



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 02:39 AM UTC

PDB ID : 7UA5 / pdb_00007ua5
EMDB ID : EMD-26415
Title : Structure of dephosphorylated human RyR2 in the closed state
Authors : Miotto, M.C.; Marks, A.R.
Deposited on : 2022-03-11
Resolution : 2.83 Å(reported)
Based on initial model : 7U9Q

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:

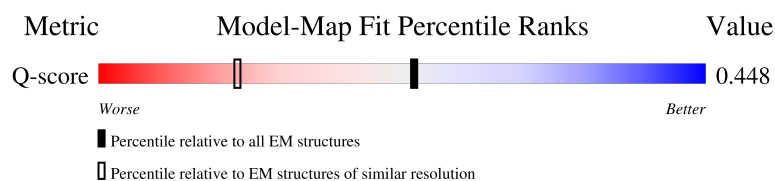
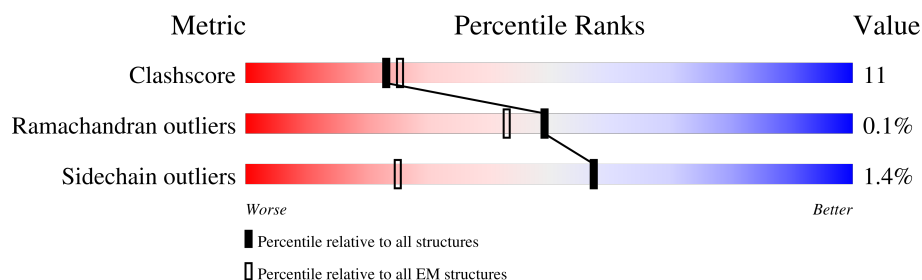
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 2.83 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	11847 (2.33 - 3.33)

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	4967	
1	B	4967	
1	C	4967	
1	D	4967	

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Mol	Chain	Length	Quality of chain
2	E	108	82%16%..
2	F	108	82%16%..
2	G	108	83%15%..
2	H	108	81%17%..

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 138608 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 Ryanodine receptor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	4224	Total	C	N	O	S	2	0
			33771	21516	5745	6280	230		
1	B	4224	Total	C	N	O	S	2	0
			33771	21516	5745	6280	230		
1	C	4224	Total	C	N	O	S	2	0
			33771	21516	5745	6280	230		
1	D	4224	Total	C	N	O	S	2	0
			33771	21516	5745	6280	230		

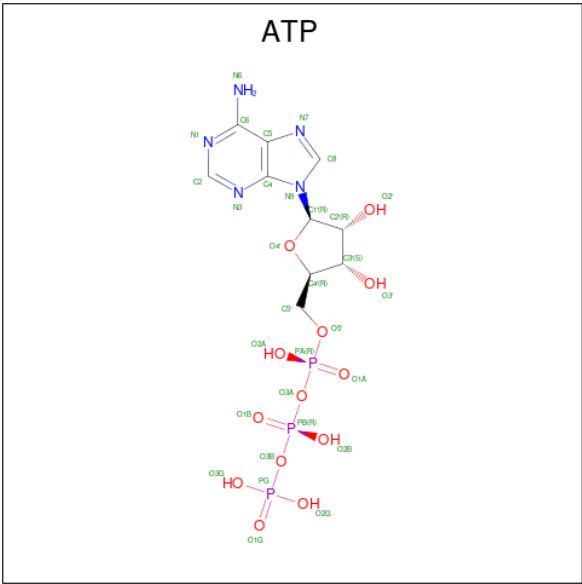
- Molecule 2 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
2	F	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
2	G	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
2	H	107	Total	C	N	O	S	0	0
			818	516	144	154	4		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Zn	0
			1	1	
3	B	1	Total	Zn	0
			1	1	
3	C	1	Total	Zn	0
			1	1	
3	D	1	Total	Zn	0
			1	1	

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



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

3 Residue-property plots

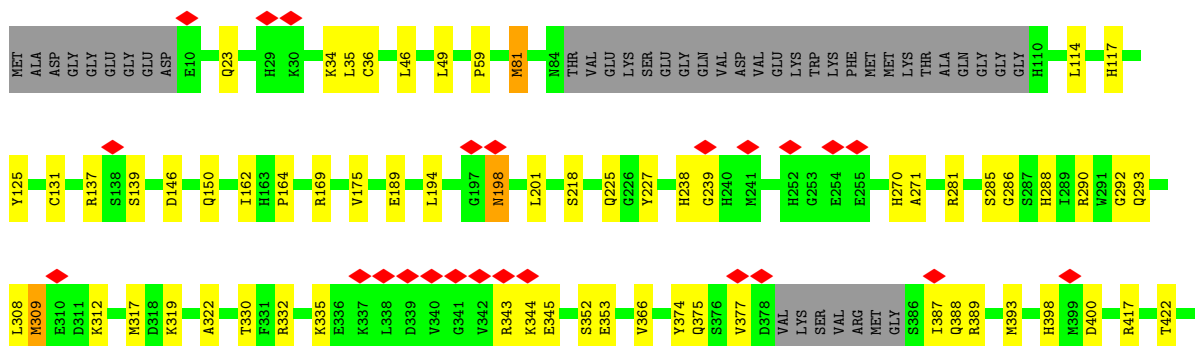
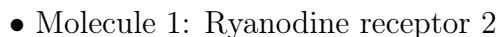
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Ryanodine receptor 2

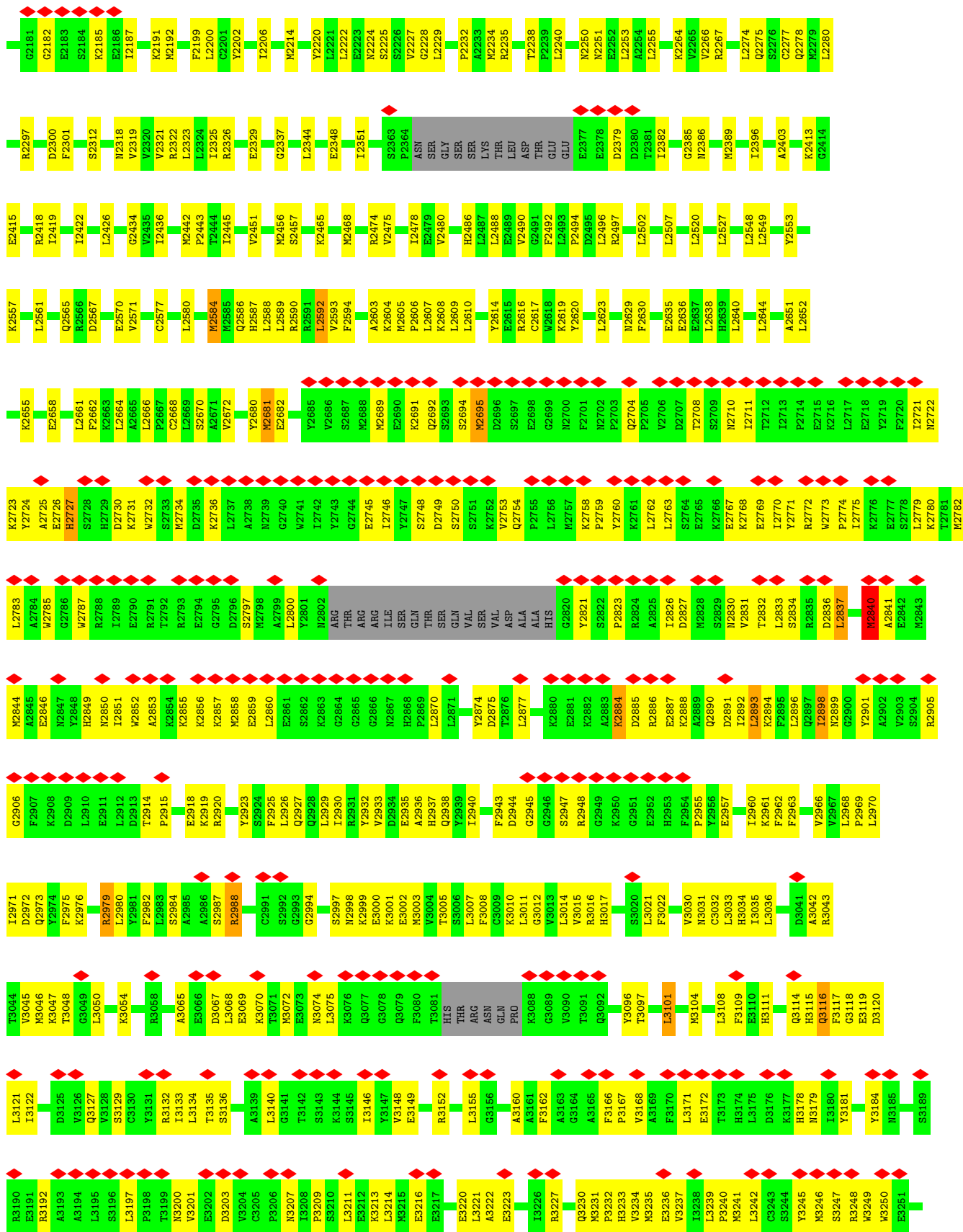


12711	E2636	L2520	D2380	E2952	M2142	LEU	M1938	F1851	S1713	T1548	TYR	ASP
T2712	E2637	L2527	T2381	L2253	R2143	LEU	M1939	K1852	Y1714	T1549	SER	ALA
12713	H2638	L2527	I2382	L2255	R2144	SER	V1947	E1853	L1719	S1550	THR	ALA
P2714	L2640	L2548	G2385	K2264	Y2156	VAL	M1948	A1854	M1722	SER	HIS	ASP
E2715	S2641	L2549	N2386	V2266	L2165	GLU	Q1949	ALA	F1555	PHE	ASP	ASP
	K2643	Y2553	M2389	V2265	G2166	THR	A1950	THR	E1732	GLU	ALA	ASP
	L2644	Y2557	I2396	R2267	Y2167	TYR	L1951	GLU	R1559	VAL	ARG	GLU
	A2651	K2557	A2403	L2274	H2168	LEU	M1952	GLU	I1560	THR	ARG	GLU
L2721	L2652	L2561	G2413	Q2275	V2171	LYS	A1955	SER	G1752	GLU	LEU	MET
K2723		Q2565	G2414	Q2276	M2175	LYS	A1956	THR	L1753	ASP	VAL	LYS
Y2724		Q2566	M2278	C2277	V2176	LYS	L1957	LEU	R1751	ASP	LEU	THR
A2725		D2567	E2415	L2280	R2177	ALA	K1961	GLU	P1759	ASP	ALA	HIS
E2726		D2567	L2280	R2287	V2178	GLU	R1966	GLU	M1761	ASP	ASP	GLY
H2727		E2570	I2419	R2287	G2181	LYS	S1967	LEU	P1766	R1414	LEU	HIS
S2728		V2571	I2422	D2300	E2182	VAL	Q1972	SER	F1767	D1415	VAL	VAL
D2730		C2577	L2426	F2301	E2183	GLU	M1975	VAL	S1768	D1416	PRO	ASP
K2731		L2580	G2434	S2312	S2184	SER	N1978	ALA	P1780	Y1417	ARG	ASP
Y2732		L2584	I2436	N2318	K2053	SER	F1979	LYS	D1785	D1418	VAL	VAL
S2733		P2585	V2435	V2320	S2054	LEU	D1982	GLN	I1786	F1419	LYS	ASP
L2734		G2586	M2442	V2321	S2055	GLU	S1983	GLY	L1787	F1433	ASP	ASP
L2735		H2587	P2443	R2321	S2056	GLY	K1983	ALA	K1788	P1434	LYS	GLU
L2737		L2588	T2444	L2323	T2057	GLU	S1984	GLY	S1789	G1435	THR	ALA
L2738		L2589	I2445	L2324	L2058	GLU	E1985	GLU	T1791	P1438	LYS	LYS
N2739		R2590	V2451	L2325	Q2059	GLU	C1986	GLU	I1792	L1618	PRO	PRO
G2740		L2592	M2456	R2326	Q2060	GLU	P1987	ALA	K1793	L1630	GLU	GLU
Y2741		V2593	S2457	E2329	L2061	LYS	C1988	LYS	M1794	L1644	PHE	ASN
L2742		F2594	K2465	L2344	Q2071	GLY	E1990	GLY	E1797	L1644	ASN	ASN
Y2743		K2604	M2468	E2348	D2077	LYS	I1991	LYS	A1806	E1649	LYS	LYS
E2745		P2606	M2468	E2348	V2081	GLU	I1992	ARG	R1807	L1650	THR	ASP
L2746		L2607	R2474	L2351	R2082	GLU	R1993	K1890	D1808	L1651	ALA	GLN
Y2747		L2610	V2475	L2351	A2083	GLU	D1994	L1898	V1819	L1667	THR	GLN
S2748		Y2614	I2478	S2363	L2222	LEU	Q1995	L1898	F1825	H1670	LYS	LYS
D2749		E2615	V2479	P2364	L2222	ASP	E2010	L1898	F1826	H1674	PRO	PRO
S2750		E2615	V2480	ASN	S2225	GLU	LEU	V1902	T1827	E1674	GLY	GLY
S2751		E2616	L2488	GLY	S2227	GLU	ASP	Q1905	T1830	E1682	SER	ARG
K2752		C2617	L2488	SER	G2228	ASP	GLU	Q1905	M1831	P1683	ARG	ARG
Y2753		L2618	F2492	LYS	L2229	GLY	GLY	L1910	F1834	Q1684	LYS	LYS
Q2754		L2619	L2493	THR	P2232	LEU	LEU	Q1911	L1839	L1685	GLN	ALA
P2755		Y2620	P2494	LEU	A2233	ASP	ASP	C1914	I1839	L1686	ARG	ARG
L2756		L2623	D2495	ASP	R2234	GLY	GLY	R1919	L1842	Q1498	PHE	LEU
L2757		L2623	L2496	THR	R2235	ASN	SER	F1928	I1842	G1499	LEU	GLY
K2758		N2629	R2497	GLU	T2238	LEU	LEU	F1928	L1845	R1500	ARG	LYS
P2759		F2630	E2377	GLU	T2238	THR	THR	D1931	L1547	L1505	THR	THR
Y2760		E2635	E2378	GLU	L2240	ILE	ILE	F1932	S1849	D1708	LYS	LYS
K2761			E2378	GLU	N2250	ARG	ARG	S1850	V1850	L1711	PRO	PRO
L2762			D2379		N2251	GLY	GLY	Q1937		S1712	ASP	ASP
L2763												
S2764												
E2765												
K2766												
E2767												
K2768												
E2769												
12770												
Y2771												
R2772												

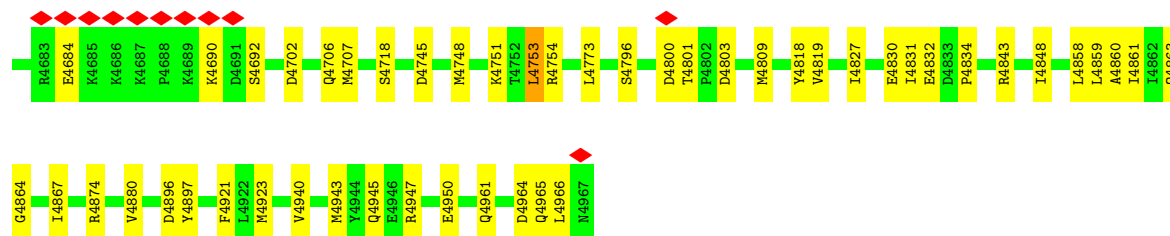




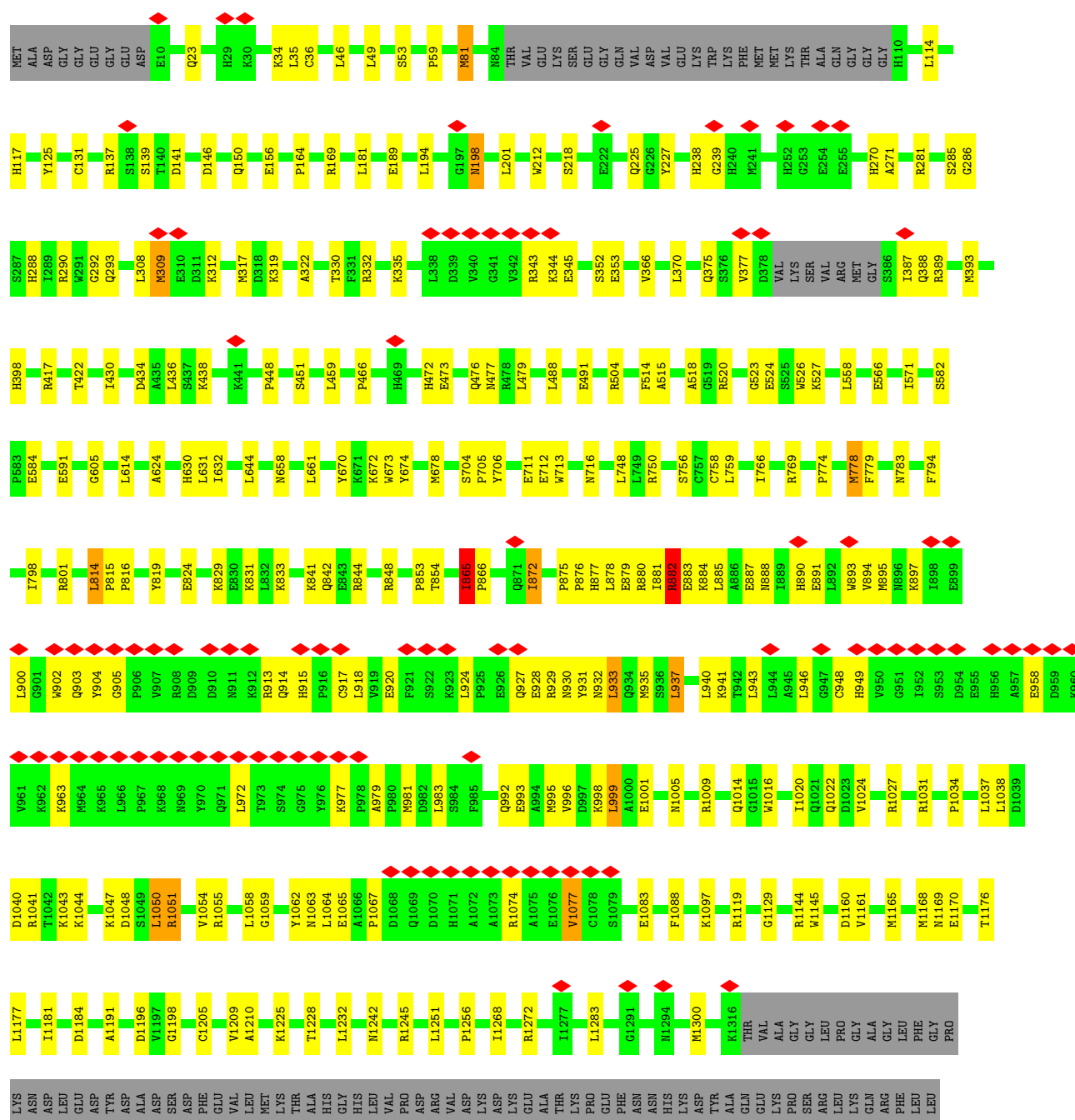








• Molecule 1: Ryanodine receptor 2







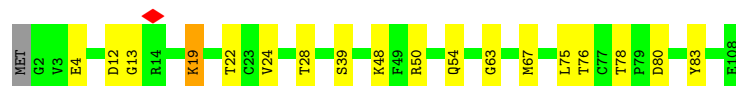
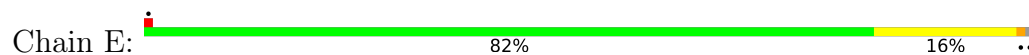


S3247	R3115	L3036	V2966	Y2901	L2837	P2774	E2687	M2889	R2267
R3248	Q3116	D3041	V2967	A2902	H2838	L2775	L2638	I2389	L2274
V3249	G3117	G3042	L2968	V2903	A2839	L2779	H2639	I2396	Q2275
N3250	G3118	R3043	P2969	S2904	M2840	K2779	L2640	A2403	S2276
E3251	D3120	T3044	D2970	R2905	A2841	T2781	S2641	K2413	C2277
	L3121	V3045	D2972	G2906		M2782	R2642	G2414	Q2278
	I3122	M3046	Q2973	F2907		L2783	K2643	R2279	L2280
		K3047	T2974	K2908	M2844	A2784	L2644	G2415	
		T3048	F2975	K2909	A2845	K2785	L2651	R2418	
		G3049	K2976	L2910	N2847	Q2786	L2652	I2419	
		L3050		E2911	Y2848	V2787	K2655	L2422	
			R2979	L2912	H2849	K2788	L2656	D2300	
			L2980	E2913	N2850	V2789	Q2566	F2301	
			T2981	T2914	I2851	L2789	L2657	D2301	
			L2982	T2915	V2852	E2790	E2658		
			S2984		A2853	R2793	L2661	L2426	
			A2985	E2918	K2854	E2794	F2662	L2426	
			A2986	K2919	K2855	G2795	K2663	G2434	
			S2987	R2920	K2856	D2796	L2664	V2435	
			R2988		K2857	S2797	P2667	I2436	
			L2989	Y2923	M2858	K2798	L2668		
			L2990	F2924	E2859	L2800	C2669	M2442	
			C2991	F2925	K2860	D2735	P2670	P2443	
			G2992	L2926	L2861	K2736	A2671	T2444	
			G2993	Q2927	S2862	L2737	V2672	I2445	
			G2994	Q2928	L2863	A2738	L2680	V2451	
				L2929	K2864	R2739	M2681	M2456	
				T2930	G2865	G2740	E2682	S2457	
				R2931	G2866	T2741		K2465	
				V2932	G2867	L2742	Y2685	M2468	
				V2933	G2868	Y2743	V2686	R2474	
				G2934	G2869	G2744	S2687	V2475	
				E2935	G2870	E2745	M2688		
				A2936	G2871	L2746	L2689	I2478	
				H2937	G2872	Y2747	E2690	E2479	
				Q2938	G2873	VAL	K2691	V2480	
				V2939	G2874	VAL	Q2692	H2486	
				L2940	G2875	ASP	K2693	L2487	
				F2943	G2876	ALA	S2694	L2488	
				D2944	G2877	ALA	S2695	L2489	
				G2945	G2878	ALA	D2696	V2490	
				S2947	G2879	ALA	L2697	C2617	
				R2948	G2880	ALA	L2698	F2491	
				Q2949	G2881	ALA	L2699	F2492	
				K2950	G2882	ALA	L2700	L2493	
				G2951	G2883	ALA	L2701	P2494	
				G2952	G2884	ALA	L2702	D2495	
				H2953	G2885	ALA	L2703	L2496	
				F2954	G2886	ALA	L2704	R2497	
				V2955	G2887	ALA	L2705	L2502	
				V2956	G2888	ALA	L2706	L2507	
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				E2957	G2890	ALA	L2708		
				I2960	G2891	ALA	L2709		
				F2961	G2892	ALA	L2710		
				F2962	G2893	ALA	L2711		
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						ALA	L2863		
						ALA	L2864		
						ALA	L2865		
						ALA	L2866		
						ALA	L2867		
						ALA	L2868		
						ALA	L2869		
						ALA	L2870		
						ALA	L2871		

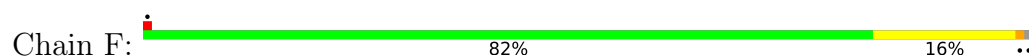




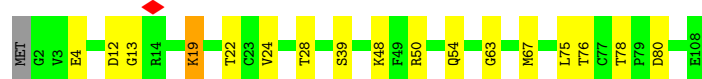
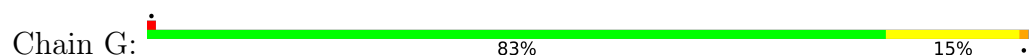
- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B



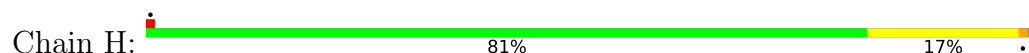
- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B



- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B



- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	90375	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	58	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.667	Depositor
Minimum map value	-0.007	Depositor
Average map value	0.013	Depositor
Map value standard deviation	0.033	Depositor
Recommended contour level	0.13	Depositor
Map size (Å)	428.544, 428.544, 428.544	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.837, 0.837, 0.837	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.16	0/34511	0.45	11/46614 (0.0%)
1	B	0.16	0/34511	0.45	11/46614 (0.0%)
1	C	0.16	0/34511	0.45	10/46614 (0.0%)
1	D	0.16	0/34511	0.45	11/46614 (0.0%)
2	E	0.17	0/834	0.41	0/1123
2	F	0.17	0/834	0.41	0/1123
2	G	0.17	0/834	0.41	0/1123
2	H	0.17	0/834	0.41	0/1123
All	All	0.16	0/141380	0.45	43/190948 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	3
1	C	0	3
1	D	0	3
All	All	0	12

There are no bond length outliers.

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	3315	LEU	CA-CB-CG	7.52	142.62	116.30
1	B	3315	LEU	CA-CB-CG	7.52	142.61	116.30
1	A	3315	LEU	CA-CB-CG	7.51	142.60	116.30
1	D	3315	LEU	CA-CB-CG	7.51	142.59	116.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	2840	MET	CB-CG-SD	6.67	132.72	112.70
1	A	2840	MET	CB-CG-SD	6.67	132.69	112.70
1	C	2840	MET	CB-CG-SD	6.66	132.67	112.70
1	B	2840	MET	CB-CG-SD	6.65	132.65	112.70
1	D	2979	ARG	CA-CB-CG	5.57	125.25	114.10
1	B	2979	ARG	CA-CB-CG	5.56	125.22	114.10
1	A	2979	ARG	CA-CB-CG	5.56	125.22	114.10
1	C	4046	ARG	CG-CD-NE	5.56	124.23	112.00
1	A	4046	ARG	CG-CD-NE	5.55	124.21	112.00
1	C	2979	ARG	CA-CB-CG	5.55	125.20	114.10
1	D	4046	ARG	CG-CD-NE	5.55	124.20	112.00
1	B	4046	ARG	CG-CD-NE	5.53	124.17	112.00
1	B	4060	GLN	CB-CG-CD	5.46	121.89	112.60
1	D	4060	GLN	CB-CG-CD	5.45	121.86	112.60
1	A	4060	GLN	CB-CG-CD	5.43	121.84	112.60
1	C	4060	GLN	CB-CG-CD	5.43	121.83	112.60
1	C	865	ILE	CB-CA-C	5.38	116.19	111.08
1	A	865	ILE	CB-CA-C	5.38	116.19	111.08
1	B	865	ILE	CB-CA-C	5.34	116.15	111.08
1	D	865	ILE	CB-CA-C	5.33	116.14	111.08
1	A	882	ARG	CG-CD-NE	-5.25	100.46	112.00
1	C	882	ARG	CG-CD-NE	-5.25	100.46	112.00
1	B	882	ARG	CG-CD-NE	-5.23	100.50	112.00
1	D	882	ARG	CG-CD-NE	-5.22	100.52	112.00
1	C	937	LEU	CA-CB-CG	5.21	134.52	116.30
1	A	937	LEU	CA-CB-CG	5.20	134.51	116.30
1	D	937	LEU	CA-CB-CG	5.20	134.49	116.30
1	B	937	LEU	CA-CB-CG	5.19	134.45	116.30
1	A	4269	LYS	CB-CG-CD	5.16	123.17	111.30
1	C	4269	LYS	CB-CG-CD	5.16	123.17	111.30
1	D	4269	LYS	CB-CG-CD	5.14	123.13	111.30
1	B	4269	LYS	CB-CG-CD	5.14	123.12	111.30
1	B	1948	MET	CB-CG-SD	5.07	127.90	112.70
1	D	1948	MET	CB-CG-SD	5.07	127.89	112.70
1	C	1948	MET	CB-CG-SD	5.05	127.86	112.70
1	B	2926	LEU	CA-C-O	-5.05	115.50	120.70
1	A	1948	MET	CB-CG-SD	5.05	127.84	112.70
1	A	2926	LEU	CA-C-O	-5.04	115.51	120.70
1	D	2926	LEU	CA-C-O	-5.02	115.53	120.70

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1051	ARG	Sidechain
1	A	4640	PHE	Peptide
1	A	882	ARG	Sidechain
1	B	1051	ARG	Sidechain
1	B	4640	PHE	Peptide
1	B	882	ARG	Sidechain
1	C	1051	ARG	Sidechain
1	C	4640	PHE	Peptide
1	C	882	ARG	Sidechain
1	D	1051	ARG	Sidechain
1	D	4640	PHE	Peptide
1	D	882	ARG	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	33771	0	33455	784	0
1	B	33771	0	33455	772	0
1	C	33771	0	33455	771	0
1	D	33771	0	33455	784	0
2	E	818	0	821	11	0
2	F	818	0	821	11	0
2	G	818	0	821	10	0
2	H	818	0	821	12	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	62	0	24	1	0
4	B	62	0	24	1	0
4	C	62	0	24	1	0
4	D	62	0	24	1	0
All	All	138608	0	137200	3061	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 11.

All (3061) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1498:GLN:NE2	1:D:2899:ASN:O	1.91	1.04
1:A:4060:GLN:HE21	1:A:4060:GLN:HA	1.21	1.04
1:A:882:ARG:NH2	1:A:933:LEU:O	1.92	1.03
1:B:4060:GLN:HA	1:B:4060:GLN:HE21	1.21	1.02
1:C:4060:GLN:HA	1:C:4060:GLN:HE21	1.21	1.01
1:D:4060:GLN:HE21	1:D:4060:GLN:HA	1.21	1.01
1:B:882:ARG:NH2	1:B:933:LEU:O	1.92	1.01
1:C:882:ARG:NH2	1:C:933:LEU:O	1.92	1.01
1:D:882:ARG:NH2	1:D:933:LEU:O	1.92	1.01
1:A:4036:ASP:HB2	1:A:4043:ILE:HD11	1.48	0.95
1:B:4036:ASP:HB2	1:B:4043:ILE:HD11	1.48	0.95
1:D:4036:ASP:HB2	1:D:4043:ILE:HD11	1.48	0.93
1:C:4036:ASP:HB2	1:C:4043:ILE:HD11	1.48	0.93
1:B:4834:PRO:HB3	1:B:4843:ARG:HD3	1.52	0.91
1:A:4834:PRO:HB3	1:A:4843:ARG:HD3	1.52	0.90
1:C:4834:PRO:HB3	1:C:4843:ARG:HD3	1.52	0.89
1:D:4834:PRO:HB3	1:D:4843:ARG:HD3	1.52	0.87
1:A:2874:TYR:HA	1:A:2877:LEU:HD12	1.58	0.85
1:B:2898:ILE:HD12	1:C:1499:GLY:HA3	1.56	0.85
1:B:983:LEU:HD11	1:B:1055:ARG:HG2	1.59	0.85
1:A:983:LEU:HD11	1:A:1055:ARG:HG2	1.59	0.85
1:B:2874:TYR:HA	1:B:2877:LEU:HD12	1.58	0.85
1:C:2927:GLN:NE2	1:C:3003:MET:SD	2.50	0.85
1:D:2874:TYR:HA	1:D:2877:LEU:HD12	1.58	0.84
1:D:2927:GLN:NE2	1:D:3003:MET:SD	2.50	0.84
1:A:2927:GLN:NE2	1:A:3003:MET:SD	2.50	0.84
1:D:983:LEU:HD11	1:D:1055:ARG:HG2	1.59	0.84
1:C:983:LEU:HD11	1:C:1055:ARG:HG2	1.59	0.84
1:A:4265:LYS:HA	1:A:4268:MET:HG3	1.60	0.83
1:B:2927:GLN:NE2	1:B:3003:MET:SD	2.50	0.83
1:C:2874:TYR:HA	1:C:2877:LEU:HD12	1.58	0.83
1:B:4265:LYS:HA	1:B:4268:MET:HG3	1.60	0.83
1:D:4265:LYS:HA	1:D:4268:MET:HG3	1.60	0.82
1:C:4265:LYS:HA	1:C:4268:MET:HG3	1.61	0.82
1:A:3235:MET:HA	1:A:3239:LEU:HD23	1.63	0.81
1:C:3235:MET:HA	1:C:3239:LEU:HD23	1.63	0.81
1:D:3235:MET:HA	1:D:3239:LEU:HD23	1.63	0.81
1:B:2899:ASN:O	1:C:1498:GLN:NE2	2.12	0.81
1:D:2884:LYS:HG3	1:D:2885:ASP:N	1.96	0.80
1:B:3246:MET:HE3	1:B:3276:LEU:HD22	1.62	0.80
1:D:3246:MET:HE3	1:D:3276:LEU:HD22	1.62	0.80
1:A:2884:LYS:HG3	1:A:2885:ASP:N	1.96	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3246:MET:HE3	1:C:3276:LEU:HD22	1.62	0.80
1:B:3235:MET:HA	1:B:3239:LEU:HD23	1.63	0.80
1:A:3246:MET:HE3	1:A:3276:LEU:HD22	1.62	0.80
1:B:2884:LYS:HG3	1:B:2885:ASP:N	1.96	0.79
1:C:2884:LYS:HG3	1:C:2885:ASP:N	1.96	0.78
1:A:2852:TRP:CD1	1:A:2856:LYS:HZ3	2.02	0.78
1:C:3231:MET:HE3	1:C:3233:HIS:HB2	1.66	0.78
1:D:1074:ARG:HH11	1:D:1077:VAL:H	1.31	0.78
1:D:2841:ALA:HA	1:D:2844:MET:HG3	1.65	0.78
1:C:981:MET:HE3	1:C:1059:GLY:HA3	1.66	0.78
1:D:2852:TRP:CD1	1:D:2856:LYS:HZ3	2.02	0.78
1:B:2841:ALA:HA	1:B:2844:MET:HG3	1.65	0.78
1:D:981:MET:HE3	1:D:1059:GLY:HA3	1.66	0.78
1:A:1074:ARG:HH11	1:A:1077:VAL:H	1.31	0.77
1:D:1947:VAL:HG22	1:D:1961:LYS:HE2	1.66	0.77
1:B:3231:MET:HE3	1:B:3233:HIS:HB2	1.66	0.77
1:A:2841:ALA:HA	1:A:2844:MET:HG3	1.65	0.77
1:C:1947:VAL:HG22	1:C:1961:LYS:HE2	1.66	0.77
1:D:3231:MET:HE3	1:D:3233:HIS:HB2	1.66	0.77
1:B:3312:PRO:HA	1:B:3315:LEU:HG	1.67	0.77
1:A:1947:VAL:HG22	1:A:1961:LYS:HE2	1.66	0.77
1:B:875:PRO:HD2	1:B:878:LEU:HD12	1.68	0.76
1:B:1074:ARG:HH11	1:B:1077:VAL:H	1.31	0.76
1:C:2852:TRP:CD1	1:C:2856:LYS:HZ3	2.03	0.76
1:B:2852:TRP:CD1	1:B:2856:LYS:HZ1	2.03	0.76
1:C:3072:MET:HE3	1:C:3136:SER:HB2	1.67	0.76
1:B:1947:VAL:HG22	1:B:1961:LYS:HE2	1.66	0.76
1:C:1074:ARG:HH11	1:C:1077:VAL:H	1.31	0.76
1:C:2841:ALA:HA	1:C:2844:MET:HG3	1.65	0.76
1:A:981:MET:HE3	1:A:1059:GLY:HA3	1.66	0.76
1:B:981:MET:HE3	1:B:1059:GLY:HA3	1.66	0.76
1:B:3072:MET:HE3	1:B:3136:SER:HB2	1.67	0.76
1:A:3231:MET:HE3	1:A:3233:HIS:HB2	1.66	0.76
1:D:3312:PRO:HA	1:D:3315:LEU:HG	1.67	0.76
1:A:875:PRO:HD2	1:A:878:LEU:HD12	1.68	0.76
1:D:2586:GLN:NE2	1:D:2636:GLU:OE1	2.19	0.75
1:D:3179:ASN:ND2	1:D:3265:CYS:SG	2.60	0.75
1:A:3227:ARG:HA	1:A:3290:ILE:HD12	1.68	0.75
1:C:2586:GLN:NE2	1:C:2636:GLU:OE1	2.19	0.75
1:A:2586:GLN:NE2	1:A:2636:GLU:OE1	2.19	0.75
1:C:3312:PRO:HA	1:C:3315:LEU:HG	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2586:GLN:NE2	1:B:2636:GLU:OE1	2.19	0.75
1:B:948:CYS:HA	1:B:1067:PRO:HD3	1.69	0.75
1:C:875:PRO:HD2	1:C:878:LEU:HD12	1.68	0.75
1:A:2142:MET:HG2	1:A:2192:MET:HE1	1.68	0.75
1:A:883:GLU:OE2	1:A:929:ARG:NH2	2.20	0.75
1:B:3227:ARG:HA	1:B:3290:ILE:HD12	1.68	0.75
1:C:3179:ASN:ND2	1:C:3265:CYS:SG	2.60	0.75
1:D:883:GLU:OE2	1:D:929:ARG:NH2	2.20	0.75
1:A:3312:PRO:HA	1:A:3315:LEU:HG	1.66	0.74
1:B:3179:ASN:ND2	1:B:3265:CYS:SG	2.60	0.74
1:C:883:GLU:OE2	1:C:929:ARG:NH2	2.20	0.74
1:A:3179:ASN:ND2	1:A:3265:CYS:SG	2.60	0.74
1:C:948:CYS:HA	1:C:1067:PRO:HD3	1.69	0.74
1:A:948:CYS:HA	1:A:1067:PRO:HD3	1.69	0.74
1:A:3072:MET:HE3	1:A:3136:SER:HB2	1.67	0.74
1:C:2142:MET:HG2	1:C:2192:MET:HE1	1.68	0.74
1:D:875:PRO:HD2	1:D:878:LEU:HD12	1.68	0.74
1:D:877:HIS:ND1	1:D:1062:TYR:OH	2.20	0.74
1:D:3227:ARG:HA	1:D:3290:ILE:HD12	1.68	0.74
1:C:3227:ARG:HA	1:C:3290:ILE:HD12	1.68	0.74
1:D:2142:MET:HG2	1:D:2192:MET:HE1	1.68	0.74
1:A:4690:LYS:HG3	1:A:4692:SER:H	1.53	0.74
1:D:3072:MET:HE3	1:D:3136:SER:HB2	1.67	0.74
1:B:2142:MET:HG2	1:B:2192:MET:HE1	1.68	0.73
1:A:877:HIS:ND1	1:A:1062:TYR:OH	2.20	0.73
1:B:2892:ILE:HG23	1:B:2893:LEU:HD23	1.71	0.73
1:C:877:HIS:ND1	1:C:1062:TYR:OH	2.20	0.73
1:D:948:CYS:HA	1:D:1067:PRO:HD3	1.69	0.73
1:B:877:HIS:ND1	1:B:1062:TYR:OH	2.20	0.73
1:C:2892:ILE:HG23	1:C:2893:LEU:HD23	1.71	0.73
1:D:2187:ILE:HG21	1:D:2227:VAL:HG13	1.71	0.73
1:D:4690:LYS:HG3	1:D:4692:SER:H	1.53	0.73
1:D:4268:MET:HA	1:D:4271:VAL:HG12	1.71	0.73
1:A:2187:ILE:HG21	1:A:2227:VAL:HG13	1.71	0.73
1:A:2758:LYS:HG3	1:A:2763:LEU:HD12	1.71	0.73
1:B:4268:MET:HA	1:B:4271:VAL:HG12	1.71	0.73
1:C:4690:LYS:HG3	1:C:4692:SER:H	1.53	0.73
1:D:2592:LEU:HD22	1:D:2610:LEU:HG	1.71	0.73
1:A:2592:LEU:HD22	1:A:2610:LEU:HG	1.71	0.72
1:A:4268:MET:HA	1:A:4271:VAL:HG12	1.71	0.72
1:B:883:GLU:OE2	1:B:929:ARG:NH2	2.20	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2592:LEU:HD22	1:C:2610:LEU:HG	1.71	0.72
1:C:4557:VAL:HG21	1:D:4790:ARG:HH22	1.54	0.72
1:B:520:ARG:NH1	1:B:524:GLU:OE2	2.23	0.72
1:A:2892:ILE:HG23	1:A:2893:LEU:HD23	1.71	0.72
1:B:2592:LEU:HD22	1:B:2610:LEU:HG	1.71	0.72
1:D:2436:ILE:O	1:D:2465:LYS:NZ	2.23	0.72
1:D:2892:ILE:HG23	1:D:2893:LEU:HD23	1.71	0.72
1:A:3111:HIS:O	1:A:3115:HIS:ND1	2.23	0.72
1:C:520:ARG:NH1	1:C:524:GLU:OE2	2.23	0.72
1:D:520:ARG:NH1	1:D:524:GLU:OE2	2.23	0.72
1:A:1499:GLY:HA3	1:D:2898:ILE:HD12	1.72	0.72
1:D:2758:LYS:HG3	1:D:2763:LEU:HD12	1.71	0.72
1:C:4268:MET:HA	1:C:4271:VAL:HG12	1.71	0.71
1:A:4652:LYS:NZ	1:A:4945:GLN:OE1	2.23	0.71
1:B:2187:ILE:HG21	1:B:2227:VAL:HG13	1.71	0.71
1:D:2998:ASN:ND2	1:D:3048:THR:OG1	2.24	0.71
1:D:3111:HIS:O	1:D:3115:HIS:ND1	2.23	0.71
1:A:2436:ILE:O	1:A:2465:LYS:NZ	2.23	0.71
1:B:2436:ILE:O	1:B:2465:LYS:NZ	2.23	0.71
1:C:2758:LYS:HG3	1:C:2763:LEU:HD12	1.71	0.71
1:B:4690:LYS:HG3	1:B:4692:SER:H	1.53	0.71
1:A:4520:TYR:HE2	1:A:4559:TYR:HB3	1.56	0.71
1:B:2758:LYS:HG3	1:B:2763:LEU:HD12	1.71	0.71
1:B:3111:HIS:O	1:B:3115:HIS:ND1	2.23	0.71
1:B:4520:TYR:HE2	1:B:4559:TYR:HB3	1.56	0.71
1:B:2998:ASN:ND2	1:B:3048:THR:OG1	2.24	0.71
1:B:4652:LYS:NZ	1:B:4945:GLN:OE1	2.23	0.71
1:C:2998:ASN:ND2	1:C:3048:THR:OG1	2.24	0.71
1:D:4520:TYR:HE2	1:D:4559:TYR:HB3	1.56	0.71
1:C:4520:TYR:HE2	1:C:4559:TYR:HB3	1.56	0.70
1:C:2436:ILE:O	1:C:2465:LYS:NZ	2.23	0.70
1:C:2758:LYS:HE3	1:C:2763:LEU:HA	1.73	0.70
1:C:3111:HIS:O	1:C:3115:HIS:ND1	2.23	0.70
1:B:2758:LYS:HE3	1:B:2763:LEU:HA	1.73	0.70
1:C:2187:ILE:HG21	1:C:2227:VAL:HG13	1.71	0.70
1:A:2998:ASN:ND2	1:A:3048:THR:OG1	2.24	0.70
1:C:4652:LYS:NZ	1:C:4945:GLN:OE1	2.24	0.70
1:D:2937:HIS:HB2	1:D:3014:LEU:HD21	1.73	0.70
1:A:2937:HIS:HB2	1:A:3014:LEU:HD21	1.72	0.70
1:D:2758:LYS:HE3	1:D:2763:LEU:HA	1.73	0.70
1:B:2937:HIS:HB2	1:B:3014:LEU:HD21	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:520:ARG:NH1	1:A:524:GLU:OE2	2.23	0.69
1:A:1473:LYS:HE3	1:A:1475:LYS:HB2	1.75	0.69
1:A:4046:ARG:NE	1:A:4046:ARG:HA	2.07	0.69
1:C:1473:LYS:HE3	1:C:1475:LYS:HB2	1.75	0.69
1:D:1473:LYS:HE3	1:D:1475:LYS:HB2	1.74	0.69
1:A:3242:LEU:HG	1:A:3246:MET:HE1	1.75	0.69
1:B:1473:LYS:HE3	1:B:1475:LYS:HB2	1.74	0.69
1:C:2937:HIS:HB2	1:C:3014:LEU:HD21	1.72	0.69
1:A:2758:LYS:HE3	1:A:2763:LEU:HA	1.73	0.69
1:A:1548:THR:O	1:D:2832:THR:OG1	2.10	0.69
1:A:3699:CYS:O	1:A:3727:GLN:NE2	2.25	0.69
1:B:3242:LEU:HG	1:B:3246:MET:HE1	1.75	0.69
1:B:3699:CYS:O	1:B:3727:GLN:NE2	2.26	0.69
1:C:4046:ARG:HA	1:C:4046:ARG:NE	2.07	0.69
1:C:3699:CYS:O	1:C:3727:GLN:NE2	2.26	0.68
1:D:678:MET:SD	1:D:801:ARG:NH2	2.66	0.68
1:D:3699:CYS:O	1:D:3727:GLN:NE2	2.26	0.68
1:A:4868:ASP:OD1	1:D:4874:ARG:NH1	2.25	0.68
1:B:4046:ARG:NE	1:B:4046:ARG:HA	2.07	0.68
1:C:3242:LEU:HG	1:C:3246:MET:HE1	1.75	0.68
1:D:3242:LEU:HG	1:D:3246:MET:HE1	1.75	0.68
1:D:4046:ARG:NE	1:D:4046:ARG:HA	2.07	0.68
1:D:3246:MET:HB3	1:D:3273:MET:HE1	1.76	0.68
1:C:678:MET:SD	1:C:801:ARG:NH2	2.66	0.68
1:B:678:MET:SD	1:B:801:ARG:NH2	2.67	0.68
1:C:59:PRO:O	1:C:319:LYS:NZ	2.26	0.68
1:D:4520:TYR:CE2	1:D:4559:TYR:HB3	2.29	0.68
1:D:713:TRP:HH2	1:D:1251:LEU:HD21	1.58	0.68
1:A:4060:GLN:HA	1:A:4060:GLN:NE2	2.02	0.68
1:D:4052:MET:HE2	1:D:4063:THR:HG23	1.76	0.67
1:A:4052:MET:HE2	1:A:4063:THR:HG23	1.76	0.67
1:C:3246:MET:HB3	1:C:3273:MET:HE1	1.76	0.67
1:D:1001:GLU:OE2	1:D:1005:ASN:ND2	2.26	0.67
1:D:4652:LYS:NZ	1:D:4945:GLN:OE1	2.24	0.67
1:B:3246:MET:O	1:B:3250:TRP:CD1	2.48	0.67
1:A:678:MET:SD	1:A:801:ARG:NH2	2.67	0.67
1:A:713:TRP:HH2	1:A:1251:LEU:HD21	1.58	0.67
1:A:4520:TYR:CE2	1:A:4559:TYR:HB3	2.29	0.67
1:C:335:LYS:NZ	1:C:398:HIS:O	2.27	0.67
1:D:59:PRO:O	1:D:319:LYS:NZ	2.26	0.67
1:A:59:PRO:O	1:A:319:LYS:NZ	2.26	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4052:MET:HE2	1:B:4063:THR:HG23	1.76	0.67
2:H:83:TYR:OH	1:D:1768:PHE:O	2.12	0.67
1:B:713:TRP:HH2	1:B:1251:LEU:HD21	1.58	0.67
1:D:3246:MET:O	1:D:3250:TRP:CD1	2.48	0.67
1:A:3246:MET:O	1:A:3250:TRP:CD1	2.48	0.67
1:B:1001:GLU:OE2	1:B:1005:ASN:ND2	2.26	0.67
1:C:713:TRP:HH2	1:C:1251:LEU:HD21	1.58	0.67
1:A:2134:MET:HE1	1:A:2192:MET:HE2	1.77	0.67
1:D:2134:MET:HE1	1:D:2192:MET:HE2	1.77	0.67
1:B:2326:ARG:HH22	1:C:189:GLU:HB3	1.60	0.66
1:B:3246:MET:HB3	1:B:3273:MET:HE1	1.76	0.66
1:D:335:LYS:NZ	1:D:398:HIS:O	2.27	0.66
1:B:854:THR:HG22	1:B:1210:ALA:HA	1.78	0.66
1:B:2134:MET:HE1	1:B:2192:MET:HE2	1.77	0.66
1:C:854:THR:HG22	1:C:1210:ALA:HA	1.78	0.66
1:D:3043:ARG:NH1	1:D:3116:GLN:O	2.29	0.66
1:C:2134:MET:HE1	1:C:2192:MET:HE2	1.77	0.66
1:C:3043:ARG:NH1	1:C:3116:GLN:O	2.29	0.66
1:D:880:ARG:NH1	1:D:881:ILE:HB	2.10	0.66
1:D:3032:CYS:HA	1:D:3035:ILE:HG12	1.78	0.66
1:D:2570:GLU:HG2	1:D:2605:MET:HG3	1.77	0.66
1:D:2670:SER:HB2	1:D:2973:GLN:HG2	1.77	0.66
1:A:2570:GLU:HG2	1:A:2605:MET:HG3	1.77	0.66
1:A:3246:MET:HB3	1:A:3273:MET:HE1	1.76	0.66
1:C:2852:TRP:CG	1:C:2856:LYS:HZ3	2.13	0.66
1:C:3032:CYS:HA	1:C:3035:ILE:HG12	1.78	0.66
1:D:3046:MET:HG3	1:D:3121:LEU:HA	1.77	0.66
1:A:1498:GLN:NE2	1:D:2795:GLY:HA2	2.11	0.66
1:A:2235:ARG:HH11	1:A:2297:ARG:HE	1.44	0.66
1:B:880:ARG:NH1	1:B:881:ILE:HB	2.10	0.66
1:B:2235:ARG:HH11	1:B:2297:ARG:HE	1.44	0.66
1:B:3043:ARG:NH1	1:B:3116:GLN:O	2.29	0.66
1:D:2235:ARG:HH11	1:D:2297:ARG:HE	1.44	0.66
1:A:335:LYS:NZ	1:A:398:HIS:O	2.27	0.66
1:A:880:ARG:NH1	1:A:881:ILE:HB	2.10	0.66
1:A:3043:ARG:NH1	1:A:3116:GLN:O	2.29	0.66
2:F:24:VAL:HG22	2:F:48:LYS:HG2	1.78	0.66
1:C:4520:TYR:CE2	1:C:4559:TYR:HB3	2.29	0.66
1:A:1001:GLU:OE2	1:A:1005:ASN:ND2	2.26	0.66
1:A:3032:CYS:HA	1:A:3035:ILE:HG12	1.78	0.66
2:E:24:VAL:HG22	2:E:48:LYS:HG2	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4052:MET:HE2	1:C:4063:THR:HG23	1.76	0.66
1:D:854:THR:HG22	1:D:1210:ALA:HA	1.78	0.66
1:B:2852:TRP:CG	1:B:2856:LYS:HZ1	2.13	0.66
1:C:3246:MET:O	1:C:3250:TRP:CD1	2.48	0.66
1:B:2570:GLU:HG2	1:B:2605:MET:HG3	1.77	0.65
1:B:2670:SER:HB2	1:B:2973:GLN:HG2	1.77	0.65
1:B:3046:MET:HG3	1:B:3121:LEU:HA	1.77	0.65
1:C:2235:ARG:HH11	1:C:2297:ARG:HE	1.44	0.65
1:D:2846:GLU:OE2	1:D:2850:ASN:ND2	2.29	0.65
1:C:2570:GLU:HG2	1:C:2605:MET:HG3	1.77	0.65
1:B:2846:GLU:OE2	1:B:2850:ASN:ND2	2.29	0.65
1:B:4520:TYR:CE2	1:B:4559:TYR:HB3	2.29	0.65
1:C:880:ARG:NH1	1:C:881:ILE:HB	2.10	0.65
1:C:2670:SER:HB2	1:C:2973:GLN:HG2	1.78	0.65
1:D:4060:GLN:HA	1:D:4060:GLN:NE2	2.02	0.65
1:C:882:ARG:HH22	1:C:937:LEU:HG	1.62	0.65
1:C:1001:GLU:OE2	1:C:1005:ASN:ND2	2.26	0.65
1:A:854:THR:HG22	1:A:1210:ALA:HA	1.78	0.65
1:B:335:LYS:NZ	1:B:398:HIS:O	2.27	0.65
1:C:2616:ARG:NE	1:C:2617:CYS:SG	2.69	0.65
1:A:3046:MET:HG3	1:A:3121:LEU:HA	1.77	0.65
1:B:2616:ARG:NE	1:B:2617:CYS:SG	2.69	0.65
1:B:4187:GLU:OE2	1:B:4947:ARG:NH2	2.30	0.65
1:C:2846:GLU:OE2	1:C:2850:ASN:ND2	2.29	0.65
1:A:2616:ARG:NE	1:A:2617:CYS:SG	2.69	0.65
1:A:2846:GLU:OE2	1:A:2850:ASN:ND2	2.29	0.65
1:B:3844:GLN:HG3	1:B:3922:GLU:HG3	1.78	0.65
2:G:24:VAL:HG22	2:G:48:LYS:HG2	1.78	0.65
1:B:59:PRO:O	1:B:319:LYS:NZ	2.26	0.65
1:B:1564:MET:HE2	1:B:1564:MET:HA	1.79	0.65
1:C:1564:MET:HA	1:C:1564:MET:HE2	1.79	0.65
1:B:3032:CYS:HA	1:B:3035:ILE:HG12	1.78	0.64
1:A:882:ARG:HH22	1:A:937:LEU:HG	1.62	0.64
1:A:2670:SER:HB2	1:A:2973:GLN:HG2	1.78	0.64
1:A:4187:GLU:OE2	1:A:4947:ARG:NH2	2.30	0.64
1:C:3046:MET:HG3	1:C:3121:LEU:HA	1.77	0.64
1:C:3135:THR:HA	1:C:3207:ASN:HD21	1.63	0.64
1:A:3171:LEU:HB3	1:A:3211:LEU:HB2	1.79	0.64
1:B:4060:GLN:HA	1:B:4060:GLN:NE2	2.02	0.64
1:C:4187:GLU:OE2	1:C:4947:ARG:NH2	2.30	0.64
1:A:3184:TYR:O	1:A:3192:ARG:NH2	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2666:LEU:HD11	1:C:2969:PRO:HB2	1.79	0.64
1:C:3844:GLN:HG3	1:C:3922:GLU:HG3	1.78	0.64
1:D:2616:ARG:NE	1:D:2617:CYS:SG	2.69	0.64
1:D:3135:THR:HA	1:D:3207:ASN:HD21	1.63	0.64
1:A:1937:GLN:NE2	1:A:3608:LEU:O	2.31	0.64
1:B:2834:SER:OG	1:B:2836:ASP:OD1	2.14	0.64
1:C:164:PRO:HB3	1:C:169:ARG:HB2	1.79	0.64
1:C:992:GLN:HA	1:C:995:MET:HE3	1.80	0.64
1:C:1937:GLN:NE2	1:C:3608:LEU:O	2.31	0.64
1:D:882:ARG:HH22	1:D:937:LEU:HG	1.62	0.64
1:A:1564:MET:HE2	1:A:1564:MET:HA	1.79	0.64
1:A:3844:GLN:HG3	1:A:3922:GLU:HG3	1.78	0.64
1:B:3222:ALA:O	1:B:3282:LYS:NZ	2.28	0.64
1:C:3222:ALA:O	1:C:3282:LYS:NZ	2.28	0.64
1:D:2277:CYS:HB3	1:D:2280:LEU:HB2	1.80	0.64
1:D:3844:GLN:HG3	1:D:3922:GLU:HG3	1.78	0.64
2:H:24:VAL:HG22	2:H:48:LYS:HG2	1.78	0.64
1:D:992:GLN:HA	1:D:995:MET:HE3	1.80	0.64
1:B:3135:THR:HA	1:B:3207:ASN:HD21	1.63	0.64
1:C:3171:LEU:HB3	1:C:3211:LEU:HB2	1.79	0.64
1:D:3184:TYR:O	1:D:3192:ARG:NH2	2.31	0.64
1:B:1144:ARG:NH1	1:B:1184:ASP:OD2	2.32	0.63
1:B:1937:GLN:NE2	1:B:3608:LEU:O	2.31	0.63
1:B:2899:ASN:C	1:C:1498:GLN:HE21	2.06	0.63
1:C:3184:TYR:O	1:C:3192:ARG:NH2	2.31	0.63
1:D:164:PRO:HB3	1:D:169:ARG:HB2	1.79	0.63
1:A:288:HIS:O	1:A:290:ARG:NH1	2.31	0.63
1:A:943:LEU:HA	1:A:946:LEU:HD12	1.80	0.63
1:A:2229:LEU:HA	1:A:2297:ARG:HH11	1.63	0.63
1:A:3135:THR:HA	1:A:3207:ASN:HD21	1.63	0.63
1:B:882:ARG:HH22	1:B:937:LEU:HG	1.62	0.63
1:C:288:HIS:O	1:C:290:ARG:NH1	2.31	0.63
1:C:2488:LEU:HD11	1:C:2548:LEU:HD13	1.81	0.63
1:D:943:LEU:HA	1:D:946:LEU:HD12	1.80	0.63
1:D:2666:LEU:HD11	1:D:2969:PRO:HB2	1.79	0.63
1:D:2834:SER:OG	1:D:2836:ASP:OD1	2.14	0.63
1:A:3043:ARG:HH11	1:A:3117:PHE:HA	1.63	0.63
1:B:3043:ARG:HH11	1:B:3117:PHE:HA	1.62	0.63
1:C:1910:LEU:HD13	1:C:2062:ILE:HG12	1.80	0.63
1:A:3914:LYS:NZ	1:A:3977:ASP:OD2	2.31	0.63
1:B:164:PRO:HB3	1:B:169:ARG:HB2	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:801:ARG:HD3	1:B:1611:ILE:HD12	1.81	0.63
1:B:3184:TYR:O	1:B:3192:ARG:NH2	2.31	0.63
1:D:1564:MET:HE2	1:D:1564:MET:HA	1.79	0.63
1:A:164:PRO:HB3	1:A:169:ARG:HB2	1.79	0.63
1:A:1498:GLN:HE21	1:D:2899:ASN:C	2.04	0.63
1:B:3914:LYS:NZ	1:B:3977:ASP:OD2	2.31	0.63
1:A:1097:LYS:NZ	1:A:1198:GLY:O	2.32	0.63
1:D:2386:ASN:ND2	1:D:2457:SER:O	2.28	0.63
1:D:3171:LEU:HB3	1:D:3211:LEU:HB2	1.79	0.63
1:C:2229:LEU:HA	1:C:2297:ARG:HH11	1.64	0.63
1:D:2229:LEU:HA	1:D:2297:ARG:HH11	1.63	0.63
1:A:801:ARG:HD3	1:A:1611:ILE:HD12	1.81	0.63
1:A:3043:ARG:NH1	1:A:3117:PHE:HA	2.14	0.63
1:B:1910:LEU:HD13	1:B:2062:ILE:HG12	1.80	0.63
1:C:1097:LYS:NZ	1:C:1198:GLY:O	2.32	0.63
1:D:2488:LEU:HD11	1:D:2548:LEU:HD13	1.81	0.63
1:D:2933:VAL:HG22	1:D:2963:PHE:HE1	1.63	0.63
1:D:3043:ARG:HH11	1:D:3117:PHE:HA	1.62	0.63
1:D:4187:GLU:OE2	1:D:4947:ARG:NH2	2.30	0.63
1:A:992:GLN:HA	1:A:995:MET:HE3	1.80	0.63
1:B:3171:LEU:HB3	1:B:3211:LEU:HB2	1.79	0.63
1:C:3914:LYS:NZ	1:C:3977:ASP:OD2	2.31	0.63
1:D:1144:ARG:NH1	1:D:1184:ASP:OD2	2.31	0.63
1:D:1937:GLN:NE2	1:D:3608:LEU:O	2.31	0.63
1:D:3043:ARG:NH1	1:D:3117:PHE:HA	2.14	0.63
1:A:2933:VAL:HG22	1:A:2963:PHE:HE1	1.63	0.62
1:A:3249:TRP:HB3	1:A:3266:THR:HG21	1.81	0.62
1:A:3846:LEU:HB3	1:A:3854:PHE:CE2	2.34	0.62
1:B:1097:LYS:NZ	1:B:1198:GLY:O	2.32	0.62
1:B:2488:LEU:HD11	1:B:2548:LEU:HD13	1.81	0.62
1:B:2975:PHE:HB2	1:B:3035:ILE:HD12	1.81	0.62
1:C:943:LEU:HA	1:C:946:LEU:HD12	1.80	0.62
1:C:2975:PHE:HB2	1:C:3035:ILE:HD12	1.81	0.62
1:D:3249:TRP:HB3	1:D:3266:THR:HG21	1.81	0.62
1:B:963:LYS:HB3	1:B:977:LYS:HE3	1.81	0.62
1:B:3043:ARG:NH1	1:B:3117:PHE:HA	2.14	0.62
1:D:963:LYS:HB3	1:D:977:LYS:HE3	1.81	0.62
1:D:3914:LYS:NZ	1:D:3977:ASP:OD2	2.32	0.62
1:A:963:LYS:HB3	1:A:977:LYS:HE3	1.81	0.62
1:A:1144:ARG:NH1	1:A:1184:ASP:OD2	2.32	0.62
1:B:2277:CYS:HB3	1:B:2280:LEU:HB2	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:801:ARG:HD3	1:C:1611:ILE:HD12	1.81	0.62
1:D:2496:LEU:HD23	1:D:2520:LEU:HD13	1.81	0.62
1:A:1910:LEU:HD13	1:A:2062:ILE:HG12	1.80	0.62
1:A:2975:PHE:HB2	1:A:3035:ILE:HD12	1.81	0.62
1:B:2666:LEU:HD11	1:B:2969:PRO:HB2	1.80	0.62
1:C:3043:ARG:NH1	1:C:3117:PHE:HA	2.14	0.62
1:C:3043:ARG:HH11	1:C:3117:PHE:HA	1.63	0.62
1:C:3846:LEU:HB3	1:C:3854:PHE:CE2	2.35	0.62
1:D:1097:LYS:NZ	1:D:1198:GLY:O	2.32	0.62
1:A:2277:CYS:HB3	1:A:2280:LEU:HB2	1.80	0.62
1:B:288:HIS:O	1:B:290:ARG:NH1	2.31	0.62
1:C:963:LYS:HB3	1:C:977:LYS:HE3	1.81	0.62
1:C:1144:ARG:NH1	1:C:1184:ASP:OD2	2.31	0.62
1:C:2277:CYS:HB3	1:C:2280:LEU:HB2	1.80	0.62
1:C:3249:TRP:HB3	1:C:3266:THR:HG21	1.81	0.62
1:B:992:GLN:HA	1:B:995:MET:HE3	1.80	0.62
1:B:2229:LEU:HA	1:B:2297:ARG:HH11	1.63	0.62
1:B:3846:LEU:HB3	1:B:3854:PHE:CE2	2.35	0.62
1:D:801:ARG:HD3	1:D:1611:ILE:HD12	1.81	0.62
1:A:2666:LEU:HD11	1:A:2969:PRO:HB2	1.80	0.62
1:B:2496:LEU:HD23	1:B:2520:LEU:HD13	1.81	0.62
1:B:2933:VAL:HG22	1:B:2963:PHE:HE1	1.63	0.62
1:D:288:HIS:O	1:D:290:ARG:NH1	2.31	0.62
1:C:2920:ARG:HH22	1:C:2997:SER:H	1.47	0.62
1:D:2975:PHE:HB2	1:D:3035:ILE:HD12	1.81	0.62
1:A:2496:LEU:HD23	1:A:2520:LEU:HD13	1.81	0.62
1:B:943:LEU:HA	1:B:946:LEU:HD12	1.80	0.62
1:B:2827:ASP:H	1:C:1501:ASN:CG	2.08	0.62
1:B:3249:TRP:HB3	1:B:3266:THR:HG21	1.82	0.61
1:C:4060:GLN:HA	1:C:4060:GLN:NE2	2.02	0.61
1:D:1129:GLY:HA3	1:D:1145:TRP:HB3	1.82	0.61
1:D:2727:HIS:CE1	1:D:2826:ILE:HG21	2.36	0.61
1:C:1268:ILE:HD11	1:C:1300:MET:HE2	1.82	0.61
1:A:2488:LEU:HD11	1:A:2548:LEU:HD13	1.81	0.61
1:C:2727:HIS:CE1	1:C:2826:ILE:HG21	2.36	0.61
1:C:3294:ALA:HA	1:C:3297:LYS:HD3	1.82	0.61
1:D:1268:ILE:HD11	1:D:1300:MET:HE2	1.82	0.61
1:D:1910:LEU:HD13	1:D:2062:ILE:HG12	1.80	0.61
1:D:3846:LEU:HB3	1:D:3854:PHE:CE2	2.35	0.61
1:A:1129:GLY:HA3	1:A:1145:TRP:HB3	1.82	0.61
1:C:1129:GLY:HA3	1:C:1145:TRP:HB3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2933:VAL:HG22	1:C:2963:PHE:HE1	1.63	0.61
1:A:2920:ARG:HH22	1:A:2997:SER:H	1.47	0.61
1:B:2920:ARG:HH22	1:B:2997:SER:H	1.47	0.61
1:A:2727:HIS:CE1	1:A:2826:ILE:HG21	2.36	0.61
1:B:2385:GLY:O	1:B:2389:MET:HG3	2.01	0.61
1:C:2496:LEU:HD23	1:C:2520:LEU:HD13	1.81	0.61
1:B:1420:LEU:HD22	1:B:1564:MET:HE3	1.83	0.61
1:D:2920:ARG:HH22	1:D:2997:SER:H	1.47	0.61
1:A:1268:ILE:HD11	1:A:1300:MET:HE2	1.82	0.61
1:B:2727:HIS:CE1	1:B:2826:ILE:HG21	2.36	0.61
1:C:2385:GLY:O	1:C:2389:MET:HG3	2.01	0.61
1:A:1420:LEU:HD22	1:A:1564:MET:HE3	1.83	0.61
1:B:1129:GLY:HA3	1:B:1145:TRP:HB3	1.82	0.61
1:D:137:ARG:NE	1:D:139:SER:OG	2.34	0.61
1:C:658:ASN:HD21	1:C:833:LYS:HG2	1.66	0.61
1:A:2385:GLY:O	1:A:2389:MET:HG3	2.01	0.60
1:B:2830:ASN:HB3	1:C:1549:SER:HB2	1.82	0.60
1:D:3294:ALA:HA	1:D:3297:LYS:HD3	1.81	0.60
1:B:882:ARG:HH21	1:B:937:LEU:N	1.99	0.60
1:B:2759:PRO:HG2	1:B:2762:LEU:HD13	1.83	0.60
1:B:4177:VAL:HG11	1:B:4880:VAL:HA	1.84	0.60
1:A:2759:PRO:HG2	1:A:2762:LEU:HD13	1.83	0.60
1:B:2337:GLY:O	1:C:141:ASP:HA	2.01	0.60
1:C:4622:SER:OG	1:C:4624:ASP:OD1	2.17	0.60
1:D:658:ASN:HD21	1:D:833:LYS:HG2	1.66	0.60
1:D:2127:ARG:NH2	1:D:2165:LEU:O	2.35	0.60
1:A:4819:VAL:HG12	1:A:4830:GLU:HG3	1.84	0.60
1:B:137:ARG:NE	1:B:139:SER:OG	2.34	0.60
1:C:137:ARG:NE	1:C:139:SER:OG	2.34	0.60
1:C:591:GLU:HG3	1:C:631:LEU:HD22	1.84	0.60
1:D:882:ARG:HH21	1:D:937:LEU:N	1.99	0.60
1:D:4751:LYS:HA	1:D:4754:ARG:HH11	1.67	0.60
1:A:977:LYS:NZ	1:A:979:ALA:O	2.34	0.60
1:B:977:LYS:NZ	1:B:979:ALA:O	2.35	0.60
1:B:3246:MET:CE	1:B:3276:LEU:HD22	2.32	0.60
1:B:3294:ALA:HA	1:B:3297:LYS:HD3	1.82	0.60
1:D:2385:GLY:O	1:D:2389:MET:HG3	2.01	0.60
1:A:658:ASN:HD21	1:A:833:LYS:HG2	1.66	0.60
1:B:1268:ILE:HD11	1:B:1300:MET:HE2	1.82	0.60
1:C:2232:PRO:HG2	1:C:2379:ASP:HA	1.84	0.60
1:C:4177:VAL:HG11	1:C:4880:VAL:HA	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2122:SER:O	1:D:2126:ILE:HG12	2.02	0.60
1:B:293:GLN:HB2	1:B:343:ARG:HH22	1.67	0.60
1:B:4819:VAL:HG12	1:B:4830:GLU:HG3	1.84	0.60
1:C:1420:LEU:HD22	1:C:1564:MET:HE3	1.83	0.60
1:C:1471:ASP:OD1	1:C:1475:LYS:N	2.34	0.60
1:C:4751:LYS:HA	1:C:4754:ARG:HH11	1.67	0.60
1:D:1471:ASP:OD1	1:D:1475:LYS:N	2.34	0.60
1:D:2852:TRP:CG	1:D:2856:LYS:HZ3	2.20	0.60
1:A:137:ARG:NE	1:A:139:SER:OG	2.34	0.60
1:A:2232:PRO:HG2	1:A:2379:ASP:HA	1.84	0.60
1:A:3269:ASN:HB2	1:A:3272:HIS:ND1	2.17	0.60
1:B:2122:SER:O	1:B:2126:ILE:HG12	2.02	0.60
1:B:2127:ARG:NH2	1:B:2165:LEU:O	2.35	0.60
1:B:3606:ALA:HB1	1:B:3610:ASN:HB2	1.84	0.60
1:D:1420:LEU:HD22	1:D:1564:MET:HE3	1.83	0.60
1:A:3287:ASN:ND2	1:A:3295:TRP:HH2	2.00	0.60
1:A:3294:ALA:HA	1:A:3297:LYS:HD3	1.81	0.60
1:A:3606:ALA:HB1	1:A:3610:ASN:HB2	1.84	0.60
1:C:977:LYS:NZ	1:C:979:ALA:O	2.35	0.60
1:D:3222:ALA:O	1:D:3282:LYS:NZ	2.28	0.60
1:D:3269:ASN:HB2	1:D:3272:HIS:ND1	2.17	0.60
1:A:882:ARG:HH21	1:A:937:LEU:N	1.99	0.60
1:A:4177:VAL:HG11	1:A:4880:VAL:HA	1.84	0.60
1:B:3269:ASN:HB2	1:B:3272:HIS:ND1	2.17	0.60
1:C:293:GLN:HB2	1:C:343:ARG:HH22	1.67	0.60
1:D:591:GLU:HG3	1:D:631:LEU:HD22	1.84	0.60
1:D:2759:PRO:HG2	1:D:2762:LEU:HD13	1.83	0.60
1:D:2851:ILE:O	1:D:2855:LYS:HE2	2.02	0.60
1:D:3287:ASN:ND2	1:D:3295:TRP:HH2	2.00	0.60
1:D:4832:GLU:O	1:D:4843:ARG:NH2	2.35	0.60
1:A:2122:SER:O	1:A:2126:ILE:HG12	2.02	0.59
1:C:3246:MET:CE	1:C:3276:LEU:HD22	2.32	0.59
1:B:3074:ASN:OD1	1:B:3075:LEU:N	2.35	0.59
1:C:882:ARG:HH21	1:C:937:LEU:N	1.99	0.59
1:C:4520:TYR:H	1:D:4809:MET:HB2	1.67	0.59
1:D:977:LYS:NZ	1:D:979:ALA:O	2.35	0.59
1:D:1074:ARG:HD3	1:D:1077:VAL:HB	1.85	0.59
1:A:4622:SER:OG	1:A:4624:ASP:OD1	2.17	0.59
1:B:658:ASN:HD21	1:B:833:LYS:HG2	1.66	0.59
1:B:2769:GLU:O	1:B:2771:TYR:N	2.31	0.59
1:C:2127:ARG:NH2	1:C:2165:LEU:O	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2759:PRO:HG2	1:C:2762:LEU:HD13	1.83	0.59
1:C:3606:ALA:HB1	1:C:3610:ASN:HB2	1.84	0.59
1:D:1495:SER:HB2	1:D:1525:LYS:HE3	1.85	0.59
1:A:4832:GLU:O	1:A:4843:ARG:NH2	2.35	0.59
1:B:2222:LEU:HB3	1:B:2264:LYS:HD2	1.84	0.59
1:C:4832:GLU:O	1:C:4843:ARG:NH2	2.35	0.59
1:D:995:MET:HA	1:D:998:LYS:HE2	1.84	0.59
1:A:2127:ARG:NH2	1:A:2165:LEU:O	2.35	0.59
1:A:2222:LEU:HB3	1:A:2264:LYS:HD2	1.84	0.59
1:A:2724:TYR:HE2	1:A:2775:ILE:HG12	1.68	0.59
1:B:1471:ASP:OD1	1:B:1475:LYS:N	2.34	0.59
1:B:2232:PRO:HG2	1:B:2379:ASP:HA	1.84	0.59
1:B:2724:TYR:HE2	1:B:2775:ILE:HG12	1.68	0.59
1:C:2122:SER:O	1:C:2126:ILE:HG12	2.02	0.59
1:C:2386:ASN:ND2	1:C:2457:SER:O	2.28	0.59
1:C:2851:ILE:O	1:C:2855:LYS:HE2	2.02	0.59
1:A:3277:LEU:HD21	1:A:3319:PHE:HZ	1.68	0.59
1:B:1074:ARG:HD3	1:B:1077:VAL:HB	1.85	0.59
1:C:3287:ASN:ND2	1:C:3295:TRP:HH2	2.00	0.59
1:D:3606:ALA:HB1	1:D:3610:ASN:HB2	1.84	0.59
1:D:4177:VAL:HG11	1:D:4880:VAL:HA	1.84	0.59
1:A:473:GLU:OE2	1:A:477:ASN:ND2	2.36	0.59
1:B:1495:SER:HB2	1:B:1525:LYS:HE3	1.85	0.59
1:B:2851:ILE:O	1:B:2855:LYS:HE2	2.02	0.59
1:B:3277:LEU:HD21	1:B:3319:PHE:HZ	1.68	0.59
1:B:4832:GLU:O	1:B:4843:ARG:NH2	2.35	0.59
1:C:769:ARG:HG2	1:C:774:PRO:HA	1.85	0.59
1:A:1074:ARG:HD3	1:A:1077:VAL:HB	1.85	0.59
1:B:769:ARG:HG2	1:B:774:PRO:HA	1.85	0.59
1:B:3140:LEU:HD13	1:B:3155:LEU:HD22	1.85	0.59
1:C:2445:ILE:HG22	1:C:2451:VAL:HG22	1.85	0.59
1:C:3269:ASN:HB2	1:C:3272:HIS:ND1	2.17	0.59
1:A:293:GLN:HB2	1:A:343:ARG:HH22	1.67	0.59
1:A:591:GLU:HG3	1:A:631:LEU:HD22	1.84	0.59
1:A:995:MET:HA	1:A:998:LYS:HE2	1.84	0.59
1:A:1495:SER:HB2	1:A:1525:LYS:HE3	1.85	0.59
1:A:2445:ILE:HG22	1:A:2451:VAL:HG22	1.85	0.59
1:A:3140:LEU:HD13	1:A:3155:LEU:HD22	1.85	0.59
1:A:4751:LYS:HA	1:A:4754:ARG:HH11	1.67	0.59
1:B:2214:MET:HA	1:B:2214:MET:HE2	1.84	0.59
1:B:3287:ASN:ND2	1:B:3295:TRP:HH2	2.00	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2834:SER:OG	1:A:2836:ASP:OD1	2.14	0.59
1:D:2222:LEU:HB3	1:D:2264:LYS:HD2	1.84	0.59
1:D:2232:PRO:HG2	1:D:2379:ASP:HA	1.84	0.59
1:D:2724:TYR:HE2	1:D:2775:ILE:HG12	1.68	0.59
1:A:769:ARG:HG2	1:A:774:PRO:HA	1.85	0.58
1:A:2275:GLN:NE2	1:A:2278:GLN:OE1	2.36	0.58
1:C:2721:ILE:HD11	1:C:2779:LEU:HD22	1.85	0.58
1:C:3074:ASN:OD1	1:C:3075:LEU:N	2.35	0.58
1:D:769:ARG:HG2	1:D:774:PRO:HA	1.85	0.58
1:D:1498:GLN:HG2	1:D:1499:GLY:H	1.68	0.58
1:D:3074:ASN:OD1	1:D:3075:LEU:N	2.36	0.58
1:D:3246:MET:CE	1:D:3276:LEU:HD22	2.32	0.58
1:D:4819:VAL:HG12	1:D:4830:GLU:HG3	1.84	0.58
1:A:3074:ASN:OD1	1:A:3075:LEU:N	2.36	0.58
2:G:22:THR:HG22	2:G:50:ARG:HG2	1.85	0.58
2:H:22:THR:HG22	2:H:50:ARG:HG2	1.85	0.58
1:B:473:GLU:OE2	1:B:477:ASN:ND2	2.36	0.58
1:C:995:MET:HA	1:C:998:LYS:HE2	1.84	0.58
1:C:2275:GLN:NE2	1:C:2278:GLN:OE1	2.36	0.58
1:C:4819:VAL:HG12	1:C:4830:GLU:HG3	1.84	0.58
1:D:2721:ILE:HD11	1:D:2779:LEU:HD22	1.85	0.58
1:A:877:HIS:HD1	1:A:1062:TYR:HH	1.44	0.58
1:A:2851:ILE:O	1:A:2855:LYS:HE2	2.02	0.58
1:B:591:GLU:HG3	1:B:631:LEU:HD22	1.84	0.58
1:B:995:MET:HA	1:B:998:LYS:HE2	1.84	0.58
1:B:2251:ASN:HB3	1:B:3819:MET:HE1	1.85	0.58
1:B:2445:ILE:HG22	1:B:2451:VAL:HG22	1.85	0.58
1:B:4751:LYS:HA	1:B:4754:ARG:HH11	1.66	0.58
1:C:1074:ARG:HD3	1:C:1077:VAL:HB	1.85	0.58
1:D:473:GLU:OE2	1:D:477:ASN:ND2	2.36	0.58
1:C:3043:ARG:HD3	1:C:3117:PHE:CD1	2.39	0.58
1:D:293:GLN:HB2	1:D:343:ARG:HH22	1.67	0.58
1:A:2852:TRP:CG	1:A:2856:LYS:HZ3	2.22	0.58
1:A:3222:ALA:O	1:A:3282:LYS:NZ	2.28	0.58
1:B:2275:GLN:NE2	1:B:2278:GLN:OE1	2.36	0.58
1:B:3043:ARG:HD3	1:B:3117:PHE:CD1	2.39	0.58
1:D:4622:SER:OG	1:D:4624:ASP:OD1	2.17	0.58
1:A:1471:ASP:OD1	1:A:1475:LYS:N	2.34	0.58
1:A:3043:ARG:HD3	1:A:3117:PHE:CD1	2.39	0.58
1:C:2214:MET:HE2	1:C:2214:MET:HA	1.84	0.58
1:A:2251:ASN:HB3	1:A:3819:MET:HE1	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4773:LEU:HD13	1:D:4753:LEU:HD21	1.84	0.58
1:C:1495:SER:HB2	1:C:1525:LYS:HE3	1.85	0.58
1:D:605:GLY:HA2	1:D:1585:ARG:HD2	1.86	0.58
1:D:2445:ILE:HG22	1:D:2451:VAL:HG22	1.85	0.58
1:A:4943:MET:HE1	1:A:4950:GLU:HB2	1.86	0.58
2:E:22:THR:HG22	2:E:50:ARG:HG2	1.85	0.58
1:B:2386:ASN:ND2	1:B:2457:SER:O	2.28	0.58
1:C:3277:LEU:HD21	1:C:3319:PHE:HZ	1.68	0.58
1:D:3043:ARG:HD3	1:D:3117:PHE:CD1	2.39	0.58
1:D:3140:LEU:HD13	1:D:3155:LEU:HD22	1.85	0.58
1:D:3277:LEU:HD21	1:D:3319:PHE:HZ	1.68	0.58
1:D:4027:THR:HA	1:D:4032:PHE:CD1	2.39	0.58
1:A:2721:ILE:HD11	1:A:2779:LEU:HD22	1.85	0.58
1:A:3653:GLU:OE2	1:A:3660:ARG:NH2	2.37	0.58
1:B:434:ASP:OD1	1:B:504:ARG:NE	2.37	0.58
1:C:605:GLY:HA2	1:C:1585:ARG:HD2	1.86	0.58
1:A:2593:VAL:HG21	1:A:2640:LEU:HD11	1.85	0.58
1:A:4027:THR:HA	1:A:4032:PHE:CD1	2.39	0.58
1:C:473:GLU:OE2	1:C:477:ASN:ND2	2.36	0.58
1:C:2724:TYR:HE2	1:C:2775:ILE:HG12	1.68	0.58
1:D:2251:ASN:HB3	1:D:3819:MET:HE1	1.85	0.58
1:D:2275:GLN:NE2	1:D:2278:GLN:OE1	2.36	0.58
1:D:2443:PRO:HG2	1:D:2502:LEU:HD21	1.86	0.58
1:D:2593:VAL:HG21	1:D:2640:LEU:HD11	1.85	0.58
1:D:2769:GLU:O	1:D:2771:TYR:N	2.31	0.58
1:A:1498:GLN:HG2	1:A:1499:GLY:H	1.68	0.57
1:A:2691:LYS:HG3	1:A:2694:SER:H	1.69	0.57
1:A:3246:MET:CE	1:A:3276:LEU:HD22	2.31	0.57
1:B:4027:THR:HA	1:B:4032:PHE:CD1	2.39	0.57
1:C:1058:LEU:HD12	1:C:1063:ASN:HB3	1.86	0.57
1:A:434:ASP:OD1	1:A:504:ARG:NE	2.37	0.57
1:A:1433:PHE:HB3	1:D:2830:ASN:HD22	1.67	0.57
1:A:2443:PRO:HG2	1:A:2502:LEU:HD21	1.86	0.57
1:B:891:GLU:O	1:B:895:MET:HG2	2.05	0.57
1:C:1498:GLN:HG2	1:C:1499:GLY:H	1.68	0.57
1:B:1498:GLN:HG2	1:B:1499:GLY:H	1.68	0.57
1:C:2251:ASN:HB3	1:C:3819:MET:HE1	1.85	0.57
1:D:2214:MET:HE2	1:D:2214:MET:HA	1.84	0.57
1:A:2214:MET:HE2	1:A:2214:MET:HA	1.84	0.57
1:B:2593:VAL:HG21	1:B:2640:LEU:HD11	1.85	0.57
1:B:4943:MET:HE1	1:B:4950:GLU:HB2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3796:LEU:HD22	1:B:3835:PHE:HZ	1.69	0.57
1:C:2222:LEU:HB3	1:C:2264:LYS:HD2	1.84	0.57
1:C:3140:LEU:HD13	1:C:3155:LEU:HD22	1.85	0.57
1:D:4943:MET:HE1	1:D:4950:GLU:HB2	1.86	0.57
1:A:891:GLU:O	1:A:895:MET:HG2	2.05	0.57
1:A:2386:ASN:ND2	1:A:2457:SER:O	2.28	0.57
2:F:22:THR:HG22	2:F:50:ARG:HG2	1.85	0.57
1:B:2721:ILE:HD11	1:B:2779:LEU:HD22	1.85	0.57
1:C:2691:LYS:HG3	1:C:2694:SER:H	1.69	0.57
1:D:434:ASP:OD1	1:D:504:ARG:NE	2.37	0.57
1:A:1498:GLN:CD	1:D:2795:GLY:HA2	2.29	0.57
1:B:2691:LYS:HG3	1:B:2694:SER:H	1.69	0.57
1:B:3653:GLU:OE2	1:B:3660:ARG:NH2	2.37	0.57
1:B:1438:PRO:HG3	1:B:1500:ARG:HH12	1.69	0.57
1:B:2443:PRO:HG2	1:B:2502:LEU:HD21	1.86	0.57
1:B:2768:LYS:O	1:B:2772:ARG:HG3	2.05	0.57
1:C:2443:PRO:HG2	1:C:2502:LEU:HD21	1.86	0.57
1:C:4027:THR:HA	1:C:4032:PHE:CD1	2.39	0.57
1:D:2768:LYS:O	1:D:2772:ARG:HG3	2.05	0.57
1:D:3653:GLU:OE2	1:D:3660:ARG:NH2	2.37	0.57
1:A:2768:LYS:O	1:A:2772:ARG:HG3	2.05	0.57
1:C:2593:VAL:HG21	1:C:2640:LEU:HD11	1.85	0.57
1:C:2834:SER:OG	1:C:2836:ASP:OD1	2.14	0.57
1:C:3653:GLU:OE2	1:C:3660:ARG:NH2	2.37	0.57
1:C:4818:TYR:HD1	1:D:4848:ILE:HD11	1.70	0.57
1:D:891:GLU:O	1:D:895:MET:HG2	2.05	0.57
1:D:2691:LYS:HG3	1:D:2694:SER:H	1.70	0.57
1:A:876:PRO:HA	1:A:879:GLU:HG3	1.87	0.57
1:A:4028:SER:O	1:A:4033:LYS:NZ	2.38	0.57
1:B:1058:LEU:HD12	1:B:1063:ASN:HB3	1.86	0.57
1:A:2971:ILE:HG23	1:A:2975:PHE:CE2	2.40	0.56
1:A:3796:LEU:HD22	1:A:3835:PHE:HZ	1.69	0.56
1:A:605:GLY:HA2	1:A:1585:ARG:HD2	1.86	0.56
1:C:876:PRO:HA	1:C:879:GLU:HG3	1.87	0.56
1:C:891:GLU:O	1:C:895:MET:HG2	2.05	0.56
1:C:1438:PRO:HG3	1:C:1500:ARG:HH12	1.69	0.56
1:C:2691:LYS:NZ	1:C:2846:GLU:OE2	2.30	0.56
1:D:1438:PRO:HG3	1:D:1500:ARG:HH12	1.69	0.56
1:D:4028:SER:O	1:D:4033:LYS:NZ	2.38	0.56
1:A:2312:SER:OG	1:A:2474:ARG:NH2	2.39	0.56
1:A:2318:ASN:O	1:A:2322:ARG:HD3	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:644:LEU:HD13	1:B:1630:LEU:HD21	1.87	0.56
1:B:3332:THR:HG22	1:B:3334:VAL:H	1.71	0.56
1:C:644:LEU:HD13	1:C:1630:LEU:HD21	1.87	0.56
1:C:1438:PRO:HB2	1:C:1494:MET:HE2	1.88	0.56
1:C:3332:THR:HG22	1:C:3334:VAL:H	1.71	0.56
1:C:3796:LEU:HD22	1:C:3835:PHE:HZ	1.69	0.56
1:D:2312:SER:OG	1:D:2474:ARG:NH2	2.39	0.56
1:D:3241:MET:O	1:D:3245:TYR:CB	2.54	0.56
1:D:3332:THR:HG22	1:D:3334:VAL:H	1.70	0.56
1:D:3796:LEU:HD22	1:D:3835:PHE:HZ	1.69	0.56
1:A:3241:MET:O	1:A:3245:TYR:CB	2.54	0.56
1:A:3332:THR:HG22	1:A:3334:VAL:H	1.71	0.56
1:B:876:PRO:HA	1:B:879:GLU:HG3	1.86	0.56
1:B:876:PRO:O	1:B:879:GLU:HG3	2.05	0.56
1:B:2312:SER:OG	1:B:2474:ARG:NH2	2.39	0.56
1:B:3241:MET:O	1:B:3245:TYR:CB	2.54	0.56
1:C:434:ASP:OD1	1:C:504:ARG:NE	2.37	0.56
1:C:4028:SER:O	1:C:4033:LYS:NZ	2.38	0.56
1:C:4943:MET:HE1	1:C:4950:GLU:HB2	1.86	0.56
1:B:605:GLY:HA2	1:B:1585:ARG:HD2	1.86	0.56
1:B:1438:PRO:HB2	1:B:1494:MET:HE2	1.88	0.56
1:B:2318:ASN:O	1:B:2322:ARG:HD3	2.05	0.56
1:C:2971:ILE:HG23	1:C:2975:PHE:CE2	2.40	0.56
1:C:3241:MET:O	1:C:3245:TYR:CB	2.54	0.56
1:D:644:LEU:HD13	1:D:1630:LEU:HD21	1.87	0.56
1:D:2318:ASN:O	1:D:2322:ARG:HD3	2.06	0.56
1:D:2651:ALA:O	1:D:2655:LYS:HB2	2.06	0.56
1:D:2971:ILE:HG23	1:D:2975:PHE:CE2	2.40	0.56
1:D:3097:THR:HA	1:D:3101:LEU:HG	1.88	0.56
1:B:3166:PHE:CE2	1:B:3168:VAL:HB	2.41	0.56
1:C:2312:SER:OG	1:C:2474:ARG:NH2	2.39	0.56
1:C:2318:ASN:O	1:C:2322:ARG:HD3	2.05	0.56
1:C:2651:ALA:O	1:C:2655:LYS:HB2	2.06	0.56
1:C:3166:PHE:CE2	1:C:3168:VAL:HB	2.41	0.56
1:D:1722:ASN:O	1:D:1919:ARG:NH2	2.39	0.56
1:A:876:PRO:O	1:A:879:GLU:HG3	2.05	0.56
1:A:1438:PRO:HG3	1:A:1500:ARG:HH12	1.69	0.56
1:B:1722:ASN:O	1:B:1919:ARG:NH2	2.39	0.56
1:C:271:ALA:HB2	1:C:488:LEU:HD22	1.88	0.56
1:A:1058:LEU:HD12	1:A:1063:ASN:HB3	1.86	0.56
1:A:1722:ASN:O	1:A:1919:ARG:NH2	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2651:ALA:O	1:A:2655:LYS:HB2	2.06	0.56
1:A:3005:THR:HG21	1:A:3045:VAL:HG11	1.87	0.56
1:C:876:PRO:O	1:C:879:GLU:HG3	2.05	0.56
1:C:2937:HIS:HA	1:C:3014:LEU:HD11	1.88	0.56
1:D:876:PRO:HA	1:D:879:GLU:HG3	1.87	0.56
1:D:3005:THR:HG21	1:D:3045:VAL:HG11	1.87	0.56
1:A:2691:LYS:O	1:A:2695:MET:HB2	2.06	0.56
1:A:3097:THR:HA	1:A:3101:LEU:HG	1.88	0.56
1:A:4268:MET:O	1:A:4272:LYS:HG2	2.06	0.56
1:B:558:LEU:HG	1:B:571:ILE:HG23	1.88	0.56
1:C:2973:GLN:HA	1:C:2976:LYS:HG2	1.88	0.56
1:C:4268:MET:O	1:C:4272:LYS:HG2	2.06	0.56
1:D:2594:PHE:HB2	1:D:2695:MET:HE1	1.88	0.56
1:D:3068:LEU:HD21	1:D:3133:ILE:HG12	1.87	0.56
1:A:2973:GLN:HA	1:A:2976:LYS:HG2	1.88	0.56
1:C:2594:PHE:HB2	1:C:2695:MET:HE1	1.88	0.56
1:D:3108:LEU:HA	1:D:3111:HIS:HD1	1.71	0.56
1:A:1144:ARG:NH1	1:A:1191:ALA:O	2.39	0.55
1:A:3068:LEU:HD21	1:A:3133:ILE:HG12	1.87	0.55
1:B:2826:ILE:HG22	1:C:1501:ASN:ND2	2.22	0.55
1:B:3068:LEU:HD21	1:B:3133:ILE:HG12	1.87	0.55
1:B:4028:SER:O	1:B:4033:LYS:NZ	2.38	0.55
1:C:1722:ASN:O	1:C:1919:ARG:NH2	2.39	0.55
1:D:1144:ARG:NH1	1:D:1191:ALA:O	2.39	0.55
1:D:2973:GLN:HA	1:D:2976:LYS:HG2	1.88	0.55
1:A:644:LEU:HD13	1:A:1630:LEU:HD21	1.87	0.55
1:A:658:ASN:ND2	1:A:833:LYS:HG2	2.21	0.55
1:A:3166:PHE:CE2	1:A:3168:VAL:HB	2.41	0.55
1:B:271:ALA:HB2	1:B:488:LEU:HD22	1.87	0.55
1:C:2768:LYS:O	1:C:2772:ARG:HG3	2.05	0.55
1:D:3152:ARG:NH1	1:D:3236:GLU:OE2	2.40	0.55
1:B:2691:LYS:O	1:B:2695:MET:HB2	2.06	0.55
1:B:2830:ASN:HD22	1:C:1433:PHE:HB3	1.71	0.55
1:B:2971:ILE:HG23	1:B:2975:PHE:CE2	2.40	0.55
1:B:3250:TRP:CE2	1:B:3309:LYS:HD3	2.41	0.55
1:B:4275:THR:HB	1:B:4278:ASP:HB2	1.89	0.55
1:C:558:LEU:HG	1:C:571:ILE:HG23	1.88	0.55
1:C:2445:ILE:HA	1:C:2451:VAL:HA	1.89	0.55
1:C:3068:LEU:HD21	1:C:3133:ILE:HG12	1.87	0.55
1:C:4520:TYR:O	1:D:4809:MET:HB2	2.06	0.55
1:A:2594:PHE:HB2	1:A:2695:MET:HE1	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2852:TRP:NE1	1:A:2856:LYS:HZ3	2.04	0.55
1:C:2769:GLU:O	1:C:2771:TYR:N	2.31	0.55
1:D:4268:MET:O	1:D:4272:LYS:HG2	2.06	0.55
1:A:1438:PRO:HB2	1:A:1494:MET:HE2	1.88	0.55
1:A:1498:GLN:HB2	1:D:2794:GLU:HG3	1.88	0.55
2:E:78:THR:HG23	2:E:80:ASP:OD1	2.07	0.55
2:H:12:ASP:OD2	2:H:13:GLY:N	2.40	0.55
1:B:2651:ALA:O	1:B:2655:LYS:HB2	2.06	0.55
1:B:4859:LEU:O	1:B:4863:GLN:HG2	2.07	0.55
1:B:4874:ARG:NH1	1:C:4868:ASP:OD1	2.39	0.55
1:D:271:ALA:HB2	1:D:488:LEU:HD22	1.88	0.55
1:D:1058:LEU:HD12	1:D:1063:ASN:HB3	1.86	0.55
1:D:1438:PRO:HB2	1:D:1494:MET:HE2	1.88	0.55
1:A:2445:ILE:HA	1:A:2451:VAL:HA	1.89	0.55
1:A:4275:THR:HB	1:A:4278:ASP:HB2	1.88	0.55
1:B:2445:ILE:HA	1:B:2451:VAL:HA	1.89	0.55
1:C:2691:LYS:O	1:C:2695:MET:HB2	2.06	0.55
1:C:3250:TRP:CE2	1:C:3309:LYS:HD3	2.42	0.55
1:D:658:ASN:ND2	1:D:833:LYS:HG2	2.21	0.55
1:D:2692:GLN:HG2	1:D:2704:GLN:CD	2.32	0.55
1:A:905:GLY:HA3	1:A:914:GLN:OE1	2.07	0.55
2:E:12:ASP:OD2	2:E:13:GLY:N	2.40	0.55
2:F:12:ASP:OD2	2:F:13:GLY:N	2.40	0.55
2:G:12:ASP:OD2	2:G:13:GLY:N	2.40	0.55
1:B:2418:ARG:NH2	1:C:156:GLU:OE1	2.27	0.55
1:D:876:PRO:O	1:D:879:GLU:HG3	2.06	0.55
1:D:2691:LYS:O	1:D:2695:MET:HB2	2.06	0.55
1:D:3250:TRP:CE2	1:D:3309:LYS:HD3	2.41	0.55
1:A:271:ALA:HB2	1:A:488:LEU:HD22	1.88	0.55
1:A:2937:HIS:HA	1:A:3014:LEU:HD11	1.88	0.55
1:B:1144:ARG:NH1	1:B:1191:ALA:O	2.39	0.55
1:B:4268:MET:O	1:B:4272:LYS:HG2	2.06	0.55
1:C:3152:ARG:NH1	1:C:3236:GLU:OE2	2.40	0.55
1:C:4737:PHE:CD1	1:D:4783:VAL:HG13	2.41	0.55
1:A:3250:TRP:CE2	1:A:3309:LYS:HD3	2.41	0.55
2:G:78:THR:HG23	2:G:80:ASP:OD1	2.07	0.55
2:H:78:THR:HG23	2:H:80:ASP:OD1	2.07	0.55
1:B:2692:GLN:HG2	1:B:2704:GLN:CD	2.32	0.55
1:C:1144:ARG:NH1	1:C:1191:ALA:O	2.39	0.55
1:C:2593:VAL:HG12	1:C:2644:LEU:HD13	1.89	0.55
1:C:2692:GLN:HG2	1:C:2704:GLN:CD	2.32	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3097:THR:HA	1:C:3101:LEU:HG	1.88	0.55
1:C:4859:LEU:O	1:C:4863:GLN:HG2	2.07	0.55
1:D:3166:PHE:CE2	1:D:3168:VAL:HB	2.41	0.55
1:A:3237:VAL:C	1:A:3240:PRO:HD2	2.32	0.55
2:F:78:THR:HG23	2:F:80:ASP:OD1	2.07	0.55
1:B:658:ASN:ND2	1:B:833:LYS:HG2	2.21	0.55
1:B:882:ARG:NH2	1:B:937:LEU:HG	2.22	0.55
1:B:2779:LEU:O	1:B:2782:MET:HG2	2.07	0.55
1:C:905:GLY:HA3	1:C:914:GLN:OE1	2.07	0.55
1:C:3005:THR:HG21	1:C:3045:VAL:HG11	1.87	0.55
1:C:4275:THR:HB	1:C:4278:ASP:HB2	1.88	0.55
1:D:882:ARG:NH2	1:D:937:LEU:HG	2.22	0.55
1:D:2445:ILE:HA	1:D:2451:VAL:HA	1.89	0.55
1:D:2936:ALA:O	1:D:2940:ILE:HG12	2.07	0.55
1:A:558:LEU:HG	1:A:571:ILE:HG23	1.88	0.54
1:A:4859:LEU:O	1:A:4863:GLN:HG2	2.07	0.54
1:B:2973:GLN:HA	1:B:2976:LYS:HG2	1.88	0.54
1:B:3005:THR:HG21	1:B:3045:VAL:HG11	1.87	0.54
1:B:3097:THR:HA	1:B:3101:LEU:HG	1.88	0.54
1:B:3152:ARG:NH1	1:B:3236:GLU:OE2	2.40	0.54
1:D:2593:VAL:HG12	1:D:2644:LEU:HD13	1.89	0.54
1:A:882:ARG:NH2	1:A:937:LEU:HG	2.22	0.54
1:A:4113:THR:O	1:A:4117:THR:HG23	2.08	0.54
1:B:2937:HIS:HA	1:B:3014:LEU:HD11	1.88	0.54
1:C:3803:LEU:HB2	1:C:3884:SER:HB2	1.90	0.54
1:D:2779:LEU:O	1:D:2782:MET:HG2	2.07	0.54
1:D:2937:HIS:HA	1:D:3014:LEU:HD11	1.88	0.54
1:B:4239:LEU:HD12	1:B:4308:ILE:HD12	1.90	0.54
1:B:4753:LEU:HD21	1:C:4773:LEU:HD13	1.89	0.54
1:A:1551:ASN:ND2	1:D:2830:ASN:OD1	2.27	0.54
1:A:3152:ARG:NH1	1:A:3236:GLU:OE2	2.40	0.54
1:A:4239:LEU:HD12	1:A:4308:ILE:HD12	1.90	0.54
1:B:3237:VAL:C	1:B:3240:PRO:HD2	2.32	0.54
1:B:3245:TYR:HA	1:B:3249:TRP:CZ3	2.43	0.54
1:D:866:PRO:HD2	1:D:1009:ARG:NH2	2.23	0.54
1:D:4113:THR:O	1:D:4117:THR:HG23	2.08	0.54
1:A:2603:ALA:C	1:A:2606:PRO:HD2	2.33	0.54
1:A:3232:PRO:HA	1:A:3235:MET:SD	2.48	0.54
1:B:2603:ALA:C	1:B:2606:PRO:HD2	2.33	0.54
1:C:658:ASN:ND2	1:C:833:LYS:HG2	2.21	0.54
1:C:3237:VAL:C	1:C:3240:PRO:HD2	2.32	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:3245:TYR:HA	1:D:3249:TRP:CZ3	2.43	0.54
1:A:866:PRO:HD2	1:A:1009:ARG:NH2	2.23	0.54
1:A:996:VAL:HB	1:A:1051:ARG:NH1	2.23	0.54
1:A:2593:VAL:HG12	1:A:2644:LEU:HD13	1.89	0.54
1:A:2898:ILE:HD12	1:B:1499:GLY:HA3	1.90	0.54
1:B:996:VAL:HB	1:B:1051:ARG:NH1	2.23	0.54
1:D:905:GLY:HA3	1:D:914:GLN:OE1	2.07	0.54
1:D:3008:PHE:CZ	1:D:3108:LEU:HD21	2.43	0.54
1:D:3232:PRO:HA	1:D:3235:MET:SD	2.48	0.54
1:D:3803:LEU:HB2	1:D:3884:SER:HB2	1.90	0.54
1:A:2692:GLN:HG2	1:A:2704:GLN:CD	2.32	0.54
1:C:2936:ALA:O	1:C:2940:ILE:HG12	2.07	0.54
1:A:2769:GLU:O	1:A:2771:TYR:N	2.31	0.54
1:A:3119:GLU:HG3	1:A:3167:PRO:HB3	1.89	0.54
1:A:4265:LYS:HA	1:A:4268:MET:CG	2.35	0.54
1:A:4640:PHE:CD2	1:A:4641:PRO:HD3	2.43	0.54
1:B:2326:ARG:NH2	1:C:189:GLU:HB3	2.22	0.54
1:B:2594:PHE:HB2	1:B:2695:MET:HE1	1.88	0.54
1:B:2936:ALA:O	1:B:2940:ILE:HG12	2.07	0.54
1:C:2779:LEU:O	1:C:2782:MET:HG2	2.07	0.54
1:C:3232:PRO:HA	1:C:3235:MET:SD	2.48	0.54
1:C:3245:TYR:HA	1:C:3249:TRP:CZ3	2.43	0.54
1:D:558:LEU:HG	1:D:571:ILE:HG23	1.88	0.54
1:D:996:VAL:HB	1:D:1051:ARG:NH1	2.23	0.54
1:D:4859:LEU:O	1:D:4863:GLN:HG2	2.07	0.54
1:A:3250:TRP:NE1	1:A:3309:LYS:HD3	2.23	0.54
1:B:198:ASN:HD22	1:B:198:ASN:C	2.16	0.54
1:B:902:TRP:NE1	1:B:915:HIS:HB2	2.23	0.54
1:B:905:GLY:HA3	1:B:914:GLN:OE1	2.07	0.54
1:B:2826:ILE:CG2	1:C:1501:ASN:ND2	2.71	0.54
1:C:902:TRP:NE1	1:C:915:HIS:HB2	2.23	0.54
1:C:3119:GLU:HG3	1:C:3167:PRO:HB3	1.90	0.54
1:C:3311:LYS:HB2	1:C:3314:LEU:HD13	1.90	0.54
1:D:2300:ASP:OD1	1:D:2301:PHE:N	2.41	0.54
1:D:3237:VAL:C	1:D:3240:PRO:HD2	2.32	0.54
1:D:4275:THR:HB	1:D:4278:ASP:HB2	1.88	0.54
1:A:2779:LEU:O	1:A:2782:MET:HG2	2.07	0.54
1:B:866:PRO:HD2	1:B:1009:ARG:NH2	2.22	0.54
1:B:2202:TYR:O	1:B:2206:ILE:HG12	2.08	0.54
1:B:2604:LYS:HD2	1:B:2664:LEU:HD23	1.90	0.54
1:B:3879:LEU:O	1:B:3882:GLN:HG3	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:624:ALA:HB2	1:C:1667:LEU:HD12	1.90	0.54
1:C:882:ARG:NH2	1:C:937:LEU:HG	2.22	0.54
1:C:2603:ALA:C	1:C:2606:PRO:HD2	2.33	0.54
1:C:3008:PHE:CZ	1:C:3108:LEU:HD21	2.43	0.54
1:C:3108:LEU:O	1:C:3111:HIS:ND1	2.41	0.54
1:C:3250:TRP:NE1	1:C:3309:LYS:HD3	2.23	0.54
1:C:4239:LEU:HD12	1:C:4308:ILE:HD12	1.90	0.54
1:D:448:PRO:HB2	1:D:451:SER:OG	2.08	0.54
1:D:2202:TYR:O	1:D:2206:ILE:HG12	2.08	0.54
1:B:2300:ASP:OD1	1:B:2301:PHE:N	2.41	0.53
1:D:2603:ALA:C	1:D:2606:PRO:HD2	2.33	0.53
1:A:2202:TYR:O	1:A:2206:ILE:HG12	2.08	0.53
1:A:2691:LYS:NZ	1:A:2846:GLU:OE2	2.30	0.53
1:A:3008:PHE:CZ	1:A:3108:LEU:HD21	2.43	0.53
1:A:4250:TYR:O	1:A:4254:THR:HG23	2.08	0.53
1:B:4640:PHE:CD2	1:B:4641:PRO:HD3	2.43	0.53
1:C:448:PRO:HB2	1:C:451:SER:OG	2.08	0.53
1:C:2202:TYR:O	1:C:2206:ILE:HG12	2.08	0.53
1:C:3072:MET:HE1	1:C:3140:LEU:CD1	2.39	0.53
1:C:4113:THR:O	1:C:4117:THR:HG23	2.08	0.53
1:D:624:ALA:HB2	1:D:1667:LEU:HD12	1.90	0.53
1:D:3119:GLU:O	1:D:3181:TYR:OH	2.27	0.53
1:D:3903:GLN:NE2	1:D:3964:GLN:OE1	2.41	0.53
1:A:2235:ARG:NH1	1:A:2297:ARG:HE	2.07	0.53
1:A:2936:ALA:O	1:A:2940:ILE:HG12	2.07	0.53
1:A:3248:ARG:HH11	1:A:3249:TRP:CD1	2.27	0.53
1:B:2666:LEU:HD13	1:B:2966:VAL:HA	1.90	0.53
1:B:3119:GLU:HG3	1:B:3167:PRO:HB3	1.90	0.53
1:C:2300:ASP:OD1	1:C:2301:PHE:N	2.41	0.53
1:C:2957:GLU:HA	1:C:2960:ILE:HG12	1.91	0.53
1:D:902:TRP:NE1	1:D:915:HIS:HB2	2.23	0.53
1:D:2235:ARG:NH1	1:D:2297:ARG:HE	2.07	0.53
1:D:3119:GLU:HG3	1:D:3167:PRO:HB3	1.89	0.53
1:D:3160:ALA:HB2	1:D:3240:PRO:HB3	1.91	0.53
1:D:4239:LEU:HD12	1:D:4308:ILE:HD12	1.90	0.53
1:A:448:PRO:HB2	1:A:451:SER:OG	2.08	0.53
1:A:2300:ASP:OD1	1:A:2301:PHE:N	2.41	0.53
1:A:2957:GLU:HA	1:A:2960:ILE:HG12	1.91	0.53
1:A:3119:GLU:O	1:A:3181:TYR:OH	2.27	0.53
1:A:3245:TYR:HA	1:A:3249:TRP:CZ3	2.43	0.53
1:B:4250:TYR:O	1:B:4254:THR:HG23	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4640:PHE:CD2	1:C:4641:PRO:HD3	2.43	0.53
1:D:2134:MET:CE	1:D:2192:MET:HE2	2.38	0.53
1:D:2957:GLU:HA	1:D:2960:ILE:HG12	1.91	0.53
1:D:3248:ARG:HD2	1:D:3249:TRP:CE2	2.44	0.53
1:D:3248:ARG:HH11	1:D:3249:TRP:CD1	2.27	0.53
1:D:4640:PHE:CD2	1:D:4641:PRO:HD3	2.43	0.53
1:A:2134:MET:CE	1:A:2192:MET:HE2	2.38	0.53
1:A:2821:TYR:CE2	1:A:2823:PRO:HG3	2.44	0.53
1:A:3248:ARG:HD2	1:A:3249:TRP:CE2	2.44	0.53
1:A:3803:LEU:HB2	1:A:3884:SER:HB2	1.90	0.53
1:A:3879:LEU:O	1:A:3882:GLN:HG3	2.08	0.53
1:B:2589:LEU:O	1:B:2593:VAL:HG13	2.09	0.53
1:B:2593:VAL:HG12	1:B:2644:LEU:HD13	1.89	0.53
1:B:3250:TRP:NE1	1:B:3309:LYS:HD3	2.23	0.53
1:D:2821:TYR:CE2	1:D:2823:PRO:HG3	2.44	0.53
1:D:2852:TRP:NE1	1:D:2856:LYS:HZ3	2.06	0.53
2:F:28:THR:HG23	2:F:39:SER:HB2	1.91	0.53
1:B:2821:TYR:CE2	1:B:2823:PRO:HG3	2.44	0.53
1:B:3008:PHE:CZ	1:B:3108:LEU:HD21	2.43	0.53
1:B:3072:MET:HE1	1:B:3140:LEU:CD1	2.38	0.53
1:B:3232:PRO:HA	1:B:3235:MET:SD	2.48	0.53
1:B:3248:ARG:HD2	1:B:3249:TRP:CE2	2.44	0.53
1:B:4113:THR:O	1:B:4117:THR:HG23	2.08	0.53
1:C:3805:LEU:HD21	1:C:3888:PHE:HA	1.91	0.53
1:C:3903:GLN:NE2	1:C:3964:GLN:OE1	2.41	0.53
1:D:3072:MET:HE1	1:D:3140:LEU:CD1	2.39	0.53
1:A:4664:ASP:OD1	1:A:4665:ARG:N	2.42	0.53
1:B:3248:ARG:HH11	1:B:3249:TRP:CD1	2.27	0.53
1:C:4250:TYR:O	1:C:4254:THR:HG23	2.08	0.53
1:C:4557:VAL:HG21	1:D:4790:ARG:NH2	2.23	0.53
1:C:4664:ASP:OD1	1:C:4665:ARG:N	2.42	0.53
1:D:3311:LYS:HB2	1:D:3314:LEU:HD13	1.90	0.53
1:A:466:PRO:HG2	1:A:479:LEU:HG	1.91	0.53
1:A:880:ARG:HH11	1:A:881:ILE:HB	1.74	0.53
1:B:3108:LEU:O	1:B:3111:HIS:ND1	2.41	0.53
1:C:198:ASN:C	1:C:198:ASN:HD22	2.16	0.53
1:C:996:VAL:HB	1:C:1051:ARG:NH1	2.23	0.53
1:C:2821:TYR:CE2	1:C:2823:PRO:HG3	2.44	0.53
1:C:2972:ASP:HA	1:C:3035:ILE:CD1	2.39	0.53
1:D:2604:LYS:HD2	1:D:2664:LEU:HD23	1.90	0.53
1:D:3250:TRP:NE1	1:D:3309:LYS:HD3	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:3805:LEU:HD21	1:D:3888:PHE:HA	1.91	0.53
1:A:902:TRP:NE1	1:A:915:HIS:HB2	2.23	0.53
1:A:2666:LEU:HD13	1:A:2966:VAL:HA	1.90	0.53
1:B:624:ALA:HB2	1:B:1667:LEU:HD12	1.90	0.53
1:C:2681:MET:HE2	1:C:2681:MET:HA	1.91	0.53
1:D:2666:LEU:HD13	1:D:2966:VAL:HA	1.90	0.53
1:D:2972:ASP:HA	1:D:3035:ILE:CD1	2.39	0.53
1:A:3160:ALA:HB2	1:A:3240:PRO:HB3	1.91	0.53
1:A:4726:MET:HE2	1:D:4288:TRP:HZ3	1.73	0.53
2:G:28:THR:HG23	2:G:39:SER:HB2	1.91	0.53
1:B:2593:VAL:HA	1:B:2644:LEU:HD13	1.91	0.53
1:B:4265:LYS:HA	1:B:4268:MET:CG	2.35	0.53
1:C:866:PRO:HD2	1:C:1009:ARG:NH2	2.23	0.53
1:C:2666:LEU:HD13	1:C:2966:VAL:HA	1.90	0.53
1:C:3906:PHE:HB3	1:C:3967:LEU:HD11	1.91	0.53
1:D:2589:LEU:O	1:D:2593:VAL:HG13	2.09	0.53
1:D:3108:LEU:O	1:D:3111:HIS:ND1	2.41	0.53
1:D:4664:ASP:OD1	1:D:4665:ARG:N	2.42	0.53
1:A:624:ALA:HB2	1:A:1667:LEU:HD12	1.90	0.52
1:A:2833:LEU:HB2	1:A:2838[B]:HIS:CE1	2.44	0.52
1:A:3072:MET:HE1	1:A:3140:LEU:CD1	2.39	0.52
1:B:2972:ASP:HA	1:B:3035:ILE:CD1	2.39	0.52
1:B:3000:GLU:HA	1:B:3003:MET:HE3	1.91	0.52
1:B:3311:LYS:HB2	1:B:3314:LEU:HD13	1.90	0.52
1:C:2604:LYS:HD2	1:C:2664:LEU:HD23	1.90	0.52
1:C:2998:ASN:HA	1:C:3001:LYS:HG2	1.91	0.52
1:D:2502:LEU:HG	1:D:2507:LEU:HD13	1.91	0.52
1:D:2833:LEU:HD13	1:D:2837:LEU:HD23	1.92	0.52
1:D:3879:LEU:O	1:D:3882:GLN:HG3	2.08	0.52
1:D:4250:TYR:O	1:D:4254:THR:HG23	2.08	0.52
1:A:1939:ASN:ND2	1:A:1989:PRO:HG2	2.25	0.52
1:A:2652:LEU:HD11	1:A:2662:PHE:CD1	2.45	0.52
1:A:3000:GLU:HA	1:A:3003:MET:HE3	1.91	0.52
1:A:3035:ILE:HG13	1:A:3036:LEU:HD12	1.91	0.52
1:A:3108:LEU:O	1:A:3111:HIS:ND1	2.41	0.52
1:A:3903:GLN:NE2	1:A:3964:GLN:OE1	2.41	0.52
1:A:3906:PHE:HB3	1:A:3967:LEU:HD11	1.91	0.52
2:H:28:THR:HG23	2:H:39:SER:HB2	1.91	0.52
1:B:448:PRO:HB2	1:B:451:SER:OG	2.08	0.52
1:B:1849:SER:HA	1:B:1852:LYS:HE2	1.92	0.52
1:B:2502:LEU:HG	1:B:2507:LEU:HD13	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2681:MET:HE2	1:B:2681:MET:HA	1.91	0.52
1:B:3906:PHE:HB3	1:B:3967:LEU:HD11	1.91	0.52
1:B:4664:ASP:OD1	1:B:4665:ARG:N	2.42	0.52
1:A:198:ASN:C	1:A:198:ASN:HD22	2.16	0.52
1:A:893:TRP:CD1	1:A:897:LYS:HZ3	2.27	0.52
1:A:1050:LEU:O	1:A:1054:VAL:HG22	2.10	0.52
1:A:1849:SER:HA	1:A:1852:LYS:HE2	1.92	0.52
1:A:2998:ASN:HA	1:A:3001:LYS:HG2	1.92	0.52
1:B:4302:PHE:HB3	1:B:4306:PHE:HE2	1.75	0.52
1:B:4622:SER:OG	1:B:4624:ASP:OD1	2.17	0.52
1:C:904:TYR:HD1	1:C:918:LEU:HD12	1.75	0.52
1:C:2589:LEU:O	1:C:2593:VAL:HG13	2.09	0.52
1:C:3248:ARG:HH11	1:C:3249:TRP:CD1	2.27	0.52
1:D:466:PRO:HG2	1:D:479:LEU:HG	1.91	0.52
1:D:2652:LEU:HD11	1:D:2662:PHE:CD1	2.45	0.52
1:A:2502:LEU:HG	1:A:2507:LEU:HD13	1.91	0.52
1:A:2589:LEU:O	1:A:2593:VAL:HG13	2.09	0.52
1:A:2833:LEU:HB2	1:A:2838[A]:HIS:CE1	2.44	0.52
1:A:2833:LEU:HD13	1:A:2837:LEU:HD23	1.92	0.52
1:B:2957:GLU:HA	1:B:2960:ILE:HG12	1.91	0.52
1:C:672:LYS:HG2	1:C:819:TYR:HA	1.92	0.52
1:C:880:ARG:HH11	1:C:881:ILE:HB	1.74	0.52
1:C:2235:ARG:NH1	1:C:2297:ARG:HE	2.07	0.52
1:C:3269:ASN:HB3	1:C:3271:GLU:HG3	1.91	0.52
1:D:672:LYS:HG2	1:D:819:TYR:HA	1.91	0.52
1:D:2918:GLU:HA	1:D:2923:TYR:CG	2.45	0.52
1:D:3000:GLU:HA	1:D:3003:MET:HE3	1.91	0.52
1:A:2658:GLU:OE2	1:A:2661:LEU:N	2.24	0.52
1:B:3803:LEU:HB2	1:B:3884:SER:HB2	1.90	0.52
1:C:794:PHE:HB2	1:C:798:ILE:HG13	1.92	0.52
1:C:2502:LEU:HG	1:C:2507:LEU:HD13	1.92	0.52
1:C:3248:ARG:HD2	1:C:3249:TRP:CE2	2.44	0.52
1:C:4302:PHE:HB3	1:C:4306:PHE:HE2	1.75	0.52
1:D:2156:TYR:HE1	1:D:2202:TYR:HE2	1.57	0.52
1:D:3035:ILE:HG13	1:D:3036:LEU:HD12	1.91	0.52
1:D:4302:PHE:HB3	1:D:4306:PHE:HE2	1.75	0.52
1:A:141:ASP:HA	1:D:2337:GLY:O	2.10	0.52
1:A:2918:GLU:HA	1:A:2923:TYR:CG	2.45	0.52
1:A:2972:ASP:HA	1:A:3035:ILE:CD1	2.39	0.52
1:A:3069:GLU:HG3	1:A:3132:ARG:NH2	2.24	0.52
1:A:3269:ASN:HB3	1:A:3271:GLU:HG3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1050:LEU:O	1:B:1054:VAL:HG22	2.10	0.52
1:B:2708:THR:HB	1:B:2780:LYS:HG2	1.92	0.52
1:C:2176:VAL:HG22	1:C:2220:TYR:CZ	2.44	0.52
1:C:2200:LEU:HD22	1:C:2214:MET:SD	2.49	0.52
1:C:2652:LEU:HD11	1:C:2662:PHE:CD1	2.45	0.52
1:C:3879:LEU:O	1:C:3882:GLN:HG3	2.08	0.52
1:D:2176:VAL:HG22	1:D:2220:TYR:CZ	2.44	0.52
1:D:2593:VAL:HA	1:D:2644:LEU:HD13	1.91	0.52
1:D:3069:GLU:HG3	1:D:3132:ARG:NH2	2.24	0.52
1:A:514:PHE:CD2	1:A:526:TRP:HB2	2.45	0.52
1:A:2176:VAL:HG22	1:A:2220:TYR:CZ	2.44	0.52
1:A:2200:LEU:HD22	1:A:2214:MET:SD	2.49	0.52
1:A:2604:LYS:HD2	1:A:2664:LEU:HD23	1.90	0.52
1:A:4110:PRO:HG3	1:A:4966:LEU:HD23	1.92	0.52
1:A:4487:TYR:HD2	1:D:4279:MET:HE3	1.75	0.52
1:B:904:TYR:HD1	1:B:918:LEU:HD12	1.75	0.52
1:C:1849:SER:HA	1:C:1852:LYS:HE2	1.92	0.52
1:C:3069:GLU:HG3	1:C:3132:ARG:NH2	2.24	0.52
1:C:3122:ILE:O	1:C:3181:TYR:OH	2.28	0.52
1:D:514:PHE:CD2	1:D:526:TRP:HB2	2.45	0.52
1:D:904:TYR:HD1	1:D:918:LEU:HD12	1.75	0.52
1:D:1819:VAL:HG13	1:D:1905:GLN:HE22	1.75	0.52
1:D:2200:LEU:HD22	1:D:2214:MET:SD	2.49	0.52
1:A:1245:ARG:NH1	1:A:1808:ASP:OD2	2.43	0.52
1:A:4086:ARG:HH21	1:A:4087:PHE:HE2	1.57	0.52
1:B:672:LYS:HG2	1:B:819:TYR:HA	1.91	0.52
1:B:2833:LEU:HD13	1:B:2837:LEU:HD23	1.92	0.52
1:C:514:PHE:CD2	1:C:526:TRP:HB2	2.45	0.52
1:C:1785:ASP:OD1	1:C:1786:ILE:N	2.43	0.52
1:C:3016:ARG:HA	1:C:3096:TYR:OH	2.10	0.52
1:D:880:ARG:HH11	1:D:881:ILE:HB	1.74	0.52
1:D:1245:ARG:NH1	1:D:1808:ASP:OD2	2.43	0.52
1:D:4086:ARG:HH21	1:D:4087:PHE:HE2	1.57	0.52
1:A:3311:LYS:HB2	1:A:3314:LEU:HD13	1.90	0.52
1:B:514:PHE:CD2	1:B:526:TRP:HB2	2.45	0.52
1:B:2134:MET:CE	1:B:2192:MET:HE2	2.38	0.52
1:B:3069:GLU:HG3	1:B:3132:ARG:NH2	2.24	0.52
1:B:3122:ILE:O	1:B:3181:TYR:OH	2.28	0.52
1:B:3805:LEU:HD21	1:B:3888:PHE:HA	1.91	0.52
1:B:4896:ASP:OD1	1:B:4897:TYR:N	2.43	0.52
1:D:4110:PRO:HG3	1:D:4966:LEU:HD23	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:672:LYS:HG2	1:A:819:TYR:HA	1.91	0.52
1:B:1685:LEU:O	1:B:1689:ILE:HG12	2.10	0.52
1:B:1785:ASP:OD1	1:B:1786:ILE:N	2.43	0.52
1:B:2652:LEU:HD11	1:B:2662:PHE:CD1	2.44	0.52
1:C:1050:LEU:O	1:C:1054:VAL:HG22	2.10	0.52
1:C:2134:MET:CE	1:C:2192:MET:HE2	2.38	0.52
1:C:2918:GLU:HA	1:C:2923:TYR:CG	2.45	0.52
1:C:4110:PRO:HG3	1:C:4966:LEU:HD23	1.92	0.52
1:D:2681:MET:HE2	1:D:2681:MET:HA	1.91	0.52
1:A:712:GLU:HG3	1:A:713:TRP:CE3	2.45	0.51
1:A:1228:THR:HG22	1:A:1232:LEU:HD22	1.92	0.51
1:A:2593:VAL:HA	1:A:2644:LEU:HD13	1.91	0.51
1:A:2681:MET:HE2	1:A:2681:MET:HA	1.91	0.51
1:A:4302:PHE:HB3	1:A:4306:PHE:HE2	1.75	0.51
2:E:28:THR:HG23	2:E:39:SER:HB2	1.91	0.51
1:B:1939:ASN:ND2	1:B:1989:PRO:HG2	2.25	0.51
1:B:2176:VAL:HG22	1:B:2220:TYR:CZ	2.44	0.51
1:B:2200:LEU:HD22	1:B:2214:MET:SD	2.49	0.51
1:C:2629:ASN:OD1	1:C:2630:PHE:N	2.44	0.51
1:C:3209:PRO:HB3	1:C:3213:LYS:HD2	1.92	0.51
1:D:1228:THR:HG22	1:D:1232:LEU:HD22	1.92	0.51
1:D:1849:SER:HA	1:D:1852:LYS:HE2	1.92	0.51
1:D:3906:PHE:HB3	1:D:3967:LEU:HD11	1.91	0.51
1:A:904:TYR:HD1	1:A:918:LEU:HD12	1.75	0.51
1:A:1819:VAL:HG13	1:A:1905:GLN:HE22	1.75	0.51
1:A:2708:THR:HB	1:A:2780:LYS:HG2	1.92	0.51
1:B:2168:HIS:CD2	1:B:2214:MET:HE3	2.45	0.51
1:B:3160:ALA:HB2	1:B:3240:PRO:HB3	1.91	0.51
1:C:466:PRO:HG2	1:C:479:LEU:HG	1.91	0.51
1:C:1228:THR:HG22	1:C:1232:LEU:HD22	1.92	0.51
1:C:1245:ARG:NH1	1:C:1808:ASP:OD2	2.43	0.51
1:C:2593:VAL:HA	1:C:2644:LEU:HD13	1.91	0.51
1:C:3000:GLU:HA	1:C:3003:MET:HE3	1.91	0.51
1:C:4265:LYS:HA	1:C:4268:MET:CG	2.36	0.51
1:D:893:TRP:CD1	1:D:897:LYS:HZ3	2.28	0.51
1:D:3287:ASN:HD21	1:D:3295:TRP:HH2	1.58	0.51
1:A:1685:LEU:O	1:A:1689:ILE:HG12	2.10	0.51
1:A:3209:PRO:HB3	1:A:3213:LYS:HD2	1.92	0.51
1:B:1245:ARG:NH1	1:B:1808:ASP:OD2	2.43	0.51
1:B:4086:ARG:HH21	1:B:4087:PHE:HE2	1.57	0.51
1:C:1119:ARG:NH2	1:C:1196:ASP:OD1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2156:TYR:HE1	1:C:2202:TYR:HE2	1.57	0.51
1:C:2833:LEU:HD13	1:C:2837:LEU:HD23	1.92	0.51
1:D:4144:ARG:HB3	1:D:4961:GLN:HE22	1.76	0.51
1:A:2168:HIS:CD2	1:A:2214:MET:HE3	2.45	0.51
1:A:2629:ASN:OD1	1:A:2630:PHE:N	2.43	0.51
1:A:3245:TYR:HD2	1:A:3246:MET:SD	2.34	0.51
1:A:3287:ASN:HD21	1:A:3295:TRP:HH2	1.58	0.51
1:A:3805:LEU:HD21	1:A:3888:PHE:HA	1.91	0.51
1:B:3035:ILE:HG13	1:B:3036:LEU:HD12	1.91	0.51
1:C:281:ARG:NH1	1:C:345:GLU:OE1	2.44	0.51
1:C:2168:HIS:CD2	1:C:2214:MET:HE3	2.45	0.51
1:C:2708:THR:HB	1:C:2780:LYS:HG2	1.92	0.51
1:C:4144:ARG:HB3	1:C:4961:GLN:HE22	1.76	0.51
1:D:2629:ASN:OD1	1:D:2630:PHE:N	2.44	0.51
1:D:3072:MET:HE1	1:D:3140:LEU:HD11	1.92	0.51
1:D:4896:ASP:OD1	1:D:4897:TYR:N	2.43	0.51
1:A:794:PHE:HB2	1:A:798:ILE:HG13	1.92	0.51
1:A:1119:ARG:NH2	1:A:1196:ASP:OD1	2.43	0.51
1:A:1988:CYS:O	1:A:1993:ARG:NE	2.38	0.51
1:A:4896:ASP:OD1	1:A:4897:TYR:N	2.43	0.51
1:B:281:ARG:NH1	1:B:345:GLU:OE1	2.44	0.51
1:B:466:PRO:HG2	1:B:479:LEU:HG	1.91	0.51
1:B:3903:GLN:NE2	1:B:3964:GLN:OE1	2.41	0.51
1:C:1685:LEU:O	1:C:1689:ILE:HG12	2.10	0.51
1:C:3035:ILE:HG13	1:C:3036:LEU:HD12	1.91	0.51
1:C:4287:TYR:HE1	1:D:4591:TYR:CD2	2.28	0.51
1:D:712:GLU:HG3	1:D:713:TRP:CE3	2.45	0.51
1:D:1119:ARG:NH2	1:D:1196:ASP:OD1	2.43	0.51
1:A:2396:ILE:HG13	1:A:2468:MET:HE1	1.93	0.51
1:B:880:ARG:HH11	1:B:881:ILE:HB	1.74	0.51
1:B:2918:GLU:HA	1:B:2923:TYR:CG	2.45	0.51
1:B:2998:ASN:HA	1:B:3001:LYS:HG2	1.92	0.51
1:B:3245:TYR:HD2	1:B:3246:MET:SD	2.33	0.51
1:C:1939:ASN:ND2	1:C:1989:PRO:HG2	2.25	0.51
1:C:2824:ARG:NH2	1:D:1502:ASN:O	2.44	0.51
1:C:3072:MET:HE1	1:C:3140:LEU:HD11	1.92	0.51
1:A:3016:ARG:HA	1:A:3096:TYR:OH	2.10	0.51
1:A:3246:MET:HG2	1:A:3273:MET:HE1	1.92	0.51
1:B:794:PHE:HB2	1:B:798:ILE:HG13	1.92	0.51
1:B:1819:VAL:HG13	1:B:1905:GLN:HE22	1.75	0.51
1:B:2629:ASN:OD1	1:B:2630:PHE:N	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3209:PRO:HB3	1:B:3213:LYS:HD2	1.92	0.51
1:C:948:CYS:SG	1:C:1064:LEU:HB3	2.51	0.51
1:C:993:GLU:OE2	1:C:1051:ARG:NE	2.44	0.51
1:C:4921:PHE:HE2	1:C:4940:VAL:HG11	1.76	0.51
1:D:1685:LEU:O	1:D:1689:ILE:HG12	2.10	0.51
1:D:1785:ASP:OD1	1:D:1786:ILE:N	2.43	0.51
1:D:4921:PHE:HE2	1:D:4940:VAL:HG11	1.76	0.51
1:A:3011:LEU:HD21	1:A:3036:LEU:HD22	1.93	0.51
1:A:4059:THR:O	1:A:4063:THR:OG1	2.22	0.51
1:B:712:GLU:HG3	1:B:713:TRP:CE3	2.46	0.51
1:B:1119:ARG:NH2	1:B:1196:ASP:OD1	2.43	0.51
1:B:4569:GLU:HB3	1:B:4570:PRO:HD3	1.93	0.51
1:C:1819:VAL:HG13	1:C:1905:GLN:HE22	1.75	0.51
1:D:2168:HIS:CD2	1:D:2214:MET:HE3	2.45	0.51
1:D:2998:ASN:HA	1:D:3001:LYS:HG2	1.92	0.51
1:D:3016:ARG:HA	1:D:3096:TYR:OH	2.10	0.51
1:D:3245:TYR:HD2	1:D:3246:MET:SD	2.33	0.51
1:D:4569:GLU:HB3	1:D:4570:PRO:HD3	1.93	0.51
1:A:1014:GLN:O	1:A:1027:ARG:NH2	2.44	0.51
1:A:2156:TYR:HE1	1:A:2202:TYR:HE2	1.57	0.51
1:B:993:GLU:OE2	1:B:1051:ARG:NE	2.44	0.51
1:B:1228:THR:HG22	1:B:1232:LEU:HD22	1.92	0.51
1:B:2984:SER:OG	1:B:2994:GLY:O	2.27	0.51
1:B:3016:ARG:HA	1:B:3096:TYR:OH	2.10	0.51
1:B:3246:MET:HG2	1:B:3273:MET:HE1	1.92	0.51
1:B:3269:ASN:HB3	1:B:3271:GLU:HG3	1.92	0.51
1:C:995:MET:O	1:C:999:LEU:HD23	2.11	0.51
1:D:281:ARG:NH1	1:D:345:GLU:OE1	2.44	0.51
1:D:3209:PRO:HB3	1:D:3213:LYS:HD2	1.92	0.51
1:A:948:CYS:SG	1:A:1064:LEU:HB3	2.51	0.51
1:A:993:GLU:OE2	1:A:1051:ARG:NE	2.44	0.51
1:A:1074:ARG:HH11	1:A:1077:VAL:N	2.06	0.51
1:A:3030:VAL:HA	1:A:3033:LEU:HB2	1.93	0.51
1:A:3072:MET:HE1	1:A:3140:LEU:HD11	1.92	0.51
1:A:3227:ARG:HB3	1:A:3230:GLN:OE1	2.11	0.51
1:B:948:CYS:SG	1:B:1064:LEU:HB3	2.51	0.51
1:B:1014:GLN:O	1:B:1027:ARG:NH2	2.44	0.51
1:B:3072:MET:HE1	1:B:3140:LEU:HD11	1.92	0.51
1:B:3245:TYR:HA	1:B:3249:TRP:HZ3	1.75	0.51
1:C:712:GLU:HG3	1:C:713:TRP:CE3	2.45	0.51
1:C:3011:LEU:HD21	1:C:3036:LEU:HD22	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1074:ARG:HH11	1:D:1077:VAL:N	2.06	0.51
1:D:3269:ASN:HB3	1:D:3271:GLU:HG3	1.91	0.51
1:A:2403:ALA:HB2	1:A:2475:VAL:HG22	1.93	0.50
1:A:2975:PHE:HD1	1:A:2982:PHE:CE1	2.29	0.50
1:B:2235:ARG:NH1	1:B:2297:ARG:HE	2.07	0.50
1:B:2396:ILE:HG13	1:B:2468:MET:HE1	1.93	0.50
1:B:2933:VAL:HG12	1:B:3010:LYS:HE2	1.93	0.50
1:C:3160:ALA:HB2	1:C:3240:PRO:HB3	1.91	0.50
1:C:3245:TYR:HD2	1:C:3246:MET:SD	2.33	0.50
1:C:4086:ARG:HH21	1:C:4087:PHE:HE2	1.57	0.50
1:C:4896:ASP:OD1	1:C:4897:TYR:N	2.43	0.50
1:D:794:PHE:HB2	1:D:798:ILE:HG13	1.92	0.50
1:D:1050:LEU:O	1:D:1054:VAL:HG22	2.10	0.50
1:D:1939:ASN:ND2	1:D:1989:PRO:HG2	2.25	0.50
1:D:3797:MET:HE1	1:D:3870:ILE:HG23	1.94	0.50
1:D:3952:ALA:HB1	1:D:4012:MET:HE2	1.94	0.50
1:A:4144:ARG:HB3	1:A:4961:GLN:HE22	1.76	0.50
1:B:4110:PRO:HG3	1:B:4966:LEU:HD23	1.92	0.50
1:B:4144:ARG:HB3	1:B:4961:GLN:HE22	1.76	0.50
1:C:2975:PHE:HD1	1:C:2982:PHE:CE1	2.29	0.50
1:C:3246:MET:HG2	1:C:3273:MET:HE1	1.92	0.50
1:D:948:CYS:SG	1:D:1064:LEU:HB3	2.51	0.50
1:D:2403:ALA:HB2	1:D:2475:VAL:HG22	1.93	0.50
1:D:2708:THR:HB	1:D:2780:LYS:HG2	1.92	0.50
1:D:3030:VAL:HA	1:D:3033:LEU:HB2	1.93	0.50
1:A:290:ARG:HG3	1:A:353:GLU:HG3	1.94	0.50
1:A:932:ASN:O	1:A:935:MET:HG3	2.12	0.50
1:A:4569:GLU:HB3	1:A:4570:PRO:HD3	1.93	0.50
1:B:2156:TYR:HE1	1:B:2202:TYR:HE2	1.57	0.50
1:B:2691:LYS:NZ	1:B:2846:GLU:OE2	2.30	0.50
1:D:932:ASN:O	1:D:935:MET:HG3	2.12	0.50
1:A:281:ARG:NH1	1:A:345:GLU:OE1	2.44	0.50
1:A:292:GLY:HA2	1:A:332:ARG:HH12	1.77	0.50
1:A:1785:ASP:OD1	1:A:1786:ILE:N	2.43	0.50
1:A:3797:MET:HE1	1:A:3870:ILE:HG23	1.93	0.50
1:A:3952:ALA:HB1	1:A:4012:MET:HE2	1.94	0.50
1:A:4921:PHE:HE2	1:A:4940:VAL:HG11	1.76	0.50
1:B:995:MET:O	1:B:999:LEU:HD23	2.11	0.50
1:B:3011:LEU:HD21	1:B:3036:LEU:HD22	1.93	0.50
1:C:1711:LEU:HB3	1:C:1831:MET:SD	2.52	0.50
1:C:1732:GLU:HB2	1:C:1753:LEU:HD21	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4562:GLU:OE1	1:C:4562:GLU:N	2.45	0.50
1:D:2238:THR:HG21	1:D:2297:ARG:HH12	1.76	0.50
1:D:2396:ILE:HG13	1:D:2468:MET:HE1	1.93	0.50
1:D:2975:PHE:HD1	1:D:2982:PHE:CE1	2.29	0.50
1:A:995:MET:O	1:A:999:LEU:HD23	2.11	0.50
1:B:4014:LEU:HD13	1:B:4122:ALA:HB2	1.92	0.50
1:B:4818:TYR:HA	1:C:4848:ILE:HD11	1.94	0.50
1:C:2403:ALA:HB2	1:C:2475:VAL:HG22	1.93	0.50
1:C:2968:LEU:HB3	1:C:2969:PRO:HD3	1.94	0.50
1:C:3245:TYR:HA	1:C:3249:TRP:HZ3	1.76	0.50
1:C:4014:LEU:HD13	1:C:4122:ALA:HB2	1.92	0.50
1:D:829:LYS:NZ	1:D:1037:LEU:O	2.45	0.50
1:D:993:GLU:OE2	1:D:1051:ARG:NE	2.44	0.50
1:D:2945:GLY:HA2	1:D:2948:ARG:NH2	2.27	0.50
1:A:3118:GLY:O	1:A:3122:ILE:HG22	2.12	0.50
1:B:1682:GLU:HG2	1:B:1683:PRO:HD3	1.94	0.50
1:B:1711:LEU:HB3	1:B:1831:MET:SD	2.52	0.50
1:B:3797:MET:HE1	1:B:3870:ILE:HG23	1.94	0.50
1:C:330:THR:HG23	1:C:366:VAL:HG22	1.94	0.50
1:C:1014:GLN:O	1:C:1027:ARG:NH2	2.44	0.50
1:C:2933:VAL:HG12	1:C:3010:LYS:HE2	1.94	0.50
1:C:3227:ARG:HB3	1:C:3230:GLN:OE1	2.11	0.50
1:C:4569:GLU:HB3	1:C:4570:PRO:HD3	1.93	0.50
1:C:4827:ILE:O	1:C:4831:ILE:HG12	2.12	0.50
1:D:711:GLU:OE1	1:D:716:ASN:ND2	2.44	0.50
1:B:2238:THR:HG21	1:B:2297:ARG:HH12	1.76	0.50
1:B:2968:LEU:HB3	1:B:2969:PRO:HD3	1.94	0.50
1:C:1793:GLN:NE2	1:C:1797:GLU:OE2	2.43	0.50
1:C:2608:LYS:HG2	1:C:2664:LEU:HD11	1.94	0.50
1:C:3030:VAL:HA	1:C:3033:LEU:HB2	1.93	0.50
1:C:4495:PHE:HD1	1:C:4502:MET:HE1	1.76	0.50
1:C:4748:MET:O	1:C:4754:ARG:NH2	2.45	0.50
1:D:1014:GLN:O	1:D:1027:ARG:NH2	2.44	0.50
1:D:1766:PRO:HG3	1:D:1780:PRO:HB3	1.94	0.50
1:D:2968:LEU:HB3	1:D:2969:PRO:HD3	1.94	0.50
1:D:4748:MET:O	1:D:4754:ARG:NH2	2.45	0.50
1:A:2608:LYS:HG2	1:A:2664:LEU:HD11	1.94	0.50
1:A:2827:ASP:H	1:B:1501:ASN:ND2	2.10	0.50
1:A:2945:GLY:HA2	1:A:2948:ARG:NH2	2.27	0.50
1:B:932:ASN:O	1:B:935:MET:HG3	2.12	0.50
1:B:2608:LYS:HG2	1:B:2664:LEU:HD11	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3140:LEU:HD13	1:B:3155:LEU:CD2	2.42	0.50
1:B:4495:PHE:HD1	1:B:4502:MET:HE1	1.76	0.50
1:B:4748:MET:O	1:B:4754:ARG:NH2	2.45	0.50
1:C:292:GLY:HA2	1:C:332:ARG:HH12	1.77	0.50
1:C:932:ASN:O	1:C:935:MET:HG3	2.12	0.50
1:C:1766:PRO:HG3	1:C:1780:PRO:HB3	1.94	0.50
1:C:3213:LYS:O	1:C:3216:GLU:HG3	2.12	0.50
1:C:3729:ALA:HA	1:C:3732:HIS:CD2	2.47	0.50
1:D:198:ASN:HD22	1:D:198:ASN:C	2.16	0.50
1:D:995:MET:O	1:D:999:LEU:HD23	2.11	0.50
1:D:2608:LYS:HG2	1:D:2664:LEU:HD11	1.94	0.50
1:D:3245:TYR:HA	1:D:3249:TRP:HZ3	1.75	0.50
1:D:3246:MET:HG2	1:D:3273:MET:HE1	1.92	0.50
1:D:4014:LEU:HD13	1:D:4122:ALA:HB2	1.92	0.50
1:A:2935:GLU:O	1:A:2938:GLN:HG3	2.12	0.50
1:A:3140:LEU:HD13	1:A:3155:LEU:CD2	2.42	0.50
1:A:4609:LYS:HD2	1:A:4615:LEU:HD22	1.94	0.50
1:B:829:LYS:NZ	1:B:1037:LEU:O	2.45	0.50
1:B:893:TRP:CD1	1:B:897:LYS:HZ3	2.30	0.50
1:B:2890:GLN:HB3	1:B:2894:LYS:HE2	1.94	0.50
1:B:3952:ALA:HB1	1:B:4012:MET:HE2	1.94	0.50
1:B:4609:LYS:HD2	1:B:4615:LEU:HD22	1.94	0.50
1:B:4827:ILE:O	1:B:4831:ILE:HG12	2.12	0.50
1:B:4921:PHE:HE2	1:B:4940:VAL:HG11	1.76	0.50
1:C:829:LYS:NZ	1:C:1037:LEU:O	2.45	0.50
1:C:1682:GLU:HG2	1:C:1683:PRO:HD3	1.94	0.50
1:C:2396:ILE:HG13	1:C:2468:MET:HE1	1.93	0.50
1:C:2945:GLY:HA2	1:C:2948:ARG:NH2	2.27	0.50
1:C:4166:LYS:NZ	4:C:5002:ATP:O2G	2.42	0.50
1:D:1711:LEU:HB3	1:D:1831:MET:SD	2.52	0.50
1:A:1711:LEU:HB3	1:A:1831:MET:SD	2.52	0.49
1:A:4495:PHE:HD1	1:A:4502:MET:HE1	1.76	0.49
1:A:4562:GLU:OE1	1:A:4562:GLU:N	2.45	0.49
1:B:292:GLY:HA2	1:B:332:ARG:HH12	1.77	0.49
1:B:972:LEU:HD23	1:B:972:LEU:H	1.77	0.49
1:B:2403:ALA:HB2	1:B:2475:VAL:HG22	1.93	0.49
1:B:2945:GLY:HA2	1:B:2948:ARG:NH2	2.27	0.49
1:B:3287:ASN:HD21	1:B:3295:TRP:HH2	1.58	0.49
1:C:972:LEU:HD23	1:C:972:LEU:H	1.77	0.49
1:C:3245:TYR:O	1:C:3249:TRP:HE3	1.95	0.49
1:C:4023:LEU:HG	1:C:4084:VAL:HG12	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:3011:LEU:HD21	1:D:3036:LEU:HD22	1.93	0.49
1:A:2238:THR:HG21	1:A:2297:ARG:HH12	1.76	0.49
1:A:3729:ALA:HA	1:A:3732:HIS:CD2	2.47	0.49
1:A:4753:LEU:HD21	1:B:4773:LEU:HD13	1.94	0.49
1:B:1732:GLU:HB2	1:B:1753:LEU:HD21	1.94	0.49
1:B:3030:VAL:HA	1:B:3033:LEU:HB2	1.93	0.49
1:B:4023:LEU:HG	1:B:4084:VAL:HG12	1.93	0.49
1:C:3952:ALA:HB1	1:C:4012:MET:HE2	1.94	0.49
1:A:705:PRO:HG2	1:A:706:TYR:CE1	2.47	0.49
1:A:972:LEU:HD23	1:A:972:LEU:H	1.77	0.49
1:A:3245:TYR:HA	1:A:3249:TRP:HZ3	1.75	0.49
1:B:1988:CYS:O	1:B:1993:ARG:NE	2.38	0.49
1:B:3729:ALA:HA	1:B:3732:HIS:CD2	2.47	0.49
1:C:2794:GLU:HG3	1:D:1498:GLN:HB2	1.94	0.49
1:C:4609:LYS:HD2	1:C:4615:LEU:HD22	1.94	0.49
1:D:3118:GLY:O	1:D:3122:ILE:HG22	2.12	0.49
1:D:3227:ARG:HB3	1:D:3230:GLN:OE1	2.11	0.49
1:A:829:LYS:NZ	1:A:1037:LEU:O	2.45	0.49
1:A:1496:PRO:CB	1:D:2798:MET:HE1	2.42	0.49
1:A:3213:LYS:O	1:A:3216:GLU:HG3	2.12	0.49
1:B:3245:TYR:O	1:B:3249:TRP:HE3	1.95	0.49
1:C:711:GLU:OE1	1:C:716:ASN:ND2	2.44	0.49
1:C:893:TRP:CD1	1:C:897:LYS:HZ3	2.30	0.49
1:C:2890:GLN:HB3	1:C:2894:LYS:HE2	1.94	0.49
1:D:1611:ILE:HD11	1:D:1618:LEU:HD22	1.94	0.49
1:D:4495:PHE:HD1	1:D:4502:MET:HE1	1.76	0.49
1:D:4827:ILE:O	1:D:4831:ILE:HG12	2.12	0.49
1:A:1766:PRO:HG3	1:A:1780:PRO:HB3	1.94	0.49
1:A:2182:GLY:HA2	1:A:2185:LYS:HE2	1.94	0.49
1:A:2918:GLU:HG3	1:A:2923:TYR:CZ	2.48	0.49
1:B:290:ARG:HG3	1:B:353:GLU:HG3	1.94	0.49
1:B:2732:TRP:O	1:B:2736:LYS:HG3	2.13	0.49
1:B:2927:GLN:HA	1:B:2930:ILE:HD12	1.94	0.49
1:B:2935:GLU:O	1:B:2938:GLN:HG3	2.12	0.49
1:B:2975:PHE:HD1	1:B:2982:PHE:CE1	2.29	0.49
1:B:3227:ARG:HB3	1:B:3230:GLN:OE1	2.11	0.49
1:C:290:ARG:HG3	1:C:353:GLU:HG3	1.94	0.49
1:C:2182:GLY:HA2	1:C:2185:LYS:HE2	1.94	0.49
1:C:2736:LYS:HE2	1:C:2754:GLN:NE2	2.28	0.49
1:C:3287:ASN:HD21	1:C:3295:TRP:HH2	1.58	0.49
1:D:3213:LYS:O	1:D:3216:GLU:HG3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2968:LEU:HB3	1:A:2969:PRO:HD3	1.94	0.49
1:A:4014:LEU:HD13	1:A:4122:ALA:HB2	1.92	0.49
1:A:4023:LEU:HG	1:A:4084:VAL:HG12	1.93	0.49
1:B:3118:GLY:O	1:B:3122:ILE:HG22	2.12	0.49
1:B:3213:LYS:O	1:B:3216:GLU:HG3	2.12	0.49
1:B:4640:PHE:CG	1:B:4641:PRO:HD3	2.48	0.49
1:C:705:PRO:HG2	1:C:706:TYR:CE1	2.48	0.49
1:C:3797:MET:HE1	1:C:3870:ILE:HG23	1.94	0.49
1:C:4271:VAL:O	1:D:4480:PHE:HZ	1.95	0.49
1:D:705:PRO:HG2	1:D:706:TYR:CE1	2.48	0.49
1:D:2732:TRP:O	1:D:2736:LYS:HG3	2.13	0.49
1:D:3140:LEU:HD13	1:D:3155:LEU:CD2	2.42	0.49
1:D:3729:ALA:HA	1:D:3732:HIS:CD2	2.47	0.49
1:A:1686:LEU:HD22	1:A:1790:LYS:HE3	1.94	0.49
1:A:2724:TYR:CE2	1:A:2775:ILE:HG12	2.47	0.49
1:A:3245:TYR:O	1:A:3249:TRP:HE3	1.95	0.49
1:A:3321:PRO:HA	1:A:3324:GLU:HG3	1.94	0.49
1:B:766:ILE:HB	1:B:779:PHE:HB2	1.95	0.49
1:B:4562:GLU:OE1	1:B:4562:GLU:N	2.45	0.49
1:C:387:ILE:HB	1:C:389:ARG:HG3	1.95	0.49
1:C:2238:THR:HG21	1:C:2297:ARG:HH12	1.76	0.49
1:D:972:LEU:HD23	1:D:972:LEU:H	1.77	0.49
1:D:1686:LEU:HD22	1:D:1790:LYS:HE3	1.94	0.49
1:D:1732:GLU:HB2	1:D:1753:LEU:HD21	1.94	0.49
1:D:2182:GLY:HA2	1:D:2185:LYS:HE2	1.94	0.49
1:A:1793:GLN:NE2	1:A:1797:GLU:OE2	2.43	0.49
1:A:2890:GLN:HB3	1:A:2894:LYS:HE2	1.94	0.49
1:B:330:THR:HG23	1:B:366:VAL:HG22	1.94	0.49
1:D:387:ILE:HB	1:D:389:ARG:HG3	1.95	0.49
1:D:3321:PRO:HA	1:D:3324:GLU:HG3	1.94	0.49
1:A:387:ILE:HB	1:A:389:ARG:HG3	1.95	0.49
1:A:2853:ALA:O	1:A:2857:LYS:HG3	2.13	0.49
1:A:2933:VAL:HG12	1:A:3010:LYS:HE2	1.94	0.49
1:A:3016:ARG:HH21	1:A:3017:HIS:HE1	1.60	0.49
1:A:4640:PHE:CG	1:A:4641:PRO:HD3	2.48	0.49
1:A:4748:MET:O	1:A:4754:ARG:NH2	2.45	0.49
1:B:2853:ALA:O	1:B:2857:LYS:HG3	2.13	0.49
1:C:1686:LEU:HD22	1:C:1790:LYS:HE3	1.94	0.49
1:C:2724:TYR:CE2	1:C:2775:ILE:HG12	2.47	0.49
1:C:3321:PRO:HA	1:C:3324:GLU:HG3	1.94	0.49
1:C:4302:PHE:O	1:C:4306:PHE:HD2	1.96	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4640:PHE:CG	1:C:4641:PRO:HD3	2.48	0.49
1:D:292:GLY:HA2	1:D:332:ARG:HH12	1.77	0.49
1:D:2933:VAL:HG12	1:D:3010:LYS:HE2	1.94	0.49
1:D:4302:PHE:O	1:D:4306:PHE:HD2	1.96	0.49
1:A:2827:ASP:H	1:B:1501:ASN:HD21	1.60	0.49
1:A:4827:ILE:O	1:A:4831:ILE:HG12	2.12	0.49
1:B:1766:PRO:HG3	1:B:1780:PRO:HB3	1.94	0.49
1:C:930:ASN:HA	1:C:933:LEU:HG	1.95	0.49
1:C:2905:ARG:HH11	1:C:2906:GLY:H	1.61	0.49
1:C:2918:GLU:HG3	1:C:2923:TYR:CZ	2.48	0.49
1:C:3016:ARG:HH21	1:C:3017:HIS:HE1	1.60	0.49
1:C:3134:LEU:HD13	1:C:3162:PHE:CE2	2.48	0.49
1:D:2724:TYR:CE2	1:D:2775:ILE:HG12	2.47	0.49
1:D:2905:ARG:HH11	1:D:2906:GLY:H	1.61	0.49
1:D:2918:GLU:HG3	1:D:2923:TYR:CZ	2.48	0.49
1:D:2935:GLU:O	1:D:2938:GLN:HG3	2.12	0.49
1:D:4023:LEU:HG	1:D:4084:VAL:HG12	1.93	0.49
1:D:4562:GLU:N	1:D:4562:GLU:OE1	2.45	0.49
1:A:3045:VAL:HG12	1:A:3046:MET:HE2	1.95	0.48
1:A:3241:MET:O	1:A:3245:TYR:HB2	2.13	0.48
1:B:387:ILE:HB	1:B:389:ARG:HG3	1.95	0.48
1:B:2724:TYR:CE2	1:B:2775:ILE:HG12	2.47	0.48
1:C:1611:ILE:HD11	1:C:1618:LEU:HD22	1.94	0.48
1:C:2658:GLU:OE2	1:C:2661:LEU:N	2.24	0.48
1:C:2927:GLN:HA	1:C:2930:ILE:HD12	1.94	0.48
1:C:2935:GLU:O	1:C:2938:GLN:HG3	2.12	0.48
1:D:330:THR:HG23	1:D:366:VAL:HG22	1.94	0.48
1:D:4640:PHE:CG	1:D:4641:PRO:HD3	2.48	0.48
1:A:766:ILE:HB	1:A:779:PHE:HB2	1.95	0.48
1:A:1611:ILE:HD11	1:A:1618:LEU:HD22	1.94	0.48
1:A:2175:MET:HA	1:A:2178:VAL:HG22	1.95	0.48
1:A:3134:LEU:HD13	1:A:3162:PHE:CE2	2.48	0.48
1:A:3232:PRO:O	1:A:3236:GLU:HG2	2.13	0.48
2:G:19:LYS:HE2	2:G:19:LYS:HA	1.95	0.48
1:B:705:PRO:HG2	1:B:706:TYR:CE1	2.48	0.48
1:B:1611:ILE:HD11	1:B:1618:LEU:HD22	1.94	0.48
1:B:3016:ARG:HH21	1:B:3017:HIS:HE1	1.60	0.48
1:C:1074:ARG:HH11	1:C:1077:VAL:N	2.06	0.48
1:C:3140:LEU:HD13	1:C:3155:LEU:CD2	2.42	0.48
1:C:3287:ASN:ND2	1:C:3295:TRP:CH2	2.81	0.48
1:D:1682:GLU:HG2	1:D:1683:PRO:HD3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4283:PHE:CE1	1:D:4287:TYR:HE2	2.31	0.48
1:A:2580:LEU:HD11	1:A:2584:MET:SD	2.53	0.48
1:A:3115:HIS:HB2	1:A:3117:PHE:H	1.79	0.48
1:A:4698:LEU:HD13	1:D:4262:LYS:HD3	1.94	0.48
2:F:19:LYS:HE2	2:F:19:LYS:HA	1.95	0.48
1:B:2182:GLY:HA2	1:B:2185:LYS:HE2	1.94	0.48
1:B:3321:PRO:HA	1:B:3324:GLU:HG3	1.94	0.48
1:C:766:ILE:HB	1:C:779:PHE:HB2	1.95	0.48
1:C:2142:MET:HG2	1:C:2192:MET:CE	2.41	0.48
1:C:3118:GLY:O	1:C:3122:ILE:HG22	2.12	0.48
1:D:877:HIS:CE1	1:D:1062:TYR:HH	2.31	0.48
1:D:930:ASN:HA	1:D:933:LEU:HG	1.95	0.48
1:D:2736:LYS:HE2	1:D:2754:GLN:NE2	2.28	0.48
1:D:2754:GLN:OE1	1:D:2754:GLN:HA	2.13	0.48
1:D:3016:ARG:HH21	1:D:3017:HIS:HE1	1.60	0.48
1:A:1732:GLU:HB2	1:A:1753:LEU:HD21	1.93	0.48
1:A:2754:GLN:OE1	1:A:2754:GLN:HA	2.13	0.48
1:A:2976:LYS:HA	1:A:2979:ARG:CZ	2.43	0.48
1:A:4252:ILE:HG21	1:B:4707:MET:HG3	1.94	0.48
1:B:930:ASN:HA	1:B:933:LEU:HG	1.95	0.48
1:B:2580:LEU:HD11	1:B:2584:MET:SD	2.53	0.48
1:C:2853:ALA:O	1:C:2857:LYS:HG3	2.13	0.48
1:C:3241:MET:O	1:C:3245:TYR:HB2	2.13	0.48
1:D:114:LEU:HB2	1:D:117:HIS:CD2	2.49	0.48
1:D:290:ARG:HG3	1:D:353:GLU:HG3	1.94	0.48
1:D:2927:GLN:HA	1:D:2930:ILE:HD12	1.94	0.48
1:A:2142:MET:HG2	1:A:2192:MET:CE	2.41	0.48
1:A:2171:VAL:HG21	1:A:2199:PHE:CE2	2.49	0.48
1:A:2824:ARG:NH2	1:B:1502:ASN:O	2.47	0.48
1:A:2905:ARG:HH11	1:A:2906:GLY:H	1.61	0.48
1:B:711:GLU:OE1	1:B:716:ASN:ND2	2.44	0.48
1:B:2736:LYS:HE2	1:B:2754:GLN:NE2	2.28	0.48
1:C:2580:LEU:HD11	1:C:2584:MET:SD	2.53	0.48
1:C:2754:GLN:OE1	1:C:2754:GLN:HA	2.13	0.48
1:C:3272:HIS:O	1:C:3276:LEU:HD23	2.14	0.48
1:C:4184:GLU:HG3	1:C:4188:LEU:HG	1.95	0.48
1:D:2853:ALA:O	1:D:2857:LYS:HG3	2.13	0.48
1:D:2976:LYS:HA	1:D:2979:ARG:CZ	2.44	0.48
1:D:3115:HIS:HB2	1:D:3117:PHE:H	1.79	0.48
1:D:3287:ASN:ND2	1:D:3295:TRP:CH2	2.81	0.48
1:A:1682:GLU:HG2	1:A:1683:PRO:HD3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2229:LEU:HD23	1:A:2297:ARG:NH1	2.29	0.48
1:A:2855:LYS:O	1:A:2859:GLU:HG3	2.14	0.48
1:A:2927:GLN:HA	1:A:2930:ILE:HD12	1.94	0.48
1:A:4184:GLU:HG3	1:A:4188:LEU:HG	1.95	0.48
1:A:4283:PHE:CE1	1:A:4287:TYR:HE2	2.31	0.48
2:E:63:GLY:HA3	2:E:75:LEU:HD21	1.96	0.48
2:F:63:GLY:HA3	2:F:75:LEU:HD21	1.96	0.48
1:B:2918:GLU:HG3	1:B:2923:TYR:CZ	2.48	0.48
1:C:853:PRO:O	1:C:1209:VAL:HA	2.14	0.48
1:C:1988:CYS:O	1:C:1993:ARG:NE	2.38	0.48
1:C:2171:VAL:HG21	1:C:2199:PHE:CE2	2.48	0.48
1:D:2171:VAL:HG21	1:D:2199:PHE:CE2	2.48	0.48
1:D:2175:MET:HA	1:D:2178:VAL:HG22	1.95	0.48
1:D:3045:VAL:HG12	1:D:3046:MET:HE2	1.95	0.48
1:D:4609:LYS:HD2	1:D:4615:LEU:HD22	1.94	0.48
1:A:114:LEU:HB2	1:A:117:HIS:CD2	2.49	0.48
1:A:2732:TRP:O	1:A:2736:LYS:HG3	2.13	0.48
1:A:3035:ILE:HG13	1:A:3036:LEU:N	2.29	0.48
1:A:4302:PHE:O	1:A:4306:PHE:HD2	1.96	0.48
2:H:63:GLY:HA3	2:H:75:LEU:HD21	1.96	0.48
1:B:1686:LEU:HD22	1:B:1790:LYS:HE3	1.94	0.48
1:C:2976:LYS:HA	1:C:2979:ARG:CZ	2.43	0.48
1:C:3119:GLU:O	1:C:3181:TYR:OH	2.27	0.48
1:C:3232:PRO:O	1:C:3236:GLU:HG2	2.13	0.48
1:C:4283:PHE:CE1	1:C:4287:TYR:HE2	2.31	0.48
1:D:2855:LYS:O	1:D:2859:GLU:HG3	2.14	0.48
1:D:3245:TYR:O	1:D:3249:TRP:HE3	1.95	0.48
1:A:194:LEU:HD11	1:A:201:LEU:HD22	1.95	0.48
1:A:330:THR:HG23	1:A:366:VAL:HG22	1.94	0.48
1:B:1931:ASP:OD1	1:B:1932:PHE:N	2.47	0.48
1:B:2171:VAL:HG21	1:B:2199:PHE:CE2	2.48	0.48
1:B:2229:LEU:HD23	1:B:2297:ARG:NH1	2.29	0.48
1:B:2905:ARG:HH11	1:B:2906:GLY:H	1.61	0.48
1:B:3134:LEU:HD13	1:B:3162:PHE:CE2	2.48	0.48
1:B:3241:MET:O	1:B:3245:TYR:HB2	2.13	0.48
1:C:1415:ASP:OD2	1:C:1559:ARG:NH2	2.45	0.48
1:C:2732:TRP:O	1:C:2736:LYS:HG3	2.13	0.48
1:C:3035:ILE:HG13	1:C:3036:LEU:N	2.29	0.48
1:D:2890:GLN:HB3	1:D:2894:LYS:HE2	1.94	0.48
1:D:3134:LEU:HD13	1:D:3162:PHE:CE2	2.48	0.48
1:D:3241:MET:O	1:D:3245:TYR:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:882:ARG:NH2	1:A:937:LEU:N	2.62	0.48
1:A:902:TRP:HA	1:A:913:ARG:HD3	1.96	0.48
1:A:2736:LYS:HE2	1:A:2754:GLN:NE2	2.28	0.48
1:A:3272:HIS:O	1:A:3276:LEU:HD23	2.14	0.48
1:B:308:LEU:HD11	1:B:312:LYS:HA	1.96	0.48
1:C:2229:LEU:HD23	1:C:2297:ARG:NH1	2.29	0.48
1:D:3035:ILE:HG13	1:D:3036:LEU:N	2.29	0.48
1:A:2326:ARG:HH22	1:B:189:GLU:HB3	1.78	0.48
1:B:853:PRO:O	1:B:1210:ALA:N	2.39	0.48
1:B:902:TRP:HA	1:B:913:ARG:HD3	1.96	0.48
1:B:2831:VAL:HG22	1:C:1435:GLY:HA2	1.95	0.48
1:B:2976:LYS:HA	1:B:2979:ARG:CZ	2.43	0.48
1:B:3031:ASN:HA	1:B:3034:HIS:ND1	2.29	0.48
1:B:4184:GLU:HG3	1:B:4188:LEU:HG	1.95	0.48
1:B:4302:PHE:O	1:B:4306:PHE:HD2	1.96	0.48
1:B:4964:ASP:OD1	1:B:4965:GLN:N	2.47	0.48
1:C:2855:LYS:O	1:C:2859:GLU:HG3	2.14	0.48
1:C:4081:GLU:HG2	1:C:4082:GLU:N	2.29	0.48
1:D:766:ILE:HB	1:D:779:PHE:HB2	1.95	0.48
1:D:3122:ILE:O	1:D:3181:TYR:OH	2.28	0.48
1:D:3192:ARG:HG3	1:D:3197:LEU:HD23	1.96	0.48
1:D:4265:LYS:HA	1:D:4268:MET:CG	2.36	0.48
1:A:853:PRO:O	1:A:1209:VAL:HA	2.14	0.47
1:A:3108:LEU:HA	1:A:3111:HIS:ND1	2.29	0.47
1:A:3287:ASN:ND2	1:A:3295:TRP:CH2	2.81	0.47
1:B:131:CYS:SG	1:B:150:GLN:HB2	2.54	0.47
1:B:882:ARG:NH2	1:B:937:LEU:N	2.62	0.47
1:C:114:LEU:HB2	1:C:117:HIS:CD2	2.49	0.47
1:C:2827:ASP:H	1:D:1501:ASN:HD21	1.62	0.47
1:D:2658:GLU:OE2	1:D:2661:LEU:N	2.24	0.47
1:A:1931:ASP:OD1	1:A:1932:PHE:N	2.47	0.47
1:A:2322:ARG:NH1	1:A:2419:ILE:HD11	2.29	0.47
1:A:3254:PRO:HD2	1:A:3267:ALA:HA	1.97	0.47
2:F:4:GLU:OE2	2:F:76:THR:OG1	2.31	0.47
2:H:19:LYS:HA	2:H:19:LYS:HE2	1.96	0.47
1:B:1074:ARG:HH11	1:B:1077:VAL:N	2.06	0.47
1:B:1415:ASP:OD2	1:B:1559:ARG:NH2	2.45	0.47
1:B:2175:MET:HA	1:B:2178:VAL:HG22	1.95	0.47
1:B:2754:GLN:OE1	1:B:2754:GLN:HA	2.13	0.47
1:B:3042:ALA:HB1	1:B:3121:LEU:HB2	1.95	0.47
1:B:4042:VAL:HG12	1:B:4077:THR:HB	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4283:PHE:CE1	1:B:4287:TYR:HE2	2.31	0.47
1:C:2998:ASN:O	1:C:3002:GLU:OE1	2.32	0.47
1:C:3045:VAL:HG12	1:C:3046:MET:HE2	1.95	0.47
1:C:3108:LEU:HA	1:C:3111:HIS:ND1	2.29	0.47
1:C:3246:MET:CB	1:C:3273:MET:HE1	2.44	0.47
1:C:4042:VAL:HG12	1:C:4077:THR:HB	1.96	0.47
1:D:1988:CYS:O	1:D:1993:ARG:NE	2.38	0.47
1:D:2142:MET:CG	1:D:2192:MET:HE1	2.43	0.47
1:D:2322:ARG:NH1	1:D:2419:ILE:HD11	2.29	0.47
1:D:3031:ASN:HA	1:D:3034:HIS:ND1	2.29	0.47
1:D:4964:ASP:OD1	1:D:4965:GLN:N	2.47	0.47
1:A:1768:PHE:O	2:E:83:TYR:OH	2.28	0.47
1:A:2710:ASN:OD1	1:A:2711:ILE:N	2.48	0.47
1:A:3192:ARG:HG3	1:A:3197:LEU:HD23	1.96	0.47
1:B:194:LEU:HD11	1:B:201:LEU:HD22	1.95	0.47
1:B:2057:THR:HB	1:B:2060:GLN:HG3	1.96	0.47
1:C:131:CYS:SG	1:C:150:GLN:HB2	2.54	0.47
1:D:194:LEU:HD11	1:D:201:LEU:HD22	1.96	0.47
1:D:902:TRP:HA	1:D:913:ARG:HD3	1.96	0.47
1:D:2229:LEU:HD23	1:D:2297:ARG:NH1	2.29	0.47
1:D:2580:LEU:HD11	1:D:2584:MET:SD	2.53	0.47
1:D:3232:PRO:O	1:D:3236:GLU:HG2	2.14	0.47
1:D:3272:HIS:O	1:D:3276:LEU:HD23	2.14	0.47
1:A:2772:ARG:HA	1:A:2775:ILE:HD12	1.96	0.47
1:A:2998:ASN:O	1:A:3002:GLU:OE1	2.32	0.47
1:A:3042:ALA:HB1	1:A:3121:LEU:HB2	1.95	0.47
2:G:63:GLY:HA3	2:G:75:LEU:HD21	1.96	0.47
1:B:3045:VAL:HG12	1:B:3046:MET:HE2	1.95	0.47
1:B:3108:LEU:HA	1:B:3111:HIS:ND1	2.29	0.47
1:B:3232:PRO:O	1:B:3236:GLU:HG2	2.13	0.47
1:C:877:HIS:CE1	1:C:1062:TYR:HH	2.31	0.47
1:C:882:ARG:NH2	1:C:937:LEU:N	2.62	0.47
1:C:2175:MET:HA	1:C:2178:VAL:HG22	1.95	0.47
1:C:2710:ASN:OD1	1:C:2711:ILE:N	2.47	0.47
1:C:2760:TYR:HA	1:C:2763:LEU:HD13	1.96	0.47
1:C:3031:ASN:HA	1:C:3034:HIS:ND1	2.29	0.47
1:D:2760:TYR:O	1:D:2768:LYS:NZ	2.46	0.47
1:A:156:GLU:OE1	1:D:2418:ARG:NH2	2.28	0.47
1:A:2235:ARG:NH2	1:A:2300:ASP:OD2	2.40	0.47
1:A:2553:TYR:HE1	1:A:2606:PRO:HG3	1.80	0.47
1:A:3031:ASN:HA	1:A:3034:HIS:ND1	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:19:LYS:HA	2:E:19:LYS:HE2	1.95	0.47
1:B:853:PRO:O	1:B:1209:VAL:HA	2.14	0.47
1:B:2172:MET:HE2	1:B:2172:MET:HB3	1.67	0.47
1:B:3287:ASN:ND2	1:B:3295:TRP:CH2	2.81	0.47
1:C:3254:PRO:HD2	1:C:3267:ALA:HA	1.97	0.47
1:D:853:PRO:O	1:D:1209:VAL:HA	2.13	0.47
1:D:2235:ARG:NH2	1:D:2300:ASP:OD2	2.41	0.47
1:D:4184:GLU:HG3	1:D:4188:LEU:HG	1.95	0.47
1:A:131:CYS:SG	1:A:150:GLN:HB2	2.54	0.47
1:B:114:LEU:HB2	1:B:117:HIS:CD2	2.49	0.47
1:B:2553:TYR:HE1	1:B:2606:PRO:HG3	1.80	0.47
1:B:3115:HIS:HB2	1:B:3117:PHE:H	1.79	0.47
1:B:3272:HIS:O	1:B:3276:LEU:HD23	2.14	0.47
1:B:3318:HIS:C	1:B:3321:PRO:HD2	2.40	0.47
1:C:281:ARG:O	1:C:285:SER:OG	2.33	0.47
1:C:2797:SER:HA	1:C:2800:LEU:HG	1.96	0.47
1:D:131:CYS:SG	1:D:150:GLN:HB2	2.54	0.47
1:D:816:PRO:HB2	1:D:819:TYR:CD1	2.50	0.47
1:D:882:ARG:NH2	1:D:937:LEU:N	2.62	0.47
1:D:1444:GLY:HA3	1:D:1487:MET:HA	1.96	0.47
1:D:2852:TRP:O	1:D:2856:LYS:HD3	2.15	0.47
1:D:2984:SER:OG	1:D:2994:GLY:O	2.27	0.47
1:A:711:GLU:OE1	1:A:716:ASN:ND2	2.44	0.47
1:A:824:GLU:HG2	1:A:1020:ILE:HG22	1.96	0.47
1:A:1031:ARG:HG3	1:A:1038:LEU:HD11	1.96	0.47
1:A:1610:ARG:HH21	1:A:1617:TRP:HZ2	1.63	0.47
1:A:2344:LEU:HD22	1:A:2434:GLY:HA3	1.97	0.47
1:A:4081:GLU:HG2	1:A:4082:GLU:N	2.29	0.47
1:B:748:LEU:O	1:B:750:ARG:HG3	2.15	0.47
1:B:2235:ARG:NH2	1:B:2300:ASP:OD2	2.41	0.47
1:B:2322:ARG:NH1	1:B:2419:ILE:HD11	2.29	0.47
1:B:2760:TYR:HA	1:B:2763:LEU:HD13	1.96	0.47
1:B:2855:LYS:O	1:B:2859:GLU:HG3	2.14	0.47
1:B:3035:ILE:HG13	1:B:3036:LEU:N	2.29	0.47
1:B:3192:ARG:HG3	1:B:3197:LEU:HD23	1.96	0.47
1:C:308:LEU:HD11	1:C:312:LYS:HA	1.96	0.47
1:C:514:PHE:HD2	1:C:526:TRP:HB2	1.80	0.47
1:C:1931:ASP:OD1	1:C:1932:PHE:N	2.47	0.47
1:C:2322:ARG:NH1	1:C:2419:ILE:HD11	2.29	0.47
1:C:2553:TYR:HE1	1:C:2606:PRO:HG3	1.80	0.47
1:C:2760:TYR:O	1:C:2768:LYS:NZ	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:824:GLU:HG2	1:D:1020:ILE:HG22	1.96	0.47
1:D:1931:ASP:OD1	1:D:1932:PHE:N	2.47	0.47
1:D:1989:PRO:HD2	1:D:1992:ILE:HD13	1.97	0.47
1:D:2225:SER:HB2	1:D:2240:LEU:HD13	1.96	0.47
1:D:2710:ASN:OD1	1:D:2711:ILE:N	2.48	0.47
1:D:3861:GLN:H	1:D:3867:THR:HG23	1.80	0.47
1:D:4081:GLU:HG2	1:D:4082:GLU:N	2.29	0.47
1:A:514:PHE:HD2	1:A:526:TRP:HB2	1.80	0.47
1:A:1016:TRP:HH2	1:A:1024:VAL:HG12	1.80	0.47
1:A:2057:THR:HB	1:A:2060:GLN:HG3	1.96	0.47
1:A:2225:SER:HB2	1:A:2240:LEU:HD13	1.96	0.47
1:A:3318:HIS:C	1:A:3321:PRO:HD2	2.40	0.47
1:A:4042:VAL:HG12	1:A:4077:THR:HB	1.96	0.47
1:B:816:PRO:HB2	1:B:819:TYR:CD1	2.50	0.47
1:B:2769:GLU:C	1:B:2771:TYR:H	2.22	0.47
1:B:3172:GLU:OE1	1:B:3267:ALA:N	2.48	0.47
1:C:902:TRP:HA	1:C:913:ARG:HD3	1.96	0.47
1:D:281:ARG:O	1:D:285:SER:OG	2.33	0.47
1:D:3108:LEU:HA	1:D:3111:HIS:ND1	2.29	0.47
1:A:930:ASN:HA	1:A:933:LEU:HG	1.95	0.47
1:A:2797:SER:HA	1:A:2800:LEU:HG	1.97	0.47
1:A:3067:ASP:OD1	1:A:3070:LYS:NZ	2.48	0.47
1:B:2142:MET:HG2	1:B:2192:MET:CE	2.41	0.47
1:B:2250:ASN:HB3	1:B:2253:LEU:HB2	1.97	0.47
1:C:3067:ASP:OD1	1:C:3070:LYS:NZ	2.48	0.47
1:D:2250:ASN:HB3	1:D:2253:LEU:HB2	1.97	0.47
1:D:2344:LEU:HD22	1:D:2434:GLY:HA3	1.97	0.47
1:D:2553:TYR:HE1	1:D:2606:PRO:HG3	1.80	0.47
1:D:2886:ARG:O	1:D:2890:GLN:HG2	2.15	0.47
1:D:2918:GLU:HA	1:D:2923:TYR:CD1	2.50	0.47
1:A:2827:ASP:N	1:B:1501:ASN:HD21	2.13	0.47
1:A:2886:ARG:O	1:A:2890:GLN:HG2	2.15	0.47
1:A:2918:GLU:HA	1:A:2923:TYR:CD1	2.50	0.47
1:A:4964:ASP:OD1	1:A:4965:GLN:N	2.47	0.47
1:B:1610:ARG:HH21	1:B:1617:TRP:HZ2	1.63	0.47
1:B:2710:ASN:OD1	1:B:2711:ILE:N	2.48	0.47
1:B:2772:ARG:HA	1:B:2775:ILE:HD12	1.96	0.47
1:B:4081:GLU:HG2	1:B:4082:GLU:N	2.29	0.47
1:C:748:LEU:O	1:C:750:ARG:HG3	2.15	0.47
1:C:816:PRO:HB2	1:C:819:TYR:CD1	2.50	0.47
1:C:1610:ARG:HH21	1:C:1617:TRP:HZ2	1.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2772:ARG:HA	1:C:2775:ILE:HD12	1.96	0.47
1:C:2918:GLU:HA	1:C:2923:TYR:CD1	2.50	0.47
1:C:4107:GLU:OE1	1:C:4149:TYR:OH	2.23	0.47
1:C:4964:ASP:OD1	1:C:4965:GLN:N	2.47	0.47
1:D:3012:GLY:HA2	1:D:3015:VAL:HG12	1.97	0.47
1:D:3318:HIS:C	1:D:3321:PRO:HD2	2.40	0.47
1:A:1549:SER:HA	1:D:2832:THR:HG21	1.98	0.46
1:A:1714:TYR:CZ	1:A:1761:MET:HB2	2.50	0.46
1:A:2763:LEU:HB3	1:A:2767:GLU:OE1	2.15	0.46
2:E:4:GLU:OE2	2:E:76:THR:OG1	2.31	0.46
1:B:514:PHE:HD2	1:B:526:TRP:HB2	1.80	0.46
1:B:1644:LEU:HD23	1:B:1651:LEU:HA	1.97	0.46
1:B:2125:GLN:OE1	1:B:2144:ARG:NH2	2.47	0.46
1:B:2344:LEU:HD22	1:B:2434:GLY:HA3	1.97	0.46
1:B:2658:GLU:OE2	1:B:2661:LEU:N	2.24	0.46
1:B:2763:LEU:HB3	1:B:2767:GLU:OE1	2.16	0.46
1:C:2852:TRP:O	1:C:2856:LYS:HD3	2.15	0.46
1:D:81:MET:O	1:D:81:MET:HG2	2.11	0.46
1:D:308:LEU:HD11	1:D:312:LYS:HA	1.96	0.46
1:D:387:ILE:HD12	1:D:389:ARG:HD3	1.97	0.46
1:D:748:LEU:O	1:D:750:ARG:HG3	2.15	0.46
1:D:2998:ASN:O	1:D:3002:GLU:OE1	2.32	0.46
1:A:748:LEU:O	1:A:750:ARG:HG3	2.15	0.46
1:A:1644:LEU:HD23	1:A:1651:LEU:HA	1.97	0.46
1:A:2852:TRP:O	1:A:2856:LYS:HD3	2.15	0.46
1:A:3861:GLN:H	1:A:3867:THR:HG23	1.80	0.46
1:A:4271:VAL:O	1:B:4480:PHE:HZ	1.98	0.46
1:B:1751:ILE:HD11	1:B:1839:LEU:HB2	1.98	0.46
1:B:2830:ASN:HB2	1:C:1434:PRO:O	2.16	0.46
1:B:3067:ASP:OD1	1:B:3070:LYS:NZ	2.48	0.46
1:B:3254:PRO:HD2	1:B:3267:ALA:HA	1.97	0.46
1:C:824:GLU:HG2	1:C:1020:ILE:HG22	1.96	0.46
1:C:1911:GLN:NE2	1:C:2090:ARG:HH11	2.14	0.46
1:C:1989:PRO:HD2	1:C:1992:ILE:HD13	1.97	0.46
1:C:2250:ASN:HB3	1:C:2253:LEU:HB2	1.97	0.46
1:D:1714:TYR:CZ	1:D:1761:MET:HB2	2.50	0.46
1:D:2763:LEU:HB3	1:D:2767:GLU:OE1	2.16	0.46
1:A:125:TYR:CZ	1:A:417:ARG:HD3	2.51	0.46
1:A:387:ILE:HD12	1:A:389:ARG:HD3	1.97	0.46
1:A:1415:ASP:OD2	1:A:1559:ARG:NH2	2.45	0.46
1:A:2652:LEU:HG	1:A:2962:PHE:HE1	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4166:LYS:NZ	4:A:5002:ATP:O2G	2.42	0.46
1:B:81:MET:O	1:B:81:MET:HG2	2.11	0.46
1:B:1031:ARG:HG3	1:B:1038:LEU:HD11	1.97	0.46
1:B:1714:TYR:CZ	1:B:1761:MET:HB2	2.50	0.46
1:B:2225:SER:HB2	1:B:2240:LEU:HD13	1.96	0.46
1:B:2918:GLU:HA	1:B:2923:TYR:CD1	2.50	0.46
1:B:3119:GLU:O	1:B:3181:TYR:OH	2.27	0.46
1:B:3296:MET:SD	1:B:3334:VAL:HG11	2.56	0.46
1:C:125:TYR:CZ	1:C:417:ARG:HD3	2.51	0.46
1:C:1714:TYR:CZ	1:C:1761:MET:HB2	2.50	0.46
1:C:1751:ILE:HD11	1:C:1839:LEU:HB2	1.98	0.46
1:C:2722:ASN:C	1:C:2724:TYR:H	2.24	0.46
1:C:2886:ARG:O	1:C:2890:GLN:HG2	2.15	0.46
1:C:3115:HIS:HB2	1:C:3117:PHE:H	1.79	0.46
1:C:3184:TYR:CE2	1:C:3201:VAL:HB	2.51	0.46
1:C:3861:GLN:H	1:C:3867:THR:HG23	1.80	0.46
1:D:3042:ALA:HB1	1:D:3121:LEU:HB2	1.96	0.46
1:D:3067:ASP:OD1	1:D:3070:LYS:NZ	2.48	0.46
1:D:4042:VAL:HG12	1:D:4077:THR:HB	1.96	0.46
1:A:816:PRO:HB2	1:A:819:TYR:CD1	2.50	0.46
1:A:2142:MET:CG	1:A:2192:MET:HE1	2.43	0.46
1:A:3012:GLY:HA2	1:A:3015:VAL:HG12	1.98	0.46
1:A:3172:GLU:OE1	1:A:3267:ALA:N	2.48	0.46
1:A:4020:PHE:CD1	1:A:4087:PHE:HB3	2.51	0.46
1:B:1016:TRP:HH2	1:B:1024:VAL:HG12	1.80	0.46
1:B:1444:GLY:HA3	1:B:1487:MET:HA	1.96	0.46
1:B:2760:TYR:O	1:B:2768:LYS:NZ	2.46	0.46
1:B:2998:ASN:O	1:B:3002:GLU:OE1	2.32	0.46
1:B:4027:THR:HA	1:B:4032:PHE:HD1	1.81	0.46
1:C:194:LEU:HD11	1:C:201:LEU:HD22	1.96	0.46
1:C:713:TRP:CE2	1:C:1600:PRO:HD3	2.51	0.46
1:C:1991:GLU:HG2	1:C:1992:ILE:HD12	1.98	0.46
1:C:3042:ALA:HB1	1:C:3121:LEU:HB2	1.95	0.46
1:C:3172:GLU:OE1	1:C:3267:ALA:N	2.48	0.46
1:C:3318:HIS:C	1:C:3321:PRO:HD2	2.40	0.46
1:C:3805:LEU:HD11	1:C:3887:ASP:HB3	1.98	0.46
1:C:4020:PHE:CD1	1:C:4087:PHE:HB3	2.51	0.46
1:C:4522:VAL:HG11	1:D:4790:ARG:CD	2.45	0.46
1:D:374:TYR:OH	1:D:400:ASP:OD1	2.32	0.46
1:D:514:PHE:HD2	1:D:526:TRP:HB2	1.80	0.46
1:D:1685:LEU:HD22	1:D:1706:LEU:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1911:GLN:NE2	1:D:2090:ARG:HH11	2.14	0.46
1:D:3297:LYS:NZ	1:D:3334:VAL:HG13	2.31	0.46
1:A:281:ARG:O	1:A:285:SER:OG	2.33	0.46
2:F:43:ARG:NH1	1:B:1766:PRO:O	2.47	0.46
1:B:387:ILE:HD12	1:B:389:ARG:HD3	1.97	0.46
1:B:2077:ASP:O	1:B:2081:VAL:HG23	2.15	0.46
1:B:2652:LEU:HG	1:B:2962:PHE:HE1	1.79	0.46
1:B:2722:ASN:C	1:B:2724:TYR:H	2.24	0.46
1:B:2797:SER:HA	1:B:2800:LEU:HG	1.97	0.46
1:B:3122:ILE:HG13	1:B:3127:GLN:HE21	1.81	0.46
1:B:3246:MET:CB	1:B:3273:MET:HE1	2.44	0.46
1:B:3861:GLN:H	1:B:3867:THR:HG23	1.80	0.46
1:C:915:HIS:NE2	1:C:917:CYS:HB2	2.31	0.46
1:C:1444:GLY:HA3	1:C:1487:MET:HA	1.96	0.46
1:C:3192:ARG:HG3	1:C:3197:LEU:HD23	1.96	0.46
1:C:3296:MET:SD	1:C:3334:VAL:HG11	2.56	0.46
1:D:915:HIS:NE2	1:D:917:CYS:HB2	2.31	0.46
1:D:2142:MET:HG2	1:D:2192:MET:CE	2.41	0.46
1:D:2652:LEU:HG	1:D:2962:PHE:HE1	1.80	0.46
1:D:3172:GLU:OE1	1:D:3267:ALA:N	2.48	0.46
1:A:2126:ILE:HD12	1:A:2142:MET:SD	2.56	0.46
1:A:2614:TYR:CD2	1:A:2672:VAL:HG22	2.51	0.46
1:A:2830:ASN:HB3	1:B:1549:SER:HB2	1.98	0.46
1:A:3184:TYR:CE2	1:A:3201:VAL:HB	2.51	0.46
1:A:3297:LYS:NZ	1:A:3334:VAL:HG13	2.31	0.46
1:B:2614:TYR:CD2	1:B:2672:VAL:HG22	2.51	0.46
1:B:4020:PHE:CD1	1:B:4087:PHE:HB3	2.51	0.46
1:B:4502:MET:SD	1:B:4585:PHE:HB3	2.56	0.46
1:C:375:GLN:HG2	1:C:377:VAL:HG13	1.98	0.46
1:C:2225:SER:HB2	1:C:2240:LEU:HD13	1.96	0.46
1:C:2652:LEU:HG	1:C:2962:PHE:HE1	1.79	0.46
1:D:125:TYR:CZ	1:D:417:ARG:HD3	2.51	0.46
1:D:238:HIS:CD2	1:D:239:GLY:H	2.34	0.46
1:A:853:PRO:O	1:A:1210:ALA:N	2.39	0.46
1:A:1435:GLY:HA2	1:D:2831:VAL:HG22	1.97	0.46
1:A:1444:GLY:HA3	1:A:1487:MET:HA	1.96	0.46
1:A:2250:ASN:HB3	1:A:2253:LEU:HB2	1.97	0.46
1:A:2749:ASP:OD1	1:A:2750:SER:N	2.49	0.46
1:A:4502:MET:SD	1:A:4585:PHE:HB3	2.56	0.46
1:B:824:GLU:HG2	1:B:1020:ILE:HG22	1.96	0.46
1:B:1991:GLU:HG2	1:B:1992:ILE:HD12	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2749:ASP:OD1	1:B:2750:SER:N	2.49	0.46
1:B:2852:TRP:O	1:B:2856:LYS:HD3	2.15	0.46
1:B:3649:ALA:HB1	1:B:3652:PRO:HB2	1.98	0.46
1:C:3650:GLU:HB2	1:C:3651:PRO:HD3	1.98	0.46
1:C:3712:LYS:O	1:C:3717:LYS:NZ	2.49	0.46
1:C:3961:ASP:OD1	1:C:3962:SER:N	2.49	0.46
1:C:4502:MET:SD	1:C:4585:PHE:HB3	2.56	0.46
1:D:1016:TRP:HH2	1:D:1024:VAL:HG12	1.80	0.46
1:D:2760:TYR:HA	1:D:2763:LEU:HD13	1.96	0.46
1:D:2772:ARG:HA	1:D:2775:ILE:HD12	1.97	0.46
1:D:2957:GLU:O	1:D:2961:LYS:HG2	2.16	0.46
1:D:3184:TYR:CE2	1:D:3201:VAL:HB	2.51	0.46
1:D:3254:PRO:HD2	1:D:3267:ALA:HA	1.97	0.46
1:D:4502:MET:SD	1:D:4585:PHE:HB3	2.56	0.46
1:A:308:LEU:HD11	1:A:312:LYS:HA	1.96	0.46
1:A:915:HIS:NE2	1:A:917:CYS:HB2	2.31	0.46
1:A:2957:GLU:O	1:A:2961:LYS:HG2	2.16	0.46
1:A:3122:ILE:O	1:A:3181:TYR:OH	2.28	0.46
1:A:3712:LYS:O	1:A:3717:LYS:NZ	2.49	0.46
1:B:125:TYR:CZ	1:B:417:ARG:HD3	2.51	0.46
1:B:915:HIS:NE2	1:B:917:CYS:HB2	2.31	0.46
1:B:1914:CYS:SG	1:B:2091:GLN:NE2	2.82	0.46
1:B:2126:ILE:HD12	1:B:2142:MET:SD	2.56	0.46
1:B:3650:GLU:HB2	1:B:3651:PRO:HD3	1.98	0.46
1:C:2057:THR:HB	1:C:2060:GLN:HG3	1.96	0.46
1:C:2266:VAL:HG11	1:C:2323:LEU:HB3	1.97	0.46
1:C:2344:LEU:HD22	1:C:2434:GLY:HA3	1.97	0.46
1:C:2763:LEU:HB3	1:C:2767:GLU:OE1	2.16	0.46
1:C:3012:GLY:HA2	1:C:3015:VAL:HG12	1.98	0.46
1:C:3122:ILE:HG13	1:C:3127:GLN:HE21	1.80	0.46
1:D:713:TRP:CE2	1:D:1600:PRO:HD3	2.51	0.46
1:D:853:PRO:O	1:D:1210:ALA:N	2.39	0.46
1:D:1610:ARG:HH21	1:D:1617:TRP:HZ2	1.63	0.46
1:D:2722:ASN:C	1:D:2724:TYR:H	2.24	0.46
1:D:3712:LYS:O	1:D:3717:LYS:NZ	2.49	0.46
1:D:4166:LYS:NZ	4:D:5002:ATP:O2G	2.42	0.46
1:A:238:HIS:CD2	1:A:239:GLY:H	2.34	0.46
1:A:877:HIS:CE1	1:A:1062:TYR:HH	2.29	0.46
1:A:3122:ILE:HG13	1:A:3127:GLN:HE21	1.81	0.46
1:A:4867:ILE:HG12	1:B:4864:GLY:HA2	1.98	0.46
1:B:1911:GLN:NE2	1:B:2090:ARG:HH11	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2077:ASP:O	1:C:2081:VAL:HG23	2.16	0.46
1:D:292:GLY:HA2	1:D:332:ARG:NH1	2.31	0.46
1:D:1793:GLN:NE2	1:D:1797:GLU:OE2	2.43	0.46
1:D:2057:THR:HB	1:D:2060:GLN:HG3	1.96	0.46
1:D:2168:HIS:HD2	1:D:2214:MET:HE3	1.81	0.46
1:D:2610:LEU:HD13	1:D:2644:LEU:HD21	1.98	0.46
1:D:3122:ILE:HG13	1:D:3127:GLN:HE21	1.81	0.46
1:D:3129:SER:O	1:D:3133:ILE:HG13	2.16	0.46
1:A:34:LYS:H	1:A:53:SER:HG	1.58	0.46
1:A:1594:VAL:HG13	1:A:1594:VAL:O	2.16	0.46
1:A:2725:ALA:HB1	1:A:2760:TYR:CZ	2.51	0.46
1:A:3296:MET:SD	1:A:3334:VAL:HG11	2.56	0.46
1:A:3649:ALA:C	1:A:3652:PRO:HD2	2.41	0.46
1:B:375:GLN:HG2	1:B:377:VAL:HG13	1.98	0.46
1:C:81:MET:O	1:C:81:MET:HG2	2.11	0.46
1:C:387:ILE:HD12	1:C:389:ARG:HD3	1.97	0.46
1:C:3649:ALA:HB1	1:C:3652:PRO:HB2	1.98	0.46
1:D:2725:ALA:HB1	1:D:2760:TYR:CZ	2.51	0.46
1:D:2797:SER:HA	1:D:2800:LEU:HG	1.96	0.46
1:D:3148:VAL:HG23	1:D:3155:LEU:HD12	1.98	0.46
1:D:3961:ASP:OD1	1:D:3962:SER:N	2.49	0.46
1:A:713:TRP:CE2	1:A:1600:PRO:HD3	2.51	0.45
1:A:1670:HIS:O	1:A:1674:HIS:ND1	2.48	0.45
1:A:1685:LEU:HD22	1:A:1706:LEU:HB2	1.98	0.45
1:A:1989:PRO:HD2	1:A:1992:ILE:HD13	1.97	0.45
1:A:2760:TYR:HA	1:A:2763:LEU:HD13	1.97	0.45
1:A:2769:GLU:C	1:A:2771:TYR:H	2.22	0.45
2:F:63:GLY:O	2:F:67:MET:HG3	2.16	0.45
2:G:63:GLY:O	2:G:67:MET:HG3	2.17	0.45
1:B:238:HIS:CD2	1:B:239:GLY:H	2.34	0.45
1:B:2725:ALA:HB1	1:B:2760:TYR:CZ	2.51	0.45
1:B:2886:ARG:O	1:B:2890:GLN:HG2	2.15	0.45
1:C:238:HIS:CD2	1:C:239:GLY:H	2.34	0.45
1:C:756:SER:OG	1:C:769:ARG:HB2	2.17	0.45
1:C:1594:VAL:HG13	1:C:1594:VAL:O	2.16	0.45
1:C:2749:ASP:OD1	1:C:2750:SER:N	2.49	0.45
1:D:1415:ASP:OD2	1:D:1559:ARG:NH2	2.45	0.45
1:D:1594:VAL:O	1:D:1594:VAL:HG13	2.16	0.45
1:D:2749:ASP:OD1	1:D:2750:SER:N	2.49	0.45
1:D:3296:MET:SD	1:D:3334:VAL:HG11	2.56	0.45
1:A:23:GLN:HB3	1:A:34:LYS:HD2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2610:LEU:HD13	1:A:2644:LEU:HD21	1.98	0.45
1:A:3961:ASP:OD1	1:A:3962:SER:N	2.49	0.45
1:A:4495:PHE:CE2	1:D:4283:PHE:HE2	2.34	0.45
1:B:1989:PRO:HD2	1:B:1992:ILE:HD13	1.97	0.45
1:B:2266:VAL:HG11	1:B:2323:LEU:HB3	1.97	0.45
1:B:3297:LYS:NZ	1:B:3334:VAL:HG13	2.31	0.45
1:B:3712:LYS:O	1:B:3717:LYS:NZ	2.49	0.45
1:B:3961:ASP:OD1	1:B:3962:SER:N	2.49	0.45
1:C:23:GLN:HB3	1:C:34:LYS:HD2	1.98	0.45
1:C:1031:ARG:HG3	1:C:1038:LEU:HD11	1.97	0.45
1:C:2984:SER:OG	1:C:2994:GLY:O	2.27	0.45
1:C:4520:TYR:HB3	1:D:4809:MET:HG2	1.98	0.45
1:D:1031:ARG:HG3	1:D:1038:LEU:HD11	1.97	0.45
1:D:4027:THR:HA	1:D:4032:PHE:HD1	1.81	0.45
1:A:1991:GLU:HG2	1:A:1992:ILE:HD12	1.98	0.45
1:A:2759:PRO:O	1:A:2762:LEU:N	2.50	0.45
1:B:865:ILE:HD12	1:B:865:ILE:HA	1.77	0.45
1:B:1793:GLN:NE2	1:B:1797:GLU:OE2	2.43	0.45
1:B:1842:ILE:HD12	1:B:1845:LEU:HD12	1.98	0.45
1:B:2587:HIS:HB3	1:B:2875:ASP:OD2	2.16	0.45
1:B:2610:LEU:HD13	1:B:2644:LEU:HD21	1.98	0.45
1:B:3015:VAL:HA	1:B:3022:PHE:HE2	1.81	0.45
1:B:3805:LEU:HD11	1:B:3887:ASP:HB3	1.98	0.45
1:C:2142:MET:CG	1:C:2192:MET:HE1	2.43	0.45
1:C:2725:ALA:HB1	1:C:2760:TYR:CZ	2.51	0.45
1:C:3015:VAL:HA	1:C:3022:PHE:HE2	1.81	0.45
1:C:3306:ILE:O	1:C:3310:VAL:HG23	2.16	0.45
1:D:877:HIS:CE1	1:D:1062:TYR:OH	2.70	0.45
1:D:2077:ASP:O	1:D:2081:VAL:HG23	2.15	0.45
1:D:3650:GLU:HB2	1:D:3651:PRO:HD3	1.98	0.45
1:A:2722:ASN:C	1:A:2724:TYR:H	2.24	0.45
1:A:3303:SER:HA	1:A:3306:ILE:HG12	1.99	0.45
1:B:2167:MET:SD	1:B:2199:PHE:HZ	2.39	0.45
1:B:2957:GLU:O	1:B:2961:LYS:HG2	2.16	0.45
1:B:3012:GLY:HA2	1:B:3015:VAL:HG12	1.98	0.45
1:B:3184:TYR:CE2	1:B:3201:VAL:HB	2.51	0.45
1:C:1644:LEU:HD23	1:C:1651:LEU:HA	1.97	0.45
1:C:2125:GLN:OE1	1:C:2144:ARG:NH2	2.47	0.45
1:C:2614:TYR:CD2	1:C:2672:VAL:HG22	2.51	0.45
1:C:3303:SER:HA	1:C:3306:ILE:HG12	1.99	0.45
1:C:4283:PHE:HB2	1:D:4488:GLN:HE22	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1751:ILE:HD11	1:D:1839:LEU:HB2	1.98	0.45
1:D:1991:GLU:HG2	1:D:1992:ILE:HD12	1.98	0.45
1:D:2732:TRP:CD2	1:D:2736:LYS:NZ	2.85	0.45
1:D:3303:SER:HA	1:D:3306:ILE:HG12	1.99	0.45
1:A:270:HIS:CE1	1:A:491:GLU:HG3	2.52	0.45
1:A:1751:ILE:HD11	1:A:1839:LEU:HB2	1.98	0.45
1:A:3129:SER:O	1:A:3133:ILE:HG13	2.16	0.45
1:A:3805:LEU:HD11	1:A:3887:ASP:HB3	1.98	0.45
2:H:63:GLY:O	2:H:67:MET:HG3	2.16	0.45
1:B:515:ALA:HB2	1:B:523:GLY:HA3	1.99	0.45
1:B:713:TRP:CE2	1:B:1600:PRO:HD3	2.51	0.45
1:B:756:SER:OG	1:B:769:ARG:HB2	2.17	0.45
1:B:3129:SER:O	1:B:3133:ILE:HG13	2.17	0.45
1:C:877:HIS:CE1	1:C:1062:TYR:OH	2.70	0.45
1:C:1914:CYS:SG	1:C:2091:GLN:NE2	2.82	0.45
1:C:4252:ILE:CG2	1:D:4707:MET:HG3	2.46	0.45
1:C:4800:ASP:OD1	1:C:4801:THR:N	2.50	0.45
1:D:1644:LEU:HD23	1:D:1651:LEU:HA	1.97	0.45
1:D:2748:SER:HB2	1:D:2753:VAL:CG2	2.46	0.45
1:D:4503:ARG:HA	1:D:4503:ARG:HD2	1.74	0.45
1:A:375:GLN:HG2	1:A:377:VAL:HG13	1.98	0.45
1:A:756:SER:OG	1:A:769:ARG:HB2	2.17	0.45
1:A:2136:LYS:HD3	1:A:2136:LYS:HA	1.83	0.45
1:A:2785:TRP:CE3	1:A:2787:TRP:CZ2	3.05	0.45
1:A:2830:ASN:HB2	1:B:1434:PRO:O	2.17	0.45
1:B:292:GLY:HA2	1:B:332:ARG:NH1	2.31	0.45
1:B:582:SER:OG	1:B:584:GLU:OE1	2.34	0.45
1:B:1594:VAL:O	1:B:1594:VAL:HG13	2.16	0.45
1:B:3148:VAL:HG23	1:B:3155:LEU:HD12	1.98	0.45
1:B:3306:ILE:O	1:B:3310:VAL:HG23	2.16	0.45
1:B:4481:TRP:HA	1:B:4484:ILE:HG12	1.99	0.45
1:C:527:LYS:HE2	1:C:566:GLU:HB2	1.98	0.45
1:C:890:HIS:HB2	1:C:932:ASN:ND2	2.32	0.45
1:C:2610:LEU:HD13	1:C:2644:LEU:HD21	1.98	0.45
1:C:2785:TRP:CE3	1:C:2787:TRP:CZ2	3.05	0.45
1:C:2966:VAL:HG12	1:C:2970:LEU:HD23	1.99	0.45
1:C:3297:LYS:NZ	1:C:3334:VAL:HG13	2.31	0.45
1:D:375:GLN:HG2	1:D:377:VAL:HG13	1.98	0.45
1:D:756:SER:OG	1:D:769:ARG:HB2	2.17	0.45
1:D:890:HIS:HB2	1:D:932:ASN:ND2	2.32	0.45
1:D:2126:ILE:HD12	1:D:2142:MET:SD	2.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2167:MET:SD	1:D:2199:PHE:HZ	2.39	0.45
1:D:3805:LEU:HD11	1:D:3887:ASP:HB3	1.98	0.45
1:D:4020:PHE:CD1	1:D:4087:PHE:HB3	2.51	0.45
1:A:292:GLY:HA2	1:A:332:ARG:NH1	2.31	0.45
1:A:1842:ILE:HD12	1:A:1845:LEU:HD12	1.98	0.45
1:A:2760:TYR:O	1:A:2768:LYS:NZ	2.46	0.45
1:A:2966:VAL:HG12	1:A:2970:LEU:HD23	1.99	0.45
1:A:3246:MET:O	1:A:3250:TRP:HD1	1.99	0.45
1:A:3650:GLU:HB2	1:A:3651:PRO:HD3	1.98	0.45
1:B:270:HIS:CE1	1:B:491:GLU:HG3	2.52	0.45
1:B:877:HIS:CE1	1:B:1062:TYR:HH	2.31	0.45
1:B:904:TYR:CD1	1:B:918:LEU:HD12	2.52	0.45
1:B:1685:LEU:HD22	1:B:1706:LEU:HB2	1.98	0.45
1:B:2264:LYS:O	1:B:2267:ARG:HG2	2.17	0.45
1:B:2748:SER:HB2	1:B:2753:VAL:CG2	2.46	0.45
1:B:3043:ARG:HA	1:B:3120:ASP:OD2	2.17	0.45
1:B:4800:ASP:OD1	1:B:4801:THR:N	2.50	0.45
1:C:582:SER:OG	1:C:584:GLU:OE1	2.34	0.45
1:C:1047:LYS:O	1:C:1051:ARG:HG2	2.17	0.45
1:C:2957:GLU:O	1:C:2961:LYS:HG2	2.16	0.45
1:C:3129:SER:O	1:C:3133:ILE:HG13	2.16	0.45
1:D:2614:TYR:CD2	1:D:2672:VAL:HG22	2.51	0.45
1:D:3043:ARG:HA	1:D:3120:ASP:OD2	2.17	0.45
1:A:515:ALA:HB2	1:A:523:GLY:HA3	1.99	0.45
1:A:1176:THR:HG22	1:A:1181:ILE:HA	1.99	0.45
1:A:2077:ASP:O	1:A:2081:VAL:HG23	2.15	0.45
1:A:2748:SER:HB2	1:A:2753:VAL:CG2	2.46	0.45
1:A:3043:ARG:HA	1:A:3120:ASP:OD2	2.17	0.45
1:B:374:TYR:OH	1:B:400:ASP:OD1	2.32	0.45
1:B:877:HIS:CE1	1:B:1062:TYR:OH	2.70	0.45
1:B:3303:SER:HA	1:B:3306:ILE:HG12	1.99	0.45
1:C:515:ALA:HB2	1:C:523:GLY:HA3	1.99	0.45
1:C:2126:ILE:HD12	1:C:2142:MET:SD	2.56	0.45
1:C:3043:ARG:HA	1:C:3120:ASP:OD2	2.17	0.45
1:C:3046:MET:HA	1:C:3054:LYS:NZ	2.32	0.45
1:D:1176:THR:HG22	1:D:1181:ILE:HA	1.99	0.45
1:A:3250:TRP:CH2	1:A:3273:MET:HG3	2.52	0.45
1:A:4027:THR:HA	1:A:4032:PHE:HD1	1.81	0.45
1:A:4089:GLU:HB2	1:A:4090:PRO:HD3	1.99	0.45
1:A:4481:TRP:HA	1:A:4484:ILE:HG12	1.99	0.45
1:B:527:LYS:HE2	1:B:566:GLU:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3250:TRP:CH2	1:B:3273:MET:HG3	2.52	0.45
1:B:3649:ALA:C	1:B:3652:PRO:HD2	2.41	0.45
1:C:2925:PHE:CE2	1:C:2929:LEU:HD11	2.52	0.45
1:D:270:HIS:CE1	1:D:491:GLU:HG3	2.52	0.45
1:D:2785:TRP:CE3	1:D:2787:TRP:CZ2	3.05	0.45
1:D:3306:ILE:O	1:D:3310:VAL:HG23	2.16	0.45
1:A:704:SER:C	1:A:706:TYR:H	2.25	0.45
1:A:2125:GLN:OE1	1:A:2144:ARG:NH2	2.47	0.45
1:A:2167:MET:SD	1:A:2199:PHE:HZ	2.39	0.45
1:A:2264:LYS:O	1:A:2267:ARG:HG2	2.17	0.45
1:A:2587:HIS:HB3	1:A:2875:ASP:OD2	2.16	0.45
1:A:3306:ILE:O	1:A:3310:VAL:HG23	2.16	0.45
2:E:63:GLY:O	2:E:67:MET:HG3	2.17	0.45
1:B:704:SER:C	1:B:706:TYR:H	2.25	0.45
1:B:2488:LEU:HA	1:B:2492:PHE:HB2	1.99	0.45
1:B:2785:TRP:CE3	1:B:2787:TRP:CZ2	3.05	0.45
1:C:270:HIS:CE1	1:C:491:GLU:HG3	2.52	0.45
1:C:1842:ILE:HD12	1:C:1845:LEU:HD12	1.98	0.45
1:D:2266:VAL:HG11	1:D:2323:LEU:HB3	1.97	0.45
1:D:2773:TRP:HB3	1:D:2774:PRO:HD3	1.99	0.45
1:D:2925:PHE:CE2	1:D:2929:LEU:HD11	2.52	0.45
1:D:3649:ALA:HB1	1:D:3652:PRO:HB2	1.98	0.45
1:D:3649:ALA:C	1:D:3652:PRO:HD2	2.41	0.45
1:D:4084:VAL:O	1:D:4088:HIS:CB	2.65	0.45
1:A:3015:VAL:HA	1:A:3022:PHE:HE2	1.81	0.44
1:A:3284:ILE:HA	1:A:3287:ASN:OD1	2.17	0.44
1:B:23:GLN:HB3	1:B:34:LYS:HD2	1.98	0.44
1:B:890:HIS:HB2	1:B:932:ASN:ND2	2.32	0.44
1:B:2732:TRP:CD2	1:B:2736:LYS:NZ	2.85	0.44
1:B:4863:GLN:OE1	1:C:4860:ALA:HB2	2.17	0.44
1:C:704:SER:C	1:C:706:TYR:H	2.25	0.44
1:C:1016:TRP:HH2	1:C:1024:VAL:HG12	1.80	0.44
1:C:1169:ASN:OD1	1:C:1170:GLU:HG2	2.17	0.44
1:C:1939:ASN:HD21	1:C:1989:PRO:HG2	1.82	0.44
1:C:2168:HIS:HD2	1:C:2214:MET:HE3	1.81	0.44
1:C:2732:TRP:CD2	1:C:2736:LYS:NZ	2.85	0.44
1:C:2896:LEU:HG	1:C:2901:TYR:HB2	2.00	0.44
1:D:23:GLN:HB3	1:D:34:LYS:HD2	1.98	0.44
1:D:527:LYS:HE2	1:D:566:GLU:HB2	1.98	0.44
1:D:2587:HIS:HA	1:D:2590:ARG:HH11	1.83	0.44
1:A:527:LYS:HE2	1:A:566:GLU:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1496:PRO:HB2	1:D:2798:MET:HE1	1.99	0.44
1:A:1788:LYS:HG3	1:A:1834:PHE:CE1	2.53	0.44
1:A:2896:LEU:HG	1:A:2901:TYR:HB2	1.99	0.44
1:A:3148:VAL:HG23	1:A:3155:LEU:HD12	1.98	0.44
1:A:3246:MET:CB	1:A:3273:MET:HE1	2.44	0.44
1:A:4800:ASP:OD1	1:A:4801:THR:N	2.50	0.44
1:B:1047:LYS:O	1:B:1051:ARG:HG2	2.17	0.44
1:B:2759:PRO:O	1:B:2762:LEU:N	2.50	0.44
1:B:3149:GLU:O	1:B:3152:ARG:HG2	2.17	0.44
1:C:2167:MET:SD	1:C:2199:PHE:HZ	2.39	0.44
1:C:2773:TRP:HB3	1:C:2774:PRO:HD3	1.99	0.44
1:C:3148:VAL:HG23	1:C:3155:LEU:HD12	1.98	0.44
1:D:515:ALA:HB2	1:D:523:GLY:HA3	1.99	0.44
1:D:2966:VAL:HG12	1:D:2970:LEU:HD23	1.99	0.44
1:D:3250:TRP:CH2	1:D:3273:MET:HG3	2.52	0.44
1:D:4800:ASP:OD1	1:D:4801:THR:N	2.50	0.44
1:A:890:HIS:HB2	1:A:932:ASN:ND2	2.32	0.44
1:A:2266:VAL:HG11	1:A:2323:LEU:HB3	1.97	0.44
1:A:3649:ALA:HB1	1:A:3652:PRO:HB2	1.98	0.44
1:A:4818:TYR:HA	1:B:4848:ILE:HD11	1.98	0.44
1:B:2322:ARG:O	1:B:2326:ARG:HG2	2.17	0.44
1:B:3284:ILE:HA	1:B:3287:ASN:OD1	2.17	0.44
1:C:2587:HIS:HB3	1:C:2875:ASP:OD2	2.16	0.44
1:C:3149:GLU:O	1:C:3152:ARG:HG2	2.17	0.44
1:C:3649:ALA:C	1:C:3652:PRO:HD2	2.41	0.44
1:C:4084:VAL:O	1:C:4088:HIS:CB	2.65	0.44
1:D:1979:PHE:HB3	1:D:1986:CYS:SG	2.57	0.44
1:A:1272:ARG:NH2	1:A:1582:CYS:SG	2.91	0.44
1:A:1825:PHE:CE1	1:A:1842:ILE:HG12	2.53	0.44
1:A:2587:HIS:HA	1:A:2590:ARG:HH11	1.82	0.44
1:A:3111:HIS:HB2	1:A:3115:HIS:HE1	1.82	0.44
1:A:3114:GLN:HE21	1:A:3115:HIS:CE1	2.36	0.44
1:B:1176:THR:HG22	1:B:1181:ILE:HA	1.99	0.44
1:B:2925:PHE:CE2	1:B:2929:LEU:HD11	2.52	0.44
1:C:181:LEU:N	1:C:212:TRP:O	2.45	0.44
1:C:292:GLY:HA2	1:C:332:ARG:NH1	2.31	0.44
1:C:1685:LEU:HD22	1:C:1706:LEU:HB2	1.98	0.44
1:C:2734:MET:HE3	1:C:2823:PRO:HB2	2.00	0.44
1:C:3994:THR:O	1:C:3998:GLN:HG3	2.18	0.44
1:D:704:SER:C	1:D:706:TYR:H	2.25	0.44
1:D:2082:ARG:HG3	1:D:3687:LEU:HD22	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2587:HIS:HB3	1:D:2875:ASP:OD2	2.16	0.44
1:D:3015:VAL:HA	1:D:3022:PHE:HE2	1.81	0.44
1:D:3284:ILE:HA	1:D:3287:ASN:OD1	2.18	0.44
1:A:2322:ARG:O	1:A:2326:ARG:HG2	2.18	0.44
1:A:3994:THR:O	1:A:3998:GLN:HG3	2.18	0.44
1:B:1169:ASN:OD1	1:B:1170:GLU:HG2	2.17	0.44
1:B:1788:LYS:HG3	1:B:1834:PHE:CE1	2.53	0.44
1:B:2422:ILE:O	1:B:2426:LEU:HG	2.18	0.44
1:B:2896:LEU:HG	1:B:2901:TYR:HB2	1.99	0.44
1:B:3046:MET:HA	1:B:3054:LYS:NZ	2.32	0.44
1:B:3994:THR:O	1:B:3998:GLN:HG3	2.18	0.44
1:B:4084:VAL:O	1:B:4088:HIS:CB	2.66	0.44
1:B:4867:ILE:HG12	1:C:4864:GLY:HA2	1.99	0.44
1:C:227:TYR:CG	1:C:352:SER:HB3	2.53	0.44
1:C:853:PRO:O	1:C:1210:ALA:N	2.39	0.44
1:C:1819:VAL:HG13	1:C:1905:GLN:NE2	2.33	0.44
1:C:2670:SER:HB2	1:C:2973:GLN:CG	2.47	0.44
1:D:1842:ILE:HD12	1:D:1845:LEU:HD12	1.98	0.44
1:D:2348:GLU:HA	1:D:2351:ILE:HG12	2.00	0.44
1:A:897:LYS:HA	1:A:900:LEU:HG	2.00	0.44
1:A:1034:PRO:HG2	1:A:1037:LEU:HB2	2.00	0.44
1:A:1911:GLN:NE2	1:A:2090:ARG:HH11	2.14	0.44
1:A:2348:GLU:HA	1:A:2351:ILE:HG12	2.00	0.44
1:B:308:LEU:HD13	1:B:393:MET:HG3	2.00	0.44
1:B:928:GLU:HA	1:B:931:TYR:HD2	1.82	0.44
1:B:1649:GLU:HG2	1:B:1650:LEU:N	2.33	0.44
1:B:2932:TYR:CE2	1:B:2963:PHE:HD1	2.36	0.44
1:C:1788:LYS:HG3	1:C:1834:PHE:CE1	2.53	0.44
1:C:2348:GLU:HA	1:C:2351:ILE:HG12	1.99	0.44
1:C:2748:SER:HB2	1:C:2753:VAL:CG2	2.46	0.44
1:C:3284:ILE:HA	1:C:3287:ASN:OD1	2.18	0.44
1:C:4089:GLU:HB2	1:C:4090:PRO:HD3	1.99	0.44
1:D:227:TYR:CG	1:D:352:SER:HB3	2.53	0.44
1:D:1788:LYS:HG3	1:D:1834:PHE:CE1	2.53	0.44
1:D:3114:GLN:HE21	1:D:3115:HIS:CE1	2.36	0.44
1:A:1169:ASN:OD1	1:A:1170:GLU:HG2	2.17	0.44
1:A:1434:PRO:O	1:D:2830:ASN:HB2	2.17	0.44
1:A:2732:TRP:CD2	1:A:2736:LYS:NZ	2.85	0.44
1:B:281:ARG:O	1:B:285:SER:OG	2.33	0.44
1:B:1272:ARG:NH2	1:B:1582:CYS:SG	2.91	0.44
1:B:2168:HIS:HD2	1:B:2214:MET:HE3	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2773:TRP:HB3	1:B:2774:PRO:HD3	1.99	0.44
1:B:2966:VAL:HG12	1:B:2970:LEU:HD23	1.99	0.44
1:C:1034:PRO:HG2	1:C:1037:LEU:HB2	2.00	0.44
1:C:1041:ARG:O	1:C:1044:LYS:HG3	2.17	0.44
1:C:3250:TRP:CH2	1:C:3273:MET:HG3	2.52	0.44
1:D:582:SER:OG	1:D:584:GLU:OE1	2.34	0.44
1:D:1041:ARG:O	1:D:1044:LYS:HG3	2.17	0.44
1:D:1169:ASN:OD1	1:D:1170:GLU:HG2	2.17	0.44
1:D:1825:PHE:CE1	1:D:1842:ILE:HG12	2.53	0.44
1:D:1967:SER:O	1:D:1972:GLN:NE2	2.49	0.44
1:D:2255:LEU:HD21	1:D:3813:LYS:HD3	2.00	0.44
1:D:2264:LYS:O	1:D:2267:ARG:HG2	2.17	0.44
1:D:2759:PRO:O	1:D:2762:LEU:N	2.50	0.44
1:D:2932:TYR:CE2	1:D:2963:PHE:HD1	2.36	0.44
1:A:841:LYS:O	1:A:848:ARG:NH2	2.50	0.44
1:A:928:GLU:HA	1:A:931:TYR:HD2	1.82	0.44
1:A:1979:PHE:HB3	1:A:1986:CYS:SG	2.57	0.44
1:A:2255:LEU:HD21	1:A:3813:LYS:HD3	2.00	0.44
1:A:2925:PHE:CE2	1:A:2929:LEU:HD11	2.52	0.44
1:A:3046:MET:HA	1:A:3054:LYS:NZ	2.32	0.44
1:B:2734:MET:HE3	1:B:2823:PRO:HB2	2.00	0.44
1:B:3114:GLN:HE21	1:B:3115:HIS:CE1	2.36	0.44
1:C:778:MET:HG2	1:C:1468:THR:HB	2.00	0.44
1:C:1989:PRO:O	1:C:1993:ARG:HG3	2.18	0.44
1:C:2255:LEU:HD21	1:C:3813:LYS:HD3	2.00	0.44
1:C:2422:ILE:O	1:C:2426:LEU:HG	2.18	0.44
1:C:2759:PRO:O	1:C:2762:LEU:N	2.50	0.44
1:D:1649:GLU:HG2	1:D:1650:LEU:N	2.33	0.44
1:D:1989:PRO:O	1:D:1993:ARG:HG3	2.18	0.44
1:D:2322:ARG:O	1:D:2326:ARG:HG2	2.18	0.44
1:D:2734:MET:HE3	1:D:2823:PRO:HB2	2.00	0.44
1:A:81:MET:O	1:A:81:MET:HG2	2.11	0.44
1:A:218:SER:HB2	1:A:286:GLY:HA3	2.00	0.44
1:A:472:HIS:O	1:A:476:GLN:HG2	2.18	0.44
1:A:877:HIS:CE1	1:A:1062:TYR:OH	2.70	0.44
1:A:1819:VAL:HG13	1:A:1905:GLN:NE2	2.33	0.44
1:A:2422:ILE:O	1:A:2426:LEU:HG	2.18	0.44
1:A:4084:VAL:O	1:A:4088:HIS:CB	2.65	0.44
1:B:1041:ARG:O	1:B:1044:LYS:HG3	2.17	0.44
1:B:1819:VAL:HG13	1:B:1905:GLN:NE2	2.33	0.44
1:B:1939:ASN:HD21	1:B:1989:PRO:HG2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1979:PHE:HB3	1:B:1986:CYS:SG	2.58	0.44
1:B:1989:PRO:O	1:B:1993:ARG:HG3	2.18	0.44
1:B:2635:GLU:HA	1:B:2638:LEU:HB2	2.00	0.44
1:B:3650:GLU:HG2	1:B:3660:ARG:CZ	2.48	0.44
1:C:1176:THR:HG22	1:C:1181:ILE:HA	1.99	0.44
1:C:1825:PHE:CE1	1:C:1842:ILE:HG12	2.53	0.44
1:C:2082:ARG:HG3	1:C:3687:LEU:HD22	2.00	0.44
1:C:2136:LYS:HA	1:C:2136:LYS:HD3	1.83	0.44
1:C:2264:LYS:O	1:C:2267:ARG:HG2	2.17	0.44
1:C:2488:LEU:HA	1:C:2492:PHE:HB2	1.99	0.44
1:C:2635:GLU:HA	1:C:2638:LEU:HB2	2.00	0.44
1:C:2668:CYS:O	1:C:2672:VAL:HG23	2.18	0.44
1:D:309:MET:HA	1:D:309:MET:HE3	2.00	0.44
1:D:903:GLN:OE1	1:D:913:ARG:HD2	2.18	0.44
1:D:1047:LYS:O	1:D:1051:ARG:HG2	2.17	0.44
1:D:2081:VAL:HA	1:D:2084:MET:HE2	2.00	0.44
1:D:2488:LEU:HA	1:D:2492:PHE:HB2	1.99	0.44
1:D:2896:LEU:HG	1:D:2901:TYR:HB2	2.00	0.44
1:D:3046:MET:HA	1:D:3054:LYS:NZ	2.32	0.44
1:B:1966:ARG:HB3	1:B:3602:CYS:HB3	2.00	0.43
1:C:999:LEU:HB3	1:C:1050:LEU:HD21	2.00	0.43
1:C:1966:ARG:HB3	1:C:3602:CYS:HB3	2.00	0.43
1:C:2943:PHE:CE1	1:C:2955:PRO:HD2	2.53	0.43
1:D:841:LYS:O	1:D:848:ARG:NH2	2.50	0.43
1:D:897:LYS:HA	1:D:900:LEU:HG	2.00	0.43
1:D:904:TYR:CD1	1:D:918:LEU:HD12	2.52	0.43
1:D:1827:THR:O	1:D:1831:MET:HG3	2.18	0.43
1:D:1914:CYS:SG	1:D:2091:GLN:NE2	2.82	0.43
1:D:2413:LYS:NZ	1:D:2415:GLU:HB3	2.33	0.43
1:D:2635:GLU:HA	1:D:2638:LEU:HB2	2.00	0.43
1:D:3111:HIS:HB2	1:D:3115:HIS:HE1	1.82	0.43
1:D:4481:TRP:HA	1:D:4484:ILE:HG12	1.99	0.43
1:A:842:GLN:HB2	1:A:1603:PHE:HB2	2.01	0.43
1:A:1040:ASP:HA	1:A:1043:LYS:HG2	2.00	0.43
1:A:1047:LYS:O	1:A:1051:ARG:HG2	2.17	0.43
1:A:1649:GLU:HG2	1:A:1650:LEU:N	2.33	0.43
1:A:2082:ARG:HG3	1:A:3687:LEU:HD22	2.00	0.43
1:A:2635:GLU:HA	1:A:2638:LEU:HB2	2.00	0.43
1:A:2984:SER:OG	1:A:2994:GLY:O	2.27	0.43
1:B:472:HIS:O	1:B:476:GLN:HG2	2.18	0.43
1:B:2057:THR:HG22	1:B:2059:GLN:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2081:VAL:HA	1:B:2084:MET:HE2	2.00	0.43
1:C:904:TYR:CD1	1:C:918:LEU:HD12	2.52	0.43
1:C:3111:HIS:HB2	1:C:3115:HIS:HE1	1.83	0.43
1:C:3305:PRO:HB2	1:C:3309:LYS:NZ	2.33	0.43
1:D:999:LEU:HB3	1:D:1050:LEU:HD21	2.00	0.43
1:D:1040:ASP:HA	1:D:1043:LYS:HG2	2.00	0.43
1:D:1272:ARG:NH2	1:D:1582:CYS:SG	2.91	0.43
1:D:2222:LEU:HD23	1:D:2222:LEU:HA	1.86	0.43
1:D:2422:ILE:O	1:D:2426:LEU:HG	2.18	0.43
1:D:2943:PHE:CE1	1:D:2955:PRO:HD2	2.53	0.43
1:A:227:TYR:CG	1:A:352:SER:HB3	2.53	0.43
1:A:1292:SER:O	1:D:2835:ARG:NH2	2.36	0.43
1:A:1551:ASN:HB2	1:D:2830:ASN:ND2	2.33	0.43
1:A:1975:MET:HA	1:A:1978:ASN:ND2	2.33	0.43
1:A:2488:LEU:HA	1:A:2492:PHE:HB2	1.99	0.43
1:A:2932:TYR:CE2	1:A:2963:PHE:HD1	2.36	0.43
1:A:3650:GLU:HG2	1:A:3660:ARG:CZ	2.48	0.43
1:B:227:TYR:CG	1:B:352:SER:HB3	2.53	0.43
1:B:778:MET:HG2	1:B:1468:THR:HB	2.00	0.43
1:B:1825:PHE:CE1	1:B:1842:ILE:HG12	2.53	0.43
1:B:2255:LEU:HD21	1:B:3813:LYS:HD3	2.00	0.43
1:B:2619:LYS:HB3	1:B:2623:LEU:HD12	1.99	0.43
1:B:2668:CYS:O	1:B:2672:VAL:HG23	2.18	0.43
1:B:4089:GLU:HB2	1:B:4090:PRO:HD3	1.99	0.43
1:B:4607:ALA:HB1	1:B:4649:VAL:HG21	2.00	0.43
1:C:472:HIS:O	1:C:476:GLN:HG2	2.18	0.43
1:C:1272:ARG:NH2	1:C:1582:CYS:SG	2.91	0.43
1:C:1649:GLU:HG2	1:C:1650:LEU:N	2.33	0.43
1:C:1979:PHE:HB3	1:C:1986:CYS:SG	2.58	0.43
1:C:3043:ARG:HB3	1:C:3047:LYS:HE2	2.01	0.43
1:C:3650:GLU:HG2	1:C:3660:ARG:CZ	2.48	0.43
1:C:4252:ILE:HG21	1:D:4707:MET:HG3	1.99	0.43
1:D:928:GLU:HA	1:D:931:TYR:HD2	1.82	0.43
1:D:3983:LEU:HD21	1:D:4100:VAL:HG12	2.00	0.43
1:A:778:MET:HG2	1:A:1468:THR:HB	2.00	0.43
1:A:903:GLN:OE1	1:A:913:ARG:HD2	2.18	0.43
1:A:904:TYR:CD1	1:A:918:LEU:HD12	2.52	0.43
1:A:2734:MET:HE3	1:A:2823:PRO:HB2	2.00	0.43
1:A:2773:TRP:HB3	1:A:2774:PRO:HD3	1.99	0.43
1:B:842:GLN:HB2	1:B:1603:PHE:HB2	2.00	0.43
1:B:1040:ASP:HA	1:B:1043:LYS:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2062:ILE:HG21	1:B:2087:LEU:HG	2.00	0.43
1:B:2348:GLU:HA	1:B:2351:ILE:HG12	2.00	0.43
1:B:3072:MET:CE	1:B:3136:SER:HB2	2.44	0.43
1:C:308:LEU:HD13	1:C:393:MET:HG3	2.00	0.43
1:C:658:ASN:ND2	1:C:831:LYS:O	2.50	0.43
1:C:917:CYS:HB3	1:C:924:LEU:HD12	2.00	0.43
1:C:1048:ASP:HA	1:C:1051:ARG:CG	2.49	0.43
1:C:1967:SER:O	1:C:1972:GLN:NE2	2.49	0.43
1:C:2587:HIS:HA	1:C:2590:ARG:HH11	1.83	0.43
1:C:2726:GLU:OE1	1:C:2726:GLU:N	2.51	0.43
1:C:2932:TYR:CE2	1:C:2963:PHE:HD1	2.36	0.43
1:C:4481:TRP:HA	1:C:4484:ILE:HG12	1.99	0.43
1:D:308:LEU:HD13	1:D:393:MET:HG3	2.00	0.43
1:D:658:ASN:ND2	1:D:831:LYS:O	2.50	0.43
1:D:1034:PRO:HG2	1:D:1037:LEU:HB2	2.00	0.43
1:D:1168:MET:HA	1:D:1168:MET:HE3	2.01	0.43
1:D:1939:ASN:HD21	1:D:1989:PRO:HG2	1.82	0.43
1:D:1966:ARG:HB3	1:D:3602:CYS:HB3	2.00	0.43
1:D:2914:THR:N	1:D:2915:PRO:HD2	2.34	0.43
1:D:3246:MET:CB	1:D:3273:MET:HE1	2.45	0.43
1:A:917:CYS:HB3	1:A:924:LEU:HD12	2.00	0.43
1:A:1041:ARG:O	1:A:1044:LYS:HG3	2.18	0.43
1:A:1168:MET:HA	1:A:1168:MET:HE3	2.01	0.43
1:A:1719:LEU:HD21	1:A:1830:ILE:HD12	2.01	0.43
1:A:1989:PRO:O	1:A:1993:ARG:HG3	2.18	0.43
1:A:2413:LYS:NZ	1:A:2415:GLU:HB3	2.33	0.43
1:A:3324:GLU:HA	1:A:3327:LYS:NZ	2.33	0.43
1:A:3983:LEU:HD21	1:A:4100:VAL:HG12	2.00	0.43
1:A:4275:THR:HG22	1:A:4278:ASP:H	1.84	0.43
1:A:4607:ALA:HB1	1:A:4649:VAL:HG21	2.00	0.43
1:B:897:LYS:HA	1:B:900:LEU:HG	2.00	0.43
1:B:1719:LEU:HD21	1:B:1830:ILE:HD12	2.01	0.43
1:B:2413:LYS:NZ	1:B:2415:GLU:HB3	2.33	0.43
1:B:3305:PRO:HB2	1:B:3309:LYS:NZ	2.34	0.43
1:B:4275:THR:HG22	1:B:4278:ASP:H	1.84	0.43
1:C:1040:ASP:HA	1:C:1043:LYS:HG2	2.00	0.43
1:C:2081:VAL:HA	1:C:2084:MET:HE2	2.00	0.43
1:C:4522:VAL:HG22	1:D:4807:ASP:O	2.18	0.43
1:D:218:SER:HB2	1:D:286:GLY:HA3	2.00	0.43
1:D:430:ILE:HG23	1:D:504:ARG:HD2	2.00	0.43
1:D:1792:ILE:HD11	1:D:1834:PHE:CE1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2668:CYS:O	1:D:2672:VAL:HG23	2.18	0.43
1:D:3994:THR:O	1:D:3998:GLN:HG3	2.18	0.43
1:A:374:TYR:OH	1:A:400:ASP:OD1	2.32	0.43
1:A:1914:CYS:SG	1:A:2091:GLN:NE2	2.82	0.43
1:A:2168:HIS:HD2	1:A:2214:MET:HE3	1.81	0.43
1:A:2779:LEU:O	1:A:2783:LEU:HG	2.19	0.43
1:A:2914:THR:N	1:A:2915:PRO:HD2	2.34	0.43
1:A:3237:VAL:O	1:A:3240:PRO:HD2	2.19	0.43
1:A:3305:PRO:HB2	1:A:3309:LYS:NZ	2.33	0.43
1:B:494:MET:HE3	1:B:494:MET:HB3	1.86	0.43
1:B:2142:MET:CG	1:B:2192:MET:HE1	2.43	0.43
1:C:1051:ARG:HG2	1:C:1051:ARG:HH21	1.84	0.43
1:C:1437:GLU:HA	1:C:1438:PRO:HD3	1.90	0.43
1:C:1765:SER:HA	1:C:1766:PRO:HD3	1.90	0.43
1:C:1827:THR:O	1:C:1831:MET:HG3	2.18	0.43
1:C:1975:MET:HA	1:C:1978:ASN:ND2	2.33	0.43
1:C:2827:ASP:H	1:D:1501:ASN:ND2	2.17	0.43
1:D:1048:ASP:HA	1:D:1051:ARG:CG	2.49	0.43
1:A:865:ILE:HD12	1:A:865:ILE:HA	1.77	0.43
1:A:1939:ASN:HD21	1:A:1989:PRO:HG2	1.82	0.43
1:A:2081:VAL:HA	1:A:2084:MET:HE2	2.00	0.43
1:A:2884:LYS:O	1:A:2887:GLU:HG3	2.19	0.43
1:A:2943:PHE:CE1	1:A:2955:PRO:HD2	2.54	0.43
1:A:4923:MET:HE2	1:A:4923:MET:HB2	1.88	0.43
1:B:903:GLN:OE1	1:B:913:ARG:HD2	2.18	0.43
1:B:1827:THR:O	1:B:1831:MET:HG3	2.18	0.43
1:B:2577:CYS:HB2	1:B:2609:LEU:HD11	2.01	0.43
1:B:3043:ARG:HB3	1:B:3047:LYS:HE2	2.01	0.43
1:C:2235:ARG:NH2	1:C:2300:ASP:OD2	2.40	0.43
1:C:2884:LYS:O	1:C:2887:GLU:HG3	2.19	0.43
1:C:3983:LEU:HD21	1:C:4100:VAL:HG12	2.00	0.43
1:D:3149:GLU:O	1:D:3152:ARG:HG2	2.18	0.43
1:D:3305:PRO:HB2	1:D:3309:LYS:NZ	2.33	0.43
1:D:4089:GLU:HB2	1:D:4090:PRO:HD3	1.99	0.43
1:A:309:MET:HA	1:A:309:MET:HE3	2.00	0.43
1:A:876:PRO:HA	1:A:879:GLU:CG	2.49	0.43
1:A:1048:ASP:HA	1:A:1051:ARG:CG	2.49	0.43
1:A:1827:THR:O	1:A:1831:MET:HG3	2.18	0.43
1:A:1966:ARG:HB3	1:A:3602:CYS:HB3	2.00	0.43
1:A:2062:ILE:HG21	1:A:2087:LEU:HG	2.00	0.43
1:A:2668:CYS:O	1:A:2672:VAL:HG23	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3149:GLU:O	1:A:3152:ARG:HG2	2.18	0.43
1:A:4046:ARG:HB3	1:A:4050:LYS:NZ	2.34	0.43
1:B:658:ASN:ND2	1:B:831:LYS:O	2.50	0.43
1:B:876:PRO:HA	1:B:879:GLU:CG	2.49	0.43
1:B:2587:HIS:HA	1:B:2590:ARG:HH11	1.82	0.43
1:B:2670:SER:HB2	1:B:2973:GLN:CG	2.47	0.43
1:B:2832:THR:OG1	1:C:1548:THR:O	2.22	0.43
1:B:3983:LEU:HD21	1:B:4100:VAL:HG12	1.99	0.43
1:C:928:GLU:HA	1:C:931:TYR:HD2	1.82	0.43
1:C:2057:THR:HG22	1:C:2059:GLN:H	1.83	0.43
1:C:2322:ARG:O	1:C:2326:ARG:HG2	2.18	0.43
1:C:2567:ASP:O	1:C:2571:VAL:HG23	2.19	0.43
1:C:2619:LYS:HB3	1:C:2623:LEU:HD12	1.99	0.43
1:C:3148:VAL:HG22	1:C:3152:ARG:NH2	2.34	0.43
1:C:3316:LYS:O	1:C:3318:HIS:ND1	2.52	0.43
1:C:3324:GLU:HA	1:C:3327:LYS:NZ	2.33	0.43
1:C:4275:THR:HG22	1:C:4278:ASP:H	1.84	0.43
1:C:4607:ALA:HB1	1:C:4649:VAL:HG21	2.00	0.43
1:D:876:PRO:HA	1:D:879:GLU:CG	2.49	0.43
1:D:2062:ILE:HG21	1:D:2087:LEU:HG	2.00	0.43
1:D:2125:GLN:OE1	1:D:2144:ARG:NH2	2.47	0.43
1:D:2605:MET:HB3	1:D:2606:PRO:HD3	2.01	0.43
1:D:2726:GLU:OE1	1:D:2726:GLU:N	2.51	0.43
1:D:3033:LEU:HD13	1:D:3104:MET:HB3	2.01	0.43
1:D:3067:ASP:HA	1:D:3070:LYS:NZ	2.34	0.43
1:D:3247:SER:HA	1:D:3309:LYS:HE2	2.01	0.43
1:D:3650:GLU:HG2	1:D:3660:ARG:CZ	2.48	0.43
1:D:4607:ALA:HB1	1:D:4649:VAL:HG21	2.00	0.43
1:A:1792:ILE:HD11	1:A:1834:PHE:CE1	2.54	0.43
1:A:2577:CYS:HB2	1:A:2609:LEU:HD11	2.01	0.43
1:A:3830:LEU:HB3	1:A:3833:ASP:OD2	2.19	0.43
1:B:1168:MET:HA	1:B:1168:MET:HE3	2.01	0.43
1:B:1517:LEU:HD12	1:B:1517:LEU:HA	1.91	0.43
1:B:2779:LEU:O	1:B:2783:LEU:HG	2.19	0.43
1:B:3111:HIS:HB2	1:B:3115:HIS:HE1	1.82	0.43
1:B:3324:GLU:HA	1:B:3327:LYS:NZ	2.33	0.43
1:B:3882:GLN:NE2	1:B:3883:GLU:HG3	2.34	0.43
1:C:903:GLN:OE1	1:C:913:ARG:HD2	2.18	0.43
1:C:3067:ASP:HA	1:C:3070:LYS:NZ	2.34	0.43
1:C:3247:SER:HA	1:C:3309:LYS:HE2	2.01	0.43
1:C:3830:LEU:HB3	1:C:3833:ASP:OD2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:422:THR:HG21	1:D:459:LEU:HD11	2.01	0.43
1:D:472:HIS:O	1:D:476:GLN:HG2	2.18	0.43
1:D:1242:ASN:HB3	1:D:1806:ALA:HA	2.01	0.43
1:D:2779:LEU:O	1:D:2783:LEU:HG	2.19	0.43
1:D:2884:LYS:O	1:D:2887:GLU:HG3	2.19	0.43
1:D:3237:VAL:O	1:D:3240:PRO:HD2	2.19	0.43
1:A:2222:LEU:HD23	1:A:2222:LEU:HA	1.86	0.43
1:A:2726:GLU:OE1	1:A:2726:GLU:N	2.51	0.43
1:A:2849:HIS:CE1	1:A:2877:LEU:HD11	2.54	0.43
1:A:3316:LYS:O	1:A:3318:HIS:ND1	2.52	0.43
1:A:3882:GLN:NE2	1:A:3883:GLU:HG3	2.34	0.43
1:B:218:SER:HB2	1:B:286:GLY:HA3	2.00	0.43
1:B:917:CYS:HB3	1:B:924:LEU:HD12	2.00	0.43
1:B:1034:PRO:HG2	1:B:1037:LEU:HB2	2.00	0.43
1:B:1048:ASP:HA	1:B:1051:ARG:CG	2.49	0.43
1:B:1242:ASN:HB3	1:B:1806:ALA:HA	2.01	0.43
1:B:1975:MET:HA	1:B:1978:ASN:ND2	2.33	0.43
1:B:2605:MET:HB3	1:B:2606:PRO:HD3	2.01	0.43
1:B:2638:LEU:HB3	1:B:2680:TYR:CE1	2.54	0.43
1:B:3247:SER:HA	1:B:3309:LYS:HE2	2.01	0.43
1:C:35:LEU:HD23	1:C:49:LEU:HB3	2.01	0.43
1:C:897:LYS:HA	1:C:900:LEU:HG	2.00	0.43
1:C:1242:ASN:HB3	1:C:1806:ALA:HA	2.01	0.43
1:C:2605:MET:HB3	1:C:2606:PRO:HD3	2.01	0.43
1:C:4027:THR:HA	1:C:4032:PHE:HD1	1.81	0.43
1:C:4255:LEU:HD23	1:D:4710:LEU:HD13	2.01	0.43
1:D:2577:CYS:HB2	1:D:2609:LEU:HD11	2.01	0.43
1:D:3127:GLN:CD	1:D:3127:GLN:H	2.27	0.43
1:D:3148:VAL:HG22	1:D:3152:ARG:NH2	2.34	0.43
1:D:3241:MET:O	1:D:3245:TYR:HB3	2.19	0.43
1:D:4046:ARG:HB3	1:D:4050:LYS:NZ	2.34	0.43
1:A:1088:PHE:HB2	1:A:1205:CYS:SG	2.59	0.42
1:A:2619:LYS:HB3	1:A:2623:LEU:HD12	1.99	0.42
1:A:2827:ASP:H	1:B:1501:ASN:CG	2.27	0.42
1:A:3033:LEU:HD13	1:A:3104:MET:HB3	2.01	0.42
1:A:3067:ASP:HA	1:A:3070:LYS:NZ	2.34	0.42
1:A:3072:MET:CE	1:A:3136:SER:HB2	2.44	0.42
1:B:430:ILE:HG23	1:B:504:ARG:HD2	2.00	0.42
1:B:853:PRO:HG3	1:B:1083:GLU:OE1	2.19	0.42
1:B:920:GLU:O	1:B:924:LEU:N	2.52	0.42
1:B:999:LEU:HB3	1:B:1050:LEU:HD21	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1758:ARG:HG3	1:B:1759:PRO:HD2	2.01	0.42
1:B:1792:ILE:HD11	1:B:1834:PHE:CE1	2.54	0.42
1:B:2849:HIS:CE1	1:B:2877:LEU:HD11	2.54	0.42
1:B:3237:VAL:O	1:B:3240:PRO:HD2	2.19	0.42
1:B:4923:MET:HE2	1:B:4923:MET:HB2	1.88	0.42
1:C:876:PRO:HA	1:C:879:GLU:CG	2.49	0.42
1:C:2156:TYR:HE1	1:C:2202:TYR:CE2	2.37	0.42
1:C:2638:LEU:HB3	1:C:2680:TYR:CE1	2.54	0.42
1:D:778:MET:HG2	1:D:1468:THR:HB	2.00	0.42
1:D:1719:LEU:HG	1:D:1830:ILE:HG21	2.01	0.42
1:D:2567:ASP:O	1:D:2571:VAL:HG23	2.19	0.42
1:D:2638:LEU:HB3	1:D:2680:TYR:CE1	2.54	0.42
1:D:3281:LEU:HA	1:D:3284:ILE:HG12	2.01	0.42
1:D:3324:GLU:HA	1:D:3327:LYS:NZ	2.33	0.42
1:D:4167:GLU:OE2	1:D:4170:ARG:NH1	2.52	0.42
1:A:308:LEU:HD13	1:A:393:MET:HG3	2.00	0.42
1:A:884:LYS:O	1:A:887:GLU:HG3	2.20	0.42
1:A:2567:ASP:O	1:A:2571:VAL:HG23	2.19	0.42
1:A:2605:MET:HB3	1:A:2606:PRO:HD3	2.01	0.42
1:A:3241:MET:O	1:A:3245:TYR:HB3	2.19	0.42
1:B:2837:LEU:HA	1:B:2840:MET:HB2	2.00	0.42
1:B:2884:LYS:O	1:B:2887:GLU:HG3	2.19	0.42
1:B:2929:LEU:HD22	1:B:2971:ILE:HD11	2.01	0.42
1:C:218:SER:HB2	1:C:286:GLY:HA3	2.00	0.42
1:C:430:ILE:HG23	1:C:504:ARG:HD2	2.00	0.42
1:C:614:LEU:HD22	1:C:632:ILE:HG12	2.02	0.42
1:C:1792:ILE:HD11	1:C:1834:PHE:CE1	2.54	0.42
1:C:2980:LEU:O	1:C:2984:SER:N	2.52	0.42
1:C:4167:GLU:OE2	1:C:4170:ARG:NH1	2.52	0.42
1:C:4279:MET:SD	1:D:4484:ILE:HB	2.59	0.42
1:D:2837:LEU:HA	1:D:2840:MET:HB2	2.00	0.42
1:D:3830:LEU:HB3	1:D:3833:ASP:OD2	2.19	0.42
1:A:46:LEU:HD11	1:A:146:ASP:HB3	2.01	0.42
1:A:1051:ARG:HG2	1:A:1051:ARG:HH21	1.84	0.42
1:A:1242:ASN:HB3	1:A:1806:ALA:HA	2.01	0.42
2:F:54:GLN:N	2:F:54:GLN:OE1	2.52	0.42
1:B:2082:ARG:HG3	1:B:3687:LEU:HD22	2.00	0.42
1:B:3178:HIS:CE1	1:B:3263:MET:HB3	2.55	0.42
1:B:3220:GLU:O	1:B:3223:GLU:HG3	2.19	0.42
1:B:3935:LEU:HD23	1:B:3940:LEU:HD22	2.01	0.42
1:B:3962:SER:OG	1:B:4071:GLU:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:842:GLN:HB2	1:C:1603:PHE:HB2	2.01	0.42
1:C:2494:PRO:HA	1:C:2497:ARG:HD3	2.02	0.42
1:C:2577:CYS:HB2	1:C:2609:LEU:HD11	2.01	0.42
1:C:3114:GLN:HE21	1:C:3115:HIS:CE1	2.36	0.42
1:D:865:ILE:HD12	1:D:1009:ARG:HH21	1.85	0.42
1:D:1051:ARG:HG2	1:D:1051:ARG:HH21	1.84	0.42
1:D:1975:MET:HA	1:D:1978:ASN:ND2	2.33	0.42
1:D:3962:SER:OG	1:D:4071:GLU:HB3	2.19	0.42
1:A:317:MET:HE2	1:A:322:ALA:HA	2.02	0.42
1:A:422:THR:HG21	1:A:459:LEU:HD11	2.01	0.42
1:A:929:ARG:HD3	1:A:933:LEU:HD23	2.01	0.42
1:A:2057:THR:HG22	1:A:2059:GLN:H	1.84	0.42
1:A:2837:LEU:HA	1:A:2840:MET:HB2	2.00	0.42
1:A:2987:SER:O	1:A:2988:ARG:HB2	2.19	0.42
1:A:3178:HIS:CE1	1:A:3263:MET:HB3	2.55	0.42
1:A:4252:ILE:CG2	1:B:4707:MET:HG3	2.49	0.42
2:G:54:GLN:OE1	2:G:54:GLN:N	2.52	0.42
1:B:929:ARG:HD3	1:B:933:LEU:HD23	2.01	0.42
1:B:1561:LYS:O	1:B:1563:VAL:HG23	2.20	0.42
1:B:2943:PHE:CE1	1:B:2955:PRO:HD2	2.53	0.42
1:B:3067:ASP:HA	1:B:3070:LYS:NZ	2.34	0.42
1:B:3148:VAL:HG22	1:B:3152:ARG:NH2	2.34	0.42
1:B:3763:ILE:HD11	1:B:3838:ASP:O	2.19	0.42
1:C:865:ILE:HD12	1:C:1009:ARG:HH21	1.85	0.42
1:C:1161:VAL:HG21	1:C:1225:LYS:HE3	2.02	0.42
1:C:2172:MET:HE2	1:C:2172:MET:HB3	1.67	0.42
1:D:317:MET:HE2	1:D:322:ALA:HA	2.02	0.42
1:D:853:PRO:HG3	1:D:1083:GLU:OE1	2.20	0.42
1:D:920:GLU:O	1:D:924:LEU:N	2.52	0.42
1:D:1088:PHE:HB2	1:D:1205:CYS:SG	2.59	0.42
1:D:1819:VAL:HG13	1:D:1905:GLN:NE2	2.33	0.42
1:D:2619:LYS:HB3	1:D:2623:LEU:HD12	1.99	0.42
1:D:3178:HIS:CE1	1:D:3263:MET:HB3	2.55	0.42
1:A:814:LEU:HD12	1:A:815:PRO:HD2	2.01	0.42
1:A:3281:LEU:HA	1:A:3284:ILE:HG12	2.01	0.42
1:A:3962:SER:OG	1:A:4071:GLU:HB3	2.19	0.42
1:A:4167:GLU:OE2	1:A:4170:ARG:NH1	2.52	0.42
1:A:4503:ARG:HA	1:A:4503:ARG:HD2	1.74	0.42
1:B:309:MET:HA	1:B:309:MET:HE3	2.00	0.42
1:B:614:LEU:HD22	1:B:632:ILE:HG12	2.01	0.42
1:B:1051:ARG:HG2	1:B:1051:ARG:HH21	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1928:PHE:HE1	1:B:1995:GLN:HG2	1.85	0.42
1:B:2830:ASN:ND2	1:C:1551:ASN:HB2	2.34	0.42
1:B:3033:LEU:HD13	1:B:3104:MET:HB3	2.01	0.42
1:C:422:THR:HG21	1:C:459:LEU:HD11	2.01	0.42
1:C:2062:ILE:HG21	1:C:2087:LEU:HG	2.00	0.42
1:C:2413:LYS:NZ	1:C:2415:GLU:HB3	2.33	0.42
1:C:2914:THR:N	1:C:2915:PRO:HD2	2.34	0.42
1:C:3241:MET:O	1:C:3245:TYR:HB3	2.19	0.42
1:C:3637:GLU:HG2	1:C:3694:ILE:HA	2.02	0.42
1:C:3763:ILE:HD11	1:C:3838:ASP:O	2.19	0.42
1:C:3962:SER:OG	1:C:4071:GLU:HB3	2.19	0.42
1:D:3637:GLU:HG2	1:D:3694:ILE:HA	2.02	0.42
1:D:3882:GLN:NE2	1:D:3883:GLU:HG3	2.34	0.42
1:A:430:ILE:HG23	1:A:504:ARG:HD2	2.00	0.42
1:A:658:ASN:ND2	1:A:831:LYS:O	2.50	0.42
1:A:783:ASN:OD1	1:A:1463:ARG:HA	2.20	0.42
1:A:881:ILE:O	1:A:885:LEU:HD23	2.20	0.42
1:A:920:GLU:O	1:A:924:LEU:N	2.52	0.42
1:B:1719:LEU:HG	1:B:1830:ILE:HG21	2.01	0.42
1:B:2494:PRO:HA	1:B:2497:ARG:HD3	2.01	0.42
1:B:2745:GLU:HG2	1:B:2746:ILE:HG23	2.02	0.42
1:B:3246:MET:O	1:B:3250:TRP:HD1	1.99	0.42
1:B:3637:GLU:HG2	1:B:3694:ILE:HA	2.02	0.42
1:B:4167:GLU:OE2	1:B:4170:ARG:NH1	2.52	0.42
1:C:884:LYS:O	1:C:887:GLU:HG3	2.19	0.42
1:C:2620:TYR:CD1	1:C:2630:PHE:HB3	2.54	0.42
1:C:3033:LEU:HD13	1:C:3104:MET:HB3	2.01	0.42
1:C:3220:GLU:O	1:C:3223:GLU:HG3	2.19	0.42
1:D:2156:TYR:HE1	1:D:2202:TYR:CE2	2.37	0.42
1:D:2849:HIS:CE1	1:D:2877:LEU:HD11	2.54	0.42
1:A:582:SER:OG	1:A:584:GLU:OE1	2.34	0.42
1:A:999:LEU:HB3	1:A:1050:LEU:HD21	2.00	0.42
1:A:1256:PRO:HG3	1:A:1593:HIS:NE2	2.35	0.42
1:A:1719:LEU:HG	1:A:1830:ILE:HG21	2.00	0.42
1:A:3127:GLN:CD	1:A:3127:GLN:H	2.28	0.42
1:A:3247:SER:HA	1:A:3309:LYS:HE2	2.01	0.42
1:A:3763:ILE:HD11	1:A:3838:ASP:O	2.19	0.42
1:A:3926:GLY:O	1:A:3927:PRO:C	2.63	0.42
1:B:841:LYS:O	1:B:848:ARG:NH2	2.50	0.42
1:B:1502:ASN:OD1	1:B:1503:ASN:N	2.52	0.42
1:B:2274:LEU:HG	1:B:2329:GLU:HG3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2567:ASP:O	1:B:2571:VAL:HG23	2.19	0.42
1:C:1283:LEU:HB2	1:C:1555:PHE:HB2	2.02	0.42
1:C:1500:ARG:HE	1:C:1505:LEU:N	2.18	0.42
1:C:2779:LEU:O	1:C:2783:LEU:HG	2.19	0.42
1:C:4046:ARG:HB3	1:C:4050:LYS:NZ	2.34	0.42
1:C:4522:VAL:HG11	1:D:4790:ARG:HD3	2.01	0.42
1:D:1438:PRO:CG	1:D:1500:ARG:HH12	2.33	0.42
1:D:2682:GLU:O	1:D:2919:LYS:HD2	2.20	0.42
1:D:3221:LEU:CD2	1:D:3234:VAL:HG11	2.50	0.42
1:D:4238:ILE:HD12	1:D:4238:ILE:H	1.85	0.42
1:A:35:LEU:HD23	1:A:49:LEU:HB3	2.01	0.42
1:A:1928:PHE:HE1	1:A:1995:GLN:HG2	1.85	0.42
1:A:2561:LEU:HD23	1:A:2565:GLN:HB3	2.02	0.42
1:A:2620:TYR:CD1	1:A:2630:PHE:HB3	2.54	0.42
1:A:2940:ILE:HG23	1:A:3021:LEU:HD23	2.02	0.42
1:A:3637:GLU:HG2	1:A:3694:ILE:HA	2.02	0.42
1:A:4858:LEU:HD23	1:A:4861:ILE:HD12	2.02	0.42
1:B:35:LEU:HD23	1:B:49:LEU:HB3	2.01	0.42
1:B:783:ASN:OD1	1:B:1463:ARG:HA	2.20	0.42
1:B:865:ILE:HD12	1:B:1009:ARG:HH21	1.85	0.42
1:B:1256:PRO:HG3	1:B:1593:HIS:NE2	2.35	0.42
1:B:1500:ARG:HE	1:B:1505:LEU:N	2.18	0.42
1:B:2682:GLU:O	1:B:2919:LYS:HD2	2.20	0.42
1:B:2980:LEU:O	1:B:2984:SER:N	2.52	0.42
1:B:3281:LEU:HA	1:B:3284:ILE:HG12	2.01	0.42
1:C:309:MET:HA	1:C:309:MET:HE3	2.00	0.42
1:C:841:LYS:O	1:C:848:ARG:NH2	2.50	0.42
1:C:1561:LYS:O	1:C:1563:VAL:HG23	2.20	0.42
1:C:1719:LEU:HD21	1:C:1830:ILE:HD12	2.01	0.42
1:C:2478:ILE:HD12	1:C:2527:LEU:HD21	2.02	0.42
1:C:2999:LYS:HA	1:C:3002:GLU:CD	2.45	0.42
1:C:3127:GLN:CD	1:C:3127:GLN:H	2.28	0.42
1:C:3312:PRO:HA	1:C:3315:LEU:CG	2.45	0.42
1:C:4021:LEU:HD22	1:C:4128:TYR:CE2	2.55	0.42
1:D:614:LEU:HD22	1:D:632:ILE:HG12	2.02	0.42
1:D:917:CYS:HB3	1:D:924:LEU:HD12	2.00	0.42
1:D:1016:TRP:HZ3	1:D:1022:GLN:HE22	1.68	0.42
1:D:1256:PRO:HG3	1:D:1593:HIS:NE2	2.35	0.42
1:D:1928:PHE:HE1	1:D:1995:GLN:HG2	1.85	0.42
1:D:2553:TYR:CE2	1:D:2557:LYS:HE2	2.55	0.42
1:D:2561:LEU:HD23	1:D:2565:GLN:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2620:TYR:CD1	1:D:2630:PHE:HB3	2.54	0.42
1:D:2940:ILE:HG23	1:D:3021:LEU:HD23	2.02	0.42
1:A:1708:ASP:HA	1:A:1712:SER:HB3	2.02	0.42
1:A:2478:ILE:HD12	1:A:2527:LEU:HD21	2.02	0.42
1:A:2682:GLU:O	1:A:2919:LYS:HD2	2.20	0.42
1:A:2745:GLU:HG2	1:A:2746:ILE:HG23	2.02	0.42
1:A:3109:PHE:CE2	1:A:3162:PHE:HD1	2.38	0.42
1:A:3208:ILE:HA	1:A:3209:PRO:HD3	1.89	0.42
1:B:434:ASP:HB3	1:B:438:LYS:NZ	2.35	0.42
1:B:872:ILE:HB	1:B:941:LYS:HE2	2.02	0.42
1:B:2620:TYR:CD1	1:B:2630:PHE:HB3	2.54	0.42
1:B:2722:ASN:O	1:B:2723:LYS:HB2	2.20	0.42
1:B:3316:LYS:O	1:B:3318:HIS:ND1	2.52	0.42
1:C:853:PRO:HG3	1:C:1083:GLU:OE1	2.20	0.42
1:C:958:GLU:OE1	1:C:958:GLU:N	2.45	0.42
1:C:1438:PRO:CG	1:C:1500:ARG:HH12	2.33	0.42
1:C:2280:LEU:HD21	1:C:2382:ILE:HD12	2.02	0.42
1:C:2745:GLU:HG2	1:C:2746:ILE:HG23	2.02	0.42
1:C:3891:TYR:HA	1:D:76:ARG:NH1	2.34	0.42
1:C:3935:LEU:HD23	1:C:3940:LEU:HD22	2.01	0.42
1:D:46:LEU:HD11	1:D:146:ASP:HB3	2.01	0.42
1:D:674:TYR:HB2	1:D:819:TYR:HB3	2.02	0.42
1:D:884:LYS:O	1:D:887:GLU:HG3	2.20	0.42
1:D:1708:ASP:HA	1:D:1712:SER:HB3	2.02	0.42
1:D:2836:ASP:OD1	1:D:2837:LEU:N	2.53	0.42
1:D:3220:GLU:O	1:D:3223:GLU:HG3	2.19	0.42
1:D:4021:LEU:HD22	1:D:4128:TYR:CE2	2.55	0.42
1:D:4275:THR:HG22	1:D:4278:ASP:H	1.84	0.42
1:A:3043:ARG:HB3	1:A:3047:LYS:HE2	2.01	0.42
1:A:3148:VAL:HG22	1:A:3152:ARG:NH2	2.34	0.42
2:E:54:GLN:OE1	2:E:54:GLN:N	2.52	0.42
2:H:54:GLN:OE1	2:H:54:GLN:N	2.52	0.42
1:B:902:TRP:HE1	1:B:915:HIS:HB2	1.85	0.42
1:B:2976:LYS:HA	1:B:2979:ARG:NH2	2.35	0.42
1:B:3272:HIS:C	1:B:3276:LEU:HD23	2.45	0.42
1:B:4021:LEU:HD22	1:B:4128:TYR:CE2	2.55	0.42
1:B:4046:ARG:HB3	1:B:4050:LYS:NZ	2.34	0.42
1:C:1928:PHE:HE1	1:C:1995:GLN:HG2	1.85	0.42
1:C:2837:LEU:HA	1:C:2840:MET:HB2	2.00	0.42
1:C:3281:LEU:HA	1:C:3284:ILE:HG12	2.01	0.42
1:C:3926:GLY:O	1:C:3927:PRO:C	2.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4796:SER:HB3	1:C:4803:ASP:HB2	2.02	0.42
1:D:34:LYS:H	1:D:53:SER:HG	1.62	0.42
1:D:842:GLN:HB2	1:D:1603:PHE:HB2	2.01	0.42
1:D:2745:GLU:HG2	1:D:2746:ILE:HG23	2.02	0.42
1:D:3935:LEU:HD23	1:D:3940:LEU:HD22	2.01	0.42
1:A:436:LEU:HD13	1:A:518:ALA:HB2	2.02	0.41
1:A:865:ILE:HD12	1:A:1009:ARG:HH21	1.85	0.41
1:A:872:ILE:HB	1:A:941:LYS:HE2	2.02	0.41
1:A:2319:VAL:O	1:A:2323:LEU:HG	2.20	0.41
1:A:2326:ARG:HA	1:A:2326:ARG:HD3	1.86	0.41
1:A:2722:ASN:O	1:A:2723:LYS:HB2	2.20	0.41
1:B:882:ARG:HA	1:B:885:LEU:HB2	2.02	0.41
1:B:983:LEU:HD11	1:B:1055:ARG:CG	2.41	0.41
1:B:1708:ASP:HA	1:B:1712:SER:HB3	2.02	0.41
1:C:436:LEU:HD13	1:C:518:ALA:HB2	2.02	0.41
1:C:1016:TRP:HZ3	1:C:1022:GLN:HE22	1.67	0.41
1:C:1168:MET:HA	1:C:1168:MET:HE3	2.01	0.41
1:C:2849:HIS:CE1	1:C:2877:LEU:HD11	2.54	0.41
1:C:2929:LEU:HD22	1:C:2971:ILE:HD11	2.01	0.41
1:C:2987:SER:O	1:C:2988:ARG:HB2	2.19	0.41
1:C:4522:VAL:HG13	1:D:4786:PHE:CZ	2.55	0.41
1:D:434:ASP:HB3	1:D:438:LYS:NZ	2.35	0.41
1:D:783:ASN:OD1	1:D:1463:ARG:HA	2.20	0.41
1:D:882:ARG:HA	1:D:885:LEU:HB2	2.02	0.41
1:D:929:ARG:HD3	1:D:933:LEU:HD23	2.01	0.41
1:D:2057:THR:HG22	1:D:2059:GLN:H	1.84	0.41
1:D:2172:MET:HB3	1:D:2172:MET:HE2	1.67	0.41
1:D:2670:SER:HB2	1:D:2973:GLN:CG	2.47	0.41
1:D:3109:PHE:CE2	1:D:3162:PHE:HD1	2.38	0.41
1:D:3763:ILE:HD11	1:D:3838:ASP:O	2.19	0.41
1:A:434:ASP:HB3	1:A:438:LYS:NZ	2.35	0.41
1:A:1283:LEU:HB2	1:A:1555:PHE:HB2	2.02	0.41
1:A:1561:LYS:O	1:A:1563:VAL:HG23	2.20	0.41
1:A:1850:VAL:HG22	1:A:2055:SER:HB3	2.02	0.41
1:A:2553:TYR:CE2	1:A:2557:LYS:HE2	2.55	0.41
1:A:2638:LEU:HB3	1:A:2680:TYR:CE1	2.54	0.41
1:A:2999:LYS:HA	1:A:3002:GLU:CD	2.45	0.41
1:A:3069:GLU:HG3	1:A:3132:ARG:CZ	2.50	0.41
1:A:4644:TYR:O	1:A:4647:LYS:NZ	2.52	0.41
1:A:4673:ASP:OD1	1:A:4676:ALA:HB3	2.20	0.41
1:A:4796:SER:HB3	1:A:4803:ASP:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:814:LEU:HD12	1:B:815:PRO:HD2	2.01	0.41
1:B:884:LYS:O	1:B:887:GLU:HG3	2.20	0.41
1:B:3127:GLN:H	1:B:3127:GLN:CD	2.28	0.41
1:B:3926:GLY:O	1:B:3927:PRO:C	2.63	0.41
1:C:783:ASN:OD1	1:C:1463:ARG:HA	2.20	0.41
1:C:882:ARG:HA	1:C:885:LEU:HB2	2.02	0.41
1:C:920:GLU:O	1:C:924:LEU:N	2.53	0.41
1:C:1719:LEU:HG	1:C:1830:ILE:HG21	2.01	0.41
1:C:1790:LYS:HG2	1:C:1794:MET:HE2	2.01	0.41
1:C:2858:MET:HE2	1:C:2858:MET:N	2.36	0.41
1:D:902:TRP:HE1	1:D:915:HIS:HB2	1.85	0.41
1:D:1790:LYS:HG2	1:D:1794:MET:HE2	2.01	0.41
1:D:2136:LYS:HA	1:D:2136:LYS:HD3	1.83	0.41
1:D:3316:LYS:O	1:D:3317:THR:OG1	2.36	0.41
1:D:3316:LYS:O	1:D:3318:HIS:ND1	2.52	0.41
1:D:4105:LEU:HB3	1:D:4115:LEU:HD21	2.02	0.41
1:A:614:LEU:HD22	1:A:632:ILE:HG12	2.02	0.41
1:A:674:TYR:HB2	1:A:819:TYR:HB3	2.02	0.41
1:A:915:HIS:HB3	1:A:918:LEU:HG	2.03	0.41
1:A:2071:GLN:CD	1:A:3648:GLY:HA3	2.45	0.41
1:A:2836:ASP:OD1	1:A:2837:LEU:N	2.53	0.41
1:A:2858:MET:N	1:A:2858:MET:HE2	2.35	0.41
1:B:2914:THR:N	1:B:2915:PRO:HD2	2.34	0.41
1:B:3293:GLY:O	1:B:3296:MET:HG2	2.20	0.41
1:B:3830:LEU:HB3	1:B:3833:ASP:OD2	2.19	0.41
1:B:4105:LEU:HB3	1:B:4115:LEU:HD21	2.02	0.41
1:B:4238:ILE:H	1:B:4238:ILE:HD12	1.85	0.41
1:B:4644:TYR:O	1:B:4647:LYS:NZ	2.53	0.41
1:B:4858:LEU:HD23	1:B:4861:ILE:HD12	2.02	0.41
1:C:881:ILE:O	1:C:885:LEU:HD23	2.20	0.41
1:C:929:ARG:HD3	1:C:933:LEU:HD23	2.01	0.41
1:C:1256:PRO:HG3	1:C:1593:HIS:NE2	2.35	0.41
1:C:2486:HIS:O	1:C:2490:VAL:HG22	2.21	0.41
1:C:2682:GLU:O	1:C:2919:LYS:HD2	2.20	0.41
1:C:2976:LYS:HA	1:C:2979:ARG:NH2	2.35	0.41
1:C:3109:PHE:CE2	1:C:3162:PHE:HD1	2.38	0.41
1:C:3171:LEU:HA	1:C:3171:LEU:HD23	1.79	0.41
1:C:3178:HIS:CE1	1:C:3263:MET:HB3	2.55	0.41
1:C:3305:PRO:O	1:C:3309:LYS:HG3	2.21	0.41
1:C:3846:LEU:HD13	1:C:3854:PHE:CZ	2.56	0.41
1:C:3882:GLN:NE2	1:C:3883:GLU:HG3	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4105:LEU:HB3	1:C:4115:LEU:HD21	2.03	0.41
1:C:4203:ALA:HA	1:C:4206:ILE:HG12	2.02	0.41
1:C:4503:ARG:NH2	1:C:4745:ASP:OD1	2.54	0.41
1:D:1161:VAL:HG21	1:D:1225:LYS:HE3	2.02	0.41
1:D:1304:LEU:HD23	1:D:1304:LEU:HA	1.91	0.41
1:D:1719:LEU:HD21	1:D:1830:ILE:HD12	2.01	0.41
1:D:2319:VAL:O	1:D:2323:LEU:HG	2.20	0.41
1:D:2976:LYS:HA	1:D:2979:ARG:NH2	2.35	0.41
1:D:3213:LYS:O	1:D:3217:GLU:OE1	2.39	0.41
1:D:3272:HIS:C	1:D:3276:LEU:HD23	2.45	0.41
1:D:4107:GLU:OE1	1:D:4149:TYR:OH	2.23	0.41
1:A:902:TRP:HE1	1:A:915:HIS:HB2	1.85	0.41
1:A:958:GLU:OE1	1:A:958:GLU:N	2.45	0.41
1:A:992:GLN:O	1:A:996:VAL:HG23	2.21	0.41
1:A:2494:PRO:HA	1:A:2497:ARG:HD3	2.01	0.41
1:A:2727:HIS:O	1:A:2730:ASP:N	2.54	0.41
1:A:4105:LEU:HB3	1:A:4115:LEU:HD21	2.02	0.41
1:A:4680:SER:HA	1:A:4684:GLU:HB2	2.02	0.41
1:B:422:THR:HG21	1:B:459:LEU:HD11	2.01	0.41
1:B:2326:ARG:HD3	1:B:2326:ARG:HA	1.86	0.41
1:B:3241:MET:O	1:B:3245:TYR:HB3	2.19	0.41
1:B:4480:PHE:O	1:B:4484:ILE:HG23	2.20	0.41
1:B:4673:ASP:OD1	1:B:4676:ALA:HB3	2.20	0.41
1:C:661:LEU:HD11	1:C:759:LEU:HD23	2.02	0.41
1:C:674:TYR:CE1	1:C:756:SER:HB2	2.55	0.41
1:C:2071:GLN:CD	1:C:3648:GLY:HA3	2.45	0.41
1:C:2274:LEU:HG	1:C:2329:GLU:HG3	2.02	0.41
1:C:2836:ASP:OD1	1:C:2837:LEU:N	2.53	0.41
1:C:3221:LEU:CD2	1:C:3234:VAL:HG11	2.50	0.41
1:D:915:HIS:HB3	1:D:918:LEU:HG	2.03	0.41
1:D:4673:ASP:OD1	1:D:4676:ALA:HB3	2.20	0.41
1:D:4796:SER:HB3	1:D:4803:ASP:HB2	2.02	0.41
1:A:853:PRO:HG3	1:A:1083:GLU:OE1	2.20	0.41
1:A:1758:ARG:HG3	1:A:1759:PRO:HD2	2.02	0.41
1:A:1898:LEU:HD13	1:A:1902:VAL:HG12	2.03	0.41
1:A:3200:ASN:HB2	1:A:3203:ASP:HB2	2.03	0.41
1:A:3220:GLU:O	1:A:3223:GLU:HG3	2.19	0.41
1:A:3846:LEU:HD13	1:A:3854:PHE:CZ	2.56	0.41
1:B:661:LEU:HD11	1:B:759:LEU:HD23	2.02	0.41
1:B:992:GLN:O	1:B:996:VAL:HG23	2.21	0.41
1:B:1048:ASP:O	1:B:1051:ARG:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1850:VAL:HG22	1:B:2055:SER:HB3	2.02	0.41
1:B:2071:GLN:CD	1:B:3648:GLY:HA3	2.45	0.41
1:B:2478:ILE:HD12	1:B:2527:LEU:HD21	2.02	0.41
1:B:2999:LYS:HA	1:B:3002:GLU:CD	2.45	0.41
1:B:3245:TYR:CD1	1:B:3249:TRP:CZ3	3.09	0.41
1:C:1088:PHE:HB2	1:C:1205:CYS:SG	2.59	0.41
1:C:2553:TYR:CE2	1:C:2557:LYS:HE2	2.55	0.41
1:C:2722:ASN:O	1:C:2723:LYS:HB2	2.20	0.41
1:D:35:LEU:HD23	1:D:49:LEU:HB3	2.01	0.41
1:D:1898:LEU:HD13	1:D:1902:VAL:HG12	2.03	0.41
1:D:2494:PRO:HA	1:D:2497:ARG:HD3	2.02	0.41
1:D:4503:ARG:NH2	1:D:4745:ASP:OD1	2.54	0.41
1:A:882:ARG:HA	1:A:885:LEU:HB2	2.02	0.41
1:A:1790:LYS:HG2	1:A:1794:MET:HE2	2.01	0.41
1:A:2976:LYS:HA	1:A:2979:ARG:NH2	2.35	0.41
1:A:3261:ALA:O	1:A:3262:GLU:HB3	2.21	0.41
1:A:4503:ARG:NH2	1:A:4745:ASP:OD1	2.54	0.41
1:B:46:LEU:HD11	1:B:146:ASP:HB3	2.01	0.41
1:B:436:LEU:HD13	1:B:518:ALA:HB2	2.02	0.41
1:B:1088:PHE:HB2	1:B:1205:CYS:SG	2.59	0.41
1:B:2054:LYS:HD2	1:B:2056:SER:N	2.36	0.41
1:B:2319:VAL:O	1:B:2323:LEU:HG	2.20	0.41
1:B:2553:TYR:CE2	1:B:2557:LYS:HE2	2.55	0.41
1:B:2652:LEU:HA	1:B:2652:LEU:HD12	1.89	0.41
1:B:2857:LYS:HA	1:B:2860:LEU:HG	2.03	0.41
1:B:3305:PRO:O	1:B:3309:LYS:HG3	2.21	0.41
1:C:872:ILE:HB	1:C:941:LYS:HE2	2.02	0.41
1:C:2857:LYS:HA	1:C:2860:LEU:HG	2.03	0.41
1:C:4858:LEU:HD23	1:C:4861:ILE:HD12	2.02	0.41
1:D:387:ILE:HG13	1:D:388:GLN:N	2.35	0.41
1:D:872:ILE:HB	1:D:941:LYS:HE2	2.02	0.41
1:D:888:ASN:C	1:D:888:ASN:HD22	2.29	0.41
1:D:1561:LYS:O	1:D:1563:VAL:HG23	2.20	0.41
1:D:1758:ARG:HG3	1:D:1759:PRO:HD2	2.01	0.41
1:D:2071:GLN:CD	1:D:3648:GLY:HA3	2.45	0.41
1:D:2224:ASN:O	1:D:2227:VAL:HG23	2.21	0.41
1:D:2478:ILE:HD12	1:D:2527:LEU:HD21	2.02	0.41
1:D:2722:ASN:O	1:D:2723:LYS:HB2	2.20	0.41
1:D:2987:SER:O	1:D:2988:ARG:HB2	2.19	0.41
1:D:3293:GLY:O	1:D:3296:MET:HG2	2.20	0.41
1:D:3926:GLY:O	1:D:3927:PRO:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1048:ASP:O	1:A:1051:ARG:HB2	2.21	0.41
1:A:1161:VAL:HG21	1:A:1225:LYS:HE3	2.01	0.41
1:A:1499:GLY:CA	1:D:2898:ILE:HD12	2.46	0.41
1:A:2274:LEU:HG	1:A:2329:GLU:HG3	2.02	0.41
1:A:3016:ARG:NH2	1:A:3017:HIS:HE1	2.19	0.41
1:A:3065:ALA:O	1:A:3068:LEU:HG	2.21	0.41
2:H:4:GLU:OE2	2:H:76:THR:OG1	2.31	0.41
1:B:23:GLN:HG2	1:B:36:CYS:SG	2.61	0.41
1:B:674:TYR:HB2	1:B:819:TYR:HB3	2.02	0.41
1:B:881:ILE:O	1:B:885:LEU:HD23	2.20	0.41
1:B:915:HIS:HB3	1:B:918:LEU:HG	2.03	0.41
1:B:2224:ASN:O	1:B:2227:VAL:HG23	2.21	0.41
1:B:2280:LEU:HD21	1:B:2382:ILE:HD12	2.02	0.41
1:B:2836:ASP:OD1	1:B:2837:LEU:N	2.53	0.41
1:B:3846:LEU:HD13	1:B:3854:PHE:CZ	2.55	0.41
1:B:4796:SER:HB3	1:B:4803:ASP:HB2	2.02	0.41
1:C:1165:MET:HE2	1:C:1176:THR:HG23	2.03	0.41
1:C:2652:LEU:HA	1:C:2652:LEU:HD12	1.89	0.41
1:C:3237:VAL:O	1:C:3240:PRO:HD2	2.19	0.41
1:C:3272:HIS:C	1:C:3276:LEU:HD23	2.45	0.41
1:C:4522:VAL:HG11	1:D:4790:ARG:NE	2.36	0.41
1:D:881:ILE:O	1:D:885:LEU:HD23	2.20	0.41
1:D:2739:ASN:HD21	1:D:2741:TRP:HE1	1.69	0.41
1:D:2999:LYS:HA	1:D:3002:GLU:CD	2.45	0.41
1:D:3043:ARG:HB3	1:D:3047:LYS:HE2	2.01	0.41
1:A:387:ILE:HG13	1:A:388:GLN:N	2.35	0.41
1:A:624:ALA:HB3	1:A:2132:VAL:HG12	2.02	0.41
1:A:2739:ASN:HD21	1:A:2741:TRP:HE1	1.69	0.41
1:A:2841:ALA:HA	1:A:2844:MET:CG	2.44	0.41
1:A:3213:LYS:O	1:A:3217:GLU:OE1	2.38	0.41
1:A:3245:TYR:CD1	1:A:3249:TRP:CZ3	3.09	0.41
2:H:43:ARG:HA	1:D:1682:GLU:OE2	2.21	0.41
1:B:758:CYS:HB3	1:B:819:TYR:CE2	2.56	0.41
1:B:2827:ASP:H	1:C:1501:ASN:ND2	2.18	0.41
1:B:2827:ASP:N	1:C:1501:ASN:OD1	2.38	0.41
1:B:2858:MET:HE2	1:B:2858:MET:N	2.36	0.41
1:B:2972:ASP:HA	1:B:3035:ILE:HD11	2.03	0.41
1:B:2987:SER:O	1:B:2988:ARG:HB2	2.19	0.41
1:B:3069:GLU:HG3	1:B:3132:ARG:CZ	2.50	0.41
1:B:4680:SER:HA	1:B:4684:GLU:HB2	2.02	0.41
1:C:434:ASP:HB3	1:C:438:LYS:NZ	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:902:TRP:HE1	1:C:915:HIS:HB2	1.85	0.41
1:C:915:HIS:HB3	1:C:918:LEU:HG	2.03	0.41
1:C:1708:ASP:HA	1:C:1712:SER:HB3	2.02	0.41
1:C:1758:ARG:HG3	1:C:1759:PRO:HD2	2.02	0.41
1:C:2224:ASN:O	1:C:2227:VAL:HG23	2.21	0.41
1:C:2319:VAL:O	1:C:2323:LEU:HG	2.20	0.41
1:C:2870:LEU:HD22	1:C:2877:LEU:CD2	2.51	0.41
1:C:3200:ASN:HB2	1:C:3203:ASP:HB2	2.03	0.41
1:C:4238:ILE:HD12	1:C:4238:ILE:H	1.85	0.41
1:C:4480:PHE:O	1:C:4484:ILE:HG23	2.20	0.41
1:C:4702:ASP:O	1:C:4706:GLN:HG2	2.21	0.41
1:D:436:LEU:HD13	1:D:518:ALA:HB2	2.02	0.41
1:D:661:LEU:HD11	1:D:759:LEU:HD23	2.02	0.41
1:D:958:GLU:OE1	1:D:958:GLU:N	2.45	0.41
1:D:2870:LEU:HD22	1:D:2877:LEU:CD2	2.51	0.41
1:D:2888:LYS:HA	1:D:2891:ASP:OD2	2.21	0.41
1:D:2929:LEU:HD22	1:D:2971:ILE:HD11	2.02	0.41
1:D:3312:PRO:HA	1:D:3315:LEU:CG	2.45	0.41
1:D:4590:TYR:OH	1:D:4718:SER:HB2	2.21	0.41
1:A:758:CYS:HB3	1:A:819:TYR:CE2	2.56	0.41
1:A:1016:TRP:HZ3	1:A:1022:GLN:HE22	1.67	0.41
1:A:1165:MET:HE2	1:A:1176:THR:HG23	2.03	0.41
1:A:1500:ARG:HE	1:A:1505:LEU:N	2.18	0.41
1:A:1967:SER:O	1:A:1972:GLN:NE2	2.49	0.41
1:A:2054:LYS:HD2	1:A:2056:SER:N	2.36	0.41
1:A:2549:LEU:HD13	1:A:2588:LEU:HD22	2.03	0.41
1:A:2669:LEU:HD23	1:A:2669:LEU:HA	1.96	0.41
1:A:2929:LEU:HD22	1:A:2971:ILE:HD11	2.02	0.41
1:A:3272:HIS:C	1:A:3276:LEU:HD23	2.45	0.41
1:A:3712:LYS:HE3	1:A:3717:LYS:HG2	2.03	0.41
1:A:3935:LEU:HD23	1:A:3940:LEU:HD22	2.01	0.41
1:A:4238:ILE:HD12	1:A:4238:ILE:H	1.85	0.41
1:A:4480:PHE:O	1:A:4484:ILE:HG23	2.20	0.41
1:B:317:MET:HE2	1:B:322:ALA:HA	2.02	0.41
1:B:670:TYR:O	1:B:673:TRP:NE1	2.54	0.41
1:B:674:TYR:CE1	1:B:756:SER:HB2	2.55	0.41
1:B:1161:VAL:HG21	1:B:1225:LYS:HE3	2.02	0.41
1:B:1165:MET:HE2	1:B:1176:THR:HG23	2.03	0.41
1:B:1304:LEU:HD23	1:B:1304:LEU:HA	1.91	0.41
1:B:1765:SER:HA	1:B:1766:PRO:HD3	1.90	0.41
1:B:2156:TYR:HE1	1:B:2202:TYR:CE2	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2570:GLU:HG2	1:B:2605:MET:CG	2.49	0.41
1:B:2726:GLU:OE1	1:B:2726:GLU:N	2.51	0.41
1:B:3109:PHE:CE2	1:B:3162:PHE:HD1	2.38	0.41
1:B:3312:PRO:HA	1:B:3315:LEU:CG	2.45	0.41
1:B:3712:LYS:HE3	1:B:3717:LYS:HG2	2.03	0.41
1:B:4166:LYS:NZ	4:B:5002:ATP:O2G	2.42	0.41
1:C:46:LEU:HD11	1:C:146:ASP:HB3	2.01	0.41
1:C:317:MET:HE2	1:C:322:ALA:HA	2.02	0.41
1:C:670:TYR:O	1:C:673:TRP:NE1	2.54	0.41
1:C:758:CYS:HB3	1:C:819:TYR:CE2	2.56	0.41
1:C:865:ILE:HD12	1:C:865:ILE:HA	1.77	0.41
1:C:992:GLN:O	1:C:996:VAL:HG23	2.21	0.41
1:C:2888:LYS:HA	1:C:2891:ASP:OD2	2.21	0.41
1:C:2972:ASP:HA	1:C:3035:ILE:HD11	2.03	0.41
1:C:3069:GLU:HG3	1:C:3132:ARG:CZ	2.50	0.41
1:C:3213:LYS:O	1:C:3217:GLU:OE1	2.39	0.41
1:C:3245:TYR:CD1	1:C:3249:TRP:CZ3	3.09	0.41
1:C:3926:GLY:O	1:C:3928:CYS:N	2.54	0.41
1:C:4831:ILE:HD12	1:C:4843:ARG:HE	1.86	0.41
1:D:225:GLN:HG2	1:D:3862:THR:O	2.21	0.41
1:D:624:ALA:HB3	1:D:2132:VAL:HG12	2.02	0.41
1:D:674:TYR:CE1	1:D:756:SER:HB2	2.55	0.41
1:D:814:LEU:HD12	1:D:815:PRO:HD2	2.01	0.41
1:D:1283:LEU:HB2	1:D:1555:PHE:HB2	2.02	0.41
1:D:1500:ARG:HE	1:D:1505:LEU:N	2.18	0.41
1:D:2280:LEU:HD21	1:D:2382:ILE:HD12	2.02	0.41
1:D:2727:HIS:O	1:D:2730:ASP:N	2.54	0.41
1:D:3016:ARG:NH2	1:D:3017:HIS:HE1	2.19	0.41
1:D:3065:ALA:O	1:D:3068:LEU:HG	2.21	0.41
1:D:3178:HIS:O	1:D:3178:HIS:CD2	2.74	0.41
1:D:3200:ASN:HB2	1:D:3203:ASP:HB2	2.03	0.41
1:D:3712:LYS:HE3	1:D:3717:LYS:HG2	2.03	0.41
1:D:3793:LEU:O	1:D:3797:MET:HG3	2.21	0.41
1:D:4203:ALA:HA	1:D:4206:ILE:HG12	2.02	0.41
1:D:4858:LEU:HD23	1:D:4861:ILE:HD12	2.02	0.41
1:A:737:ILE:HG21	1:A:1534:GLU:OE1	2.21	0.41
1:A:1517:LEU:HD12	1:A:1517:LEU:HA	1.91	0.41
1:A:2980:LEU:O	1:A:2984:SER:N	2.52	0.41
1:A:3221:LEU:CD2	1:A:3234:VAL:HG11	2.50	0.41
1:A:3926:GLY:O	1:A:3928:CYS:N	2.54	0.41
1:A:4590:TYR:OH	1:A:4718:SER:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1437:GLU:HA	1:B:1438:PRO:HD3	1.90	0.41
1:B:2486:HIS:O	1:B:2490:VAL:HG22	2.21	0.41
1:B:2898:ILE:HD12	1:B:2898:ILE:HA	1.80	0.41
1:B:2944:ASP:O	1:B:2947:SER:OG	2.39	0.41
1:B:2976:LYS:HA	1:B:2979:ARG:NH1	2.36	0.41
1:B:3016:ARG:NH2	1:B:3017:HIS:HE1	2.19	0.41
1:B:3171:LEU:HD23	1:B:3171:LEU:HA	1.79	0.41
1:B:3200:ASN:HB2	1:B:3203:ASP:HB2	2.03	0.41
1:B:3221:LEU:CD2	1:B:3234:VAL:HG11	2.50	0.41
1:B:4702:ASP:O	1:B:4706:GLN:HG2	2.21	0.41
1:C:23:GLN:HG2	1:C:36:CYS:SG	2.61	0.41
1:C:225:GLN:HG2	1:C:3862:THR:O	2.21	0.41
1:C:387:ILE:HG13	1:C:388:GLN:N	2.35	0.41
1:C:814:LEU:HD12	1:C:815:PRO:HD2	2.01	0.41
1:C:2054:LYS:HD2	1:C:2056:SER:N	2.36	0.41
1:C:2727:HIS:O	1:C:2730:ASP:N	2.54	0.41
1:C:3016:ARG:NH2	1:C:3017:HIS:HE1	2.19	0.41
1:C:3261:ALA:O	1:C:3262:GLU:HB3	2.21	0.41
1:C:4680:SER:HA	1:C:4684:GLU:HB2	2.02	0.41
1:D:281:ARG:NE	1:D:283:ALA:O	2.48	0.41
1:D:370:LEU:HB2	1:D:393:MET:HE3	2.03	0.41
1:D:670:TYR:O	1:D:673:TRP:NE1	2.54	0.41
1:D:992:GLN:O	1:D:996:VAL:HG23	2.21	0.41
1:D:3171:LEU:HD23	1:D:3171:LEU:HA	1.79	0.41
1:A:874:LEU:HA	1:A:875:PRO:HD3	1.83	0.40
1:A:888:ASN:C	1:A:888:ASN:HD22	2.29	0.40
1:A:2280:LEU:HD21	1:A:2382:ILE:HD12	2.02	0.40
1:A:2321:VAL:O	1:A:2325:ILE:HG12	2.22	0.40
1:A:3312:PRO:HA	1:A:3315:LEU:CG	2.45	0.40
1:A:3793:LEU:O	1:A:3797:MET:HG3	2.21	0.40
1:A:3967:LEU:HD12	1:A:3967:LEU:HA	1.92	0.40
1:A:4702:ASP:O	1:A:4706:GLN:HG2	2.21	0.40
2:G:4:GLU:OE2	2:G:76:THR:OG1	2.31	0.40
1:B:894:VAL:O	1:B:898:ILE:HG12	2.22	0.40
1:B:1016:TRP:HZ3	1:B:1022:GLN:HE22	1.67	0.40
1:B:1790:LYS:HG2	1:B:1794:MET:HE2	2.01	0.40
1:B:1967:SER:O	1:B:1972:GLN:NE2	2.49	0.40
1:B:4590:TYR:OH	1:B:4718:SER:HB2	2.21	0.40
1:C:370:LEU:HB2	1:C:393:MET:HE3	2.03	0.40
1:C:927:GLN:HG2	1:C:928:GLU:N	2.37	0.40
1:C:2852:TRP:NE1	1:C:2856:LYS:HZ3	2.18	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2940:ILE:HG23	1:C:3021:LEU:HD23	2.02	0.40
1:D:758:CYS:HB3	1:D:819:TYR:CE2	2.56	0.40
1:D:894:VAL:O	1:D:898:ILE:HG12	2.22	0.40
1:D:2789:ILE:HA	1:D:2902:ALA:O	2.21	0.40
1:D:3245:TYR:CD1	1:D:3249:TRP:CZ3	3.09	0.40
1:D:4806:CYS:HA	1:D:4812:CYS:HB2	2.03	0.40
1:A:274:LEU:HD23	1:A:274:LEU:HA	1.93	0.40
1:A:661:LEU:HD11	1:A:759:LEU:HD23	2.02	0.40
1:A:2789:ILE:HA	1:A:2902:ALA:O	2.22	0.40
1:A:2870:LEU:HD22	1:A:2877:LEU:CD2	2.51	0.40
1:A:3178:HIS:CD2	1:A:3178:HIS:O	2.74	0.40
1:A:4021:LEU:HD22	1:A:4128:TYR:CE2	2.55	0.40
1:A:4107:GLU:OE1	1:A:4149:TYR:OH	2.23	0.40
1:A:4863:GLN:OE1	1:B:4860:ALA:HB2	2.21	0.40
1:B:225:GLN:HG2	1:B:3862:THR:O	2.21	0.40
1:B:890:HIS:O	1:B:894:VAL:HG12	2.21	0.40
1:B:1283:LEU:HB2	1:B:1555:PHE:HB2	2.02	0.40
1:B:2321:VAL:O	1:B:2325:ILE:HG12	2.22	0.40
1:B:2549:LEU:HD13	1:B:2588:LEU:HD22	2.03	0.40
1:B:2561:LEU:HD23	1:B:2565:GLN:HB3	2.02	0.40
1:B:2888:LYS:HA	1:B:2891:ASP:OD2	2.21	0.40
1:B:3261:ALA:O	1:B:3262:GLU:HB3	2.21	0.40
1:B:4203:ALA:HA	1:B:4206:ILE:HG12	2.02	0.40
1:C:949:HIS:O	1:C:1065:GLU:HB2	2.21	0.40
1:C:1850:VAL:HG22	1:C:2055:SER:HB3	2.02	0.40
1:C:3793:LEU:O	1:C:3797:MET:HG3	2.21	0.40
1:D:737:ILE:HG21	1:D:1534:GLU:OE1	2.21	0.40
1:D:1800:LYS:HD3	1:D:1890:LYS:HE2	2.04	0.40
1:D:2857:LYS:HA	1:D:2860:LEU:HG	2.03	0.40
1:D:3284:ILE:O	1:D:3288:LEU:HG	2.21	0.40
1:D:3305:PRO:O	1:D:3309:LYS:HG3	2.21	0.40
1:D:4480:PHE:O	1:D:4484:ILE:HG23	2.20	0.40
1:D:4680:SER:HA	1:D:4684:GLU:HB2	2.02	0.40
1:A:23:GLN:HG2	1:A:36:CYS:SG	2.61	0.40
1:A:670:TYR:O	1:A:673:TRP:NE1	2.54	0.40
1:A:1438:PRO:CG	1:A:1500:ARG:HH12	2.33	0.40
1:A:2156:TYR:HE1	1:A:2202:TYR:CE2	2.37	0.40
1:A:2228:GLY:HA3	1:A:2234:MET:SD	2.61	0.40
1:A:2642:ARG:NH1	1:A:2682:GLU:HB2	2.36	0.40
1:A:2857:LYS:HA	1:A:2860:LEU:HG	2.03	0.40
1:A:3284:ILE:O	1:A:3288:LEU:HG	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4079:ASP:O	1:A:4082:GLU:HG3	2.22	0.40
1:A:4698:LEU:HB2	1:D:4262:LYS:NZ	2.36	0.40
1:B:387:ILE:HG13	1:B:388:GLN:N	2.36	0.40
1:B:2228:GLY:HA3	1:B:2234:MET:SD	2.61	0.40
1:B:2830:ASN:ND2	1:C:1433:PHE:HB3	2.35	0.40
1:B:2940:ILE:HG23	1:B:3021:LEU:HD23	2.02	0.40
1:B:3065:ALA:O	1:B:3068:LEU:HG	2.21	0.40
1:C:630:HIS:CE1	1:C:1671:ARG:HE	2.39	0.40
1:C:674:TYR:HB2	1:C:819:TYR:HB3	2.02	0.40
1:C:3284:ILE:O	1:C:3288:LEU:HG	2.21	0.40
1:C:4590:TYR:OH	1:C:4718:SER:HB2	2.21	0.40
1:C:4673:ASP:OD1	1:C:4676:ALA:HB3	2.20	0.40
1:D:1850:VAL:HG22	1:D:2055:SER:HB3	2.02	0.40
1:D:2274:LEU:HG	1:D:2329:GLU:HG3	2.02	0.40
1:D:2642:ARG:NH1	1:D:2682:GLU:HB2	2.36	0.40
1:D:2858:MET:HE2	1:D:2858:MET:N	2.35	0.40
1:D:2980:LEU:O	1:D:2984:SER:N	2.52	0.40
1:D:3655:ASP:OD1	1:D:3656:GLU:N	2.55	0.40
1:A:674:TYR:CE1	1:A:756:SER:HB2	2.55	0.40
1:A:890:HIS:O	1:A:894:VAL:HG12	2.21	0.40
1:A:927:GLN:HG2	1:A:928:GLU:N	2.37	0.40
1:A:2913:ASP:CG	1:A:2916:SER:HB2	2.47	0.40
1:A:3104:MET:HG3	1:A:3105:LEU:N	2.37	0.40
1:A:3293:GLY:O	1:A:3296:MET:HG2	2.20	0.40
1:B:2727:HIS:O	1:B:2730:ASP:N	2.54	0.40
1:B:2870:LEU:HD22	1:B:2877:LEU:CD2	2.51	0.40
1:B:3178:HIS:CD2	1:B:3178:HIS:O	2.74	0.40
1:B:4107:GLU:OE1	1:B:4149:TYR:OH	2.23	0.40
1:B:4503:ARG:NH2	1:B:4745:ASP:OD1	2.54	0.40
1:C:890:HIS:O	1:C:894:VAL:HG12	2.21	0.40
1:C:1678:SER:HB2	1:C:1768:PHE:CE2	2.57	0.40
1:C:2228:GLY:HA3	1:C:2234:MET:SD	2.61	0.40
1:C:2739:ASN:HD21	1:C:2741:TRP:HE1	1.69	0.40
1:C:3065:ALA:O	1:C:3068:LEU:HG	2.21	0.40
1:C:3712:LYS:HE3	1:C:3717:LYS:HG2	2.03	0.40
1:D:23:GLN:HG2	1:D:36:CYS:SG	2.61	0.40
1:D:331:PHE:HE1	1:D:363:ILE:HG12	1.86	0.40
1:D:356:TYR:CZ	1:D:407:ARG:HB2	2.57	0.40
1:D:630:HIS:CE1	1:D:1671:ARG:HE	2.39	0.40
1:D:1048:ASP:O	1:D:1051:ARG:HB2	2.21	0.40
1:D:2228:GLY:HA3	1:D:2234:MET:SD	2.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2486:HIS:O	1:D:2490:VAL:HG22	2.21	0.40
1:D:3012:GLY:O	1:D:3016:ARG:HG3	2.21	0.40
1:D:3069:GLU:HG3	1:D:3132:ARG:CZ	2.50	0.40
1:A:2133:ARG:HG2	1:A:2134:MET:N	2.37	0.40
1:A:2888:LYS:HA	1:A:2891:ASP:OD2	2.21	0.40
1:A:2976:LYS:HA	1:A:2979:ARG:NH1	2.36	0.40
1:A:3900:GLU:O	1:A:3904:ARG:HG2	2.22	0.40
1:B:162:ILE:HD12	1:B:175:VAL:HG21	2.03	0.40
1:B:2133:ARG:HG2	1:B:2134:MET:N	2.37	0.40
1:B:3072:MET:HE3	1:B:3136:SER:CB	2.46	0.40
1:B:3783:GLU:OE2	1:B:3784:LYS:NZ	2.55	0.40
1:B:3926:GLY:O	1:B:3928:CYS:N	2.54	0.40
1:C:34:LYS:H	1:C:53:SER:HG	1.59	0.40
1:C:866:PRO:HD2	1:C:1009:ARG:CZ	2.52	0.40
1:C:888:ASN:HD22	1:C:888:ASN:C	2.29	0.40
1:C:1160:ASP:HB3	1:C:1177:LEU:HD11	2.04	0.40
1:D:2976:LYS:HA	1:D:2979:ARG:NH1	2.36	0.40
1:D:3261:ALA:O	1:D:3262:GLU:HB3	2.21	0.40
1:D:3900:GLU:O	1:D:3904:ARG:HG2	2.22	0.40
1:D:4035:TYR:HE1	1:D:4050:LYS:HE2	1.87	0.40
1:D:4618:THR:HG22	1:D:4661:TYR:OH	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	4198/4967 (84%)	4067 (97%)	127 (3%)	4 (0%)	48	69
1	B	4198/4967 (84%)	4065 (97%)	129 (3%)	4 (0%)	48	69
1	C	4198/4967 (84%)	4064 (97%)	130 (3%)	4 (0%)	48	69
1	D	4198/4967 (84%)	4063 (97%)	131 (3%)	4 (0%)	48	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	105/108 (97%)	102 (97%)	3 (3%)	0	100	100
2	F	105/108 (97%)	102 (97%)	3 (3%)	0	100	100
2	G	105/108 (97%)	102 (97%)	3 (3%)	0	100	100
2	H	105/108 (97%)	102 (97%)	3 (3%)	0	100	100
All	All	17212/20300 (85%)	16667 (97%)	529 (3%)	16 (0%)	49	69

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2988	ARG
1	A	3927	PRO
1	A	4641	PRO
1	B	2988	ARG
1	B	3927	PRO
1	B	4641	PRO
1	C	2988	ARG
1	C	3927	PRO
1	C	4641	PRO
1	D	2988	ARG
1	D	3927	PRO
1	D	4641	PRO
1	A	2770	ILE
1	B	2770	ILE
1	D	2770	ILE
1	C	2770	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	3708/4358 (85%)	3656 (99%)	52 (1%)	59	78
1	B	3708/4358 (85%)	3656 (99%)	52 (1%)	59	78
1	C	3708/4358 (85%)	3656 (99%)	52 (1%)	59	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	3708/4358 (85%)	3654 (98%)	54 (2%)	57	77
2	E	88/89 (99%)	87 (99%)	1 (1%)	65	81
2	F	88/89 (99%)	87 (99%)	1 (1%)	65	81
2	G	88/89 (99%)	87 (99%)	1 (1%)	65	81
2	H	88/89 (99%)	87 (99%)	1 (1%)	65	81
All	All	15184/17788 (85%)	14970 (99%)	214 (1%)	57	78

All (214) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	81	MET
1	A	198	ASN
1	A	309	MET
1	A	344	LYS
1	A	778	MET
1	A	814	LEU
1	A	844	ARG
1	A	865	ILE
1	A	872	ILE
1	A	882	ARG
1	A	933	LEU
1	A	940	LEU
1	A	999	LEU
1	A	1050	LEU
1	A	1077	VAL
1	A	1564	MET
1	A	1948	MET
1	A	2191	LYS
1	A	2442	MET
1	A	2456	MET
1	A	2480	VAL
1	A	2584	MET
1	A	2592	LEU
1	A	2607	LEU
1	A	2681	MET
1	A	2689	MET
1	A	2695	MET
1	A	2727	HIS
1	A	2731	LYS
1	A	2837	LEU

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Mol	Chain	Res	Type
1	A	2840	MET
1	A	2884	LYS
1	A	2893	LEU
1	A	2898	ILE
1	A	3007	LEU
1	A	3050	LEU
1	A	3101	LEU
1	A	3116	GLN
1	A	3146	ILE
1	A	3214	LEU
1	A	3315	LEU
1	A	3316	LYS
1	A	3719	MET
1	A	3819	MET
1	A	3978	MET
1	A	4019	MET
1	A	4046	ARG
1	A	4060	GLN
1	A	4264	LEU
1	A	4269	LYS
1	A	4753	LEU
1	A	4809	MET
2	E	19	LYS
2	F	19	LYS
2	G	19	LYS
2	H	19	LYS
1	B	81	MET
1	B	198	ASN
1	B	309	MET
1	B	344	LYS
1	B	778	MET
1	B	814	LEU
1	B	844	ARG
1	B	865	ILE
1	B	872	ILE
1	B	882	ARG
1	B	933	LEU
1	B	940	LEU
1	B	999	LEU
1	B	1050	LEU
1	B	1077	VAL
1	B	1564	MET

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Mol	Chain	Res	Type
1	B	1948	MET
1	B	2191	LYS
1	B	2442	MET
1	B	2456	MET
1	B	2480	VAL
1	B	2584	MET
1	B	2592	LEU
1	B	2607	LEU
1	B	2681	MET
1	B	2689	MET
1	B	2695	MET
1	B	2727	HIS
1	B	2731	LYS
1	B	2837	LEU
1	B	2840	MET
1	B	2884	LYS
1	B	2893	LEU
1	B	2898	ILE
1	B	3007	LEU
1	B	3050	LEU
1	B	3101	LEU
1	B	3116	GLN
1	B	3146	ILE
1	B	3214	LEU
1	B	3315	LEU
1	B	3316	LYS
1	B	3719	MET
1	B	3819	MET
1	B	3978	MET
1	B	4019	MET
1	B	4046	ARG
1	B	4060	GLN
1	B	4264	LEU
1	B	4269	LYS
1	B	4753	LEU
1	B	4809	MET
1	C	81	MET
1	C	198	ASN
1	C	309	MET
1	C	344	LYS
1	C	778	MET
1	C	814	LEU

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Mol	Chain	Res	Type
1	C	844	ARG
1	C	865	ILE
1	C	872	ILE
1	C	882	ARG
1	C	933	LEU
1	C	940	LEU
1	C	999	LEU
1	C	1050	LEU
1	C	1077	VAL
1	C	1564	MET
1	C	1948	MET
1	C	2191	LYS
1	C	2442	MET
1	C	2456	MET
1	C	2480	VAL
1	C	2584	MET
1	C	2592	LEU
1	C	2607	LEU
1	C	2681	MET
1	C	2689	MET
1	C	2695	MET
1	C	2727	HIS
1	C	2731	LYS
1	C	2837	LEU
1	C	2840	MET
1	C	2884	LYS
1	C	2893	LEU
1	C	2898	ILE
1	C	3007	LEU
1	C	3050	LEU
1	C	3101	LEU
1	C	3116	GLN
1	C	3146	ILE
1	C	3214	LEU
1	C	3315	LEU
1	C	3316	LYS
1	C	3719	MET
1	C	3819	MET
1	C	3978	MET
1	C	4019	MET
1	C	4046	ARG
1	C	4060	GLN

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Mol	Chain	Res	Type
1	C	4264	LEU
1	C	4269	LYS
1	C	4753	LEU
1	C	4809	MET
1	D	81	MET
1	D	198	ASN
1	D	309	MET
1	D	344	LYS
1	D	778	MET
1	D	814	LEU
1	D	844	ARG
1	D	865	ILE
1	D	872	ILE
1	D	882	ARG
1	D	933	LEU
1	D	940	LEU
1	D	999	LEU
1	D	1050	LEU
1	D	1077	VAL
1	D	1564	MET
1	D	1948	MET
1	D	2191	LYS
1	D	2442	MET
1	D	2456	MET
1	D	2480	VAL
1	D	2584	MET
1	D	2592	LEU
1	D	2607	LEU
1	D	2681	MET
1	D	2689	MET
1	D	2695	MET
1	D	2727	HIS
1	D	2731	LYS
1	D	2837	LEU
1	D	2838[A]	HIS
1	D	2838[B]	HIS
1	D	2840	MET
1	D	2884	LYS
1	D	2893	LEU
1	D	2898	ILE
1	D	3007	LEU
1	D	3050	LEU

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Mol	Chain	Res	Type
1	D	3101	LEU
1	D	3116	GLN
1	D	3146	ILE
1	D	3214	LEU
1	D	3315	LEU
1	D	3316	LYS
1	D	3719	MET
1	D	3819	MET
1	D	3978	MET
1	D	4019	MET
1	D	4046	ARG
1	D	4060	GLN
1	D	4264	LEU
1	D	4269	LYS
1	D	4753	LEU
1	D	4809	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (159) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	GLN
1	A	193	HIS
1	A	198	ASN
1	A	604	HIS
1	A	651	HIS
1	A	890	HIS
1	A	1002	ASN
1	A	1123	GLN
1	A	1126	GLN
1	A	1211	GLN
1	A	1233	GLN
1	A	1581	GLN
1	A	1939	ASN
1	A	1972	GLN
1	A	2217	HIS
1	A	2250	ASN
1	A	2541	HIS
1	A	2802	ASN
1	A	2850	ASN
1	A	3017	HIS
1	A	3114	GLN
1	A	3178	HIS

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Mol	Chain	Res	Type
1	A	3179	ASN
1	A	3252	HIS
1	A	3622	GLN
1	A	3767	ASN
1	A	3770	ASN
1	A	3775	GLN
1	A	3869	ASN
1	A	3901	GLN
1	A	3953	HIS
1	A	4060	GLN
1	A	4178	ASN
1	A	4489	GLN
1	A	4629	GLN
1	A	4638	GLN
1	A	4879	GLN
2	E	26	HIS
2	F	26	HIS
2	G	26	HIS
2	G	88	HIS
2	H	26	HIS
1	B	71	GLN
1	B	193	HIS
1	B	198	ASN
1	B	604	HIS
1	B	651	HIS
1	B	890	HIS
1	B	1002	ASN
1	B	1123	GLN
1	B	1126	GLN
1	B	1211	GLN
1	B	1581	GLN
1	B	1972	GLN
1	B	2217	HIS
1	B	2250	ASN
1	B	2541	HIS
1	B	2802	ASN
1	B	2830	ASN
1	B	2850	ASN
1	B	3017	HIS
1	B	3114	GLN
1	B	3179	ASN
1	B	3252	HIS

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Mol	Chain	Res	Type
1	B	3614	HIS
1	B	3622	GLN
1	B	3767	ASN
1	B	3770	ASN
1	B	3775	GLN
1	B	3869	ASN
1	B	3901	GLN
1	B	3953	HIS
1	B	4060	GLN
1	B	4178	ASN
1	B	4488	GLN
1	B	4489	GLN
1	B	4638	GLN
1	B	4879	GLN
1	C	71	GLN
1	C	193	HIS
1	C	604	HIS
1	C	651	HIS
1	C	890	HIS
1	C	1002	ASN
1	C	1123	GLN
1	C	1126	GLN
1	C	1211	GLN
1	C	1233	GLN
1	C	1551	ASN
1	C	1581	GLN
1	C	1836	ASN
1	C	1972	GLN
1	C	2217	HIS
1	C	2250	ASN
1	C	2541	HIS
1	C	2613	HIS
1	C	2802	ASN
1	C	2850	ASN
1	C	3017	HIS
1	C	3114	GLN
1	C	3179	ASN
1	C	3252	HIS
1	C	3304	GLN
1	C	3614	HIS
1	C	3767	ASN
1	C	3775	GLN

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Mol	Chain	Res	Type
1	C	3869	ASN
1	C	3901	GLN
1	C	3933	GLN
1	C	3953	HIS
1	C	4060	GLN
1	C	4178	ASN
1	C	4488	GLN
1	C	4489	GLN
1	C	4638	GLN
1	C	4879	GLN
1	C	4903	HIS
1	D	71	GLN
1	D	193	HIS
1	D	270	HIS
1	D	604	HIS
1	D	651	HIS
1	D	890	HIS
1	D	1002	ASN
1	D	1123	GLN
1	D	1126	GLN
1	D	1151	HIS
1	D	1211	GLN
1	D	1233	GLN
1	D	1581	GLN
1	D	1972	GLN
1	D	2217	HIS
1	D	2250	ASN
1	D	2541	HIS
1	D	2613	HIS
1	D	2802	ASN
1	D	2850	ASN
1	D	3017	HIS
1	D	3114	GLN
1	D	3127	GLN
1	D	3178	HIS
1	D	3179	ASN
1	D	3252	HIS
1	D	3614	HIS
1	D	3622	GLN
1	D	3767	ASN
1	D	3770	ASN
1	D	3775	GLN

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Mol	Chain	Res	Type
1	D	3869	ASN
1	D	3901	GLN
1	D	3933	GLN
1	D	3953	HIS
1	D	4060	GLN
1	D	4178	ASN
1	D	4488	GLN
1	D	4489	GLN
1	D	4638	GLN
1	D	4699	ASN
1	D	4879	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	ATP	D	5002	-	32,33,33	0.27	0	48,52,52	0.31	0
4	ATP	C	5002	-	32,33,33	0.27	0	48,52,52	0.31	0
4	ATP	B	5002	-	32,33,33	0.27	0	48,52,52	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	ATP	D	5003	-	32,33,33	0.26	0	48,52,52	0.28	0
4	ATP	A	5003	-	32,33,33	0.25	0	48,52,52	0.28	0
4	ATP	C	5003	-	32,33,33	0.26	0	48,52,52	0.28	0
4	ATP	B	5003	-	32,33,33	0.25	0	48,52,52	0.28	0
4	ATP	A	5002	-	32,33,33	0.26	0	48,52,52	0.31	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ATP	D	5002	-	-	4/22/38/38	0/3/3/3
4	ATP	C	5002	-	-	4/22/38/38	0/3/3/3
4	ATP	B	5002	-	-	4/22/38/38	0/3/3/3
4	ATP	D	5003	-	-	13/22/38/38	0/3/3/3
4	ATP	A	5003	-	-	13/22/38/38	0/3/3/3
4	ATP	C	5003	-	-	13/22/38/38	0/3/3/3
4	ATP	B	5003	-	-	13/22/38/38	0/3/3/3
4	ATP	A	5002	-	-	4/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (68) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	5002	ATP	PB-O3A-PA-O5'
4	A	5003	ATP	C5'-O5'-PA-O1A
4	A	5003	ATP	C5'-O5'-PA-O2A
4	A	5003	ATP	O4'-C4'-C5'-O5'
4	B	5002	ATP	PB-O3A-PA-O5'
4	B	5003	ATP	C5'-O5'-PA-O1A
4	B	5003	ATP	C5'-O5'-PA-O2A
4	B	5003	ATP	O4'-C4'-C5'-O5'
4	C	5002	ATP	PB-O3A-PA-O5'
4	C	5003	ATP	C5'-O5'-PA-O1A
4	C	5003	ATP	C5'-O5'-PA-O2A
4	C	5003	ATP	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
4	D	5002	ATP	PB-O3A-PA-O5'
4	D	5003	ATP	C5'-O5'-PA-O1A
4	D	5003	ATP	C5'-O5'-PA-O2A
4	D	5003	ATP	O4'-C4'-C5'-O5'
4	A	5002	ATP	C3'-C4'-C5'-O5'
4	B	5002	ATP	C3'-C4'-C5'-O5'
4	C	5002	ATP	C3'-C4'-C5'-O5'
4	D	5002	ATP	C3'-C4'-C5'-O5'
4	A	5003	ATP	C3'-C4'-C5'-O5'
4	B	5003	ATP	C3'-C4'-C5'-O5'
4	C	5003	ATP	C3'-C4'-C5'-O5'
4	D	5003	ATP	C3'-C4'-C5'-O5'
4	A	5002	ATP	O4'-C4'-C5'-O5'
4	B	5002	ATP	O4'-C4'-C5'-O5'
4	C	5002	ATP	O4'-C4'-C5'-O5'
4	D	5002	ATP	O4'-C4'-C5'-O5'
4	A	5003	ATP	PG-O3B-PB-O3A
4	B	5003	ATP	PG-O3B-PB-O3A
4	C	5003	ATP	PG-O3B-PB-O3A
4	D	5003	ATP	PG-O3B-PB-O3A
4	A	5003	ATP	C2'-C1'-N9-C8
4	B	5003	ATP	C2'-C1'-N9-C8
4	C	5003	ATP	C2'-C1'-N9-C8
4	D	5003	ATP	C2'-C1'-N9-C8
4	A	5003	ATP	PB-O3A-PA-O2A
4	B	5003	ATP	PB-O3A-PA-O2A
4	C	5003	ATP	PB-O3A-PA-O2A
4	D	5003	ATP	PB-O3A-PA-O2A
4	A	5003	ATP	C5'-O5'-PA-O3A
4	B	5003	ATP	C5'-O5'-PA-O3A
4	C	5003	ATP	C5'-O5'-PA-O3A
4	D	5003	ATP	C5'-O5'-PA-O3A
4	A	5003	ATP	C2'-C1'-N9-C4
4	B	5003	ATP	C2'-C1'-N9-C4
4	C	5003	ATP	C2'-C1'-N9-C4
4	D	5003	ATP	C2'-C1'-N9-C4
4	A	5003	ATP	O4'-C1'-N9-C4
4	B	5003	ATP	O4'-C1'-N9-C4
4	C	5003	ATP	O4'-C1'-N9-C4
4	D	5003	ATP	O4'-C1'-N9-C4
4	A	5003	ATP	O4'-C1'-N9-C8
4	B	5003	ATP	O4'-C1'-N9-C8

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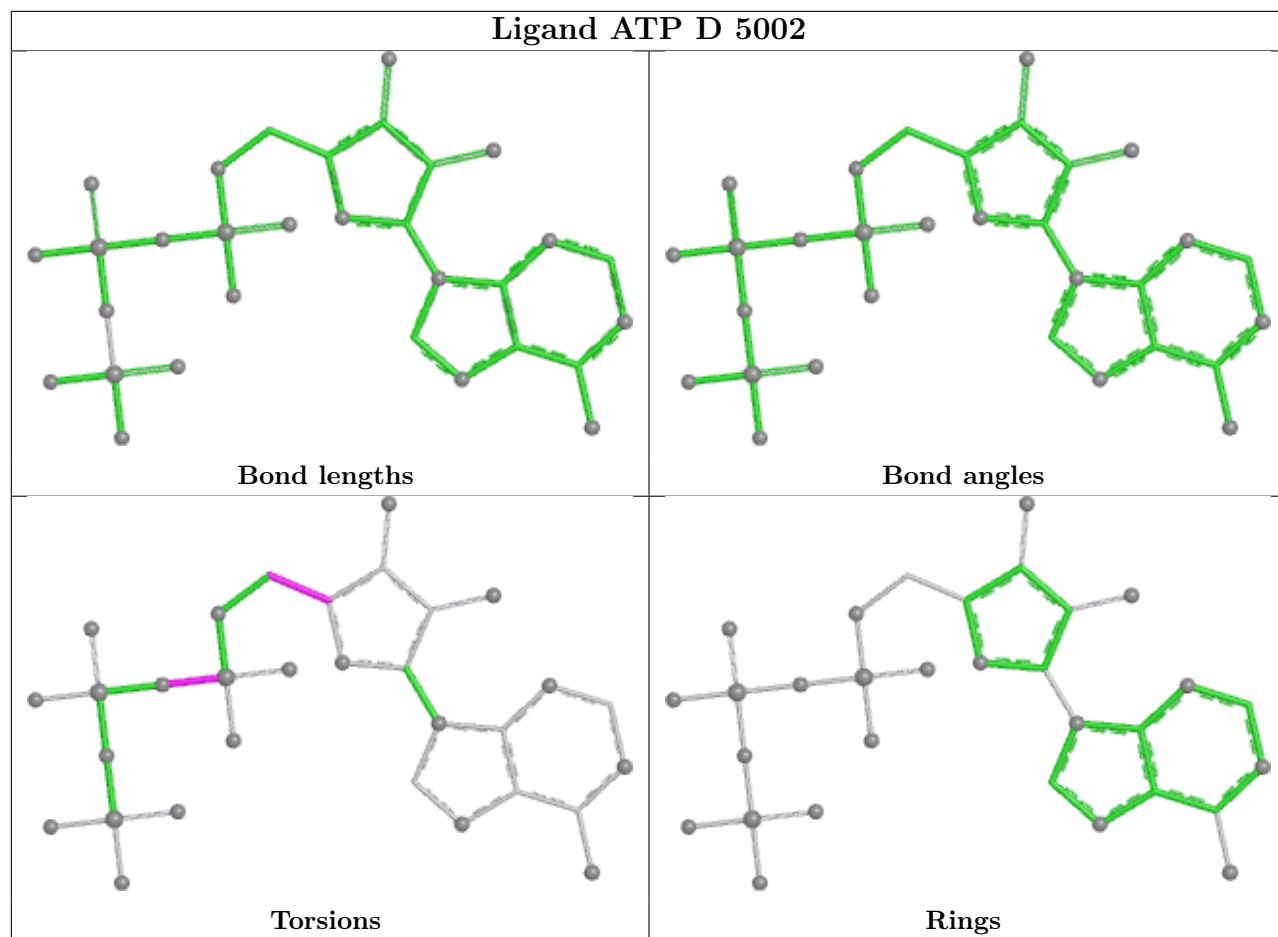
Mol	Chain	Res	Type	Atoms
4	C	5003	ATP	O4'-C1'-N9-C8
4	D	5003	ATP	O4'-C1'-N9-C8
4	A	5003	ATP	PB-O3B-PG-O2G
4	B	5003	ATP	PB-O3B-PG-O2G
4	C	5003	ATP	PB-O3B-PG-O2G
4	D	5003	ATP	PB-O3B-PG-O2G
4	A	5002	ATP	PB-O3A-PA-O1A
4	A	5003	ATP	PB-O3A-PA-O1A
4	B	5002	ATP	PB-O3A-PA-O1A
4	B	5003	ATP	PB-O3A-PA-O1A
4	C	5002	ATP	PB-O3A-PA-O1A
4	C	5003	ATP	PB-O3A-PA-O1A
4	D	5002	ATP	PB-O3A-PA-O1A
4	D	5003	ATP	PB-O3A-PA-O1A

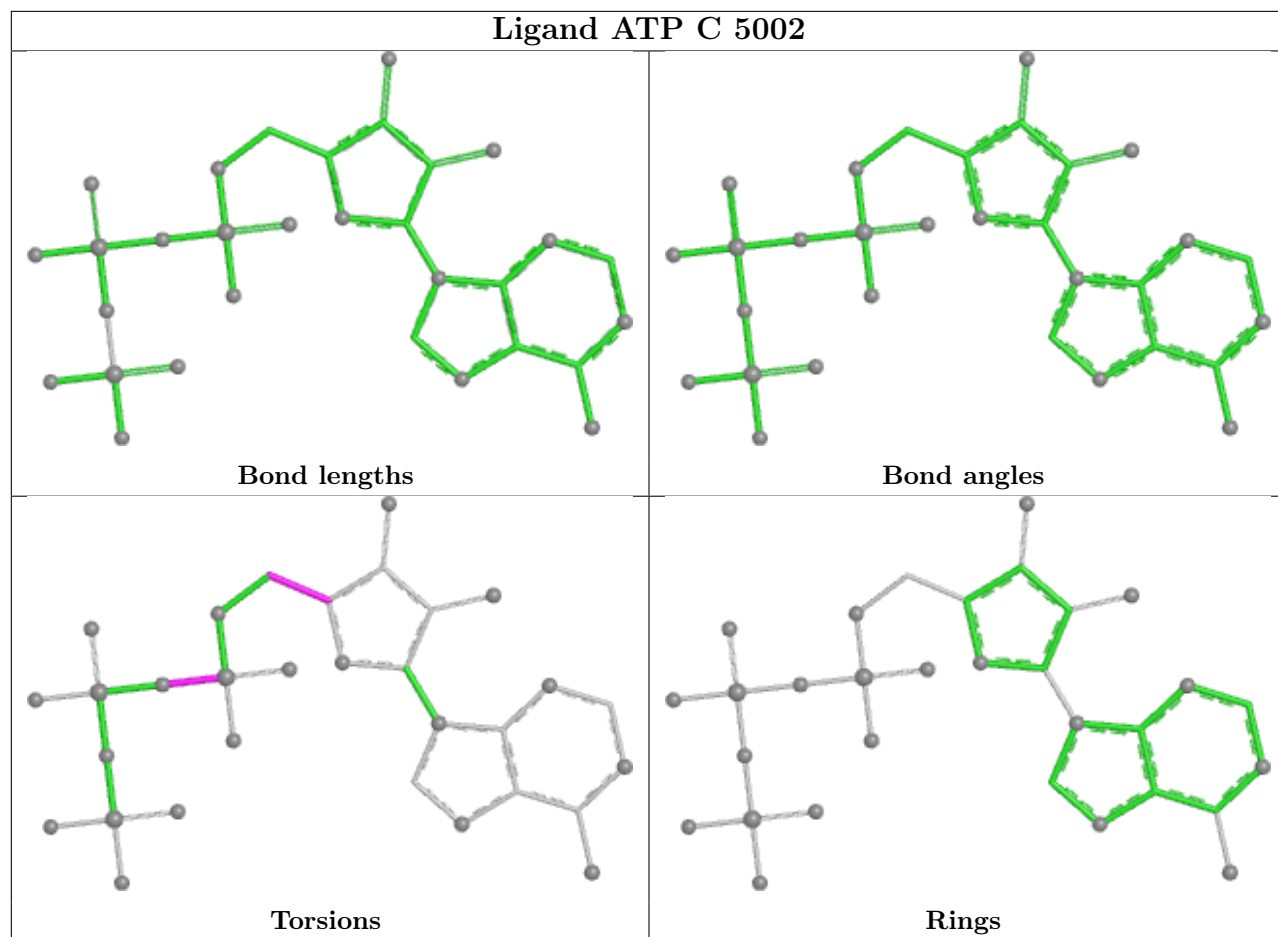
There are no ring outliers.

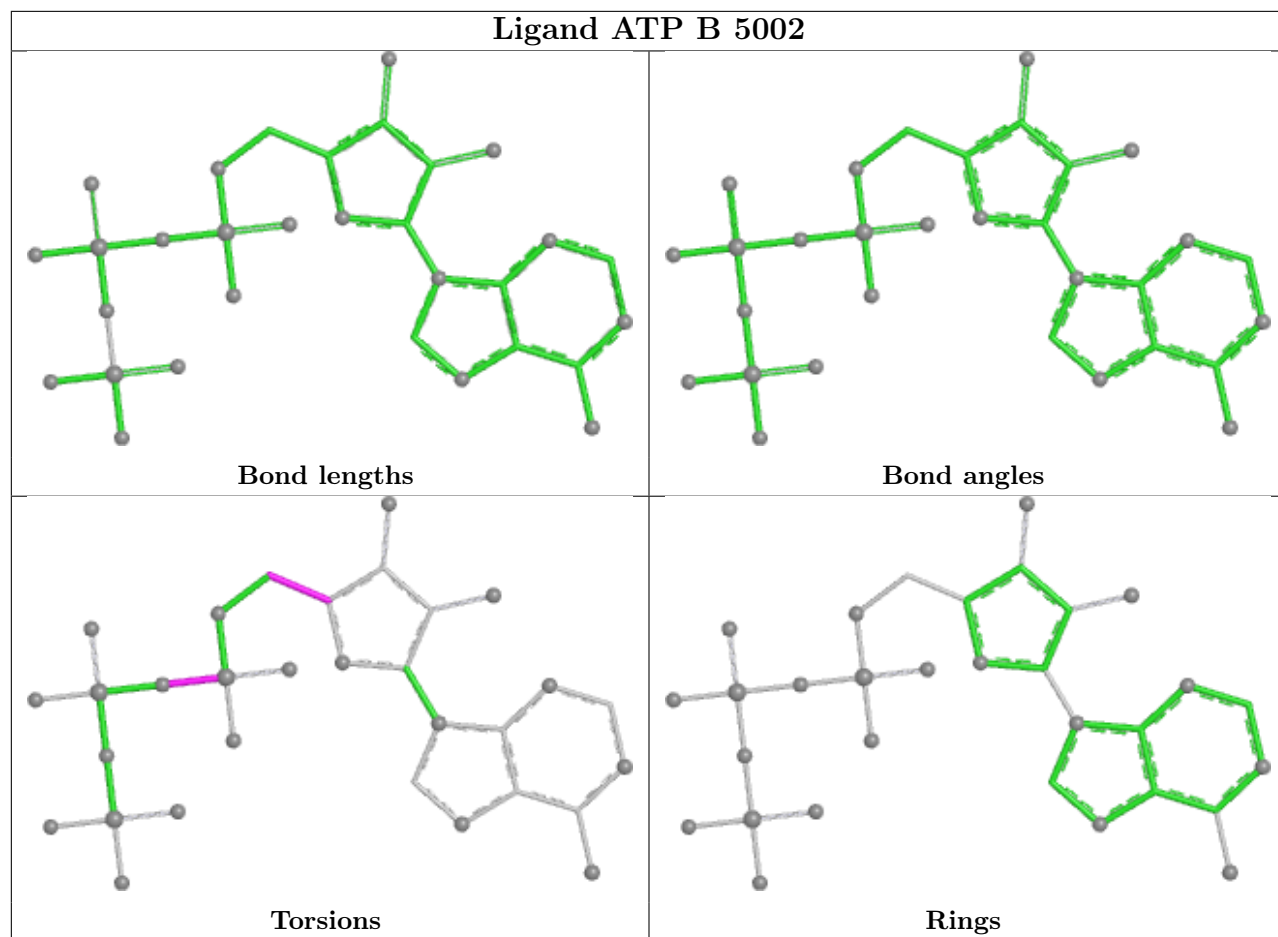
4 monomers are involved in 4 short contacts:

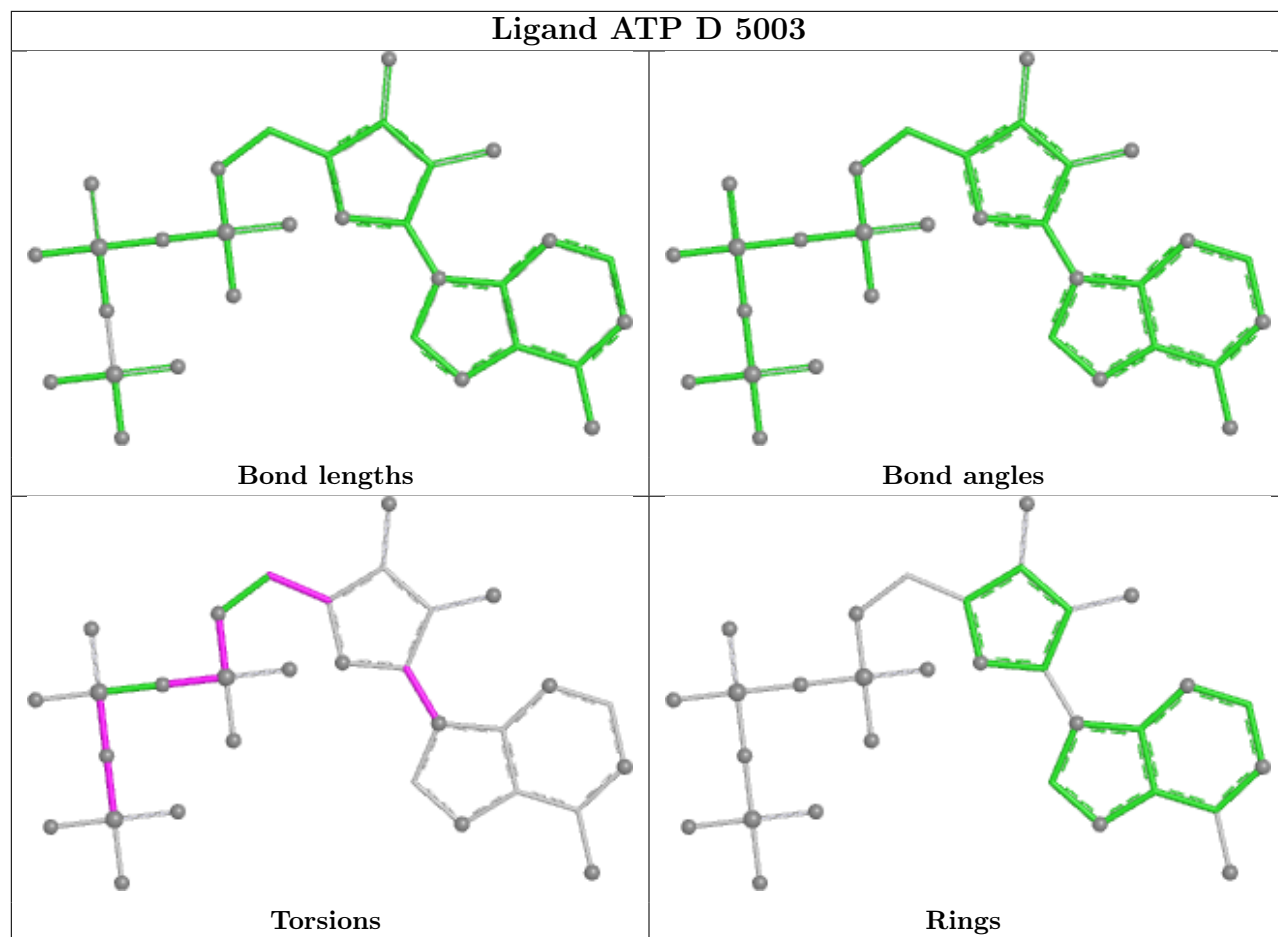
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	5002	ATP	1	0
4	C	5002	ATP	1	0
4	B	5002	ATP	1	0
4	A	5002	ATP	1	0

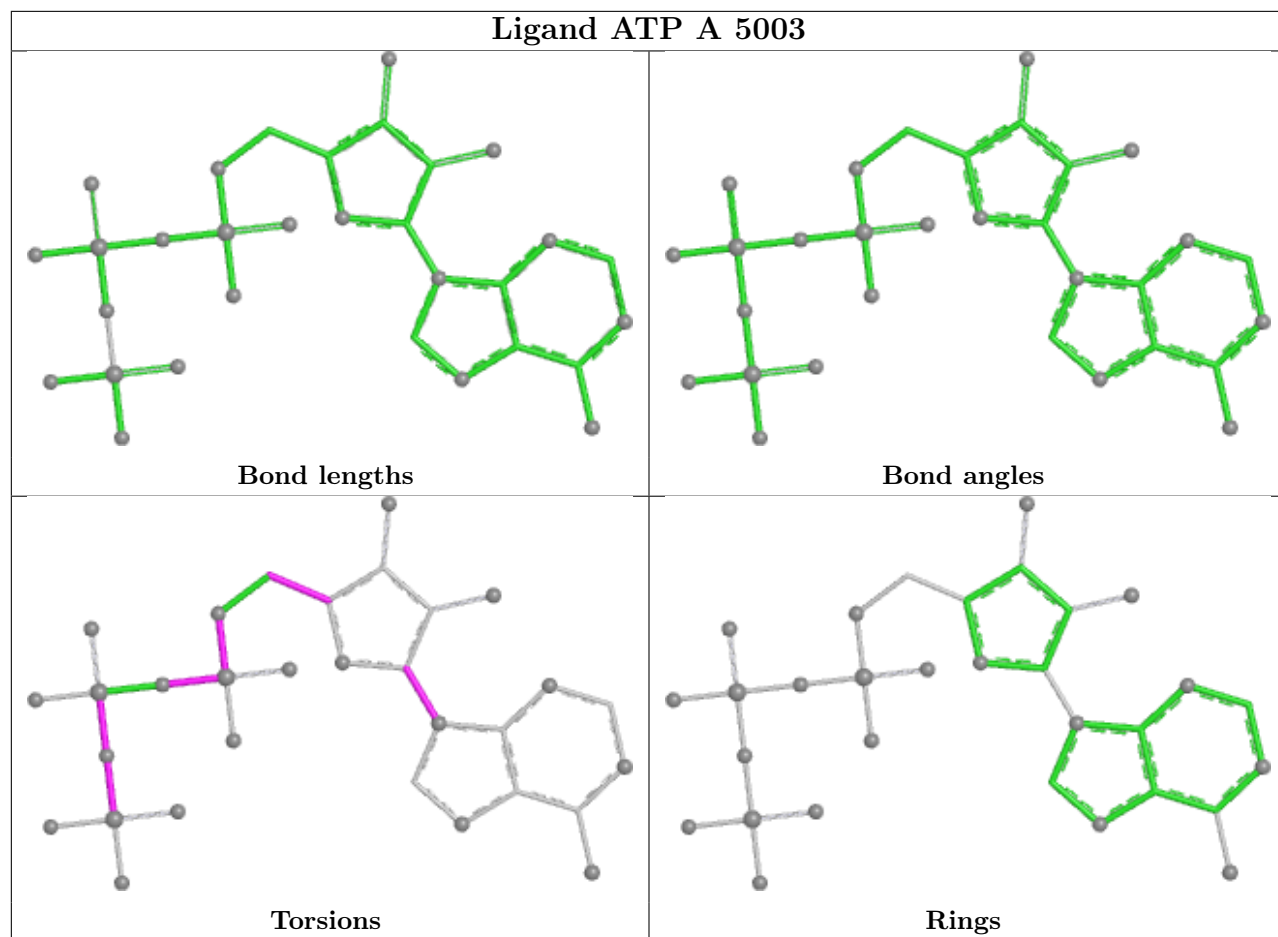
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

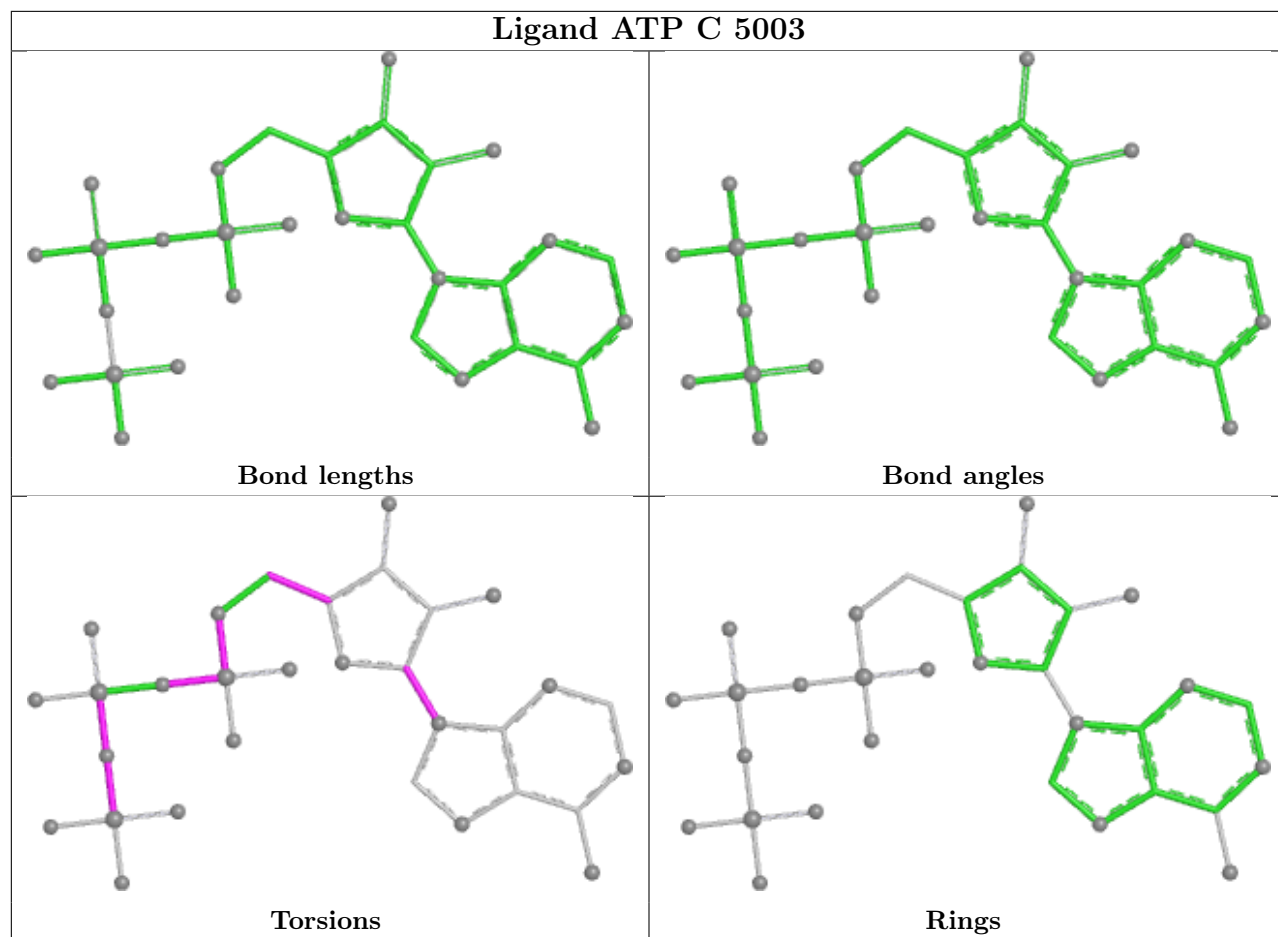


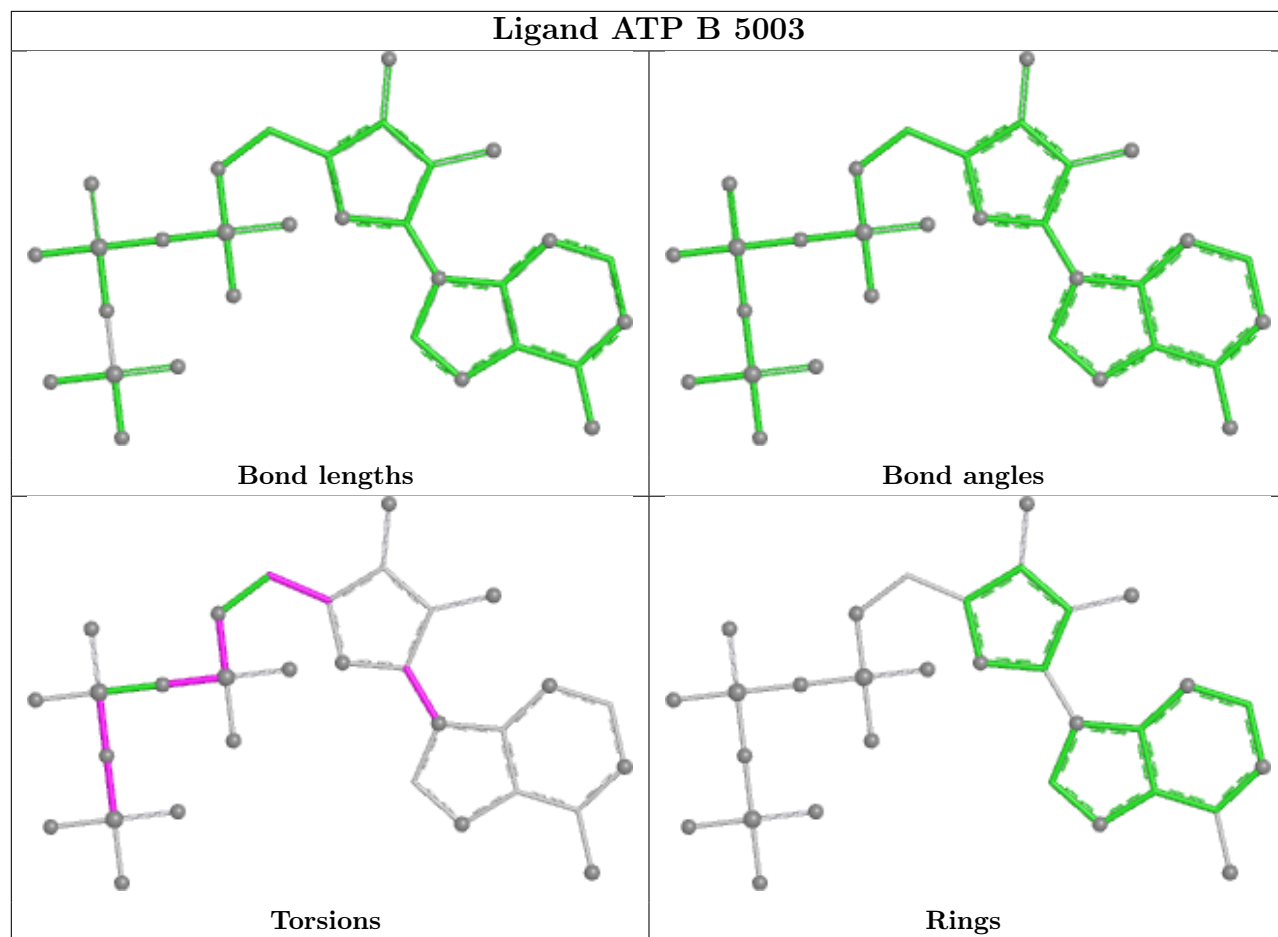


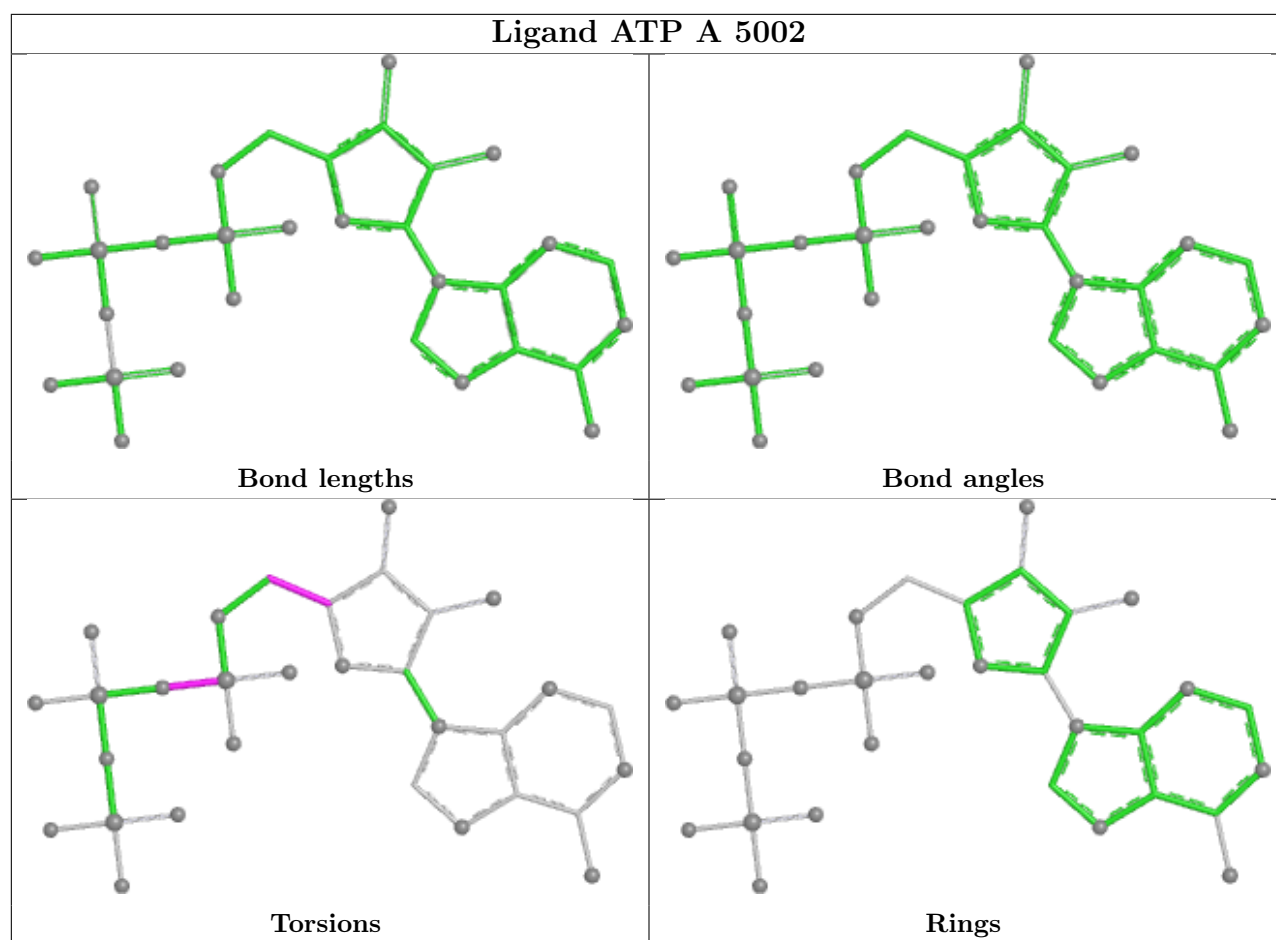












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

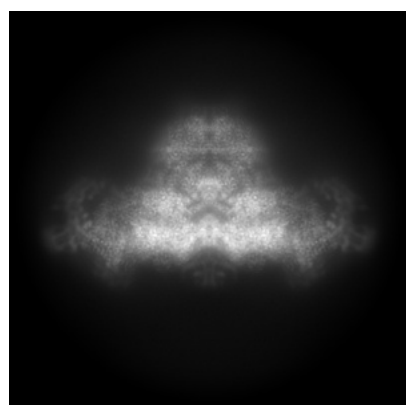
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26415. These allow visual inspection of the internal detail of the map and identification of artifacts.

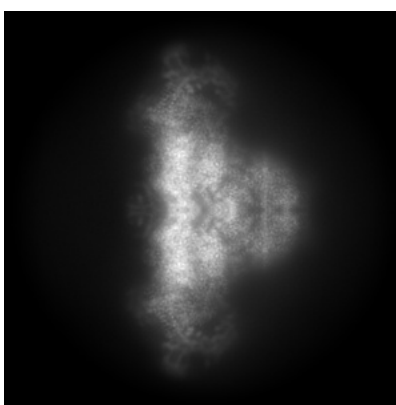
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

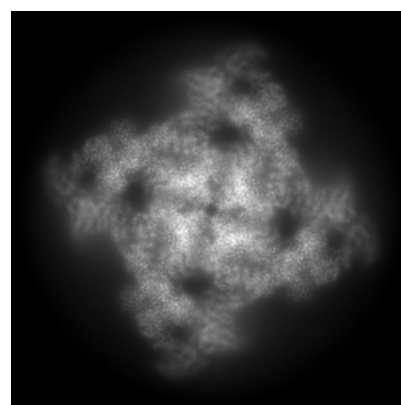
6.1.1 Primary map



X



Y

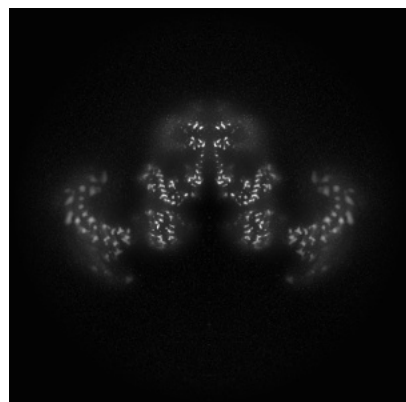


Z

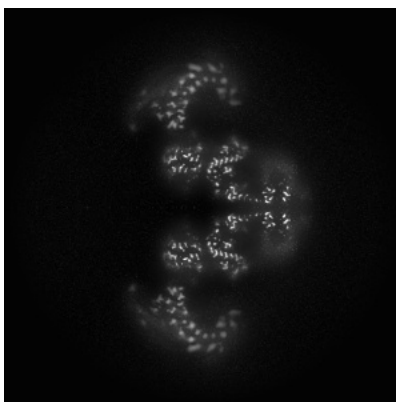
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

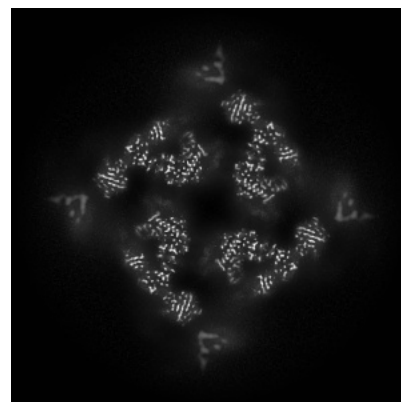
6.2.1 Primary map



X Index: 256



Y Index: 256

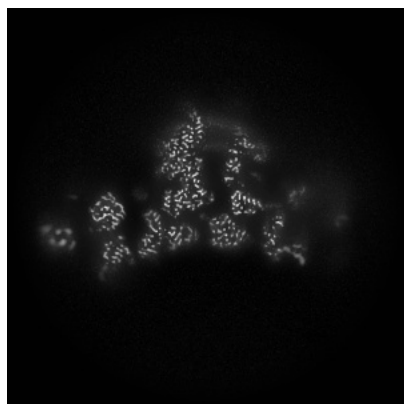


Z Index: 256

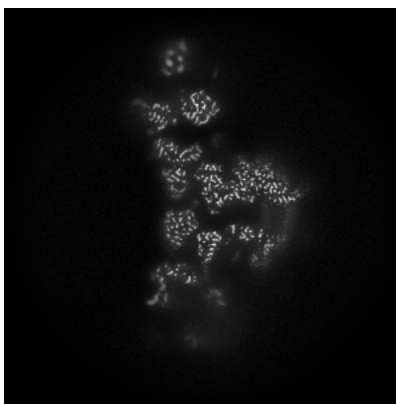
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

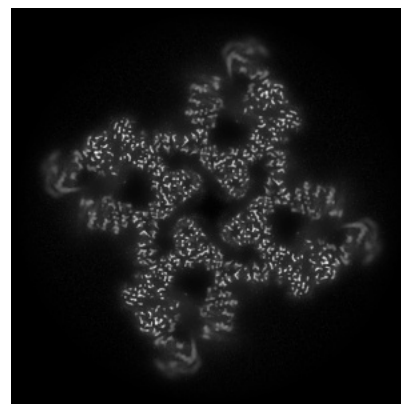
6.3.1 Primary map



X Index: 219



Y Index: 219

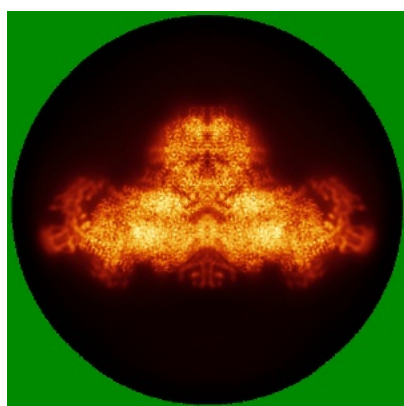


Z Index: 223

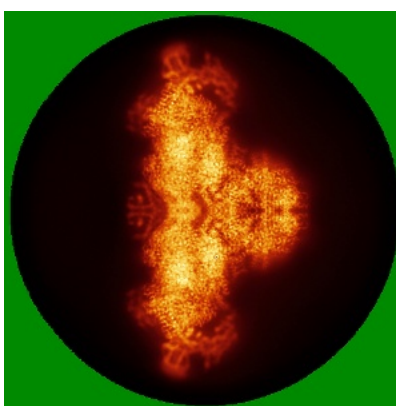
The images above show the largest variance slices of the map in three orthogonal directions.

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

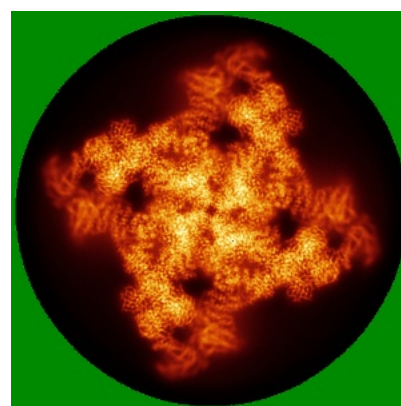
6.4.1 Primary map



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

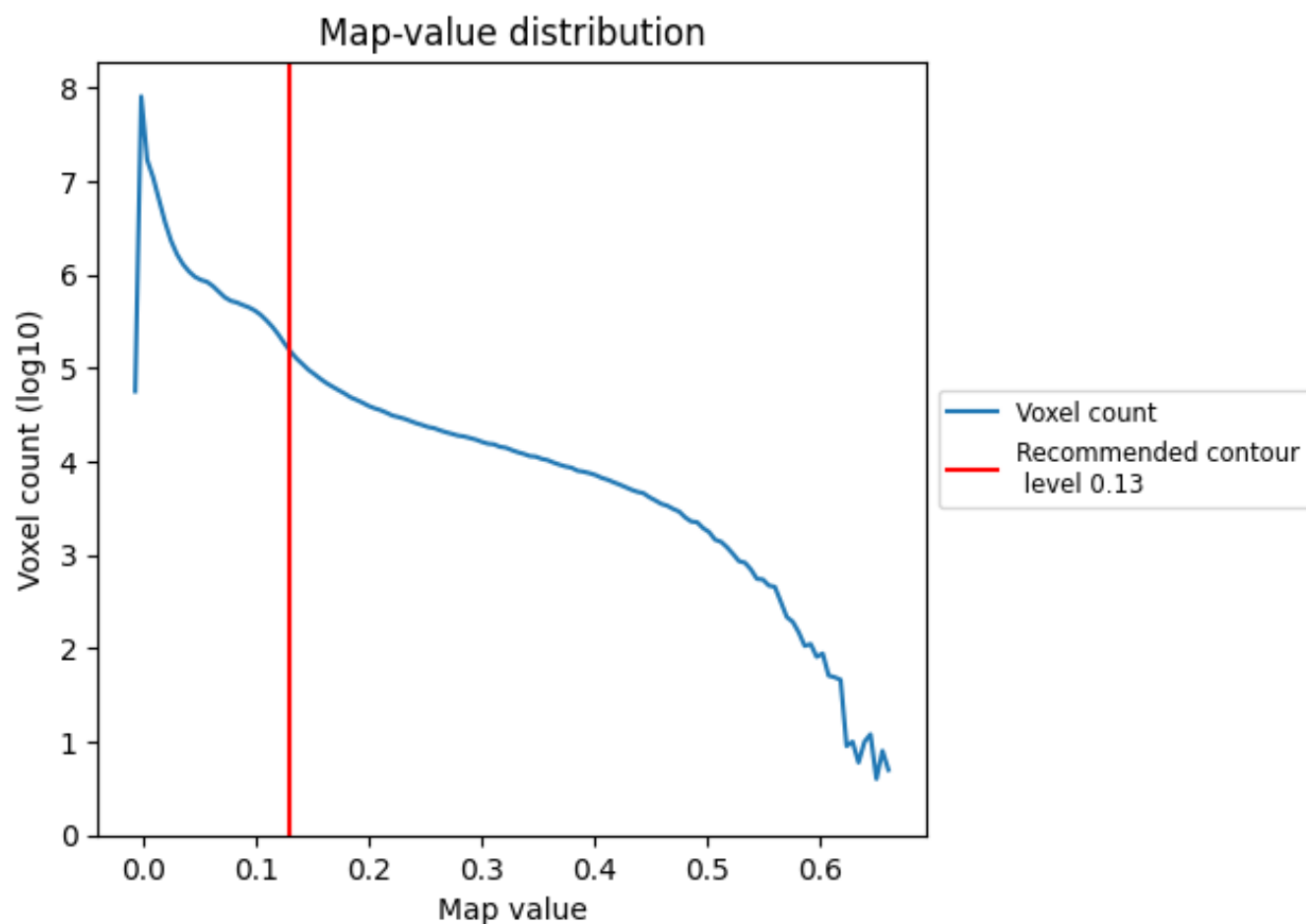
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

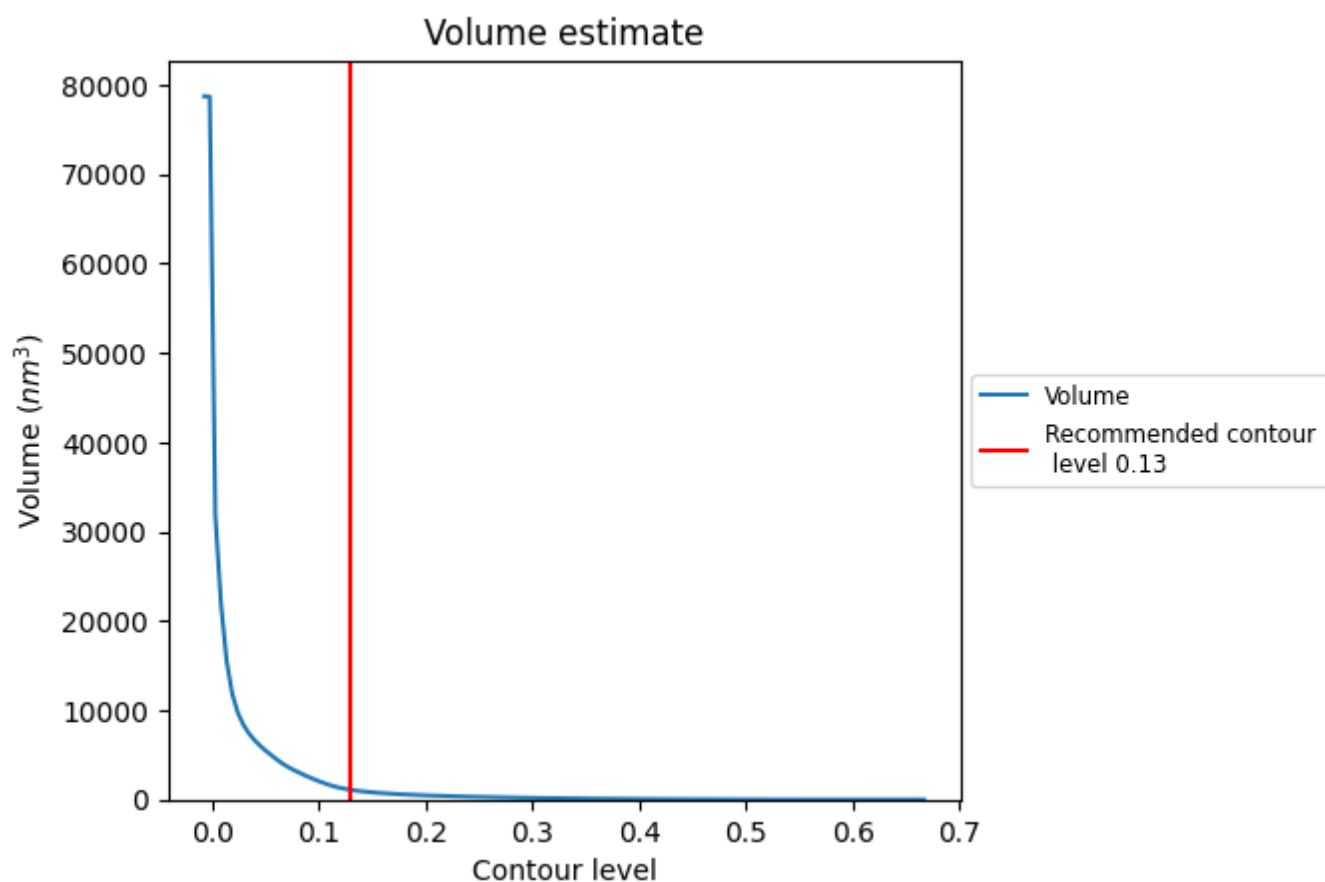
This section contains the results of statistical analysis of the map.

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.

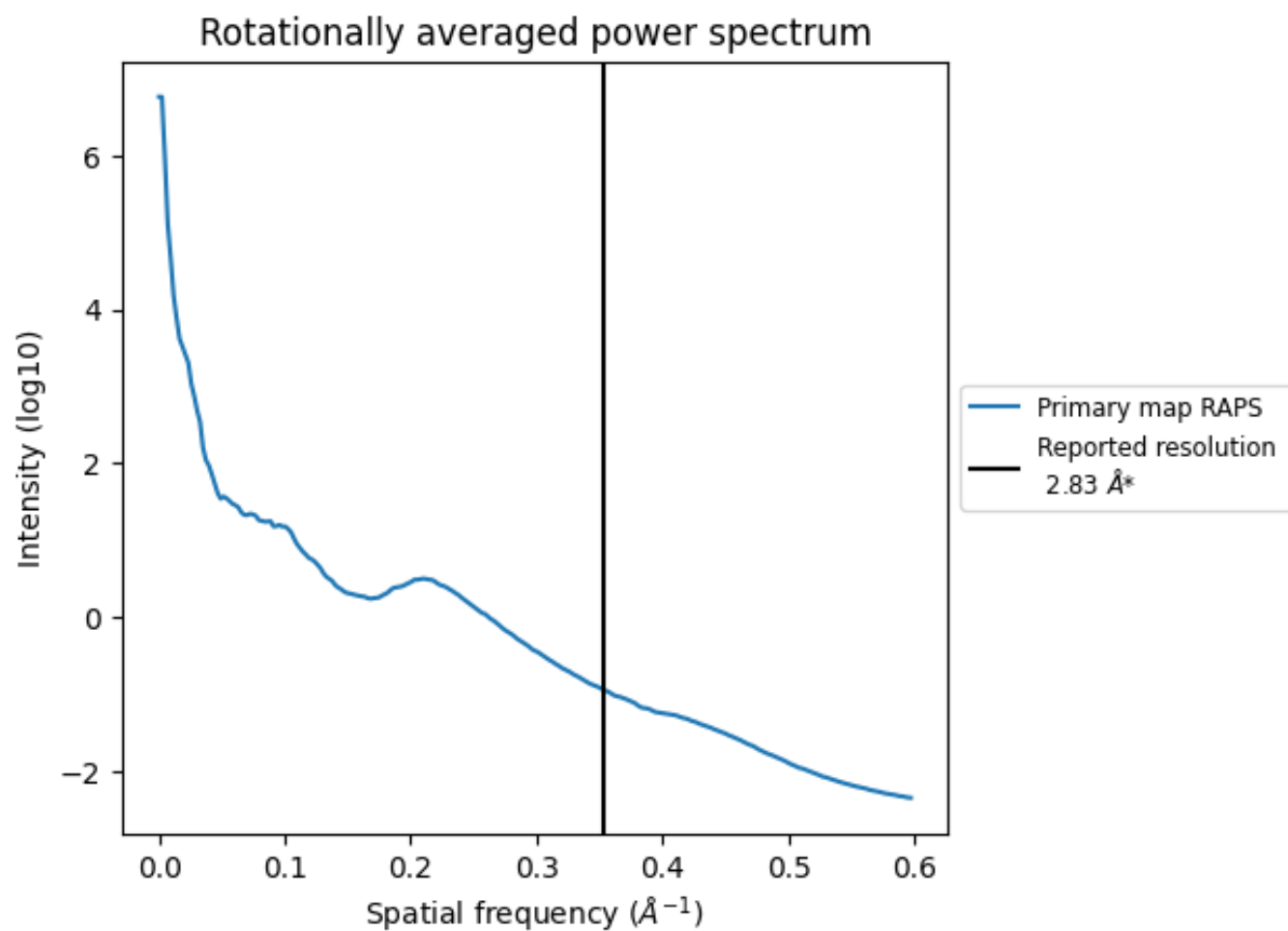
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1083 nm³; this corresponds to an approximate mass of 978 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 0.353 Å⁻¹

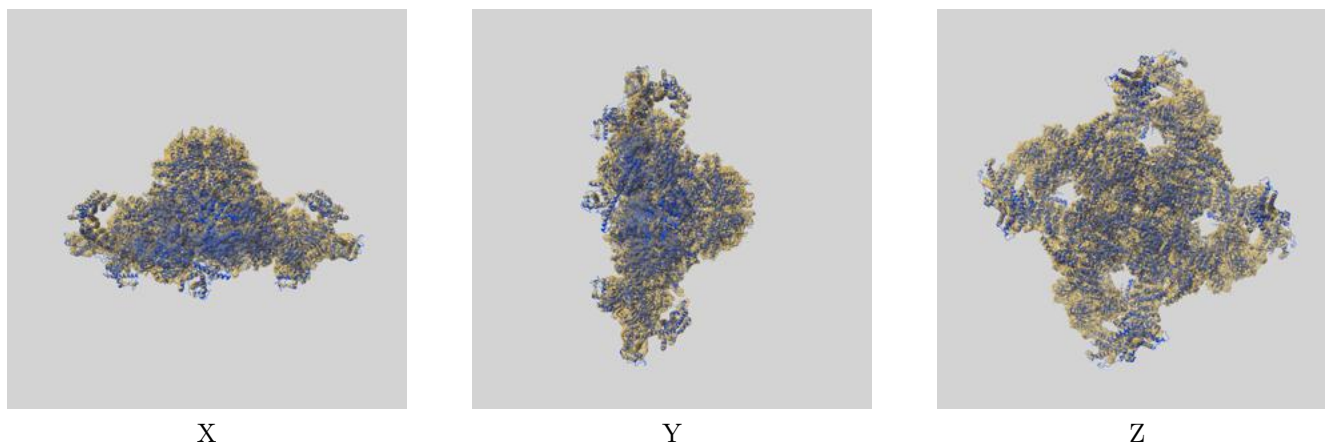
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

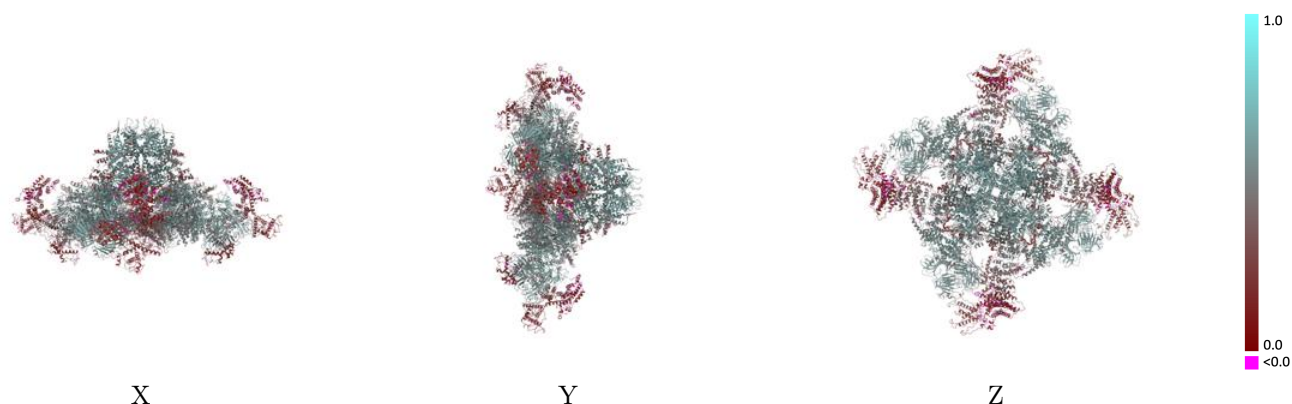
This section contains information regarding the fit between EMDB map EMD-26415 and PDB model 7UA5. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



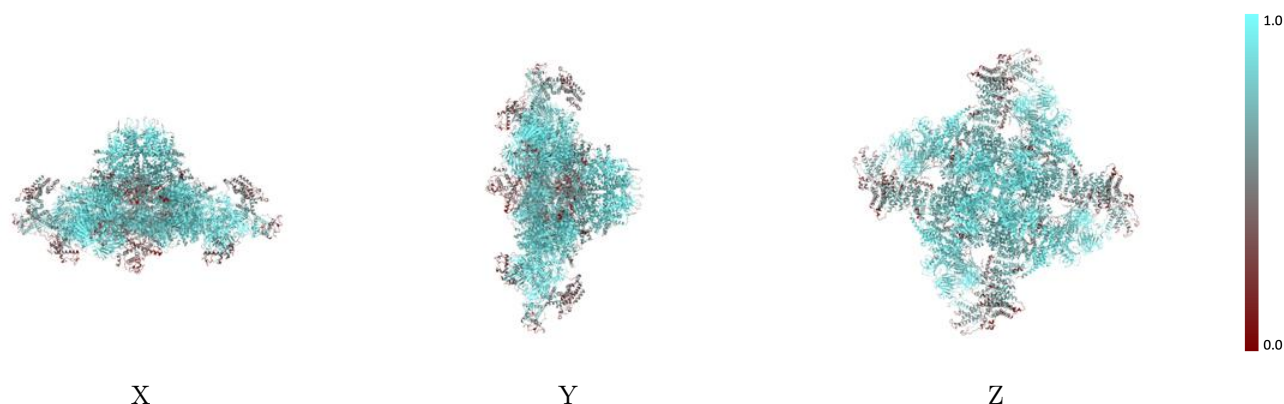
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



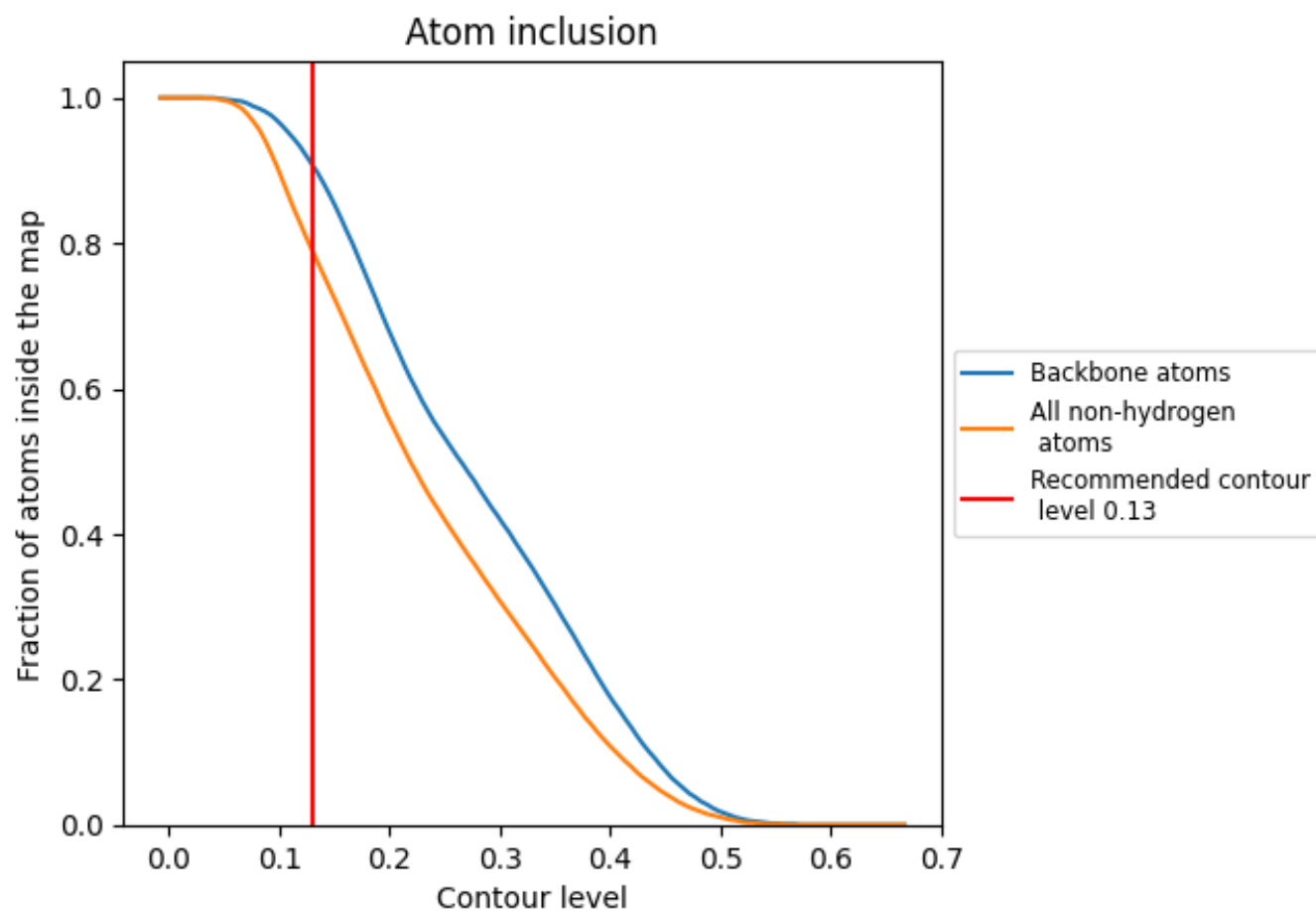
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.13).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 79% 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 (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7910	0.4480
A	0.7880	0.4490
B	0.7880	0.4480
C	0.7880	0.4470
D	0.7850	0.4380
E	0.9220	0.5670
F	0.9260	0.5600
G	0.9220	0.5650
H	0.9230	0.5640

1.0

0.0

<0.0