	2.82	0.42
2:B:708:GLU:O	2:B:709:ASP:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:900:ALA:O	2:B:901:PRO:C	2.62	0.42
4:D:52:LEU:O	4:D:54:GLU:N	2.46	0.42
5:E:14:ARG:O	5:E:15:ALA:C	2.62	0.42
7:G:30:LEU:HD13	7:G:72:VAL:HG11	2.01	0.42
10:J:6:ARG:HB3	10:J:11:GLY:O	2.20	0.42
1:A:254:GLU:H	2:B:935:ARG:NH1	2.18	0.41
1:A:515:GLN:HB2	1:A:1071:SER:HB3	2.02	0.41
1:A:515:GLN:HB3	1:A:1071:SER:OG	2.20	0.41
1:A:523:ILE:HD12	1:A:622:VAL:CG2	2.49	0.41
1:A:598:LEU:CD2	8:H:25:ARG:NH1	2.83	0.41
1:A:735:VAL:O	1:A:735:VAL:HG12	2.18	0.41
2:B:57:TYR:O	2:B:58:THR:C	2.63	0.41
2:B:247:GLY:C	2:B:249:ARG:N	2.78	0.41
2:B:293:PRO:CG	2:B:296:GLU:OE1	2.68	0.41
2:B:386:LEU:O	2:B:387:LEU:C	2.63	0.41
2:B:581:PHE:HB2	2:B:624:LEU:O	2.20	0.41
2:B:824:ILE:HG22	2:B:1087:PHE:CE2	2.55	0.41
2:B:952:VAL:CG1	2:B:953:LEU:H	2.31	0.41
7:G:27:LYS:HE2	7:G:54:ILE:HB	2.02	0.41
8:H:58:THR:HG22	8:H:59:ILE:N	2.34	0.41
9:I:90:GLN:O	9:I:92:ARG:N	2.48	0.41
10:J:47:ARG:HH11	10:J:47:ARG:HG2	1.85	0.41
1:A:58:LEU:O	1:A:59:GLY:O	2.36	0.41
1:A:90:VAL:HG12	1:A:91:PHE:O	2.20	0.41
1:A:125:ALA:C	1:A:127:ALA:N	2.78	0.41
1:A:262:LEU:HD22	1:A:303:TYR:CE1	2.55	0.41
1:A:320:ARG:HH21	1:A:323:LYS:NZ	2.18	0.41
1:A:483:ASP:OD2	1:A:485:ASP:OD1	2.38	0.41
1:A:527:THR:O	1:A:653:VAL:HG11	2.19	0.41
1:A:540:PHE:CB	1:A:571:LEU:HD23	2.39	0.41
1:A:738:LYS:NZ	3:C:194:GLU:C	2.78	0.41
1:A:845:LEU:O	1:A:846:GLU:C	2.61	0.41
2:B:31:TRP:CE3	2:B:31:TRP:HA	2.55	0.41
2:B:247:GLY:N	2:B:418:LYS:HZ3	2.16	0.41
2:B:570:VAL:HA	2:B:571:PRO:HD2	1.78	0.41
2:B:628:THR:O	2:B:629:ASP:O	2.38	0.41
2:B:770:GLN:OE1	2:B:983:ARG:HA	2.20	0.41
2:B:976:ILE:HG22	2:B:977:GLY:N	2.34	0.41
2:B:1115:THR:O	2:B:1116:ARG:CB	2.65	0.41
2:B:1147:LEU:C	2:B:1147:LEU:CD2	2.93	0.41
7:G:132:SER:C	7:G:134:GLU:N	2.77	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:115:TYR:CE2	8:H:124:ARG:HG3	2.54	0.41
11:K:24:ASP:CG	11:K:74:ARG:HH11	2.28	0.41
1:A:53:LEU:HD23	1:A:53:LEU:C	2.42	0.41
1:A:503:GLN:HE21	6:F:90:ARG:NH2	2.02	0.41
1:A:825:ILE:O	1:A:827:THR:N	2.52	0.41
1:A:900:ASP:HA	1:A:926:GLN:NE2	2.35	0.41
2:B:57:TYR:HD1	2:B:57:TYR:H	1.67	0.41
2:B:90:ILE:HD11	2:B:432:MET:SD	2.60	0.41
2:B:508:LEU:HB3	2:B:510:LYS:N	2.25	0.41
2:B:542:MET:HE3	2:B:636:PRO:CG	2.50	0.41
2:B:634:TYR:HE1	2:B:692:TYR:CD1	2.38	0.41
2:B:637:LEU:HD21	2:B:742:GLU:OE2	2.20	0.41
2:B:798:TYR:HE2	3:C:62:PHE:CE2	2.37	0.41
2:B:849:GLY:O	2:B:852:ARG:HG3	2.20	0.41
2:B:898:LEU:HB2	12:L:58:LYS:HZ3	1.81	0.41
2:B:1032:SER:O	2:B:1034:VAL:N	2.53	0.41
2:B:1098:MET:O	2:B:1101:ASP:HB2	2.19	0.41
3:C:217:ASP:HA	3:C:218:PRO:HD3	1.95	0.41
8:H:104:PHE:HZ	8:H:135:LEU:O	2.04	0.41
1:A:216:VAL:O	1:A:219:PHE:HB2	2.20	0.41
1:A:299:HIS:C	1:A:301:ALA:H	2.28	0.41
1:A:639:PRO:HG2	1:A:640:GLN:H	1.85	0.41
1:A:714:PHE:HD2	9:I:97:MET:HE1	1.81	0.41
1:A:870:GLU:HG2	5:E:208:TYR:CE2	2.55	0.41
1:A:900:ASP:HA	1:A:926:GLN:HE22	1.84	0.41
1:A:1164:PRO:C	1:A:1166:ASP:H	2.28	0.41
1:A:1192:LEU:CG	1:A:1193:LEU:N	2.81	0.41
2:B:121:ASN:HA	2:B:207:GLY:HA2	2.02	0.41
3:C:66:ARG:NH2	10:J:5:VAL:CG2	2.84	0.41
3:C:98:VAL:O	3:C:99:LEU:HD23	2.18	0.41
3:C:241:ASP:HB3	11:K:109:TRP:CH2	2.55	0.41
4:D:50:LEU:HD11	7:G:4:ILE:CG1	2.51	0.41
5:E:42:PHE:CE1	5:E:58:MET:HE3	2.55	0.41
5:E:137:GLU:C	5:E:139:ALA:H	2.29	0.41
5:E:147:HIS:HD2	5:E:149:LEU:H	1.68	0.41
6:F:90:ARG:HG3	6:F:91:ALA:N	2.35	0.41
10:J:21:TYR:HB2	10:J:39:LEU:CD1	2.51	0.41
11:K:58:PHE:CB	11:K:76:GLN:HE21	2.32	0.41
11:K:65:HIS:NE2	11:K:67:PHE:CG	2.88	0.41
12:L:50:ASP:HB3	12:L:51:CYS:H	1.58	0.41
1:A:596:THR:O	1:A:597:LEU:C	2.61	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:186:GLU:O	2:B:189:LEU:HB2	2.21	0.41
2:B:233:PRO:HG2	2:B:234:ILE:HD12	2.03	0.41
2:B:240:ILE:CG2	2:B:240:ILE:O	2.69	0.41
2:B:258:LEU:HG	2:B:258:LEU:O	2.19	0.41
2:B:295:GLY:HA2	2:B:298:LEU:HB2	2.01	0.41
2:B:515:HIS:HD2	2:B:517:THR:N	2.12	0.41
2:B:515:HIS:CG	2:B:516:ASN:N	2.88	0.41
2:B:792:MET:O	2:B:793:ALA:HB2	2.20	0.41
2:B:809:MET:O	2:B:811:TYR:N	2.54	0.41
2:B:1152:MET:C	2:B:1154:ALA:N	2.79	0.41
2:B:1216:LEU:C	2:B:1217:TYR:HD1	2.28	0.41
3:C:187:LYS:HG3	3:C:219:PHE:CE1	2.55	0.41
3:C:249:ASP:O	3:C:252:GLN:N	2.53	0.41
5:E:124:VAL:HB	5:E:125:PRO:CD	2.50	0.41
7:G:13:LEU:HD12	7:G:26:LEU:HD21	2.03	0.41
7:G:101:VAL:HG12	7:G:102:GLN:N	2.32	0.41
10:J:18:TRP:HA	10:J:18:TRP:HE3	1.85	0.41
1:A:16:GLU:HB3	1:A:1418:LEU:HD11	2.02	0.41
1:A:42:ASP:HB3	1:A:45:GLN:N	2.33	0.41
1:A:52:GLY:N	1:A:56:PRO:HG3	2.35	0.41
1:A:69:THR:O	1:A:70:CYS:C	2.63	0.41
1:A:92:HIS:HB3	1:A:95:PHE:HB2	2.02	0.41
1:A:493:GLN:HE21	1:A:493:GLN:CA	2.33	0.41
1:A:518:LYS:HE2	1:A:624:SER:O	2.20	0.41
1:A:562:THR:HA	1:A:563:PRO:HD3	1.84	0.41
1:A:630:ILE:HG23	1:A:642:CYS:SG	2.60	0.41
1:A:723:ASN:O	1:A:724:GLU:C	2.64	0.41
1:A:785:PRO:O	2:B:702:LEU:HD12	2.21	0.41
1:A:1006:ILE:CD1	5:E:163:GLU:HG3	2.51	0.41
1:A:1157:ASP:C	1:A:1159:ARG:N	2.78	0.41
1:A:1369:ALA:O	1:A:1370:LEU:C	2.64	0.41
2:B:274:PRO:CG	2:B:359:GLU:HB3	2.51	0.41
2:B:410:GLY:O	2:B:411:PRO:C	2.62	0.41
2:B:418:LYS:O	2:B:419:THR:C	2.64	0.41
2:B:785:TYR:HE2	10:J:60:PHE:CZ	2.38	0.41
2:B:866:TYR:O	2:B:868:MET:N	2.53	0.41
2:B:952:VAL:O	2:B:953:LEU:HB3	2.20	0.41
2:B:973:ILE:CG2	2:B:974:PRO:HD2	2.51	0.41
2:B:1072:MET:CE	2:B:1085:ILE:HB	2.50	0.41
2:B:1115:THR:CG2	2:B:1117:GLN:HB2	2.50	0.41
2:B:1145:SER:O	2:B:1146:PHE:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1192:TYR:CD1	2:B:1192:TYR:N	2.89	0.41
4:D:52:LEU:C	4:D:54:GLU:N	2.75	0.41
5:E:114:ASN:O	5:E:115:ASN:CB	2.68	0.41
8:H:96:VAL:HA	8:H:142:LEU:O	2.21	0.41
9:I:16:PRO:HA	9:I:26:LEU:O	2.21	0.41
10:J:14:VAL:CG1	10:J:50:ILE:CD1	2.90	0.41
12:L:53:HIS:O	12:L:55:ILE:HG12	2.20	0.41
1:A:96:ILE:O	1:A:97:ALA:C	2.63	0.41
1:A:322:VAL:CG1	1:A:323:LYS:N	2.82	0.41
1:A:334:GLY:O	1:A:335:ARG:C	2.63	0.41
1:A:370:ILE:HG22	1:A:374:LEU:HD12	2.00	0.41
1:A:455:MET:HE1	2:B:1134:GLU:HB3	2.03	0.41
1:A:704:ALA:O	1:A:705:LYS:CB	2.66	0.41
1:A:726:ARG:O	1:A:729:ALA:N	2.53	0.41
1:A:1291:VAL:HG13	1:A:1292:PRO:N	2.36	0.41
1:A:1362:TYR:CE1	1:A:1364:ASN:HA	2.56	0.41
1:A:1451:VAL:O	1:A:1453:TYR:N	2.54	0.41
2:B:544:CYS:O	2:B:545:ILE:CG1	2.68	0.41
2:B:788:ARG:HE	2:B:788:ARG:HB3	1.52	0.41
2:B:830:TYR:CE2	2:B:1000:PRO:CD	2.93	0.41
2:B:1013:ASN:OD1	2:B:1014:PRO:HD2	2.21	0.41
3:C:59:ALA:O	3:C:62:PHE:CB	2.67	0.41
3:C:167:HIS:CD2	3:C:167:HIS:C	2.98	0.41
9:I:101:PHE:O	9:I:102:VAL:CG2	2.67	0.41
11:K:50:LEU:HD11	11:K:75:ILE:HD11	2.03	0.41
11:K:83:PRO:O	11:K:84:LYS:C	2.63	0.41
1:A:44:THR:O	1:A:45:GLN:CB	2.65	0.41
1:A:107:CYS:HB2	1:A:171:GLN:HG2	2.01	0.41
1:A:208:LEU:O	1:A:209:ASN:C	2.64	0.41
1:A:899:VAL:O	1:A:929:LEU:HD12	2.21	0.41
1:A:1279:ILE:CD1	1:A:1316:VAL:HG21	2.48	0.41
1:A:1436:ILE:HD13	2:B:1139:ILE:CG2	2.45	0.41
2:B:216:GLU:HB2	2:B:406:LEU:CD2	2.51	0.41
2:B:329:THR:O	2:B:332:ASP:HB3	2.21	0.41
2:B:360:PHE:CE2	2:B:361:LEU:HB2	2.55	0.41
2:B:408:LEU:HD12	2:B:408:LEU:HA	1.75	0.41
2:B:526:GLU:HG2	2:B:538:ASN:HB2	2.01	0.41
3:C:18:VAL:O	3:C:20:PHE:CD2	2.73	0.41
3:C:61:GLU:HG2	3:C:62:PHE:N	2.36	0.41
3:C:235:VAL:HG21	10:J:6:ARG:HH21	1.85	0.41
4:D:26:THR:C	4:D:28:GLN:N	2.75	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:34:GLN:O	4:D:47:LEU:HD23	2.21	0.41
4:D:40:HIS:CG	4:D:41:GLN:N	2.89	0.41
5:E:66:GLU:HA	5:E:69:ILE:HD12	2.02	0.41
7:G:39:THR:HB	7:G:42:PHE:H	1.86	0.41
9:I:45:ARG:HE	9:I:47:GLU:HG3	1.85	0.41
1:A:41:MET:HB2	1:A:42:ASP:H	1.46	0.41
1:A:225:ASN:HD21	1:A:228:PHE:H	1.54	0.41
1:A:335:ARG:NE	1:A:339:ASN:ND2	2.57	0.41
1:A:420:ARG:O	1:A:424:ILE:HG13	2.21	0.41
1:A:501:LEU:HD11	2:B:1146:PHE:CE2	2.56	0.41
1:A:546:VAL:HG21	1:A:572:TRP:CD2	2.55	0.41
1:A:763:ALA:C	1:A:803:SER:HB3	2.45	0.41
1:A:863:VAL:CG1	1:A:864:ILE:N	2.84	0.41
1:A:1037:LEU:N	1:A:1037:LEU:HD23	2.36	0.41
1:A:1142:THR:O	1:A:1143:LEU:C	2.62	0.41
1:A:1212:VAL:O	1:A:1213:GLY:C	2.63	0.41
1:A:1438:THR:CG2	2:B:1144:ALA:HB3	2.51	0.41
2:B:102:VAL:O	2:B:109:THR:HG23	2.21	0.41
2:B:419:THR:HG21	2:B:468:GLU:OE2	2.20	0.41
2:B:510:LYS:HE2	2:B:513:GLN:OE1	2.21	0.41
2:B:515:HIS:HD2	2:B:517:THR:OG1	2.03	0.41
2:B:535:LEU:HD23	2:B:535:LEU:HA	1.87	0.41
2:B:624:LEU:HD12	2:B:624:LEU:HA	1.79	0.41
2:B:642:ASP:HB3	2:B:649:LYS:HG3	2.03	0.41
2:B:642:ASP:C	2:B:644:GLU:N	2.79	0.41
2:B:824:ILE:CG1	10:J:48:ARG:NH1	2.79	0.41
2:B:857:ARG:O	2:B:858:SER:HB3	2.21	0.41
2:B:996:ARG:HH22	3:C:175:ALA:CA	2.34	0.41
2:B:1039:GLY:HA2	10:J:51:LEU:CD2	2.50	0.41
2:B:1065:GLN:HG3	2:B:1068:GLY:N	2.35	0.41
3:C:191:TYR:HB3	3:C:201:TRP:CD1	2.56	0.41
4:D:29:LEU:O	4:D:30:GLY:O	2.39	0.41
4:D:50:LEU:HD11	7:G:4:ILE:HG13	2.03	0.41
5:E:112:TYR:CE1	5:E:136:ASN:HB2	2.56	0.41
5:E:143:ASN:ND2	5:E:146:HIS:ND1	2.68	0.41
6:F:143:PHE:C	6:F:143:PHE:HD1	2.28	0.41
7:G:1:MET:SD	7:G:1:MET:C	3.04	0.41
7:G:1:MET:SD	7:G:79:PHE:CE1	3.14	0.41
7:G:45:ILE:HD13	7:G:45:ILE:HA	1.99	0.41
7:G:80:LYS:CE	7:G:82:PHE:CZ	2.98	0.41
7:G:80:LYS:HA	7:G:81:PRO:HD2	1.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:97:HIS:CD2	7:G:97:HIS:N	2.88	0.41
7:G:132:SER:O	7:G:134:GLU:N	2.54	0.41
9:I:40:SER:HB2	9:I:41:PRO:HD2	2.03	0.41
10:J:43:ARG:HG2	10:J:46:CYS:SG	2.61	0.41
10:J:57:ILE:CG2	10:J:58:GLU:N	2.84	0.41
11:K:12:LEU:HD11	11:K:18:LYS:HE2	2.02	0.41
1:A:7:SER:CB	2:B:1175:LEU:HD22	2.51	0.41
1:A:114:LEU:O	1:A:115:LEU:HG	2.20	0.41
1:A:239:LEU:HA	1:A:240:PRO:HD2	1.88	0.41
1:A:547:LEU:HD22	11:K:58:PHE:HD1	1.85	0.41
1:A:1315:GLU:C	1:A:1317:MET:H	2.29	0.41
1:A:1327:ILE:HG22	5:E:147:HIS:HE1	1.85	0.41
1:A:1365:TYR:O	1:A:1367:HIS:N	2.54	0.41
1:A:1419:ASP:OD1	1:A:1426:GLU:OE1	2.39	0.41
2:B:27:ALA:O	2:B:30:SER:OG	2.29	0.41
2:B:179:CYS:C	2:B:181:LEU:N	2.78	0.41
2:B:311:LEU:O	2:B:312:GLU:C	2.64	0.41
2:B:349:ILE:O	2:B:349:ILE:HG22	2.20	0.41
2:B:1004:GLU:CB	2:B:1006:ILE:HD11	2.51	0.41
2:B:1187:ASN:HD21	2:B:1190:ASP:HB3	1.86	0.41
3:C:69:LEU:O	3:C:70:ILE:C	2.63	0.41
3:C:80:LEU:CD1	3:C:95:CYS:CA	2.99	0.41
3:C:247:GLY:C	3:C:249:ASP:H	2.29	0.41
4:D:33:PHE:CD1	7:G:80:LYS:HE3	2.55	0.41
4:D:151:PHE:O	4:D:152:SER:O	2.38	0.41
4:D:217:LEU:O	4:D:219:THR:N	2.54	0.41
5:E:29:PHE:N	5:E:63:ASN:O	2.47	0.41
5:E:116:ILE:HG22	5:E:117:THR:N	2.35	0.41
6:F:75:PRO:HG3	6:F:78:GLN:OE1	2.21	0.41
8:H:3:ASN:HB3	8:H:4:THR:H	1.61	0.41
1:A:34:LYS:H	1:A:34:LYS:HD3	1.86	0.40
1:A:40:THR:CG2	1:A:259:GLU:OE2	2.64	0.40
1:A:88:LYS:HA	1:A:89:PRO:HD2	1.72	0.40
1:A:151:ASP:OD1	1:A:163:SER:CB	2.68	0.40
1:A:218:ASP:HA	1:A:221:SER:OG	2.21	0.40
1:A:310:GLY:C	1:A:312:PRO:HD2	2.45	0.40
1:A:391:LEU:O	1:A:394:ASN:HB2	2.21	0.40
1:A:1007:ILE:H	1:A:1007:ILE:HG12	1.73	0.40
1:A:1027:ALA:O	1:A:1030:ARG:N	2.54	0.40
1:A:1114:PRO:O	1:A:1115:SER:O	2.38	0.40
1:A:1120:LEU:N	1:A:1120:LEU:HD12	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1217:LYS:C	1:A:1219:THR:H	2.28	0.40
1:A:1450:LEU:HD21	7:G:19:GLY:O	2.20	0.40
2:B:113:TYR:CB	2:B:114:PRO:HD2	2.38	0.40
2:B:408:LEU:O	2:B:412:LEU:HG	2.21	0.40
2:B:510:LYS:HG3	2:B:512:ARG:HD2	2.03	0.40
2:B:661:LEU:C	2:B:663:ALA:H	2.29	0.40
2:B:903:VAL:O	2:B:948:ILE:HG23	2.21	0.40
2:B:1060:ARG:C	2:B:1062:HIS:N	2.76	0.40
4:D:173:HIS:HA	4:D:174:PRO:HD3	1.95	0.40
5:E:112:TYR:HE1	5:E:136:ASN:HD22	1.69	0.40
5:E:159:ASP:C	5:E:161:LYS:N	2.76	0.40
6:F:134:ILE:N	6:F:146:TRP:O	2.50	0.40
7:G:143:ILE:HG22	7:G:144:ARG:H	1.86	0.40
10:J:1:MET:N	10:J:55:ASP:HA	2.36	0.40
10:J:2:ILE:HG12	10:J:57:ILE:CD1	2.46	0.40
11:K:85:ASP:O	11:K:89:ASN:ND2	2.53	0.40
12:L:32:ALA:HB3	12:L:55:ILE:CG1	2.52	0.40
1:A:519:PRO:HG2	1:A:624:SER:C	2.46	0.40
1:A:541:ILE:CD1	1:A:577:ILE:HD11	2.51	0.40
1:A:651:LYS:O	1:A:652:VAL:C	2.64	0.40
1:A:786:HIS:N	1:A:786:HIS:HD2	2.17	0.40
1:A:788:SER:O	1:A:789:LYS:C	2.63	0.40
1:A:825:ILE:O	1:A:828:ALA:N	2.49	0.40
1:A:839:ARG:O	1:A:842:VAL:HB	2.21	0.40
1:A:1187:GLN:HG3	1:A:1188:GLN:H	1.85	0.40
1:A:1191:TRP:HD1	1:A:1256:GLU:CB	2.35	0.40
2:B:38:PHE:CE2	2:B:43:LEU:HD23	2.57	0.40
2:B:187:SER:O	2:B:188:ASP:C	2.64	0.40
2:B:331:LEU:HD12	2:B:331:LEU:N	2.37	0.40
2:B:530:GLY:O	2:B:532:ALA:N	2.54	0.40
2:B:711:GLU:N	2:B:712:PRO:HD2	2.35	0.40
2:B:843:GLN:HA	2:B:846:ILE:HG13	2.02	0.40
2:B:847:ASP:O	2:B:849:GLY:N	2.55	0.40
2:B:873:THR:CG2	2:B:874:PHE:N	2.84	0.40
2:B:1007:VAL:HG23	2:B:1008:PRO:HD2	1.96	0.40
2:B:1183:LYS:HA	2:B:1186:ASP:HA	2.04	0.40
3:C:8:VAL:CG1	3:C:9:LYS:N	2.83	0.40
3:C:143:LEU:C	3:C:143:LEU:CD1	2.94	0.40
4:D:55:ALA:O	4:D:56:ARG:C	2.64	0.40
4:D:173:HIS:NE2	4:D:201:LYS:NZ	2.68	0.40
10:J:57:ILE:O	10:J:58:GLU:C	2.63	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:20:LYS:HB2	11:K:20:LYS:HE3	1.89	0.40
1:A:135:PHE:O	1:A:137:ALA:N	2.54	0.40
1:A:206:GLU:O	1:A:207:ILE:C	2.64	0.40
1:A:241:VAL:HA	1:A:242:PRO:HD2	1.92	0.40
1:A:289:ILE:HG22	1:A:290:GLU:N	2.37	0.40
1:A:351:THR:CG2	2:B:1103:ILE:HA	2.39	0.40
1:A:356:ASP:C	1:A:358:ASN:N	2.80	0.40
1:A:369:SER:HB3	11:K:2:ASN:HD21	1.86	0.40
1:A:470:LEU:HD12	1:A:470:LEU:C	2.46	0.40
1:A:477:PRO:HG3	1:A:521:MET:HG2	2.03	0.40
1:A:889:SER:C	1:A:891:ALA:H	2.29	0.40
1:A:932:GLU:HG3	1:A:936:LEU:HD21	2.02	0.40
1:A:1063:MET:SD	1:A:1436:ILE:HG23	2.61	0.40
1:A:1138:ILE:CG2	1:A:1316:VAL:HG13	2.52	0.40
1:A:1164:PRO:CG	1:A:1165:GLU:H	2.33	0.40
2:B:351:TYR:O	2:B:355:ILE:HG13	2.20	0.40
2:B:842:ASN:O	2:B:846:ILE:HG13	2.21	0.40
2:B:912:ILE:O	2:B:938:SER:HB3	2.22	0.40
2:B:1027:ILE:HD13	2:B:1052:VAL:CG2	2.51	0.40
2:B:1147:LEU:C	2:B:1149:GLU:N	2.76	0.40
3:C:61:GLU:HA	3:C:64:ALA:CB	2.52	0.40
3:C:229:TYR:CD1	3:C:229:TYR:N	2.89	0.40
5:E:114:ASN:HD22	5:E:114:ASN:HA	1.65	0.40
6:F:79:ARG:NH1	6:F:79:ARG:HG2	2.35	0.40
6:F:106:PRO:HG2	7:G:18:PHE:C	2.46	0.40
7:G:5:LYS:CG	7:G:7:LEU:HD21	2.51	0.40
8:H:13:SER:O	8:H:14:GLU:HB2	2.22	0.40
11:K:84:LYS:H	11:K:84:LYS:HG3	1.70	0.40
1:A:605:MET:HB2	1:A:605:MET:HE3	1.74	0.40
1:A:711:ARG:O	1:A:714:PHE:HB3	2.21	0.40
1:A:741:ASN:ND2	1:A:743:VAL:HB	2.36	0.40
1:A:1016:THR:C	1:A:1018:PHE:N	2.80	0.40
1:A:1061:GLY:O	1:A:1062:GLU:C	2.64	0.40
1:A:1067:LEU:HD12	1:A:1067:LEU:C	2.46	0.40
1:A:1211:GLN:O	1:A:1214:GLU:HB2	2.21	0.40
2:B:218:SER:HB3	2:B:241:ARG:HH11	1.87	0.40
2:B:1083:ALA:C	2:B:1084:GLN:NE2	2.80	0.40
3:C:88:CYS:HB3	3:C:92:CYS:HB3	2.02	0.40
3:C:102:GLN:HA	3:C:153:LEU:O	2.22	0.40
3:C:166:GLU:C	11:K:6:ARG:NH1	2.80	0.40
6:F:97:ARG:O	6:F:100:GLN:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:34:TYR:HE2	9:I:36:GLU:CB	2.32	0.40
10:J:35:ALA:O	10:J:38:ARG:HB3	2.21	0.40
11:K:87:LEU:O	11:K:88:LYS:C	2.65	0.40
12:L:32:ALA:HB3	12:L:55:ILE:HG13	2.03	0.40
1:A:57:ARG:C	1:A:58:LEU:O	2.64	0.40
1:A:114:LEU:HD13	1:A:171:GLN:HE22	1.86	0.40
1:A:335:ARG:HA	1:A:339:ASN:HD22	1.86	0.40
1:A:706:HIS:CD2	1:A:706:HIS:H	2.38	0.40
1:A:867:ILE:HG22	1:A:871:ASP:H	1.85	0.40
1:A:967:ALA:HA	1:A:1044:TRP:CZ3	2.56	0.40
1:A:1147:THR:HG22	1:A:1148:ILE:N	2.36	0.40
1:A:1260:LEU:HG	1:A:1260:LEU:O	2.20	0.40
1:A:1427:ASN:C	1:A:1429:ILE:N	2.77	0.40
2:B:121:ASN:HA	2:B:207:GLY:CA	2.51	0.40
2:B:619:ILE:C	2:B:621:GLU:N	2.80	0.40
2:B:635:ARG:HH11	2:B:635:ARG:CG	2.33	0.40
2:B:814:PHE:C	2:B:816:GLU:N	2.76	0.40
2:B:1072:MET:HE2	2:B:1085:ILE:HB	2.02	0.40
3:C:92:CYS:SG	3:C:95:CYS:N	2.95	0.40
4:D:188:ALA:O	4:D:191:ALA:N	2.55	0.40
7:G:5:LYS:HG3	7:G:7:LEU:HD21	2.03	0.40
8:H:87:ARG:HB3	8:H:88:SER:H	1.81	0.40
9:I:8:ARG:HB2	9:I:9:ASP:OD1	2.22	0.40
11:K:55:LYS:O	11:K:77:THR:HG22	2.20	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	1418/1455 (98%)	914 (64%)	316 (22%)	188 (13%)	0 4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	1096/1224 (90%)	725 (66%)	223 (20%)	148 (14%)	0	4
3	C	264/268 (98%)	169 (64%)	62 (24%)	33 (12%)	0	4
4	D	173/221 (78%)	129 (75%)	27 (16%)	17 (10%)	0	7
5	E	212/215 (99%)	141 (66%)	50 (24%)	21 (10%)	0	7
6	F	82/84 (98%)	60 (73%)	15 (18%)	7 (8%)	0	9
7	G	169/171 (99%)	123 (73%)	34 (20%)	12 (7%)	1	11
8	H	129/146 (88%)	93 (72%)	25 (19%)	11 (8%)	0	9
9	I	117/122 (96%)	80 (68%)	22 (19%)	15 (13%)	0	4
10	J	63/70 (90%)	36 (57%)	14 (22%)	13 (21%)	0	2
11	K	112/120 (93%)	82 (73%)	25 (22%)	5 (4%)	2	17
12	L	44/46 (96%)	18 (41%)	14 (32%)	12 (27%)	0	0
All	All	3879/4142 (94%)	2570 (66%)	827 (21%)	482 (12%)	1	4

All (482) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	GLN
1	A	48	ALA
1	A	55	ASP
1	A	58	LEU
1	A	62	ASP
1	A	70	CYS
1	A	73	GLY
1	A	76	GLU
1	A	93	VAL
1	A	130	ASP
1	A	286	HIS
1	A	311	GLN
1	A	322	VAL
1	A	385	ILE
1	A	399	HIS
1	A	423	ASP
1	A	516	SER
1	A	525	GLN
1	A	536	LEU
1	A	567	LYS
1	A	583	PRO
1	A	626	ASN

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Mol	Chain	Res	Type
1	A	708	MET
1	A	709	THR
1	A	780	VAL
1	A	821	ARG
1	A	920	LEU
1	A	1002	GLY
1	A	1036	ARG
1	A	1115	SER
1	A	1122	PRO
1	A	1124	HIS
1	A	1165	GLU
1	A	1167	GLU
1	A	1212	VAL
1	A	1223	ASP
1	A	1231	ASP
1	A	1242	VAL
1	A	1281	ARG
1	A	1308	THR
1	A	1309	ASP
1	A	1335	ILE
1	A	1341	ILE
1	A	1366	ARG
1	A	1377	THR
1	A	1378	GLN
1	A	1386	ARG
1	A	1392	SER
1	A	1396	ALA
1	A	1397	LEU
1	A	1403	GLU
1	A	1405	THR
1	A	1424	VAL
2	B	43	LEU
2	B	45	SER
2	B	58	THR
2	B	67	SER
2	B	108	VAL
2	B	124	TYR
2	B	186	GLU
2	B	219	ALA
2	B	261	ARG
2	B	367	LEU
2	B	391	ASP

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Mol	Chain	Res	Type
2	B	466	TRP
2	B	467	GLY
2	B	468	GLU
2	B	474	SER
2	B	510	LYS
2	B	530	GLY
2	B	531	GLN
2	B	571	PRO
2	B	591	ARG
2	B	620	ARG
2	B	629	ASP
2	B	636	PRO
2	B	643	ASP
2	B	648	HIS
2	B	709	ASP
2	B	727	LYS
2	B	731	VAL
2	B	751	VAL
2	B	752	ALA
2	B	818	PRO
2	B	901	PRO
2	B	903	VAL
2	B	943	SER
2	B	958	GLN
2	B	992	ILE
2	B	1046	PRO
2	B	1108	ARG
2	B	1157	ALA
2	B	1167	GLY
2	B	1171	VAL
2	B	1175	LEU
2	B	1181	GLU
2	B	1188	LYS
2	B	1211	ASN
3	C	10	ILE
3	C	60	ASP
3	C	81	GLU
3	C	83	SER
3	C	87	PHE
3	C	110	THR
3	C	149	LYS
3	C	167	HIS

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Mol	Chain	Res	Type
3	C	175	ALA
3	C	184	ASN
3	C	213	PRO
3	C	214	ASN
3	C	215	GLU
3	C	216	GLY
4	D	12	ARG
4	D	15	LEU
4	D	20	GLU
4	D	152	SER
5	E	130	ALA
5	E	158	SER
6	F	81	THR
7	G	118	ASP
8	H	81	PRO
8	H	84	ALA
8	H	140	ALA
9	I	9	ASP
9	I	11	ASN
9	I	84	VAL
10	J	6	ARG
10	J	15	GLY
10	J	53	HIS
10	J	64	ASN
12	L	50	ASP
12	L	53	HIS
12	L	59	ALA
12	L	60	ARG
1	A	42	ASP
1	A	44	THR
1	A	45	GLN
1	A	54	ASN
1	A	57	ARG
1	A	61	ILE
1	A	74	MET
1	A	79	GLY
1	A	111	GLY
1	A	126	LEU
1	A	131	SER
1	A	154	SER
1	A	219	PHE
1	A	223	GLY

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Mol	Chain	Res	Type
1	A	244	PRO
1	A	290	GLU
1	A	317	LYS
1	A	318	SER
1	A	331	GLY
1	A	332	LYS
1	A	335	ARG
1	A	400	PRO
1	A	415	LEU
1	A	418	SER
1	A	419	LYS
1	A	424	ILE
1	A	473	SER
1	A	557	ASP
1	A	594	GLY
1	A	598	LEU
1	A	619	LYS
1	A	716	ASP
1	A	720	ARG
1	A	738	LYS
1	A	760	GLN
1	A	765	VAL
1	A	775	ILE
1	A	824	LEU
1	A	846	GLU
1	A	847	ASP
1	A	859	SER
1	A	864	ILE
1	A	875	ALA
1	A	929	LEU
1	A	968	GLN
1	A	979	SER
1	A	1006	ILE
1	A	1016	THR
1	A	1052	GLN
1	A	1084	PHE
1	A	1089	VAL
1	A	1104	ILE
1	A	1105	LEU
1	A	1126	ALA
1	A	1128	GLN
1	A	1164	PRO

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Mol	Chain	Res	Type
1	A	1168	GLU
1	A	1169	ILE
1	A	1170	ILE
1	A	1224	LEU
1	A	1314	SER
1	A	1365	TYR
1	A	1376	THR
2	B	21	GLU
2	B	46	GLN
2	B	65	GLU
2	B	68	THR
2	B	114	PRO
2	B	229	ALA
2	B	258	LEU
2	B	260	GLY
2	B	266	ALA
2	B	294	ASP
2	B	322	PHE
2	B	504	ARG
2	B	509	ALA
2	B	526	GLU
2	B	534	GLY
2	B	559	SER
2	B	605	ARG
2	B	613	VAL
2	B	641	GLU
2	B	810	GLU
2	B	867	GLY
2	B	869	SER
2	B	880	THR
2	B	881	ASN
2	B	891	ASP
2	B	902	GLY
2	B	907	GLY
2	B	1018	PRO
2	B	1041	GLU
2	B	1096	ARG
2	B	1099	VAL
2	B	1150	ARG
2	B	1156	ASP
2	B	1170	THR
2	B	1183	LYS

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Mol	Chain	Res	Type
2	B	1186	ASP
2	B	1190	ASP
3	C	74	SER
3	C	141	GLY
3	C	161	LYS
4	D	6	SER
4	D	8	PHE
4	D	16	LYS
4	D	19	GLU
4	D	30	GLY
4	D	199	ASN
4	D	218	GLU
5	E	36	GLU
5	E	45	LYS
5	E	59	SER
5	E	106	GLN
5	E	145	THR
5	E	189	GLY
5	E	206	GLY
6	F	131	PRO
7	G	83	LYS
7	G	154	VAL
8	H	59	ILE
8	H	77	ARG
8	H	82	PRO
8	H	108	SER
8	H	128	ASN
9	I	3	THR
9	I	34	TYR
9	I	62	ILE
9	I	89	GLN
9	I	106	CYS
9	I	107	SER
10	J	2	ILE
10	J	62	ARG
11	K	37	LYS
11	K	103	THR
12	L	43	THR
12	L	51	CYS
12	L	56	LEU
1	A	59	GLY
1	A	66	LYS

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Mol	Chain	Res	Type
1	A	89	PRO
1	A	124	GLN
1	A	167	CYS
1	A	283	GLY
1	A	394	ASN
1	A	396	PRO
1	A	517	ASN
1	A	543	LEU
1	A	592	ASP
1	A	640	GLN
1	A	647	GLY
1	A	707	GLY
1	A	731	ARG
1	A	774	ARG
1	A	903	ASN
1	A	1017	LEU
1	A	1060	PRO
1	A	1062	GLU
1	A	1131	ALA
1	A	1221	LYS
1	A	1229	SER
1	A	1452	LYS
2	B	115	GLN
2	B	131	ASP
2	B	176	SER
2	B	206	ASN
2	B	295	GLY
2	B	308	TRP
2	B	334	ILE
2	B	365	THR
2	B	369	GLY
2	B	469	GLN
2	B	480	SER
2	B	551	PRO
2	B	598	GLU
2	B	645	SER
2	B	688	GLY
2	B	711	GLU
2	B	712	PRO
2	B	738	PHE
2	B	761	HIS
2	B	792	MET

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Mol	Chain	Res	Type
2	B	822	ASN
2	B	996	ARG
2	B	1017	ILE
2	B	1153	GLU
2	B	1155	SER
2	B	1189	ILE
3	C	6	PRO
3	C	28	ALA
3	C	91	HIS
3	C	169	LYS
3	C	202	PRO
3	C	212	PRO
3	C	218	PRO
3	C	264	GLN
4	D	52	LEU
5	E	8	ASN
5	E	44	ALA
5	E	56	LYS
5	E	74	ASP
7	G	17	PHE
7	G	139	ILE
7	G	147	ILE
9	I	7	CYS
9	I	113	ASP
10	J	22	LEU
12	L	35	SER
12	L	49	LYS
1	A	35	ILE
1	A	67	CYS
1	A	100	LYS
1	A	196	GLU
1	A	253	ASN
1	A	312	PRO
1	A	465	TYR
1	A	526	ASP
1	A	605	MET
1	A	986	ILE
1	A	1040	GLN
1	A	1139	GLU
1	A	1206	ASP
1	A	1266	THR
1	A	1280	GLU

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Mol	Chain	Res	Type
2	B	387	LEU
2	B	409	ALA
2	B	430	ARG
2	B	682	SER
2	B	754	SER
2	B	848	ARG
2	B	884	ARG
2	B	946	ASN
2	B	1029	CYS
2	B	1143	ALA
2	B	1178	ASN
2	B	1202	LEU
3	C	90	ASP
3	C	198	ALA
3	C	227	THR
3	C	240	VAL
4	D	131	GLU
4	D	168	LYS
5	E	73	PRO
5	E	115	ASN
5	E	192	ARG
6	F	73	ALA
6	F	112	GLU
7	G	133	SER
8	H	92	ASP
9	I	32	CYS
9	I	73	ARG
9	I	86	PHE
9	I	95	THR
10	J	9	SER
10	J	29	GLU
10	J	51	LEU
10	J	63	TYR
11	K	64	GLU
12	L	42	ARG
1	A	84	ILE
1	A	197	PRO
1	A	696	GLU
1	A	759	ALA
1	A	789	LYS
1	A	795	GLU
1	A	808	LEU

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Mol	Chain	Res	Type
1	A	817	ALA
1	A	958	VAL
1	A	1160	SER
1	A	1188	GLN
1	A	1302	PRO
1	A	1435	PRO
2	B	22	SER
2	B	56	ASP
2	B	368	GLU
2	B	483	LEU
2	B	490	SER
2	B	565	PRO
2	B	878	GLN
2	B	879	ARG
2	B	883	LEU
2	B	1019	SER
2	B	1100	ASP
3	C	148	ARG
4	D	27	LEU
4	D	142	LYS
5	E	40	GLU
5	E	172	GLU
5	E	183	PRO
6	F	108	PHE
7	G	30	LEU
7	G	124	GLY
7	G	165	GLU
8	H	52	GLN
11	K	70	ARG
1	A	599	SER
1	A	641	VAL
1	A	719	VAL
1	A	1162	VAL
1	A	1338	VAL
2	B	171	PRO
2	B	259	TYR
2	B	282	ILE
2	B	450	ALA
2	B	543	SER
2	B	694	ASP
2	B	758	PHE
2	B	906	SER

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Mol	Chain	Res	Type
2	B	1103	ILE
2	B	1118	PRO
3	C	126	GLY
3	C	171	GLY
4	D	201	LYS
6	F	139	PRO
8	H	8	ASP
10	J	18	TRP
12	L	26	THR
12	L	46	VAL
1	A	507	VAL
1	A	1057	VAL
2	B	635	ARG
3	C	142	VAL
6	F	93	ILE
1	A	9	ALA
1	A	653	VAL
1	A	886	ILE
1	A	963	ILE
1	A	1158	PRO
2	B	985	GLY
5	E	37	LEU
7	G	63	PRO
1	A	392	VAL
1	A	673	GLY
1	A	1379	GLY
2	B	410	GLY
2	B	502	ILE
2	B	552	MET
2	B	974	PRO
1	A	250	ILE
1	A	649	ILE
1	A	1031	VAL
10	J	14	VAL
11	K	43	GLY
1	A	357	PRO
1	A	1061	GLY
2	B	575	PRO
7	G	157	ILE
5	E	129	PRO

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	1246/1270 (98%)	1116 (90%)	130 (10%)	7	22
2	B	964/1061 (91%)	865 (90%)	99 (10%)	7	23
3	C	234/236 (99%)	207 (88%)	27 (12%)	5	18
4	D	140/200 (70%)	121 (86%)	19 (14%)	3	14
5	E	196/197 (100%)	183 (93%)	13 (7%)	15	37
6	F	74/74 (100%)	65 (88%)	9 (12%)	5	17
7	G	152/152 (100%)	143 (94%)	9 (6%)	18	39
8	H	117/128 (91%)	112 (96%)	5 (4%)	26	47
9	I	113/116 (97%)	99 (88%)	14 (12%)	4	17
10	J	60/65 (92%)	57 (95%)	3 (5%)	22	43
11	K	99/102 (97%)	90 (91%)	9 (9%)	9	27
12	L	40/40 (100%)	34 (85%)	6 (15%)	3	12
All	All	3435/3641 (94%)	3092 (90%)	343 (10%)	9	24

All (343) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	VAL
1	A	13	THR
1	A	14	VAL
1	A	18	GLN
1	A	30	ILE
1	A	34	LYS
1	A	41	MET
1	A	54	ASN
1	A	62	ASP
1	A	93	VAL
1	A	108	MET
1	A	195	ASP
1	A	208	LEU
1	A	215	SER

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Mol	Chain	Res	Type
1	A	220	THR
1	A	227	VAL
1	A	270	LEU
1	A	308	ILE
1	A	326	ARG
1	A	329	LEU
1	A	335	ARG
1	A	348	SER
1	A	354	SER
1	A	364	VAL
1	A	370	ILE
1	A	375	THR
1	A	381	THR
1	A	385	ILE
1	A	406	ILE
1	A	408	ASP
1	A	425	GLN
1	A	434	ARG
1	A	443	LEU
1	A	445	ASN
1	A	450	LEU
1	A	451	HIS
1	A	454	SER
1	A	460	VAL
1	A	461	LYS
1	A	466	SER
1	A	469	ARG
1	A	481	ASP
1	A	487	MET
1	A	489	LEU
1	A	493	GLN
1	A	497	THR
1	A	498	ARG
1	A	501	LEU
1	A	503	GLN
1	A	505	CYS
1	A	518	LYS
1	A	523	ILE
1	A	524	VAL
1	A	560	ILE
1	A	562	THR
1	A	596	THR

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Mol	Chain	Res	Type
1	A	618	GLU
1	A	629	LEU
1	A	648	ASN
1	A	652	VAL
1	A	666	ILE
1	A	718	VAL
1	A	734	GLU
1	A	739	ASP
1	A	740	LEU
1	A	754	SER
1	A	762	SER
1	A	786	HIS
1	A	791	ASP
1	A	795	GLU
1	A	821	ARG
1	A	829	VAL
1	A	830	LYS
1	A	831	THR
1	A	833	GLU
1	A	845	LEU
1	A	852	TYR
1	A	854	ASN
1	A	858	ASN
1	A	867	ILE
1	A	879	GLU
1	A	886	ILE
1	A	890	ASP
1	A	897	TYR
1	A	920	LEU
1	A	929	LEU
1	A	936	LEU
1	A	949	ASP
1	A	969	GLN
1	A	1029	ARG
1	A	1035	TYR
1	A	1037	LEU
1	A	1048	ASN
1	A	1050	GLU
1	A	1052	GLN
1	A	1058	VAL
1	A	1081	LEU
1	A	1082	ASN

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Mol	Chain	Res	Type
1	A	1110	ASN
1	A	1111	MET
1	A	1114	PRO
1	A	1116	LEU
1	A	1117	THR
1	A	1122	PRO
1	A	1127	ASP
1	A	1136	SER
1	A	1142	THR
1	A	1155	ASP
1	A	1166	ASP
1	A	1236	LEU
1	A	1242	VAL
1	A	1264	GLU
1	A	1271	ILE
1	A	1274	ARG
1	A	1276	VAL
1	A	1291	VAL
1	A	1295	THR
1	A	1297	GLU
1	A	1300	LYS
1	A	1317	MET
1	A	1325	THR
1	A	1333	ILE
1	A	1353	TYR
1	A	1358	SER
1	A	1370	LEU
1	A	1372	VAL
1	A	1376	THR
1	A	1398	MET
1	A	1445	ILE
1	A	1447	GLU
2	B	44	VAL
2	B	57	TYR
2	B	63	ILE
2	B	128	LEU
2	B	175	ARG
2	B	194	GLU
2	B	213	ILE
2	B	223	VAL
2	B	261	ARG
2	B	268	THR

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Mol	Chain	Res	Type
2	B	286	PHE
2	B	294	ASP
2	B	298	LEU
2	B	365	THR
2	B	371	GLU
2	B	378	LEU
2	B	393	LYS
2	B	401	PHE
2	B	408	LEU
2	B	419	THR
2	B	427	ASP
2	B	429	PHE
2	B	463	THR
2	B	466	TRP
2	B	476	ARG
2	B	482	VAL
2	B	485	ARG
2	B	496	ARG
2	B	498	THR
2	B	510	LYS
2	B	511	PRO
2	B	555	ILE
2	B	582	VAL
2	B	599	THR
2	B	603	LEU
2	B	615	MET
2	B	616	ILE
2	B	628	THR
2	B	629	ASP
2	B	635	ARG
2	B	636	PRO
2	B	644	GLU
2	B	658	ILE
2	B	682	SER
2	B	724	ASP
2	B	737	THR
2	B	742	GLU
2	B	743	ILE
2	B	748	ILE
2	B	751	VAL
2	B	766	ARG
2	B	807	ARG

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Mol	Chain	Res	Type
2	B	815	ARG
2	B	830	TYR
2	B	835	GLN
2	B	839	MET
2	B	855	PHE
2	B	856	PHE
2	B	859	TYR
2	B	878	GLN
2	B	901	PRO
2	B	909	ASP
2	B	918	ILE
2	B	939	THR
2	B	953	LEU
2	B	986	GLN
2	B	987	LYS
2	B	990	ILE
2	B	993	THR
2	B	997	GLU
2	B	999	MET
2	B	1002	THR
2	B	1006	ILE
2	B	1010	LEU
2	B	1017	ILE
2	B	1018	PRO
2	B	1026	LEU
2	B	1034	VAL
2	B	1047	PHE
2	B	1051	THR
2	B	1055	ILE
2	B	1076	HIS
2	B	1084	GLN
2	B	1095	LEU
2	B	1096	ARG
2	B	1103	ILE
2	B	1104	HIS
2	B	1137	CYS
2	B	1138	MET
2	B	1159	ARG
2	B	1169	MET
2	B	1170	THR
2	B	1183	LYS
2	B	1185	CYS

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Mol	Chain	Res	Type
2	B	1202	LEU
2	B	1212	ILE
2	B	1216	LEU
2	B	1218	THR
2	B	1224	PHE
3	C	23	SER
3	C	44	LEU
3	C	54	ASN
3	C	55	THR
3	C	56	THR
3	C	57	VAL
3	C	58	LEU
3	C	74	SER
3	C	77	ILE
3	C	89	GLU
3	C	99	LEU
3	C	100	THR
3	C	108	GLU
3	C	129	ILE
3	C	138	GLU
3	C	140	ASN
3	C	143	LEU
3	C	147	LEU
3	C	156	THR
3	C	166	GLU
3	C	186	LEU
3	C	214	ASN
3	C	233	GLU
3	C	240	VAL
3	C	245	VAL
3	C	250	THR
3	C	266	ASP
4	D	35	LEU
4	D	47	LEU
4	D	61	GLU
4	D	63	LEU
4	D	70	PHE
4	D	137	ASN
4	D	139	LYS
4	D	148	LEU
4	D	149	THR
4	D	152	SER

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Mol	Chain	Res	Type
4	D	177	VAL
4	D	182	SER
4	D	187	THR
4	D	192	LYS
4	D	193	THR
4	D	197	SER
4	D	202	ILE
4	D	206	GLU
4	D	208	GLU
5	E	40	GLU
5	E	60	PHE
5	E	72	PHE
5	E	78	LEU
5	E	83	CYS
5	E	114	ASN
5	E	132	ILE
5	E	135	PHE
5	E	169	ARG
5	E	183	PRO
5	E	207	ARG
5	E	211	TYR
5	E	212	ARG
6	F	79	ARG
6	F	81	THR
6	F	84	TYR
6	F	86	THR
6	F	90	ARG
6	F	96	THR
6	F	119	ARG
6	F	148	VAL
6	F	153	VAL
7	G	38	CYS
7	G	39	THR
7	G	49	LEU
7	G	70	PHE
7	G	78	VAL
7	G	80	LYS
7	G	96	GLN
7	G	126	ASN
7	G	171	ILE
8	H	10	PHE
8	H	86	ASP

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Mol	Chain	Res	Type
8	H	102	TYR
8	H	130	ARG
8	H	134	ASN
9	I	6	PHE
9	I	8	ARG
9	I	9	ASP
9	I	10	CYS
9	I	13	MET
9	I	32	CYS
9	I	46	HIS
9	I	75	CYS
9	I	78	CYS
9	I	84	VAL
9	I	85	PHE
9	I	100	PHE
9	I	101	PHE
9	I	106	CYS
10	J	2	ILE
10	J	46	CYS
10	J	55	ASP
11	K	10	PHE
11	K	25	THR
11	K	35	PHE
11	K	47	ARG
11	K	49	GLU
11	K	64	GLU
11	K	70	ARG
11	K	78	THR
11	K	114	LEU
12	L	33	GLU
12	L	51	CYS
12	L	55	ILE
12	L	63	ARG
12	L	65	VAL
12	L	68	GLU

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

Mol	Chain	Res	Type
1	A	54	ASN
1	A	80	HIS
1	A	83	HIS

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Mol	Chain	Res	Type
1	A	119	ASN
1	A	213	HIS
1	A	225	ASN
1	A	256	GLN
1	A	299	HIS
1	A	316	GLN
1	A	339	ASN
1	A	394	ASN
1	A	435	HIS
1	A	493	GLN
1	A	503	GLN
1	A	587	HIS
1	A	611	GLN
1	A	631	HIS
1	A	659	HIS
1	A	706	HIS
1	A	741	ASN
1	A	742	ASN
1	A	745	GLN
1	A	757	ASN
1	A	768	GLN
1	A	786	HIS
1	A	851	HIS
1	A	858	ASN
1	A	877	HIS
1	A	903	ASN
1	A	926	GLN
1	A	1048	ASN
1	A	1070	GLN
1	A	1085	HIS
1	A	1106	ASN
1	A	1140	HIS
1	A	1173	HIS
1	A	1265	ASN
1	A	1378	GLN
1	A	1432	GLN
2	B	52	ASN
2	B	60	GLN
2	B	121	ASN
2	B	178	ASN
2	B	236	HIS
2	B	325	GLN

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Mol	Chain	Res	Type
2	B	465	ASN
2	B	513	GLN
2	B	515	HIS
2	B	516	ASN
2	B	518	HIS
2	B	538	ASN
2	B	657	HIS
2	B	744	HIS
2	B	821	GLN
2	B	835	GLN
2	B	842	ASN
2	B	975	GLN
2	B	984	HIS
2	B	1015	HIS
2	B	1065	GLN
2	B	1076	HIS
2	B	1084	GLN
2	B	1117	GLN
2	B	1179	GLN
2	B	1193	GLN
3	C	65	HIS
3	C	73	GLN
3	C	79	GLN
3	C	91	HIS
3	C	112	ASN
3	C	123	ASN
3	C	167	HIS
3	C	252	GLN
4	D	39	ASN
4	D	40	HIS
4	D	41	GLN
4	D	51	ASN
4	D	137	ASN
4	D	216	ASN
5	E	101	GLN
5	E	104	ASN
5	E	114	ASN
5	E	143	ASN
5	E	147	HIS
7	G	10	ASN
7	G	14	HIS
7	G	53	ASN

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Mol	Chain	Res	Type
7	G	57	GLN
7	G	97	HIS
7	G	102	GLN
7	G	122	ASN
7	G	126	ASN
7	G	153	GLN
7	G	158	HIS
8	H	131	ASN
9	I	12	ASN
9	I	23	ASN
9	I	79	HIS
9	I	83	ASN
10	J	64	ASN
11	K	65	HIS
11	K	76	GLN
11	K	89	ASN
11	K	92	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](#)

Of 10 ligands modelled in this entry, 10 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5343. These allow visual inspection of the internal detail of the map and identification of artifacts.

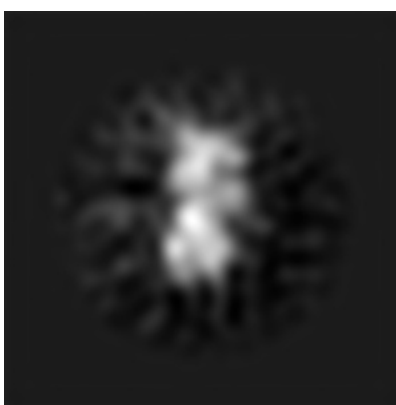
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

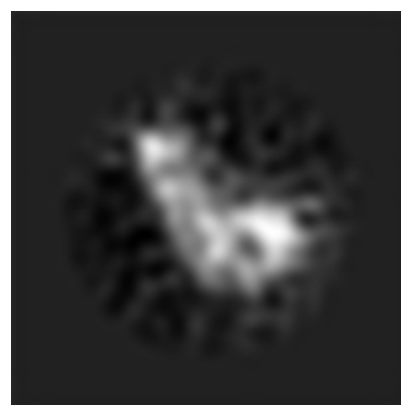
6.1.1 Primary map



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: 80



Y Index: 80



Z Index: 80

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: 104



Y Index: 71

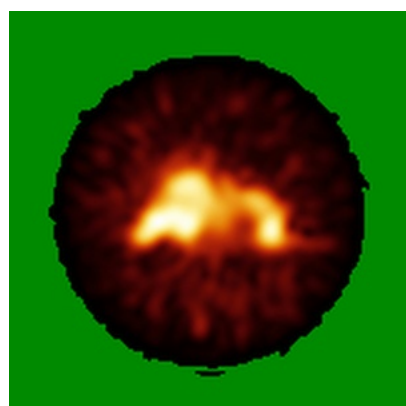


Z Index: 76

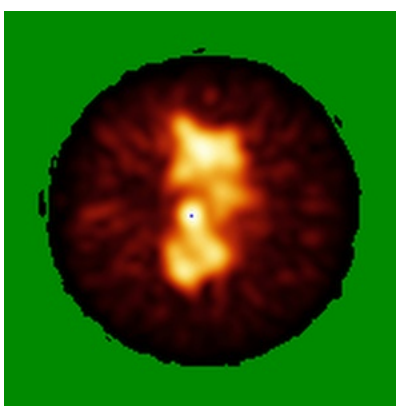
The images above show the largest variance slices of the map in three orthogonal directions.

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

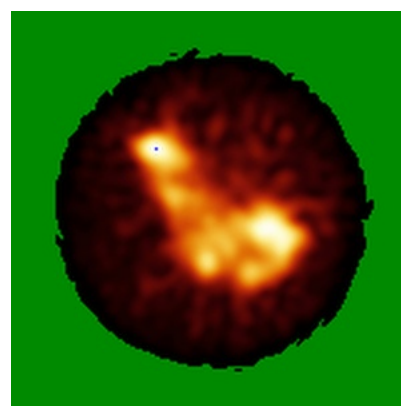
6.4.1 Primary map



X



Y

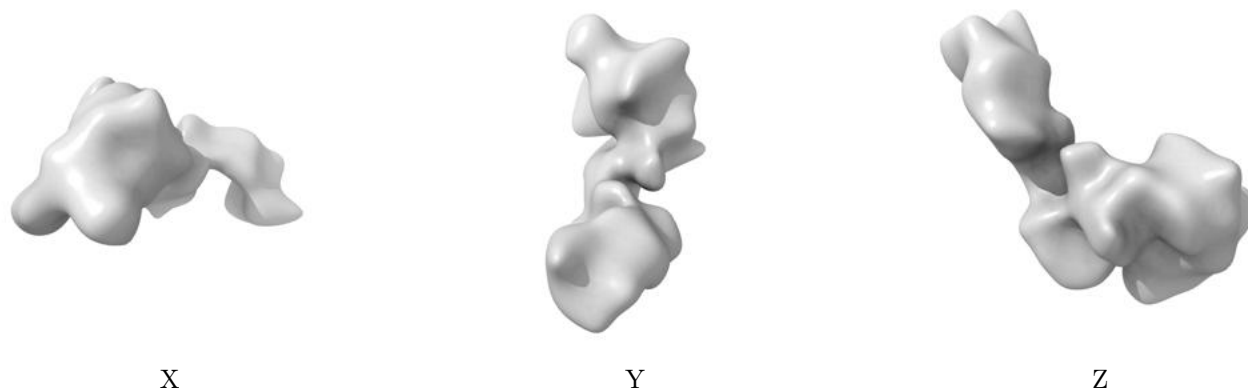


Z

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 0.0284. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

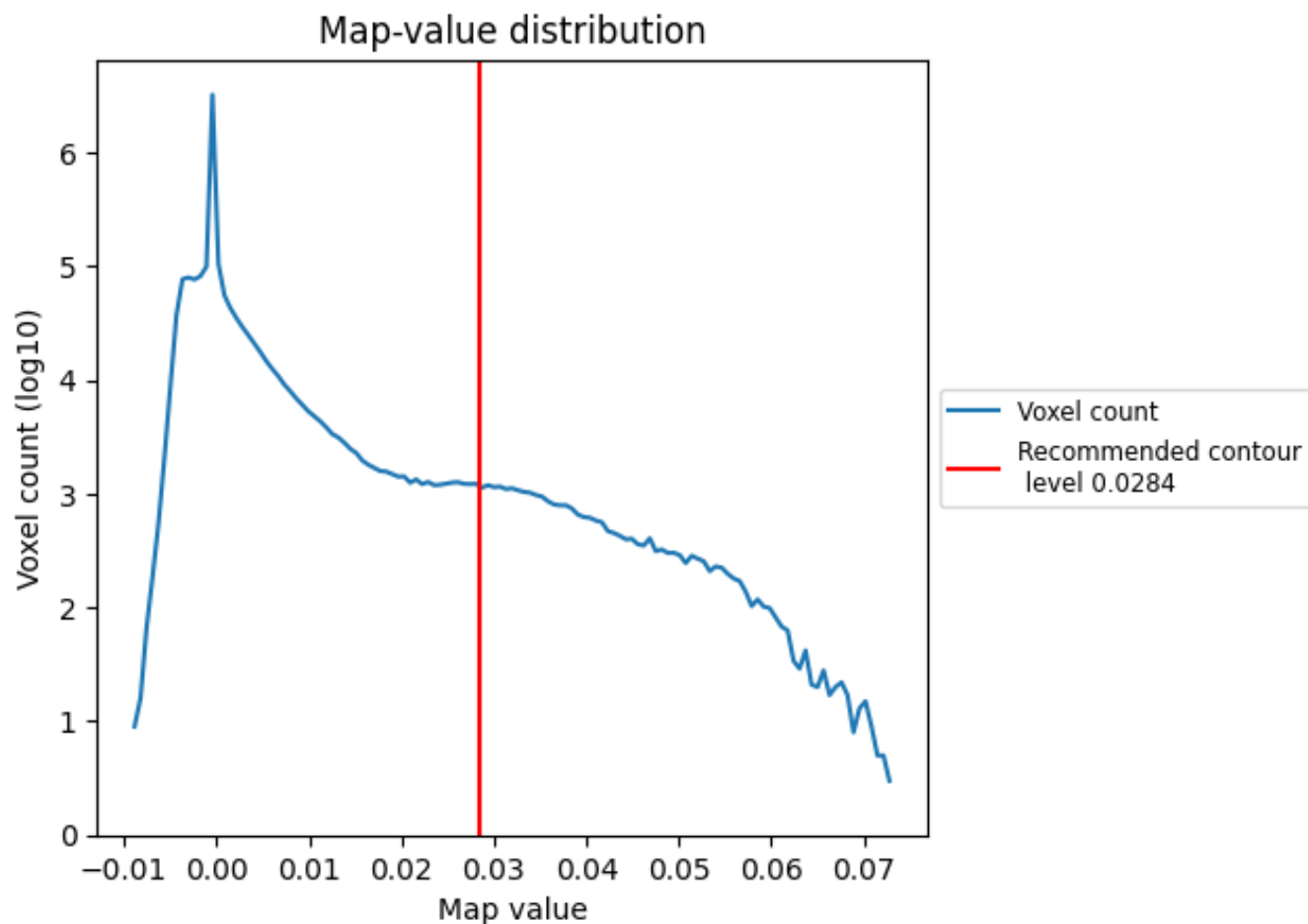
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

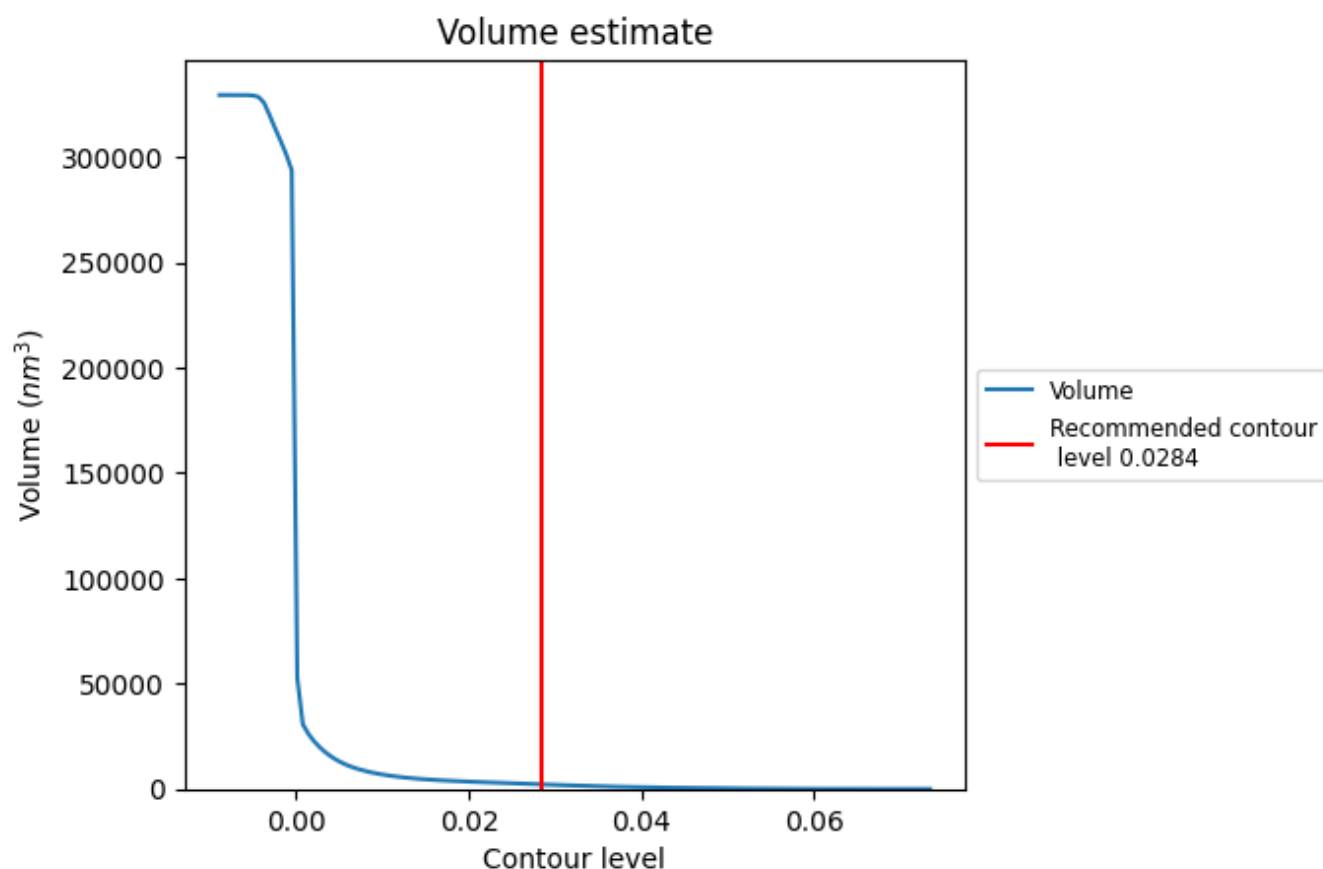
This section contains the results of statistical analysis of the map.

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.

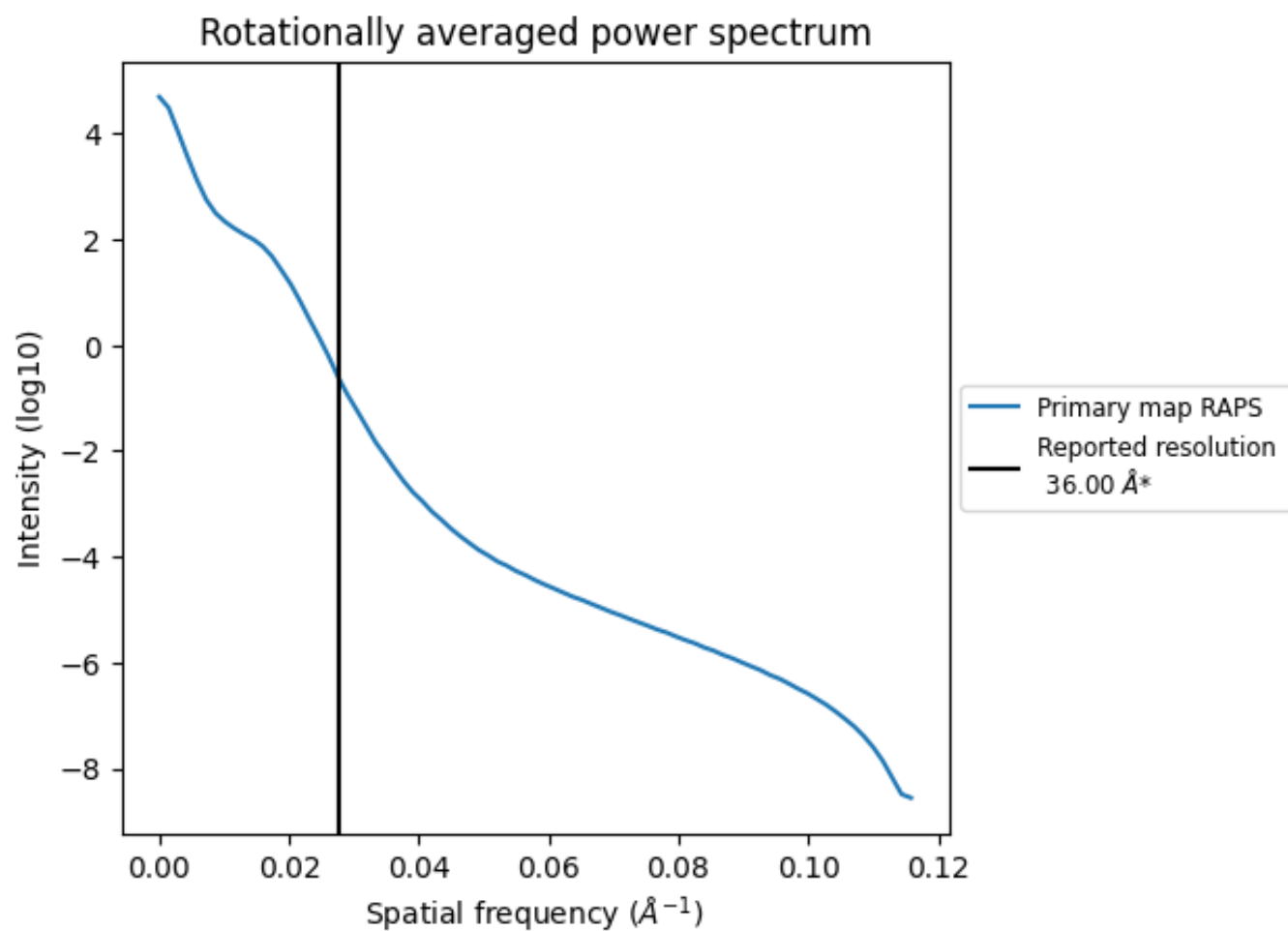
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2188 nm³; this corresponds to an approximate mass of 1977 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 0.028 Å⁻¹

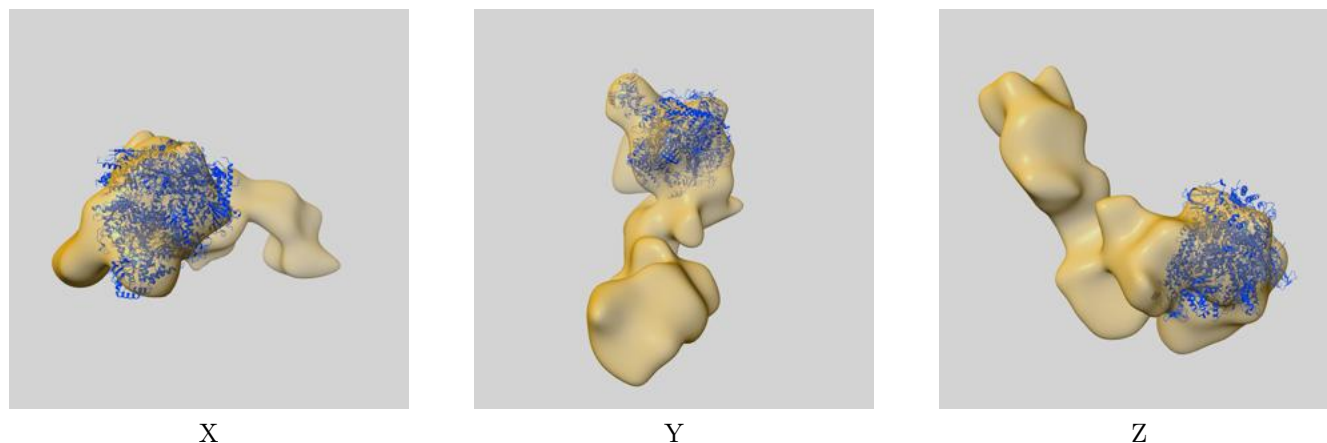
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

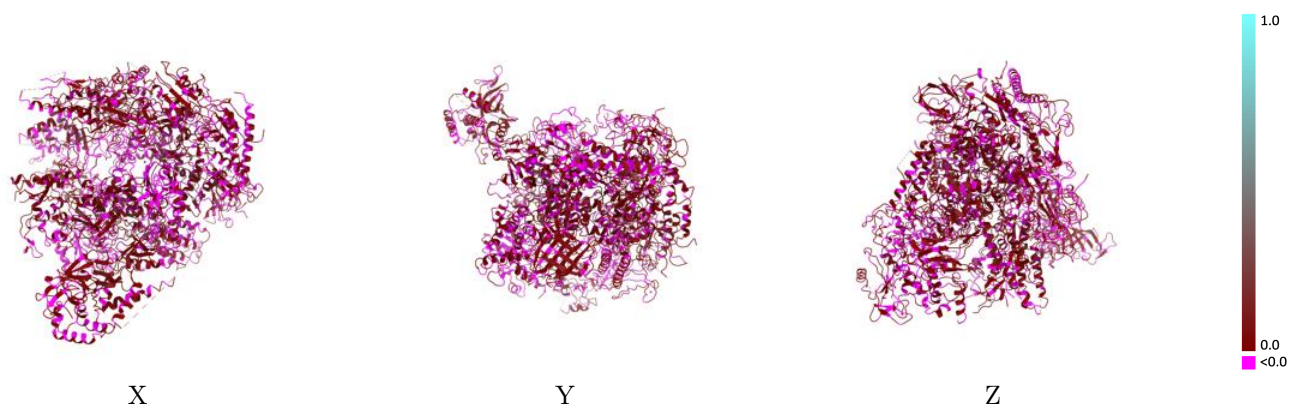
This section contains information regarding the fit between EMDB map EMD-5343 and PDB model 3J0K. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



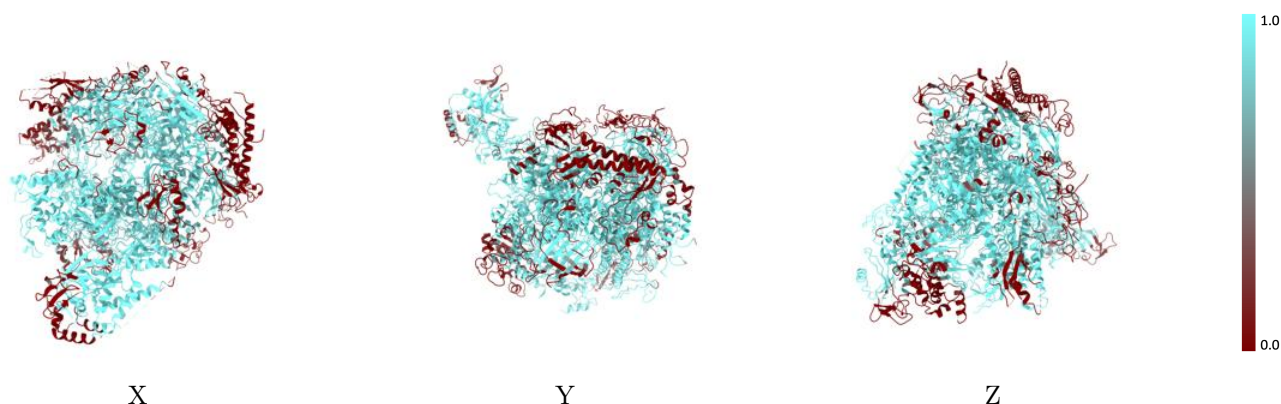
The images above show the 3D surface view of the map at the recommended contour level 0.0284 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



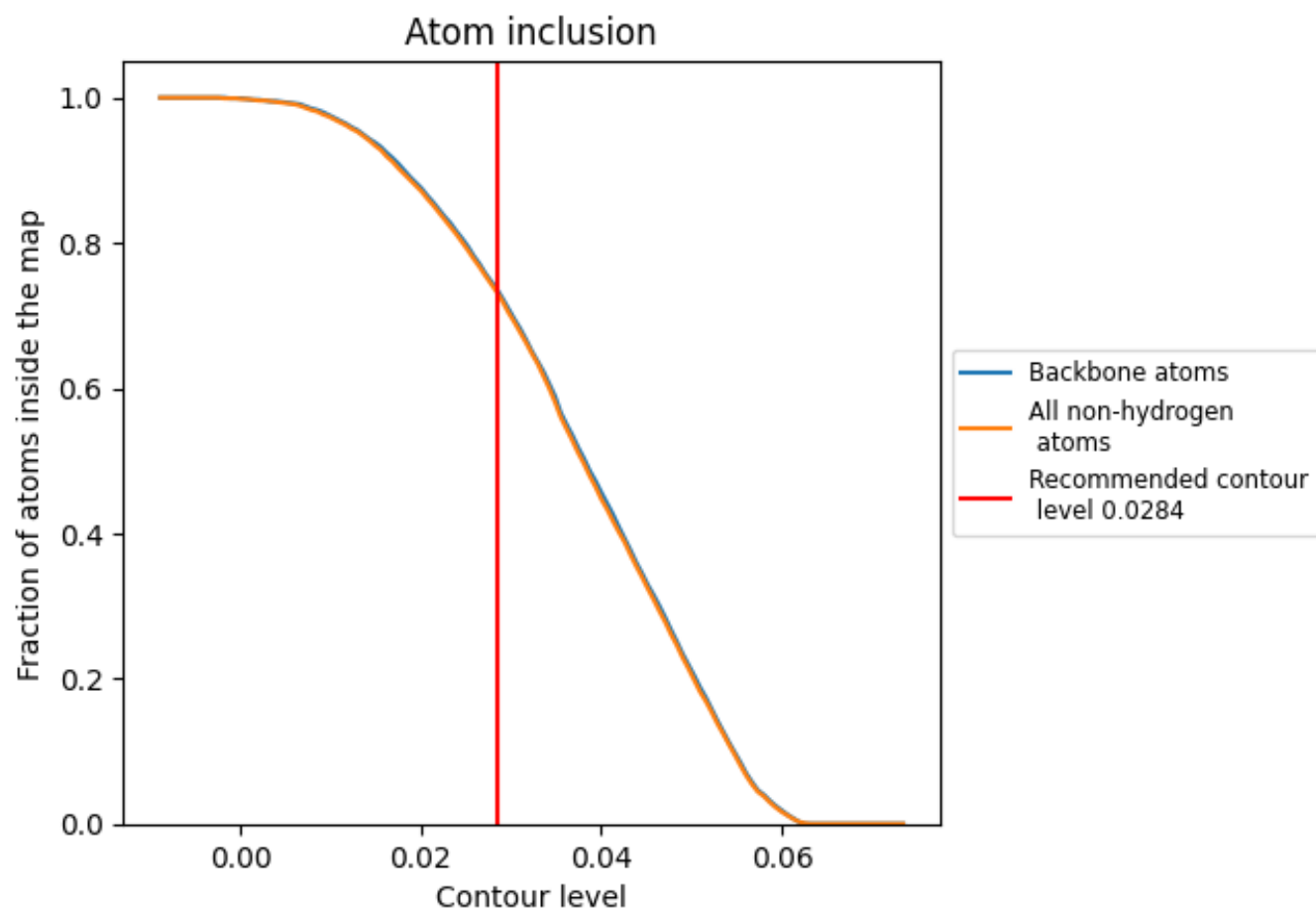
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0284).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 73% 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 (0.0284) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7330	0.0260
A	0.8980	0.0290
B	0.7610	0.0340
C	0.3730	0.0210
D	0.7520	0.0200
E	0.4560	-0.0130
F	0.7490	0.0060
G	0.7880	0.0470
H	0.4850	0.0300
I	0.6210	-0.0000
J	0.7080	0.0350
K	0.3020	0.0010
L	0.2440	0.0090

1.0

0.0

<0.0