



Full wwPDB EM Validation Report ⓘ

Nov 7, 2022 – 10:12 AM JST

PDB ID : 5GKZ
EMDB ID : EMD-9519
Title : Structure of RyR1 in a closed state (C3 conformer)
Authors : Bai, X.C.; Yan, Z.; Wu, J.P.; Yan, N.
Deposited on : 2016-07-07
Resolution : 4.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

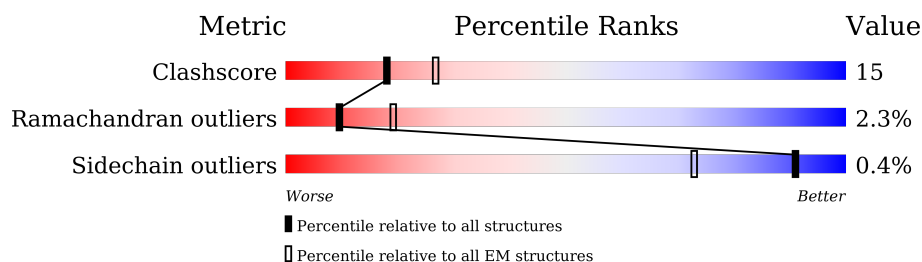
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	5037	<div> <div>14%</div> <div>49%</div> <div>22%</div> <div>•</div> <div>27%</div> </div>
1	C	5037	<div> <div>14%</div> <div>48%</div> <div>23%</div> <div>•</div> <div>27%</div> </div>
1	E	5037	<div> <div>14%</div> <div>48%</div> <div>23%</div> <div>•</div> <div>27%</div> </div>
1	G	5037	<div> <div>14%</div> <div>49%</div> <div>22%</div> <div>•</div> <div>27%</div> </div>
2	B	108	<div> <div>19%</div> <div>67%</div> <div>32%</div> <div>•</div> </div>
2	D	108	<div> <div>19%</div> <div>65%</div> <div>34%</div> <div>•</div> </div>
2	F	108	<div> <div>19%</div> <div>68%</div> <div>31%</div> <div>•</div> </div>
2	H	108	<div> <div>19%</div> <div>69%</div> <div>30%</div> <div>•</div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 111000 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 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3660	Total	C	N	O	S	0	0
			26917	17107	4682	4971	157		
1	C	3660	Total	C	N	O	S	0	0
			26917	17107	4682	4971	157		
1	E	3660	Total	C	N	O	S	0	0
			26917	17107	4682	4971	157		
1	G	3660	Total	C	N	O	S	0	0
			26917	17107	4682	4971	157		

- Molecule 2 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	107	Total	C	N	O	S	0	0
			832	527	146	155	4		
2	D	107	Total	C	N	O	S	0	0
			832	527	146	155	4		
2	F	107	Total	C	N	O	S	0	0
			832	527	146	155	4		
2	H	107	Total	C	N	O	S	0	0
			832	527	146	155	4		

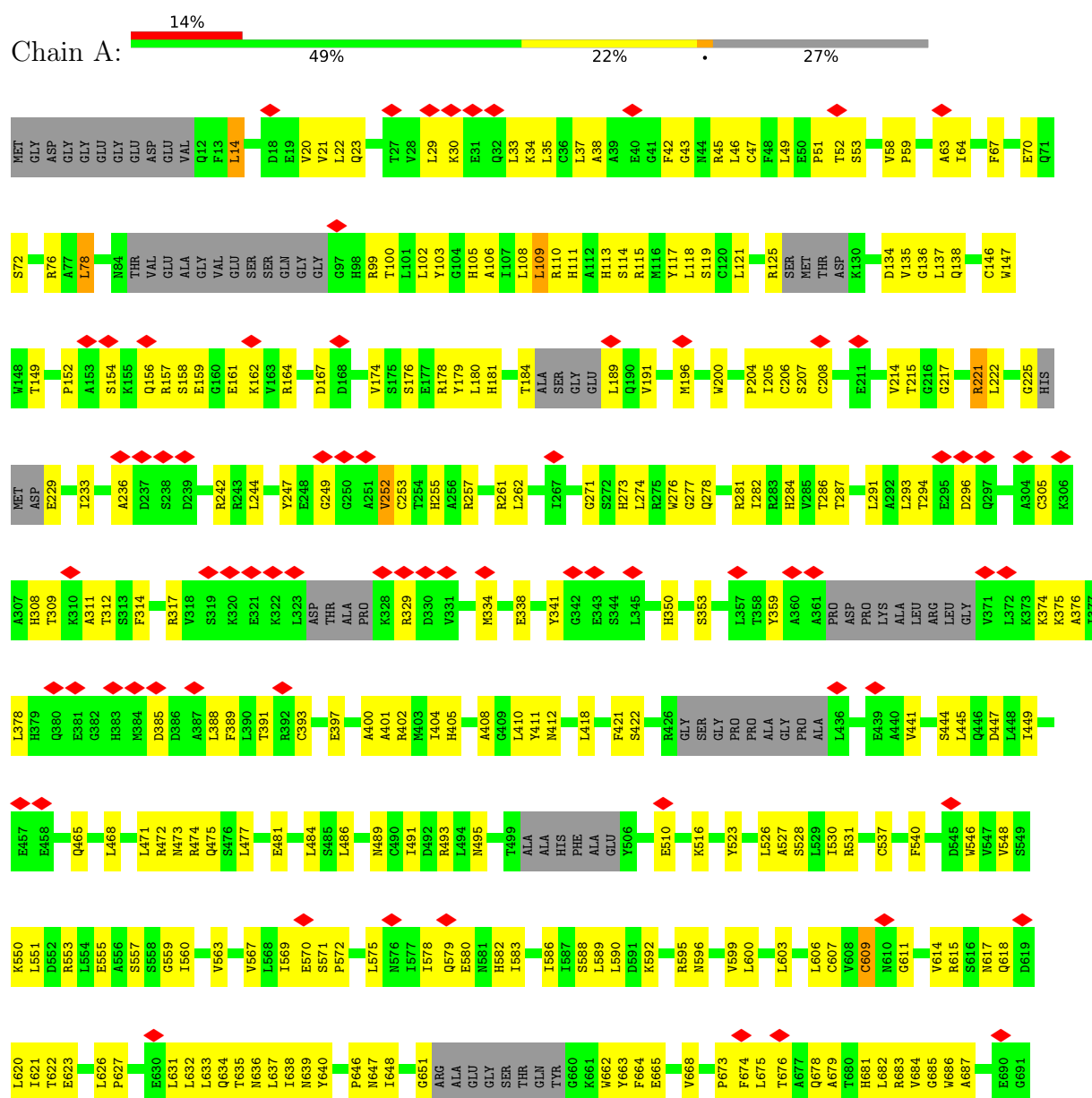
- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Zn	0
			1	1	
3	C	1	Total	Zn	0
			1	1	
3	E	1	Total	Zn	0
			1	1	
3	G	1	Total	Zn	0
			1	1	

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 1

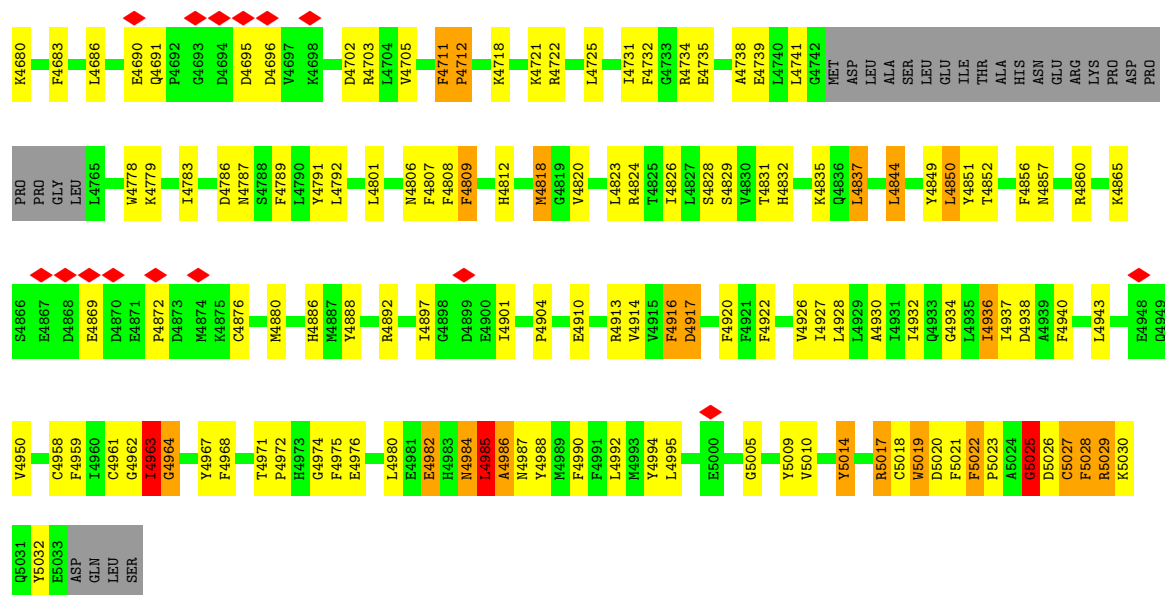




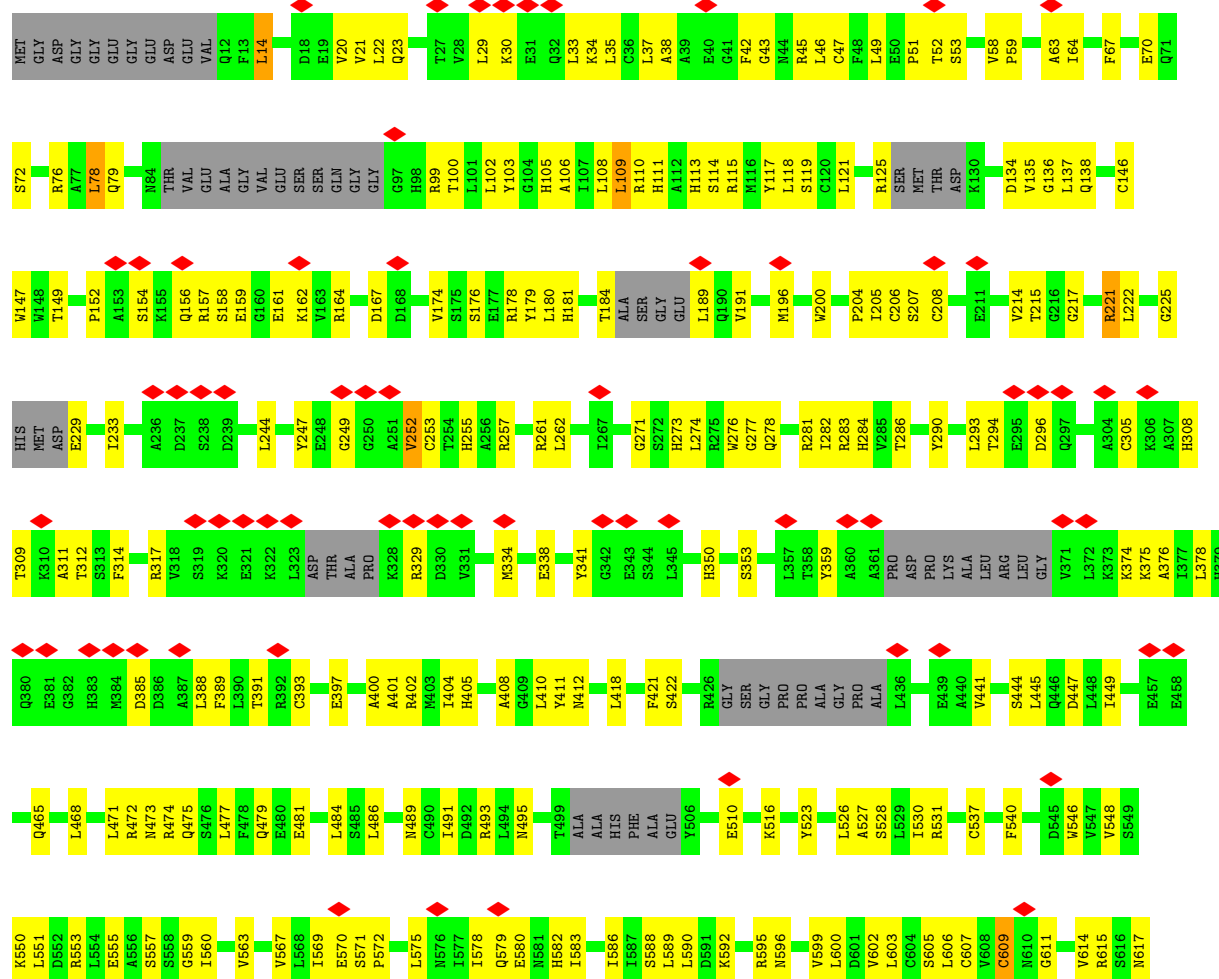


TYR	ARG	GLY	LEU	PRO	GLY	ARG	GLU	GLU	ASP	ASP	ASP	PRO	GLU	LYS	ILE	VAL	ARG	ARG	VAL	GLN	GLU	GLU	VAL	SER	ALA	VAL	LEU	TYR	HIS	LEU	GLU	GLN	THR	GLU	LEU	ALA	HIS	PRO	TYR	LYS	SER	LYS	LYS	ALA	VAL	TRP	HIS	LYS	LYS	VAL													
K3495	K3496	K3497	S3504	VAL	GLN	THR	SER	LEU	ILE	VAL	T3513	K3516	M3517	L3518	P3519	M3524	C3525	A3526	P3527	THR	ASP	GLN	ASP	LEU	ILE	ALA	K3537	T3538	A3541	L3542	K3543	D3544	THR	ASP	GLU	V3549	R3550	Q3554	H3558	P3567	S3568	L3569	R3570	W3571	Q3572	MET	ALA	LEU															
R3403	D3404	L3405	Y3406	P3410	L3411	L3412	I3413	N3418	N3419	R3420	A3421	K3422	W3423	L3424	THR	GLU	P3427	N3428	A3431	E3432	F3435	R3437	V3438	E3455	GLN	N3457	V3460	N3465	S3468	F3469	L3470	THR	ALA	ASP	SER	SER	SER	LYS	N3478	G3482	S3486	S3489	D3490	Q3491	GLU	ARG	T3494																
C3304	N3313	SER	LEU	LEU	G3317	N3318	I3319	L3320	R3321	D3330	E3331	A3339	VAL	PHE	ALA	GLN	PRO	ILE	V3346	P3351	L3354	H3355	S3356	H3357	F3358	I3359	P3360	T3361	I3362	G3363	ARG	LEU	ARG	K3367	K3371	Q3378	E3386	G3390	E3391	L3392	L3393	V3394	R3395	D3396	E3397	PHE	SER	VAL	LEU	C3402													
PRO	ASP	ILE	PRO	VAL	LEU	ASP	ARG	LEU	MET	ALA	ASP	ILE	ALA	ALA	THR	TVR	THR	GLU	MET	HIS	ILE	ILE	ILE	T3273	L3274	P3275	M3276	L3277	C3278	S3279	Y3280	L3281	P3282	R3283	R3287	G3288	P3289	E3290	ALA	PRO	PRO	Y3294	A3295	L3296	P3297	A3298	P3301	P3302	P3303														
S3171	I3172	L3175	T3178	LYS	ASN	THR	TYR	V3183	K3185	L3186	R3187	P3188	A3189	L3190	A3195	R3196	A3199	A3200	MET	PRO	VAL	A3204	F3205	P3208	E3212	Y3213	N3214	S3217	VAL	TYR	THR	LYS	SER	PRO	ARG	GLU	ARG	GLY	ILE	LEU	GLY	LEU	PRO	ASN	SER	VAL	GLU	MET	CYS														
I3087	A3090	GLY	LEU	ARG	SER	F3095	F3096	E3097	S3098	E3104	K3105	M3106	V3107	E3108	R3111	L3112	G3113	K3114	V3115	S3116	GLN	ALA	ARG	THR	GLN	VAL	LYS	GLY	VAL	GLY	ASN	LEU	THR	TYR	T3132	L3137	P3138	Q3151	F3152	GLY	ASP	VAL	VAL	L3158	D3159	V3163	S3164	C3165	Y3166	R3167													
GLU	ILE	PHE	PHE	ALA	LYS	ILE	LEU	PRO	LEU	ILE	ASN	GLN	TYR	PHE	ASN	HIS	CYS	Y3016	F3017	L3018	S3019	T3020	P3021	A3022	K3023	V3024	S3027	S3032	N3033	K3036	T3039	THR	SER	LEU	F3043	P3062	ALA	VAL	VAL	ASN	CYS	L3068	H3069	I3070	L3071	S3074	P3085	E3086															
G2934	Y2935	A2936	V2937	T2938	R2939	G2940	LEU	LYS	ASP	MET	GLU	LEU	THR	SER	SER	ILE	GLU	ARG	PHE	ALA	PHE	GLY	LEU	GLN	LEU	ARG	TRP	MET	ASP	ILE	SER	GLN	THR	L2904	L2905	V2906	P2907	Y2908	D2909	T2910	L2911	T2912	A2913	K2914	E2915	K2916	A2917	D2918	R2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	M2932	N2933
M2874	A2875	E2876	Q2877	L2878	A2879	E2880	N2881	Y2882	H2883	M2884	T2885	W2886	G2887	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	A2896	K2897	G2898	G2899	G2900	T2901	H2902	P2903	L2904	L2905	V2906	P2907	Y2908	D2909	T2910	L2911	T2912	A2913	K2914	E2915	K2916	A2917	D2918	R2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	M2932	N2933				
K2814	A2815	M2816	I2817	A2818	W2819	E2820	W2821	T2822	L2823	E2824	K2825	A2826	R2827	E2828	G2829	E2830	GLU	ARG	THR	GLU	LYS	LYS	THR	ARG	LYS	ILE	GLN	THR	ALA	GLN	THR	Y2849	D2850	P2851	R2852	E2853	G2854	N2856	P2857	Q2858	P2859	D2860	D2861	L2862	S2863	G2864	V2865	D2866	T2867	S2868	R2869	E2870	Q2872	A2873									
F2754	I2755	N2756	K2757	F2758	A2759	E2760	Y2761	T2762	H2763	E2764	K2765	W2766	A2767	F2768	D2769	K2770	I2771	Q2772	N2773	N2774	W2775	S2776	Y2777	G2778	E2779	N2780	V2781	D2782	E2783	E2784	L2785	K2786	T2787	H2788	P2789	M2790	R2792	P2793	P2794	K2795	T2796	F2797	S2798	E2799	K2800	D2801	K2802	E2803	I2804	Y2805	R2806	W2807	P2808	I2809	K2810	E2811	S2812	L2813					
I2682	L2686	ALA	HIS	LYS	LYS	Y2691	P2701	12706	A2707	G2708	A2709	L2710	P2711	P2712	ASP	TYR	VAL	ASP	ALA	SER	TVR	SER	SER	LYS	LYS	GLU	ALA	ALA	THR	VAL	ASP	GLU	GLY	N2734	F2735	D2736	P2737	R2738	P2739	E2741	T2742	L2743	N2744	V2745	I2746	I2747	P2748	E2749	K2750	L2751	D2752	S2753											





• Molecule 1: Ryanodine receptor 1

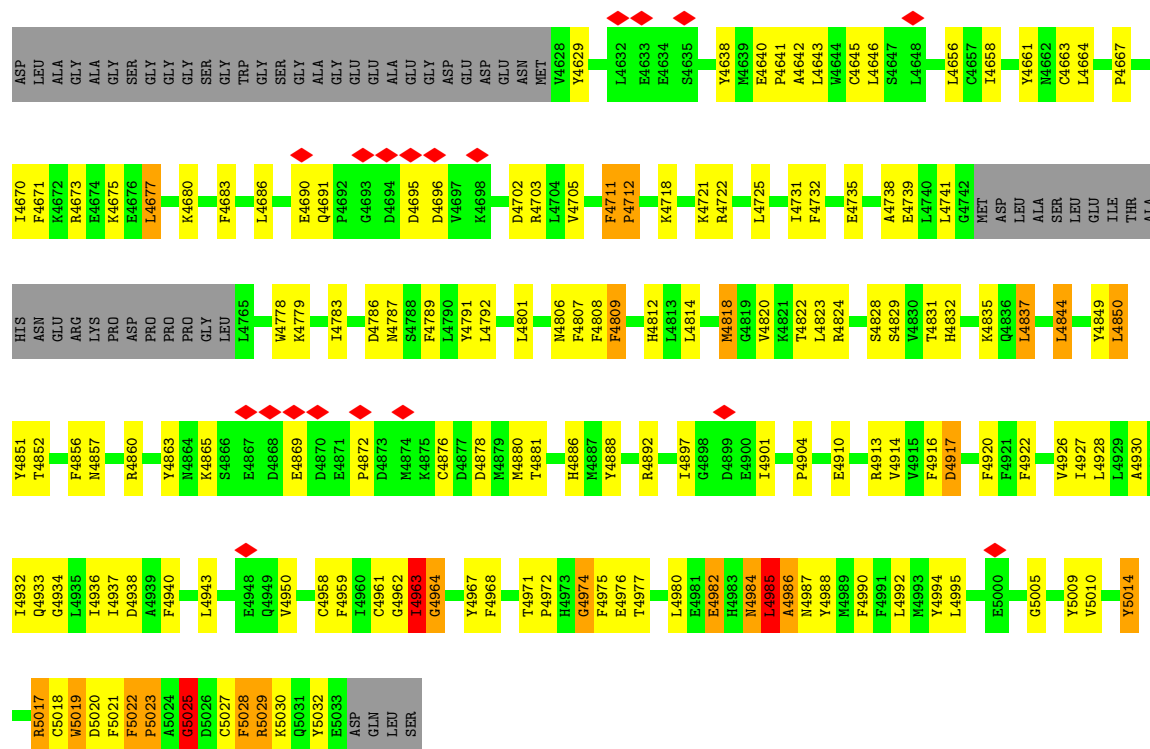




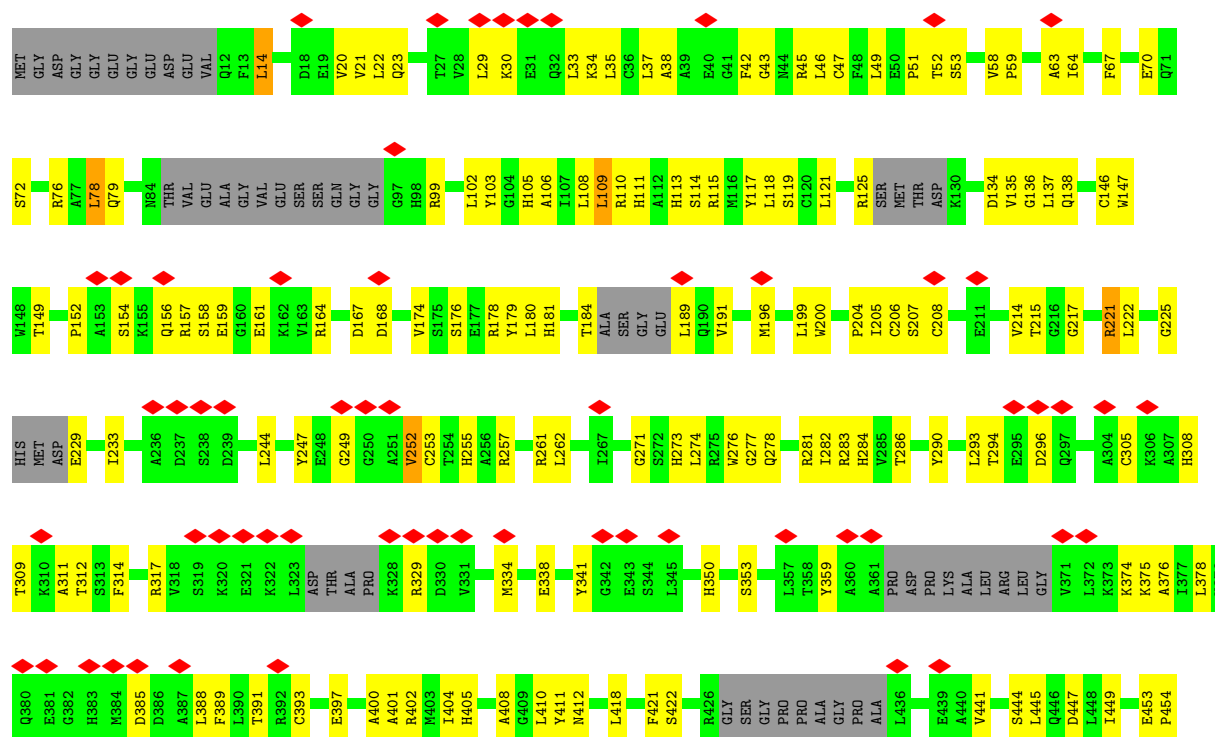


THR	ALA	ALA	THR	PHE	GLY	SER	THR	T2544	A2547	L2550	N2551	Y2553	L2554	L2561	L2562	THR	LYS	CYS	ALA	L2567	L2583	H2584	T2585	V2586	R2591	D2601	A2609	LEU	CYS	ARG	TYR	ARG	LEU	SER	R2591	D2601	A2609	LEU	CYS	TYR	ILE	R2615	P2616	P2631	I2634	GLU	PHE	ALA	R2638	H2639	P2640	L2657	P2658	T2659	G2660	TRP			
ALA	ASN	PHE	GLY	VAL	T2667	F2679	I2682	L2686	ALA	L2686	L2686	L2686	L2686	Y2691	P2701	I2706	A2707	G2708	A2709	L2710	P2711	P2712	ASP	TYR	TRP	VAL	ASP	ALA	SER	THR	SER	SER	LYS	ALA	GLU	VAL	THR	GLY	N2734	F2735	D2736	P2737	R2738	P2739	V2740	E2741	T2742	L2743	N2744	V2745									
I2746	I2747	P2748	E2749	K2750	L2751	D2752	S2753	T2754	N2755	N2756	K2757	A2758	A2759	E2760	Y2761	T2762	H2763	E2764	K2765	A2766	A2767	F2768	D2769	I2770	I2771	Q2772	N2773	N2774	N2775	S2776	Y2777	G2778	E2779	N2780	V2781	D2782	E2783	E2784	L2785	K2786	T2787	H2788	P2789	M2790	L2791	R2792	P2793	Y2794	K2795	T2796	F2797	S2798	E2799	K2800	D2801	E2802	E2803	T2804	Y2805
R2806	H2807	P2808	L2809	K2810	E2811	S2812	L2813	K2814	A2815	M2816	L2817	A2818	E2819	E2820	H2821	T2822	L2823	E2824	K2825	A2826	R2827	E2828	G2829	E2830	GLU	GLU	THR	GLU	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	Y2849	D2850	P2851	R2852	E2853	G2854	Y2855	N2856	P2857	Q2858	P2859	P2860	D2861	L2862	G2864	V2865			
L2866	L2867	S2868	R2869	E2870	L2871	Q2872	A2873	M2874	A2875	E2876	Q2877	L2878	A2879	E2880	N2881	Y2882	H2883	N2884	T2885	T2886	G2887	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	A2896	K2897	G2898	G2899	G2900	T2901	H2902	L2903	L2904	L2905	V2906	P2907	Y2908	D2909	T2910	L2911	T2912	A2913	K2914	E2915	K2916	A2917	R2918	D2919	R2920	E2921	K2922	A2923	Q2924	E2925
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VAL	GLU	LYS	SER	PRO	HIS	GLU	GLN	ILE	LYS	PHE	PHE	ALA	LYS	LEU	PRO	LEU	ILE	ASN	GLN	TYR	PHE	THR	ASN	HIS	LEU	Y3016	F3017	L3018	S3019	T3020	A3022	K3023	V3024	S3027	S3032	N3033	K3036	I3039	THR	SER	LEU	F3043	P3062	ALA	VAL	VAL	ASN	CYS	L3068										
H3069	I3070	L3071	S3074	P3085	E3086	I3087	A3090	GLY	LEU	ARG	SER	F3095	F3096	E3097	S3098	E3104	K3105	L3106	V3107	E3108	R3111	L3112	G3113	K3114	V3115	S3116	GLN	ALA	ARG	THR	GLN	VAL	LYS	GLY	VAL	GLN	ASN	THR	TYR	T3132	L3137	P3138	Q3151	F3152	GLY	ASP	ASP	VAL	ILE	L3158									
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PRO	ASN	SER	VAL	GLU	MET	CYS	PRO	ASP	ILE	VAL	LEU	ASP	ARG	LEU	MET	ALA	GLU	SER	ALA	ALA	TYR	THR	GLU	MET	PRO	HIS	VAL	ILE	GLU	ILE	T3273	L3274	P3275	M3276	L3277	C3278	S3279	Y3280	L3281	P3282	R3283	R3287	G3288	P3289	E3290	ALA	PRO	PRO	P3294										
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R3395	D3396	E3397	PHE	SER	VAL	LEU	C3402	R3403	D3404	L3405	Y3406	P3410	L3411	L3412	I3413	N3418	N3419	R3420	A3421	V3423	L3424	THR	GLU	P3427	N3428	A3431	E3432	F3435	M3437	V3438	E3455	GLN	N3457	V3460	N3465	S3468	F3469	L3470	THR	ALA	ASP	SER	LYS	SER	LYS	M3478	G3482												
S3486	S3489	D3490	D3491	GLU	ARG	THR	L3494	K3495	K3496	K3497	S3504	VAL	GLN	THR	SER	LEU	ILE	ALA	T3513	K3516	M3517	L3518	P3519	K3524	C3525	A3526	P3527	THR	ASP	GLN	ASP	LEU	ILE	MET	LEU	ALA	K3537	T3538	A3541	L3542	K3543	D3544	THR	ASP	GLU	GLU	V3549	P3550	Q3554	H3558	P3567								





• Molecule 1: Ryanodine receptor 1









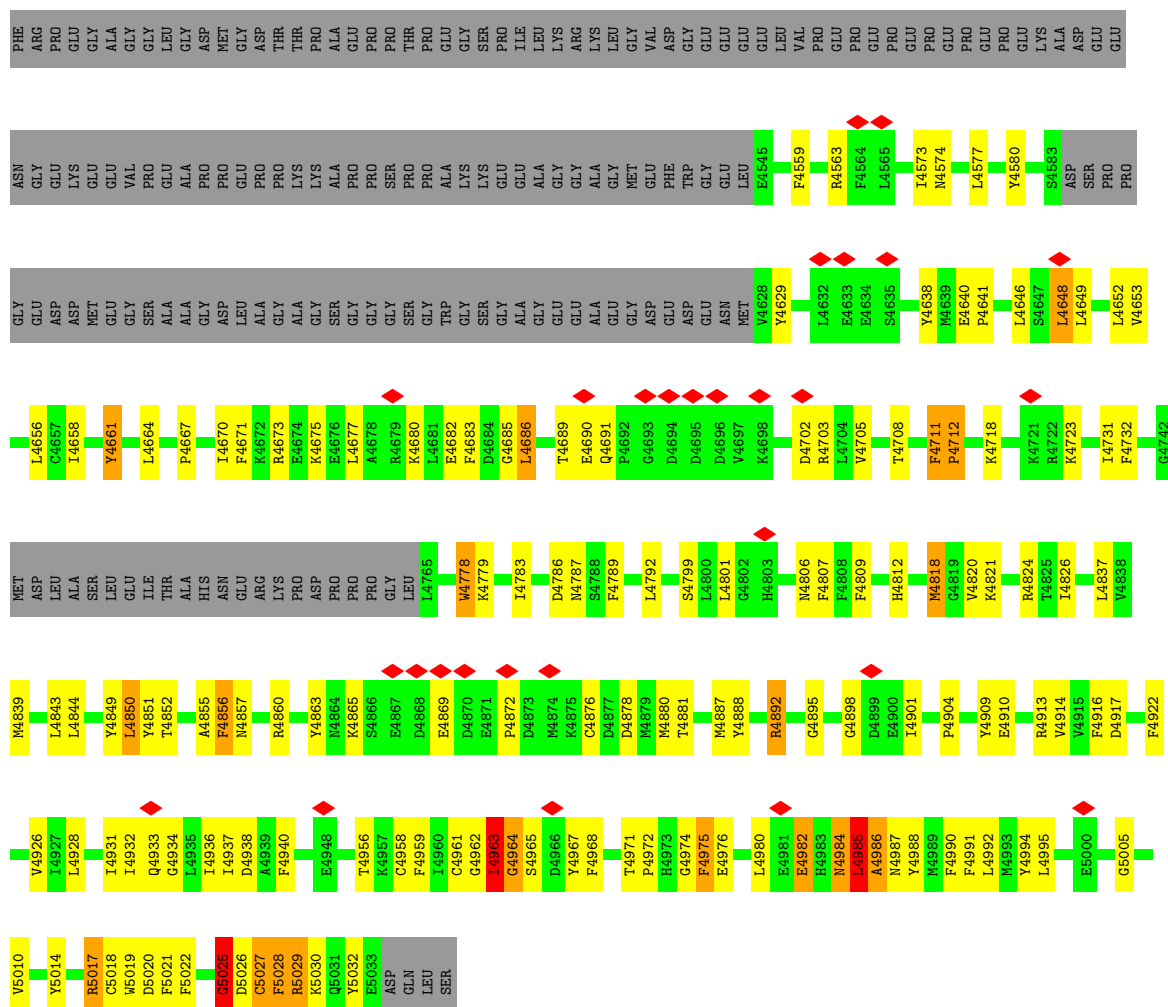




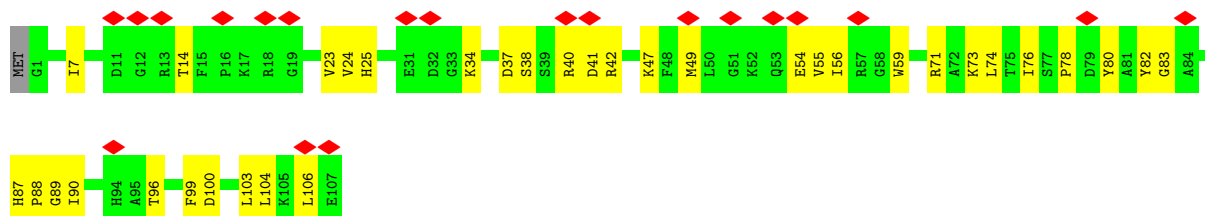


P3275	M3276	L3277	C3278	S3279	Y3280	L3281	P3282	R3283	W3284	R3287	G3288	P3289	E3290	ALA	PRO	PRO	P3294	A3295	L3296	P3297	P3301	P3302	P3303	C3304	N3313	SER	LEU	LEU	G3317	N3318	L3319	L3320	R3321	D3330	E3331	R3337	L3338	A3339	VAL	PHE	ALA	GLN	PRO	ILE	W3346	P3351	E3352	L3353	L3354	H3355	S3356	H3357	F3358							
N3214	S3217	VAL	TYR	THR	THR	LYS	PRO	SER	ARG	ARG	GLU	ARG	ALA	ILE	LEU	GLY	LEU	ASP	ASP	VAL	ILE	SER	VAL	GLU	CYS	PRO	ASP	ILE	LEU	ASP	ARG	GLY	THR	TYR	ALA	GLU	SER	GLY	ALA	GLY	VAL	MET	ASP	GLU	ILE	T3273	L3274	GLU	VAL	GLY	GLN	GLY	GLN							
ASN	LEU	THR	TYR	T3132	L3137	P3138	V3139	L3140	H3146	P3062	ALA	VAL	VAL	ASN	CYS	L3068	G3074	A3077	P3085	A3090	GLY	LEU	ARG	S3097	S3098	A3099	D3102	I3103	E3104	K3105	M3106	N3109	L3110	L3111	L3112	G3113	K3114	V3115	S3116	GLN	ALA	ARG	THR	GLN	VAL	LYS	GLY	VAL	GLY	GLN										
E3037	M3038	I3039	THR	SER	LEU	F3043	R3053	P3062	ALA	VAL	VAL	ASN	CYS	L3068	G3074	A3077	P3085	A3090	GLY	LEU	ARG	S3097	S3098	A3099	D3102	I3103	E3104	K3105	M3106	N3109	L3110	L3111	L3112	G3113	K3114	V3115	S3116	GLN	ALA	ARG	THR	GLN	VAL	LYS	GLY	VAL	GLY	GLN												
GLN	GLU	PHE	ILE	ALA	HIS	LEU	GLU	ALA	VAL	VAL	SER	GLY	ARG	VAL	GLY	GLY	VAL	PRO	HIS	GLN	GLN	ILE	LYS	PHE	PHE	ALA	ASN	THR	ASN	THR	ASN	THR	ASN	THR	ASN	THR	ASN	THR	ASN	THR	ASN	THR	ASN	THR	ASN	THR	ASN	THR												
L2911	T2912	A2913	K2914	E2915	K2916	A2917	R2918	D2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	N2932	N2933	Q2934	Y2935	A2936	V2937	T2938	R2939	G2940	LEU	LYS	ASP	THR	SER	ILE	GLU	LEU	ASP	THR	SER	ILE	GLU	LEU	ASP	THR	SER	ILE													
P2851	R2852	E2853	G2854	Y2855	N2856	P2857	Q2858	P2859	P2860	D2861	L2862	S2863	G2864	V2865	T2866	L2867	S2868	R2869	E2870	L2871	Q2872	A2873	M2874	A2875	E2876	Q2877	L2878	A2879	E2880	N2881	Y2882	H2883	N2884	T2885	W2886	G2887	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	A2896	K2897	G2898	G2899	G2900	T2901	H2902	P2903	L2904	L2905	V2906	P2907	Y2908	D2909	T2910	
L2791	R2792	P2793	Y2794	K2795	T2796	F2797	S2798	E2799	K2800	D2801	E2802	K2803	L2804	Y2805	R2806	W2807	P2808	L2809	K2810	E2811	S2812	L2813	K2814	A2815	M2816	L2817	A2818	W2819	E2820	W2821	T2822	L2823	E2824	K2825	A2826	R2827	E2828	G2829	E2830	GLU	GLU	ARG	THR	THR	GLY	LYS	LYS	THR	ARG	LYS	THR	ILE	SER	GLN	THR	ALA	GLN	THR	Y2849	D2850
ALA	GLU	GLY	N2734	F2735	D2736	P2737	R2738	P2739	V2740	E2741	L2743	N2744	V2745	I2747	P2748	E2749	K2750	L2751	H2752	S2753	F2754	I2755	N2756	K2757	F2758	A2759	E2760	Y2761	T2762	H2763	E2764	K2765	W2766	A2767	F2768	D2769	K2770	I2771	Q2772	N2773	N2774	W2775	S2776	Y2777	G2778	E2779	N2780	V2781	D2782	E2783	E2784	L2785	K2786	T2787	H2788	P2789	M2790			
W2634	GLU	PHE	ALA	K2638	W2639	P2640	L2657	P2658	T2659	G2660	TRP	ALA	ASN	PHE	GLY	VAL	T2667	F2679	I2682	L2686	ALA	HIS	LYS	Y2691	P2701	C2704	A2705	I2706	A2707	G2708	A2709	L2710	P2711	P2712	ASP	TYR	VAL	ASP	ALA	SER	TYR	SER	SER	LYS	LYS	GLU	LYS	LYS	THR	VAL	ASP									
GLU	N2514	L2522	ASP	V2525	G2526	F2527	A2533	L2537	THR	ALA	ALA	THR	PHE	GLY	SER	THR	T2544	A2547	L2550	N2551	R2552	L2554	L2561	I2562	THR	LYS	CYS	ALA	P2567	L2583	H2584	T2585	V2586	TYR	ARG	LEU	SER	R2591	D2601	A2609	LEU	CYS	ARG	TYR	ILE	R2615	P2616	P2631												
LEU	ILE	GLN	ALA	GLY	LYS	GLY	E2449	A2450	L2451	R2452	I2453	R2454	R2458	S2459	L2460	VAL	PRO	L2463	D2464	D2465	L2466	V2467	S2471	L2472	P2473	L2474	Q2475	I2476	THR	THR	GLY	LYS	ASP	GLY	PRO	HIS	PHE	GLY	GLU	PRO	ALA	ALA	SER	F2494	D2497	H2498	K2499	F2505	V2509	Y2510	GLY	ILE								
ARG	GLY	GLN	GLY	SER	SER	E2375	A2379	I2380	E2381	I2384	R2385	L2386	SER	GLU	ASP	PRO	ALA	ALA	ARG	GLY	PRO	GLY	VAL	VAL	ARG	ASP	ARG	ARG	ARG	ARG	ASN	ASN	VAL	HIS	VAL	SER	LEU	E2419	M2423	D2431	R2435	C2436	A2437	PRO	GLU	MET	HIS													

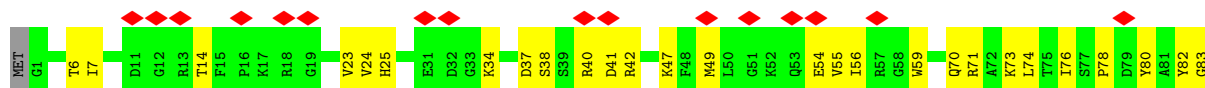


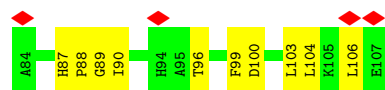


• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

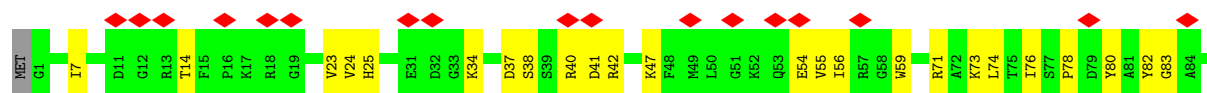


• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

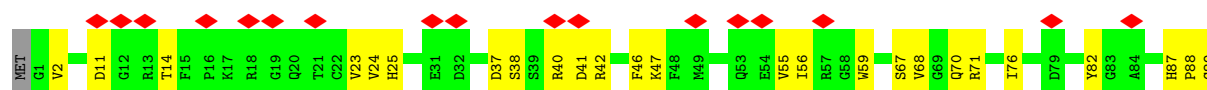




- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A



- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	64000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.428	Depositor
Minimum map value	-0.192	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.085	Depositor
Map size (\AA)	482.40002, 482.40002, 482.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.34, 1.34, 1.34	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

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	0.98	87/27385 (0.3%)	0.88	108/37104 (0.3%)
1	C	0.98	89/27385 (0.3%)	0.88	114/37104 (0.3%)
1	E	0.98	87/27385 (0.3%)	0.88	108/37104 (0.3%)
1	G	0.99	94/27385 (0.3%)	0.88	112/37104 (0.3%)
2	B	0.63	0/851	0.63	0/1146
2	D	0.63	0/851	0.63	0/1146
2	F	0.63	0/851	0.63	0/1146
2	H	0.63	0/851	0.62	0/1146
All	All	0.98	357/112944 (0.3%)	0.88	442/153000 (0.3%)

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	20
1	C	0	20
1	E	0	20
1	G	0	20
All	All	0	80

All (357) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	4988	TYR	CG-CD2	-20.55	1.12	1.39
1	E	4988	TYR	CG-CD2	-19.42	1.14	1.39
1	C	4988	TYR	CG-CD2	-19.41	1.14	1.39
1	A	4988	TYR	CG-CD2	-19.37	1.14	1.39
1	G	4988	TYR	CE1-CZ	-17.94	1.15	1.38
1	E	4988	TYR	CE1-CZ	-14.63	1.19	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	4988	TYR	CE1-CZ	-14.61	1.19	1.38
1	A	4988	TYR	CE1-CZ	-14.58	1.19	1.38
1	G	4988	TYR	CG-CD1	-13.87	1.21	1.39
1	G	4988	TYR	CE2-CZ	-12.60	1.22	1.38
1	C	4988	TYR	CG-CD1	-11.96	1.23	1.39
1	A	4988	TYR	CG-CD1	-11.95	1.23	1.39
1	E	4988	TYR	CG-CD1	-11.94	1.23	1.39
1	A	5021	PHE	CG-CD2	-11.06	1.22	1.38
1	C	5021	PHE	CG-CD2	-10.94	1.22	1.38
1	E	5021	PHE	CG-CD2	-10.91	1.22	1.38
1	G	5021	PHE	CG-CD2	-10.77	1.22	1.38
1	A	4988	TYR	CE2-CZ	-10.50	1.25	1.38
1	C	4988	TYR	CE2-CZ	-10.47	1.25	1.38
1	E	4988	TYR	CE2-CZ	-10.39	1.25	1.38
1	C	3922	TYR	CG-CD2	-10.29	1.25	1.39
1	A	3922	TYR	CG-CD2	-10.22	1.25	1.39
1	E	3922	TYR	CG-CD2	-10.22	1.25	1.39
1	G	4851	TYR	CE1-CZ	-10.01	1.25	1.38
1	C	3922	TYR	CE2-CZ	-9.93	1.25	1.38
1	A	3922	TYR	CE2-CZ	-9.90	1.25	1.38
1	A	5014	TYR	CG-CD1	-9.86	1.26	1.39
1	E	3922	TYR	CE2-CZ	-9.86	1.25	1.38
1	G	3922	TYR	CG-CD2	-9.78	1.26	1.39
1	G	4234	PHE	CG-CD1	-9.67	1.24	1.38
1	G	3922	TYR	CE2-CZ	-9.64	1.26	1.38
1	A	5022	PHE	CG-CD1	-9.62	1.24	1.38
1	E	5022	PHE	CG-CD1	-9.62	1.24	1.38
1	C	5022	PHE	CG-CD1	-9.56	1.24	1.38
1	C	5014	TYR	CG-CD1	-9.50	1.26	1.39
1	E	3886	ARG	CZ-NH1	9.48	1.45	1.33
1	A	3886	ARG	CZ-NH1	9.38	1.45	1.33
1	C	3886	ARG	CZ-NH1	9.34	1.45	1.33
1	E	5014	TYR	CG-CD1	-9.29	1.27	1.39
1	G	3922	TYR	CE1-CZ	-9.11	1.26	1.38
1	G	5022	PHE	CG-CD1	-9.08	1.25	1.38
1	E	4234	PHE	CG-CD1	-8.71	1.25	1.38
1	C	4234	PHE	CG-CD1	-8.50	1.26	1.38
1	C	4234	PHE	CG-CD2	-8.49	1.26	1.38
1	A	4234	PHE	CG-CD1	-8.48	1.26	1.38
1	A	4234	PHE	CG-CD2	-8.47	1.26	1.38
1	E	4234	PHE	CG-CD2	-8.47	1.26	1.38
1	G	5014	TYR	CG-CD1	-8.39	1.28	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	3937	TYR	CG-CD1	-8.37	1.28	1.39
1	G	3922	TYR	CG-CD1	-8.25	1.28	1.39
1	E	5019	TRP	CE3-CZ3	-8.21	1.24	1.38
1	A	4177	TYR	CB-CG	-8.19	1.39	1.51
1	E	4177	TYR	CB-CG	-8.19	1.39	1.51
1	A	5019	TRP	CE3-CZ3	-8.12	1.24	1.38
1	C	4177	TYR	CB-CG	-8.08	1.39	1.51
1	A	3919	THR	CB-CG2	-8.02	1.25	1.52
1	E	3919	THR	CB-CG2	-7.99	1.25	1.52
1	C	3919	THR	CB-CG2	-7.88	1.26	1.52
1	A	4671	PHE	CG-CD1	-7.87	1.26	1.38
1	C	4671	PHE	CG-CD1	-7.86	1.26	1.38
1	C	5019	TRP	CE3-CZ3	-7.86	1.25	1.38
1	G	4671	PHE	CG-CD1	-7.75	1.27	1.38
1	G	3722	TYR	CE1-CZ	-7.73	1.28	1.38
1	E	4671	PHE	CG-CD1	-7.72	1.27	1.38
1	G	4177	TYR	CB-CG	-7.72	1.40	1.51
1	G	4234	PHE	CG-CD2	-7.67	1.27	1.38
1	A	5014	TYR	CE2-CZ	-7.65	1.28	1.38
1	G	4982	GLU	C-O	-7.58	1.08	1.23
1	E	5014	TYR	CE2-CZ	-7.55	1.28	1.38
1	C	5014	TYR	CE2-CZ	-7.55	1.28	1.38
1	G	4958	CYS	CB-SG	-7.46	1.69	1.82
1	E	4195	PHE	CG-CD2	-7.46	1.27	1.38
1	G	5019	TRP	CE3-CZ3	-7.42	1.25	1.38
1	G	3885	PHE	CG-CD2	-7.41	1.27	1.38
1	C	4559	PHE	CG-CD1	-7.40	1.27	1.38
1	A	4195	PHE	CG-CD2	-7.38	1.27	1.38
1	C	4195	PHE	CG-CD2	-7.37	1.27	1.38
1	A	4559	PHE	CG-CD1	-7.34	1.27	1.38
1	E	4559	PHE	CG-CD1	-7.34	1.27	1.38
1	A	3922	TYR	CG-CD1	-7.26	1.29	1.39
1	E	3922	TYR	CG-CD1	-7.26	1.29	1.39
1	C	3922	TYR	CG-CD1	-7.17	1.29	1.39
1	G	3968	TYR	CE1-CZ	-7.14	1.29	1.38
1	E	3968	TYR	CE2-CZ	-7.13	1.29	1.38
1	C	4174	PHE	CG-CD2	-7.12	1.28	1.38
1	A	4174	PHE	CG-CD2	-7.08	1.28	1.38
1	G	4195	PHE	CG-CD2	-7.05	1.28	1.38
1	G	4174	PHE	CG-CD2	-7.03	1.28	1.38
1	E	4174	PHE	CG-CD2	-7.03	1.28	1.38
1	C	3968	TYR	CE2-CZ	-7.00	1.29	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	3968	TYR	CE2-CZ	-6.99	1.29	1.38
1	E	4217	PHE	CG-CD1	-6.97	1.28	1.38
1	A	5019	TRP	CB-CG	-6.95	1.37	1.50
1	E	5019	TRP	CB-CG	-6.94	1.37	1.50
1	G	4032	GLU	CD-OE1	-6.93	1.18	1.25
1	G	4968	PHE	CG-CD2	-6.92	1.28	1.38
1	C	5019	TRP	CB-CG	-6.90	1.37	1.50
1	C	4180	ARG	CZ-NH2	-6.89	1.24	1.33
1	E	4180	ARG	CZ-NH2	-6.87	1.24	1.33
1	G	5014	TYR	CE2-CZ	-6.87	1.29	1.38
1	A	4968	PHE	CG-CD2	-6.83	1.28	1.38
1	A	4217	PHE	CG-CD1	-6.82	1.28	1.38
1	G	3725	TYR	CG-CD2	-6.82	1.30	1.39
1	C	4217	PHE	CG-CD1	-6.82	1.28	1.38
1	G	5019	TRP	CB-CG	-6.80	1.38	1.50
1	C	4968	PHE	CG-CD2	-6.78	1.28	1.38
1	E	4968	PHE	CG-CD2	-6.74	1.28	1.38
1	A	4180	ARG	CZ-NH2	-6.70	1.24	1.33
1	E	4958	CYS	CB-SG	-6.66	1.71	1.82
1	G	3919	THR	CB-CG2	-6.65	1.30	1.52
1	A	4180	ARG	C-O	-6.63	1.10	1.23
1	A	4963	ILE	C-O	6.62	1.35	1.23
1	E	4963	ILE	C-O	6.61	1.35	1.23
1	C	3722	TYR	CE1-CZ	-6.57	1.30	1.38
1	C	4778	TRP	CE3-CZ3	-6.56	1.27	1.38
1	E	4778	TRP	CE3-CZ3	-6.56	1.27	1.38
1	E	5032	TYR	CE1-CZ	-6.55	1.30	1.38
1	G	4851	TYR	CG-CD2	-6.55	1.30	1.39
1	G	4559	PHE	CG-CD1	-6.54	1.28	1.38
1	A	3968	TYR	CG-CD1	-6.51	1.30	1.39
1	C	3968	TYR	CG-CD1	-6.51	1.30	1.39
1	C	3929	SER	CA-CB	-6.51	1.43	1.52
1	A	3722	TYR	CE1-CZ	-6.51	1.30	1.38
1	A	5032	TYR	CE1-CZ	-6.51	1.30	1.38
1	E	3722	TYR	CE1-CZ	-6.50	1.30	1.38
1	A	3929	SER	CA-CB	-6.50	1.43	1.52
1	C	4963	ILE	C-O	6.50	1.35	1.23
1	C	4974	GLY	CA-C	-6.48	1.41	1.51
1	C	4180	ARG	C-O	-6.48	1.11	1.23
1	A	4778	TRP	CE3-CZ3	-6.46	1.27	1.38
1	E	3929	SER	CA-CB	-6.46	1.43	1.52
1	E	3968	TYR	CG-CD1	-6.45	1.30	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	4958	CYS	CB-SG	-6.45	1.71	1.82
1	E	4180	ARG	C-O	-6.44	1.11	1.23
1	A	3885	PHE	CG-CD2	-6.42	1.29	1.38
1	A	4982	GLU	C-O	-6.42	1.11	1.23
1	C	3885	PHE	CG-CD2	-6.42	1.29	1.38
1	E	4974	GLY	CA-C	-6.39	1.41	1.51
1	C	5032	TYR	CE1-CZ	-6.38	1.30	1.38
1	G	3929	SER	CA-CB	-6.38	1.43	1.52
1	A	4958	CYS	CB-SG	-6.33	1.71	1.82
1	E	3885	PHE	CG-CD2	-6.29	1.29	1.38
1	C	4982	GLU	C-O	-6.27	1.11	1.23
1	A	4974	GLY	CA-C	-6.27	1.41	1.51
1	G	4963	ILE	C-O	6.27	1.35	1.23
1	G	3935	TRP	CG-CD1	-6.24	1.28	1.36
1	E	4982	GLU	C-O	-6.23	1.11	1.23
1	A	3899	PHE	CG-CD2	-6.22	1.29	1.38
1	E	3899	PHE	CG-CD2	-6.21	1.29	1.38
1	G	3968	TYR	CD2-CE2	-6.18	1.30	1.39
1	G	5032	TYR	CE1-CZ	-6.17	1.30	1.38
1	G	4988	TYR	CB-CG	-6.17	1.42	1.51
1	C	3899	PHE	CG-CD2	-6.16	1.29	1.38
1	G	3887	PHE	CD2-CE2	-6.14	1.26	1.39
1	G	3922	TYR	CA-CB	-6.11	1.40	1.53
1	C	4975	PHE	CG-CD2	-6.09	1.29	1.38
1	E	4975	PHE	CG-CD2	-6.09	1.29	1.38
1	G	5028	PHE	CG-CD2	-6.08	1.29	1.38
1	C	4173	TYR	CG-CD1	-6.07	1.31	1.39
1	C	4851	TYR	CE2-CZ	-6.07	1.30	1.38
1	G	4964	GLY	C-O	-6.07	1.14	1.23
1	A	4975	PHE	CG-CD2	-6.05	1.29	1.38
1	E	4851	TYR	CE2-CZ	-6.04	1.30	1.38
1	G	3964	SER	CA-CB	-6.04	1.43	1.52
1	G	4974	GLY	CA-C	-6.04	1.42	1.51
1	A	4851	TYR	CE2-CZ	-6.03	1.30	1.38
1	C	4032	GLU	CD-OE1	-6.02	1.19	1.25
1	A	4173	TYR	CG-CD1	-6.01	1.31	1.39
1	E	4173	TYR	CG-CD1	-6.01	1.31	1.39
1	A	3968	TYR	CE1-CZ	-6.00	1.30	1.38
1	G	3968	TYR	CE2-CZ	-6.00	1.30	1.38
1	G	4243	PHE	CG-CD2	-5.99	1.29	1.38
1	A	4032	GLU	CD-OE1	-5.97	1.19	1.25
1	A	5028	PHE	CG-CD2	-5.97	1.29	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	3968	TYR	CE1-CZ	-5.97	1.30	1.38
1	C	5028	PHE	CG-CD2	-5.95	1.29	1.38
1	C	4986	ALA	CA-CB	-5.92	1.40	1.52
1	G	3722	TYR	CG-CD1	-5.88	1.31	1.39
1	E	4190	ILE	C-O	-5.85	1.12	1.23
1	A	4190	ILE	C-O	-5.84	1.12	1.23
1	G	4217	PHE	CG-CD1	-5.84	1.29	1.38
1	A	3887	PHE	CD2-CE2	-5.83	1.27	1.39
1	G	4994	TYR	CG-CD1	-5.83	1.31	1.39
1	E	5028	PHE	CG-CD2	-5.82	1.30	1.38
1	E	4986	ALA	CA-CB	-5.81	1.40	1.52
1	E	5025	GLY	C-O	-5.81	1.14	1.23
1	A	4986	ALA	CA-CB	-5.80	1.40	1.52
1	E	3937	TYR	CG-CD2	-5.80	1.31	1.39
1	E	3887	PHE	CD2-CE2	-5.79	1.27	1.39
1	C	3887	PHE	CD2-CE2	-5.78	1.27	1.39
1	E	3968	TYR	CE1-CZ	-5.78	1.31	1.38
1	E	4032	GLU	CD-OE1	-5.78	1.19	1.25
1	G	4990	PHE	CB-CG	-5.77	1.41	1.51
1	A	3937	TYR	CG-CD2	-5.75	1.31	1.39
1	E	4936	ILE	C-O	5.74	1.34	1.23
1	G	5025	GLY	C-O	-5.74	1.14	1.23
1	C	3885	PHE	CD1-CE1	-5.73	1.27	1.39
1	E	1104	TRP	CG-CD1	-5.73	1.28	1.36
1	A	3922	TYR	CA-CB	-5.73	1.41	1.53
1	E	3922	TYR	CA-CB	-5.73	1.41	1.53
1	A	1104	TRP	CG-CD1	-5.72	1.28	1.36
1	C	4180	ARG	CA-C	-5.72	1.38	1.52
1	C	3922	TYR	CA-CB	-5.72	1.41	1.53
1	E	3885	PHE	CD1-CE1	-5.72	1.27	1.39
1	G	3722	TYR	CG-CD2	-5.72	1.31	1.39
1	C	3892	CYS	C-O	-5.71	1.12	1.23
1	G	5018	CYS	CB-SG	-5.71	1.72	1.81
1	A	4936	ILE	C-O	5.70	1.34	1.23
1	A	3892	CYS	C-O	-5.70	1.12	1.23
1	G	3957	VAL	CB-CG1	-5.70	1.40	1.52
1	E	3892	CYS	C-O	-5.70	1.12	1.23
1	A	3885	PHE	CD1-CE1	-5.70	1.27	1.39
1	C	3937	TYR	CG-CD2	-5.70	1.31	1.39
1	A	3935	TRP	CB-CG	-5.70	1.40	1.50
1	C	4190	ILE	C-O	-5.68	1.12	1.23
1	C	4936	ILE	C-O	5.67	1.34	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	3935	TRP	CB-CG	-5.65	1.40	1.50
1	E	4959	PHE	CG-CD2	-5.64	1.30	1.38
1	E	3935	TRP	CB-CG	-5.64	1.40	1.50
1	G	4173	TYR	CG-CD1	-5.63	1.31	1.39
1	G	4975	PHE	CG-CD2	-5.61	1.30	1.38
1	C	1104	TRP	CG-CD1	-5.61	1.28	1.36
1	C	3968	TYR	CD2-CE2	-5.59	1.30	1.39
1	E	4195	PHE	CG-CD1	-5.58	1.30	1.38
1	E	4192	ARG	CZ-NH1	-5.58	1.25	1.33
1	C	4994	TYR	CG-CD1	-5.57	1.31	1.39
1	G	4180	ARG	CA-C	-5.57	1.38	1.52
1	G	4190	ILE	C-O	-5.56	1.12	1.23
1	C	3922	TYR	CE1-CZ	-5.56	1.31	1.38
1	G	3885	PHE	CD1-CE1	-5.56	1.28	1.39
1	A	4195	PHE	CG-CD1	-5.55	1.30	1.38
1	A	4180	ARG	CA-C	-5.54	1.38	1.52
1	C	4959	PHE	CG-CD2	-5.54	1.30	1.38
1	A	4711	PHE	CG-CD2	-5.54	1.30	1.38
1	E	4711	PHE	CG-CD2	-5.54	1.30	1.38
1	G	4778	TRP	CE3-CZ3	-5.53	1.29	1.38
1	A	5029	ARG	CZ-NH2	-5.52	1.25	1.33
1	A	4994	TYR	CG-CD1	-5.52	1.31	1.39
1	G	3922	TYR	CB-CG	-5.52	1.43	1.51
1	A	4192	ARG	CZ-NH1	-5.51	1.25	1.33
1	A	5025	GLY	C-O	-5.51	1.14	1.23
1	E	3968	TYR	CD2-CE2	-5.51	1.31	1.39
1	C	4711	PHE	CG-CD2	-5.50	1.30	1.38
1	A	3968	TYR	CD2-CE2	-5.50	1.31	1.39
1	E	4180	ARG	CA-C	-5.50	1.38	1.52
1	G	4195	PHE	CG-CD1	-5.50	1.30	1.38
1	C	4195	PHE	CG-CD1	-5.50	1.30	1.38
1	E	3922	TYR	CE1-CZ	-5.49	1.31	1.38
1	G	1104	TRP	CG-CD1	-5.49	1.29	1.36
1	A	3922	TYR	CE1-CZ	-5.49	1.31	1.38
1	E	4182	GLU	CA-C	-5.48	1.38	1.52
1	C	5025	GLY	C-O	-5.47	1.14	1.23
1	C	117	TYR	CE1-CZ	-5.47	1.31	1.38
1	C	4192	ARG	CZ-NH1	-5.46	1.25	1.33
1	E	117	TYR	CE1-CZ	-5.46	1.31	1.38
1	G	4936	ILE	C-O	5.43	1.33	1.23
1	E	5029	ARG	CZ-NH2	-5.43	1.25	1.33
1	C	3968	TYR	CD1-CE1	-5.42	1.31	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	5019	TRP	CG-CD1	-5.41	1.29	1.36
1	C	5029	ARG	CZ-NH2	-5.41	1.26	1.33
1	C	4964	GLY	C-O	-5.41	1.15	1.23
1	A	3902	TYR	CG-CD2	-5.40	1.32	1.39
1	A	3968	TYR	CD1-CE1	-5.39	1.31	1.39
1	G	4177	TYR	CG-CD1	-5.39	1.32	1.39
1	A	4959	PHE	CG-CD2	-5.39	1.30	1.38
1	G	3937	TYR	CE2-CZ	-5.38	1.31	1.38
1	G	117	TYR	CE1-CZ	-5.38	1.31	1.38
1	G	3828	PHE	CG-CD2	-5.37	1.30	1.38
1	C	4182	GLU	C-O	-5.36	1.13	1.23
1	A	117	TYR	CE1-CZ	-5.35	1.31	1.38
1	E	3968	TYR	CD1-CE1	-5.35	1.31	1.39
1	E	4964	GLY	C-O	-5.35	1.15	1.23
1	A	4182	GLU	CA-C	-5.34	1.39	1.52
1	G	4191	GLU	CG-CD	5.33	1.59	1.51
1	C	4182	GLU	CA-C	-5.33	1.39	1.52
1	E	4243	PHE	CG-CD2	-5.33	1.30	1.38
1	A	4243	PHE	CG-CD2	-5.33	1.30	1.38
1	E	4661	TYR	CG-CD1	-5.33	1.32	1.39
1	C	4243	PHE	CG-CD2	-5.33	1.30	1.38
1	E	1076	ARG	CZ-NH2	-5.32	1.26	1.33
1	A	5018	CYS	CB-SG	-5.31	1.73	1.81
1	C	4661	TYR	CG-CD1	-5.31	1.32	1.39
1	E	1162	PHE	CG-CD1	-5.31	1.30	1.38
1	G	3899	PHE	CG-CD2	-5.31	1.30	1.38
1	E	4994	TYR	CG-CD1	-5.29	1.32	1.39
1	A	1162	PHE	CG-CD1	-5.28	1.30	1.38
1	G	4179	GLY	CA-C	-5.28	1.43	1.51
1	G	4182	GLU	C-O	-5.28	1.13	1.23
1	G	4988	TYR	N-CA	-5.27	1.35	1.46
1	G	4180	ARG	CZ-NH2	-5.27	1.26	1.33
1	A	692	TYR	CE1-CZ	-5.27	1.31	1.38
1	E	692	TYR	CE1-CZ	-5.27	1.31	1.38
1	A	4038	GLY	C-O	-5.25	1.15	1.23
1	C	692	TYR	CE1-CZ	-5.25	1.31	1.38
1	G	3902	TYR	CG-CD2	-5.25	1.32	1.39
1	C	3902	TYR	CG-CD2	-5.24	1.32	1.39
1	G	4975	PHE	CG-CD1	-5.24	1.30	1.38
1	G	5029	ARG	CZ-NH2	-5.23	1.26	1.33
1	C	3964	SER	CA-CB	-5.23	1.45	1.52
1	G	4991	PHE	CG-CD2	-5.23	1.30	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	5021	PHE	CE1-CZ	-5.23	1.27	1.37
1	C	4038	GLY	C-O	-5.22	1.15	1.23
1	E	5009	TYR	CG-CD1	-5.22	1.32	1.39
1	A	4661	TYR	CG-CD1	-5.22	1.32	1.39
1	G	3816	MET	CG-SD	-5.22	1.67	1.81
1	G	692	TYR	CE1-CZ	-5.21	1.31	1.38
1	C	5018	CYS	CB-SG	-5.20	1.73	1.81
1	E	3964	SER	CA-CB	-5.20	1.45	1.52
1	G	1162	PHE	CG-CD1	-5.20	1.30	1.38
1	A	4964	GLY	C-O	-5.19	1.15	1.23
1	A	4990	PHE	CB-CG	-5.19	1.42	1.51
1	E	4988	TYR	CB-CG	-5.18	1.43	1.51
1	E	4990	PHE	CB-CG	-5.18	1.42	1.51
1	C	1162	PHE	CG-CD1	-5.18	1.30	1.38
1	C	5009	TYR	CG-CD1	-5.18	1.32	1.39
1	E	4975	PHE	CG-CD1	-5.18	1.30	1.38
1	A	5022	PHE	CE2-CZ	-5.17	1.27	1.37
1	A	4975	PHE	CG-CD1	-5.16	1.31	1.38
1	C	4990	PHE	CB-CG	-5.16	1.42	1.51
1	G	5020	ASP	CB-CG	5.16	1.62	1.51
1	A	5009	TYR	CG-CD1	-5.15	1.32	1.39
1	E	4182	GLU	C-O	-5.15	1.13	1.23
1	A	4182	GLU	C-O	-5.15	1.13	1.23
1	G	4202	ARG	CZ-NH2	5.15	1.39	1.33
1	A	3964	SER	CA-CB	-5.14	1.45	1.52
1	E	4038	GLY	C-O	-5.14	1.15	1.23
1	E	3902	TYR	CG-CD2	-5.13	1.32	1.39
1	A	4988	TYR	CB-CG	-5.13	1.44	1.51
1	E	4191	GLU	CD-OE1	-5.12	1.20	1.25
1	C	4988	TYR	CB-CG	-5.12	1.44	1.51
1	A	4191	GLU	CD-OE1	-5.12	1.20	1.25
1	E	5020	ASP	CB-CG	5.11	1.62	1.51
1	C	5020	ASP	CB-CG	5.11	1.62	1.51
1	C	5022	PHE	CE2-CZ	-5.11	1.27	1.37
1	C	4975	PHE	CG-CD1	-5.10	1.31	1.38
1	G	4711	PHE	CG-CD2	-5.10	1.31	1.38
1	E	4851	TYR	CG-CD1	-5.10	1.32	1.39
1	G	1275	ARG	CZ-NH1	-5.10	1.26	1.33
1	G	4179	GLY	C-O	5.10	1.31	1.23
1	E	4232	GLU	CD-OE1	5.10	1.31	1.25
1	G	4661	TYR	CG-CD1	-5.09	1.32	1.39
1	G	4194	TYR	CB-CG	-5.09	1.44	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	4959	PHE	CG-CD2	-5.09	1.31	1.38
1	E	4177	TYR	CG-CD1	-5.08	1.32	1.39
1	E	1275	ARG	CZ-NH1	-5.07	1.26	1.33
1	A	5020	ASP	CB-CG	5.06	1.62	1.51
1	G	4968	PHE	CE1-CZ	-5.05	1.27	1.37
1	A	1275	ARG	CZ-NH1	-5.04	1.26	1.33
1	C	4177	TYR	CG-CD1	-5.04	1.32	1.39
1	A	5019	TRP	CG-CD1	-5.03	1.29	1.36
1	C	1275	ARG	CZ-NH1	-5.03	1.26	1.33
1	C	4863	TYR	CE1-CZ	-5.03	1.32	1.38
1	G	4967	TYR	CG-CD1	-5.02	1.32	1.39
1	C	4191	GLU	CD-OE1	-5.02	1.20	1.25
1	C	5023	PRO	C-O	5.01	1.33	1.23
1	C	4093	PHE	CB-CG	5.00	1.59	1.51
1	A	4851	TYR	CE1-CZ	-5.00	1.32	1.38

All (442) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	5029	ARG	NE-CZ-NH1	10.79	125.69	120.30
1	E	5029	ARG	NE-CZ-NH1	10.60	125.60	120.30
1	E	4988	TYR	CB-CG-CD1	10.56	127.34	121.00
1	A	4988	TYR	CB-CG-CD1	10.55	127.33	121.00
1	C	4988	TYR	CB-CG-CD1	10.53	127.32	121.00
1	C	5029	ARG	NE-CZ-NH1	10.31	125.46	120.30
1	E	5017	ARG	NE-CZ-NH2	-10.20	115.20	120.30
1	C	5017	ARG	NE-CZ-NH2	-10.19	115.20	120.30
1	A	5017	ARG	NE-CZ-NH2	-10.19	115.21	120.30
1	A	1076	ARG	NE-CZ-NH1	10.16	125.38	120.30
1	G	1076	ARG	NE-CZ-NH1	10.13	125.36	120.30
1	A	5029	ARG	NE-CZ-NH1	10.12	125.36	120.30
1	E	1076	ARG	NE-CZ-NH1	10.07	125.34	120.30
1	G	4231	MET	CG-SD-CE	9.87	116.00	100.20
1	C	1076	ARG	NE-CZ-NH1	9.60	125.10	120.30
1	G	4988	TYR	CB-CG-CD1	9.33	126.60	121.00
1	G	5010	VAL	CG1-CB-CG2	-9.18	96.21	110.90
1	G	3729	MET	CG-SD-CE	-8.96	85.86	100.20
1	A	4231	MET	CG-SD-CE	8.91	114.46	100.20
1	C	4231	MET	CG-SD-CE	8.78	114.25	100.20
1	C	4146	LEU	CB-CG-CD1	-8.71	96.19	111.00
1	E	4231	MET	CG-SD-CE	8.69	114.10	100.20
1	E	5029	ARG	NE-CZ-NH2	-8.65	115.97	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	4146	LEU	CB-CG-CD1	-8.63	96.33	111.00
1	G	4850	LEU	CB-CG-CD1	8.62	125.65	111.00
1	A	4146	LEU	CB-CG-CD1	-8.55	96.47	111.00
1	C	3729	MET	CG-SD-CE	-8.42	86.72	100.20
1	E	3729	MET	CG-SD-CE	-8.39	86.77	100.20
1	G	4985	LEU	CB-CG-CD1	-8.39	96.73	111.00
1	A	3729	MET	CG-SD-CE	-8.36	86.83	100.20
1	A	5029	ARG	NE-CZ-NH2	-8.27	116.17	120.30
1	E	3886	ARG	NE-CZ-NH2	-8.20	116.20	120.30
1	C	5029	ARG	NE-CZ-NH2	-8.09	116.25	120.30
1	G	5029	ARG	NE-CZ-NH2	-8.00	116.30	120.30
1	A	3886	ARG	NE-CZ-NH2	-7.97	116.32	120.30
1	C	3886	ARG	NE-CZ-NH2	-7.94	116.33	120.30
1	C	1275	ARG	NE-CZ-NH2	7.90	124.25	120.30
1	G	1275	ARG	NE-CZ-NH2	7.88	124.24	120.30
1	A	1275	ARG	NE-CZ-NH2	7.86	124.23	120.30
1	G	4013	LEU	CB-CG-CD1	7.86	124.35	111.00
1	E	1275	ARG	NE-CZ-NH2	7.85	124.22	120.30
1	E	3841	VAL	CA-CB-CG1	7.81	122.62	110.90
1	C	3841	VAL	CA-CB-CG1	7.79	122.59	110.90
1	C	5010	VAL	CG1-CB-CG2	-7.79	98.44	110.90
1	A	3841	VAL	CA-CB-CG1	7.76	122.54	110.90
1	C	4184	MET	CB-CG-SD	-7.75	89.14	112.40
1	E	5010	VAL	CG1-CB-CG2	-7.72	98.55	110.90
1	A	5010	VAL	CG1-CB-CG2	-7.69	98.59	110.90
1	A	4184	MET	CB-CG-SD	-7.68	89.37	112.40
1	C	5021	PHE	CB-CG-CD2	-7.65	115.45	120.80
1	G	4184	MET	CB-CG-SD	-7.64	89.48	112.40
1	A	4850	LEU	CB-CG-CD1	7.59	123.91	111.00
1	G	4563	ARG	NE-CZ-NH1	-7.52	116.54	120.30
1	A	5021	PHE	CB-CG-CD2	-7.46	115.58	120.80
1	E	3891	LEU	CB-CG-CD2	-7.44	98.36	111.00
1	A	3891	LEU	CB-CG-CD2	-7.42	98.38	111.00
1	A	2168	VAL	CG1-CB-CG2	7.42	122.77	110.90
1	G	3841	VAL	CA-CB-CG1	7.42	122.03	110.90
1	G	2168	VAL	CG1-CB-CG2	7.39	122.73	110.90
1	E	4850	LEU	CB-CG-CD1	7.39	123.56	111.00
1	C	4850	LEU	CB-CG-CD1	7.38	123.54	111.00
1	E	5021	PHE	CB-CG-CD2	-7.38	115.64	120.80
1	E	2168	VAL	CG1-CB-CG2	7.34	122.65	110.90
1	C	2168	VAL	CG1-CB-CG2	7.34	122.64	110.90
1	A	4985	LEU	CB-CG-CD1	-7.31	98.57	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	4184	MET	CB-CG-SD	-7.30	90.50	112.40
1	A	808	TYR	N-CA-CB	7.29	123.72	110.60
1	E	808	TYR	N-CA-CB	7.28	123.71	110.60
1	G	808	TYR	N-CA-CB	7.26	123.66	110.60
1	C	808	TYR	N-CA-CB	7.25	123.65	110.60
1	C	3891	LEU	CB-CG-CD2	-7.23	98.70	111.00
1	G	4988	TYR	CB-CG-CD2	-7.21	116.67	121.00
1	G	4856	PHE	CB-CG-CD2	-7.20	115.76	120.80
1	A	4995	LEU	CB-CG-CD1	-7.18	98.79	111.00
1	E	4995	LEU	CB-CG-CD1	-7.13	98.88	111.00
1	C	4995	LEU	CB-CG-CD1	-7.09	98.94	111.00
1	C	4985	LEU	CB-CG-CD1	-7.06	99.00	111.00
1	A	4578	LEU	CB-CG-CD1	-7.04	99.03	111.00
1	C	3903	LEU	CB-CG-CD1	7.04	122.96	111.00
1	G	3782	MET	CG-SD-CE	7.02	111.43	100.20
1	E	4985	LEU	CB-CG-CD1	-6.92	99.23	111.00
1	A	3903	LEU	CB-CG-CD1	6.92	122.76	111.00
1	C	3567	PRO	N-CA-CB	6.88	111.56	103.30
1	A	3567	PRO	N-CA-CB	6.88	111.56	103.30
1	G	4183	ILE	CG1-CB-CG2	-6.88	96.27	111.40
1	C	4916	PHE	CB-CG-CD1	-6.87	115.99	120.80
1	E	3138	PRO	N-CA-CB	6.86	111.53	103.30
1	E	3567	PRO	N-CA-CB	6.85	111.53	103.30
1	A	3138	PRO	N-CA-CB	6.85	111.52	103.30
1	C	3138	PRO	N-CA-CB	6.84	111.51	103.30
1	G	4217	PHE	CB-CG-CD1	-6.81	116.03	120.80
1	E	3664	THR	N-CA-CB	6.81	123.24	110.30
1	G	4995	LEU	CB-CG-CD1	-6.80	99.44	111.00
1	E	3903	LEU	CB-CG-CD1	6.79	122.55	111.00
1	E	1493	TYR	N-CA-CB	6.79	122.81	110.60
1	A	4916	PHE	CB-CG-CD1	-6.78	116.06	120.80
1	A	3664	THR	N-CA-CB	6.76	123.14	110.30
1	G	3567	PRO	N-CA-CB	6.72	111.37	103.30
1	A	1493	TYR	N-CA-CB	6.71	122.68	110.60
1	C	3664	THR	N-CA-CB	6.71	123.05	110.30
1	E	3903	LEU	CD1-CG-CD2	-6.71	90.38	110.50
1	G	1493	TYR	N-CA-CB	6.70	122.66	110.60
1	C	1493	TYR	N-CA-CB	6.69	122.64	110.60
1	E	4916	PHE	CB-CG-CD1	-6.66	116.14	120.80
1	A	3903	LEU	CD1-CG-CD2	-6.66	90.53	110.50
1	G	3062	PRO	N-CA-CB	6.65	111.28	103.30
1	C	3903	LEU	CD1-CG-CD2	-6.63	90.60	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	5021	PHE	CB-CG-CD1	6.57	125.40	120.80
1	E	3773	ARG	NE-CZ-NH2	-6.54	117.03	120.30
1	C	3773	ARG	NE-CZ-NH2	-6.52	117.04	120.30
1	A	4183	ILE	CG1-CB-CG2	-6.52	97.05	111.40
1	C	4578	LEU	CB-CG-CD1	-6.50	99.95	111.00
1	E	4578	LEU	CB-CG-CD1	-6.48	99.98	111.00
1	A	4818	MET	CG-SD-CE	6.48	110.56	100.20
1	A	4844	LEU	CB-CG-CD2	-6.47	100.00	111.00
1	A	5021	PHE	CB-CG-CD1	6.46	125.32	120.80
1	C	5019	TRP	CB-CA-C	-6.43	97.54	110.40
1	E	3297	PRO	N-CA-CB	6.42	111.00	103.30
1	A	3297	PRO	N-CA-CB	6.42	111.00	103.30
1	C	4844	LEU	CB-CG-CD2	-6.41	100.10	111.00
1	E	5019	TRP	CB-CA-C	-6.41	97.58	110.40
1	C	3297	PRO	N-CA-CB	6.40	110.98	103.30
1	C	4818	MET	CG-SD-CE	6.39	110.43	100.20
1	C	4183	ILE	CG1-CB-CG2	-6.39	97.35	111.40
1	E	4183	ILE	CG1-CB-CG2	-6.38	97.36	111.40
1	E	5021	PHE	CB-CG-CD1	6.38	125.27	120.80
1	A	3773	ARG	NE-CZ-NH2	-6.37	117.11	120.30
1	E	3519	PRO	N-CA-CB	6.37	110.94	103.30
1	A	5019	TRP	CB-CA-C	-6.36	97.68	110.40
1	A	3519	PRO	N-CA-CB	6.35	110.92	103.30
1	C	3519	PRO	N-CA-CB	6.35	110.92	103.30
1	G	3926	LEU	CB-CG-CD2	-6.33	100.23	111.00
1	C	3021	PRO	N-CA-CB	6.32	110.88	103.30
1	A	3275	PRO	N-CA-CB	6.31	110.87	103.30
1	A	3021	PRO	N-CA-CB	6.29	110.85	103.30
1	E	2631	PRO	N-CA-CB	6.29	110.85	103.30
1	E	4818	MET	CG-SD-CE	6.29	110.27	100.20
1	E	3021	PRO	N-CA-CB	6.28	110.84	103.30
1	G	3965	LEU	CB-CG-CD1	-6.28	100.32	111.00
1	E	3289	PRO	N-CA-CB	6.26	110.81	103.30
1	G	2631	PRO	N-CA-CB	6.26	110.81	103.30
1	A	2712	PRO	N-CA-CB	6.25	110.80	103.30
1	E	3275	PRO	N-CA-CB	6.25	110.80	103.30
1	A	2631	PRO	N-CA-CB	6.25	110.80	103.30
1	C	2631	PRO	N-CA-CB	6.23	110.78	103.30
1	C	3275	PRO	N-CA-CB	6.23	110.78	103.30
1	A	3289	PRO	N-CA-CB	6.22	110.77	103.30
1	C	3289	PRO	N-CA-CB	6.22	110.77	103.30
1	C	2712	PRO	N-CA-CB	6.22	110.77	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	4173	TYR	CB-CG-CD1	-6.21	117.27	121.00
1	G	2640	PRO	N-CA-CB	6.21	110.76	103.30
1	E	2712	PRO	N-CA-CB	6.21	110.75	103.30
1	C	2640	PRO	N-CA-CB	6.21	110.75	103.30
1	G	2712	PRO	N-CA-CB	6.21	110.75	103.30
1	A	2640	PRO	N-CA-CB	6.20	110.74	103.30
1	G	3904	ARG	NE-CZ-NH2	-6.20	117.20	120.30
1	A	3188	PRO	N-CA-CB	6.19	110.72	103.30
1	E	3188	PRO	N-CA-CB	6.18	110.72	103.30
1	C	3188	PRO	N-CA-CB	6.17	110.70	103.30
1	E	2640	PRO	N-CA-CB	6.17	110.70	103.30
1	E	4173	TYR	CB-CG-CD1	-6.16	117.31	121.00
1	G	3519	PRO	N-CA-CB	6.16	110.69	103.30
1	G	3275	PRO	N-CA-CB	6.14	110.67	103.30
1	A	3360	PRO	N-CA-CB	6.12	110.64	103.30
1	A	4809	PHE	CB-CG-CD2	-6.12	116.52	120.80
1	A	4988	TYR	CB-CG-CD2	-6.11	117.33	121.00
1	E	3360	PRO	N-CA-CB	6.11	110.63	103.30
1	G	3297	PRO	N-CA-CB	6.11	110.63	103.30
1	C	3360	PRO	N-CA-CB	6.10	110.62	103.30
1	G	3903	LEU	CB-CG-CD2	6.10	121.36	111.00
1	E	3903	LEU	CB-CG-CD2	6.09	121.36	111.00
1	G	3903	LEU	CD1-CG-CD2	-6.08	92.25	110.50
1	C	1076	ARG	NE-CZ-NH2	-6.07	117.26	120.30
1	G	4648	LEU	CB-CG-CD2	6.06	121.30	111.00
1	A	3698	LEU	CB-CG-CD2	-6.05	100.71	111.00
1	C	3903	LEU	CB-CG-CD2	6.05	121.29	111.00
1	G	3282	PRO	N-CA-CB	6.05	110.56	103.30
1	E	3698	LEU	CB-CG-CD2	-6.05	100.72	111.00
1	A	4173	TYR	CB-CG-CD1	-6.04	117.37	121.00
1	E	4988	TYR	CB-CG-CD2	-6.04	117.38	121.00
1	G	2701	PRO	N-CA-CB	6.04	110.55	103.30
1	G	3289	PRO	N-CA-CB	6.04	110.55	103.30
1	E	2701	PRO	N-CA-CB	6.04	110.54	103.30
1	C	2701	PRO	N-CA-CB	6.04	110.54	103.30
1	E	3410	PRO	N-CA-CB	6.04	110.54	103.30
1	G	3138	PRO	N-CA-CB	6.03	110.54	103.30
1	E	3301	PRO	N-CA-CB	6.03	110.54	103.30
1	E	3282	PRO	N-CA-CB	6.03	110.54	103.30
1	C	3282	PRO	N-CA-CB	6.03	110.53	103.30
1	G	3303	PRO	N-CA-CB	6.02	110.53	103.30
1	A	2701	PRO	N-CA-CB	6.02	110.53	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	3832	ILE	CG1-CB-CG2	-6.02	98.16	111.40
1	A	3282	PRO	N-CA-CB	6.01	110.52	103.30
1	G	4028	LEU	CB-CG-CD1	-6.01	100.78	111.00
1	G	3410	PRO	N-CA-CB	6.01	110.52	103.30
1	C	3698	LEU	CB-CG-CD2	-6.01	100.78	111.00
1	E	3351	PRO	N-CA-CB	6.01	110.51	103.30
1	G	3957	VAL	CG1-CB-CG2	-6.01	101.28	110.90
1	C	2711	PRO	N-CA-CB	6.00	110.50	103.30
1	A	3410	PRO	N-CA-CB	6.00	110.50	103.30
1	G	3021	PRO	N-CA-CB	6.00	110.50	103.30
1	C	221	ARG	NE-CZ-NH2	-5.99	117.30	120.30
1	A	2711	PRO	N-CA-CB	5.98	110.48	103.30
1	C	4988	TYR	CB-CG-CD2	-5.98	117.41	121.00
1	E	2711	PRO	N-CA-CB	5.98	110.47	103.30
1	C	3301	PRO	N-CA-CB	5.97	110.46	103.30
1	E	221	ARG	NE-CZ-NH2	-5.97	117.32	120.30
1	C	3410	PRO	N-CA-CB	5.96	110.45	103.30
1	G	4880	MET	CG-SD-CE	5.96	109.74	100.20
1	G	3891	LEU	CB-CG-CD2	-5.96	100.88	111.00
1	C	3527	PRO	N-CA-CB	5.95	110.44	103.30
1	G	4703	ARG	NE-CZ-NH2	-5.95	117.33	120.30
1	A	3527	PRO	N-CA-CB	5.94	110.43	103.30
1	E	3527	PRO	N-CA-CB	5.93	110.42	103.30
1	G	3527	PRO	N-CA-CB	5.93	110.42	103.30
1	A	3301	PRO	N-CA-CB	5.93	110.42	103.30
1	A	3351	PRO	N-CA-CB	5.93	110.41	103.30
1	G	2711	PRO	N-CA-CB	5.92	110.41	103.30
1	C	3351	PRO	N-CA-CB	5.92	110.40	103.30
1	C	3302	PRO	N-CA-CB	5.91	110.39	103.30
1	E	3302	PRO	N-CA-CB	5.91	110.39	103.30
1	E	4844	LEU	CB-CG-CD2	-5.91	100.96	111.00
1	G	3188	PRO	N-CA-CB	5.91	110.39	103.30
1	G	3933	PHE	CB-CG-CD1	-5.90	116.67	120.80
1	A	3302	PRO	N-CA-CB	5.89	110.37	103.30
1	G	3301	PRO	N-CA-CB	5.89	110.37	103.30
1	G	221	ARG	NE-CZ-NH2	-5.87	117.36	120.30
1	C	109	LEU	CB-CG-CD2	-5.86	101.04	111.00
1	G	1659	LEU	CB-CG-CD1	-5.85	101.05	111.00
1	A	3903	LEU	CB-CG-CD2	5.84	120.94	111.00
1	G	3302	PRO	N-CA-CB	5.84	110.31	103.30
1	E	3933	PHE	CB-CG-CD1	-5.84	116.71	120.80
1	G	4801	LEU	CB-CG-CD2	5.84	120.92	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	4818	MET	CG-SD-CE	5.83	109.53	100.20
1	A	1659	LEU	CB-CG-CD1	-5.82	101.10	111.00
1	A	3303	PRO	N-CA-CB	5.82	110.29	103.30
1	A	4988	TYR	CE1-CZ-OH	5.82	135.81	120.10
1	E	3303	PRO	N-CA-CB	5.82	110.28	103.30
1	G	3360	PRO	N-CA-CB	5.82	110.28	103.30
1	E	3995	VAL	CA-CB-CG2	-5.81	102.18	110.90
1	G	4967	TYR	CB-CG-CD1	-5.81	117.51	121.00
1	E	4180	ARG	NE-CZ-NH2	-5.81	117.40	120.30
1	G	5017	ARG	NE-CZ-NH2	-5.81	117.40	120.30
1	A	3990	VAL	CG1-CB-CG2	-5.80	101.62	110.90
1	C	3995	VAL	CA-CB-CG2	-5.80	102.20	110.90
1	E	1659	LEU	CB-CG-CD1	-5.80	101.14	111.00
1	A	3995	VAL	CA-CB-CG2	-5.79	102.21	110.90
1	C	4988	TYR	CE1-CZ-OH	5.79	135.74	120.10
1	E	4988	TYR	CE1-CZ-OH	5.79	135.74	120.10
1	G	3351	PRO	N-CA-CB	5.79	110.24	103.30
1	C	3303	PRO	N-CA-CB	5.79	110.24	103.30
1	C	1659	LEU	CB-CG-CD1	-5.78	101.17	111.00
1	G	3427	PRO	N-CA-CB	5.78	110.23	103.30
1	G	1076	ARG	NE-CZ-NH2	-5.75	117.42	120.30
1	A	3933	PHE	CB-CG-CD1	-5.74	116.78	120.80
1	G	4986	ALA	CB-CA-C	-5.74	101.49	110.10
1	G	109	LEU	CB-CG-CD2	-5.74	101.25	111.00
1	A	221	ARG	NE-CZ-NH2	-5.72	117.44	120.30
1	A	3427	PRO	N-CA-CB	5.72	110.17	103.30
1	G	4629	TYR	CB-CG-CD2	-5.72	117.57	121.00
1	G	4990	PHE	CB-CG-CD1	-5.71	116.80	120.80
1	A	3085	PRO	N-CA-CB	5.71	110.15	103.30
1	A	4703	ARG	NE-CZ-NH2	-5.70	117.45	120.30
1	G	3294	PRO	N-CA-CB	5.70	110.14	103.30
1	C	3933	PHE	CB-CG-CD1	-5.70	116.81	120.80
1	E	3990	VAL	CG1-CB-CG2	-5.69	101.79	110.90
1	G	5021	PHE	CB-CG-CD2	-5.69	116.81	120.80
1	G	5017	ARG	CG-CD-NE	-5.69	99.85	111.80
1	E	3085	PRO	N-CA-CB	5.69	110.13	103.30
1	C	3085	PRO	N-CA-CB	5.68	110.12	103.30
1	A	45	ARG	NE-CZ-NH2	-5.68	117.46	120.30
1	C	3294	PRO	N-CA-CB	5.68	110.12	103.30
1	G	5028	PHE	CB-CG-CD1	5.68	124.78	120.80
1	A	3294	PRO	N-CA-CB	5.68	110.12	103.30
1	C	3427	PRO	N-CA-CB	5.68	110.11	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	3926	LEU	CB-CG-CD2	-5.68	101.35	111.00
1	C	3990	VAL	CG1-CB-CG2	-5.67	101.82	110.90
1	E	3427	PRO	N-CA-CB	5.67	110.11	103.30
1	A	109	LEU	CB-CG-CD2	-5.67	101.36	111.00
1	G	4851	TYR	CB-CG-CD1	5.67	124.40	121.00
1	C	4629	TYR	CB-CG-CD1	5.67	124.40	121.00
1	G	3880	PHE	CB-CG-CD1	-5.66	116.83	120.80
1	E	3887	PHE	CB-CG-CD2	-5.65	116.84	120.80
1	A	4217	PHE	CB-CG-CD1	-5.65	116.85	120.80
1	E	3294	PRO	N-CA-CB	5.64	110.07	103.30
1	A	4673	ARG	NE-CZ-NH2	-5.64	117.48	120.30
1	E	4703	ARG	NE-CZ-NH2	-5.64	117.48	120.30
1	E	109	LEU	CB-CG-CD2	-5.63	101.42	111.00
1	C	3962	PHE	CB-CG-CD2	-5.63	116.86	120.80
1	G	4629	TYR	CB-CG-CD1	5.63	124.38	121.00
1	C	45	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	C	4673	ARG	NE-CZ-NH2	-5.61	117.49	120.30
1	G	3208	PRO	N-CA-CB	5.61	110.03	103.30
1	E	45	ARG	NE-CZ-NH2	-5.60	117.50	120.30
1	E	14	LEU	CB-CG-CD1	-5.60	101.47	111.00
1	E	3962	PHE	CB-CG-CD2	-5.60	116.88	120.80
1	A	14	LEU	CB-CG-CD1	-5.59	101.49	111.00
1	G	3989	VAL	CG1-CB-CG2	-5.58	101.96	110.90
1	A	5028	PHE	CB-CG-CD1	5.58	124.71	120.80
1	A	3962	PHE	CB-CG-CD2	-5.58	116.90	120.80
1	C	14	LEU	CB-CG-CD1	-5.57	101.52	111.00
1	G	3962	PHE	CB-CG-CD2	-5.56	116.91	120.80
1	A	3887	PHE	CB-CG-CD2	-5.56	116.91	120.80
1	A	4837	LEU	CB-CG-CD2	-5.56	101.55	111.00
1	G	45	ARG	NE-CZ-NH2	-5.55	117.52	120.30
1	E	5017	ARG	NH1-CZ-NH2	5.54	125.49	119.40
1	G	3721	LEU	CB-CG-CD1	5.54	120.41	111.00
1	G	4892	ARG	NE-CZ-NH1	-5.54	117.53	120.30
1	A	4215	ARG	NE-CZ-NH2	-5.53	117.53	120.30
1	A	2616	PRO	N-CA-CB	5.53	109.94	103.30
1	C	4703	ARG	NE-CZ-NH2	-5.53	117.54	120.30
1	E	4217	PHE	CB-CG-CD1	-5.53	116.93	120.80
1	G	14	LEU	CB-CG-CD1	-5.53	101.61	111.00
1	C	4629	TYR	CB-CG-CD2	-5.52	117.69	121.00
1	C	4112	LEU	CB-CG-CD1	-5.52	101.62	111.00
1	A	2658	PRO	N-CA-CB	5.51	109.92	103.30
1	A	4112	LEU	CB-CG-CD1	-5.51	101.62	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	4217	PHE	CB-CG-CD1	-5.51	116.94	120.80
1	G	2658	PRO	N-CA-CB	5.51	109.91	103.30
1	E	4112	LEU	CB-CG-CD1	-5.51	101.64	111.00
1	A	3926	LEU	CB-CG-CD2	-5.50	101.64	111.00
1	E	2658	PRO	N-CA-CB	5.50	109.90	103.30
1	A	4943	LEU	CB-CG-CD1	5.50	120.34	111.00
1	E	3832	ILE	CG1-CB-CG2	-5.49	99.32	111.40
1	E	4673	ARG	NE-CZ-NH2	-5.49	117.56	120.30
1	E	4629	TYR	CB-CG-CD1	5.49	124.29	121.00
1	G	2616	PRO	N-CA-CB	5.49	109.88	103.30
1	C	4180	ARG	NE-CZ-NH2	-5.48	117.56	120.30
1	E	2616	PRO	N-CA-CB	5.48	109.88	103.30
1	C	2658	PRO	N-CA-CB	5.48	109.87	103.30
1	C	3832	ILE	CG1-CB-CG2	-5.47	99.38	111.40
1	C	2616	PRO	N-CA-CB	5.46	109.86	103.30
1	E	3926	LEU	CB-CG-CD2	-5.46	101.72	111.00
1	G	78	LEU	CB-CG-CD2	-5.46	101.72	111.00
1	A	3832	ILE	CG1-CB-CG2	-5.46	99.40	111.40
1	C	78	LEU	CB-CG-CD2	-5.46	101.73	111.00
1	E	4215	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	G	3918	CYS	CA-CB-SG	-5.45	104.19	114.00
1	C	3887	PHE	CB-CG-CD2	-5.45	116.98	120.80
1	G	5019	TRP	CB-CA-C	-5.45	99.51	110.40
1	C	3208	PRO	N-CA-CB	5.44	109.83	103.30
1	E	3208	PRO	N-CA-CB	5.44	109.83	103.30
1	E	3999	MET	CG-SD-CE	5.44	108.91	100.20
1	C	5028	PHE	CB-CG-CD1	5.44	124.61	120.80
1	A	3999	MET	CG-SD-CE	5.43	108.89	100.20
1	C	3999	MET	CG-SD-CE	5.43	108.89	100.20
1	A	3208	PRO	N-CA-CB	5.43	109.81	103.30
1	A	4178	LEU	CB-CG-CD2	5.42	120.22	111.00
1	G	3995	VAL	CA-CB-CG2	-5.42	102.77	110.90
1	E	4809	PHE	CB-CG-CD2	-5.40	117.02	120.80
1	G	4992	LEU	CB-CG-CD1	-5.39	101.84	111.00
1	G	5021	PHE	CB-CG-CD1	5.38	124.56	120.80
1	C	5017	ARG	NH1-CZ-NH2	5.38	125.31	119.40
1	G	4217	PHE	CB-CG-CD2	5.37	124.56	120.80
1	G	3085	PRO	N-CA-CB	5.37	109.74	103.30
1	A	5017	ARG	NH1-CZ-NH2	5.36	125.30	119.40
1	C	4992	LEU	CB-CG-CD1	-5.36	101.89	111.00
1	C	4215	ARG	NE-CZ-NH2	-5.36	117.62	120.30
1	G	4237	PHE	CB-CG-CD1	-5.36	117.05	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	4677	LEU	CB-CG-CD1	-5.35	101.90	111.00
1	E	4629	TYR	CB-CG-CD2	-5.35	117.79	121.00
1	E	4838	VAL	CG1-CB-CG2	5.34	119.45	110.90
1	E	5028	PHE	CB-CG-CD1	5.34	124.54	120.80
1	E	4920	PHE	CB-CG-CD2	-5.34	117.06	120.80
1	C	4880	MET	CG-SD-CE	5.32	108.71	100.20
1	C	5017	ARG	CG-CD-NE	-5.32	100.63	111.80
1	E	4992	LEU	CB-CG-CD1	-5.31	101.97	111.00
1	A	4992	LEU	CB-CG-CD1	-5.31	101.98	111.00
1	E	5017	ARG	CG-CD-NE	-5.31	100.66	111.80
1	C	4809	PHE	CB-CG-CD2	-5.30	117.09	120.80
1	A	4677	LEU	CB-CG-CD1	-5.30	102.00	111.00
1	E	78	LEU	CB-CG-CD2	-5.27	102.05	111.00
1	E	4178	LEU	CB-CG-CD2	5.27	119.95	111.00
1	A	3816	MET	CG-SD-CE	5.26	108.62	100.20
1	A	4180	ARG	NE-CZ-NH2	-5.26	117.67	120.30
1	G	4180	ARG	CD-NE-CZ	-5.25	116.25	123.60
1	C	4173	TYR	CB-CG-CD2	5.25	124.15	121.00
1	A	78	LEU	CB-CG-CD2	-5.24	102.09	111.00
1	E	4677	LEU	CB-CG-CD1	-5.23	102.11	111.00
1	E	4180	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	E	3816	MET	CG-SD-CE	5.22	108.55	100.20
1	C	4163	PHE	CB-CG-CD1	-5.22	117.15	120.80
1	E	4173	TYR	CB-CG-CD2	5.21	124.13	121.00
1	C	4943	LEU	CB-CG-CD1	5.20	119.84	111.00
1	A	4173	TYR	CB-CG-CD2	5.20	124.12	121.00
1	G	3915	ILE	CG1-CB-CG2	-5.20	99.96	111.40
1	C	3062	PRO	N-CA-CB	5.20	109.53	103.30
1	C	3918	CYS	CA-CB-SG	-5.20	104.65	114.00
1	A	4163	PHE	CB-CG-CD1	-5.19	117.17	120.80
1	C	4178	LEU	CB-CG-CD2	5.19	119.83	111.00
1	C	3816	MET	CG-SD-CE	5.19	108.50	100.20
1	E	3062	PRO	N-CA-CB	5.18	109.52	103.30
1	G	4170	ILE	CG1-CB-CG2	-5.18	100.00	111.40
1	G	4245	MET	CG-SD-CE	-5.18	91.91	100.20
1	C	3934	TYR	CB-CG-CD1	-5.18	117.89	121.00
1	E	4837	LEU	CB-CG-CD2	-5.18	102.20	111.00
1	E	3969	ILE	CG1-CB-CG2	-5.16	100.04	111.40
1	A	3062	PRO	N-CA-CB	5.16	109.49	103.30
1	C	3904	ARG	NE-CZ-NH2	-5.16	117.72	120.30
1	G	4686	LEU	CB-CG-CD2	-5.16	102.23	111.00
1	G	4844	LEU	CB-CG-CD2	-5.15	102.24	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3918	CYS	CA-CB-SG	-5.15	104.74	114.00
1	E	3918	CYS	CA-CB-SG	-5.15	104.74	114.00
1	A	4967	TYR	CB-CG-CD1	-5.14	117.92	121.00
1	A	5017	ARG	CG-CD-NE	-5.14	101.01	111.80
1	G	4673	ARG	NE-CZ-NH2	-5.14	117.73	120.30
1	C	4823	LEU	CB-CG-CD1	-5.13	102.27	111.00
1	G	4112	LEU	CB-CG-CD1	-5.13	102.27	111.00
1	C	4917	ASP	CB-CG-OD2	5.13	122.91	118.30
1	A	3904	ARG	NE-CZ-NH2	-5.12	117.74	120.30
1	C	3969	ILE	CG1-CB-CG2	-5.12	100.13	111.40
1	A	4180	ARG	NE-CZ-NH1	5.12	122.86	120.30
1	G	4711	PHE	CB-CG-CD2	-5.11	117.22	120.80
1	A	3934	TYR	CB-CG-CD1	-5.11	117.93	121.00
1	G	4887	MET	CG-SD-CE	5.11	108.38	100.20
1	A	4917	ASP	CB-CG-OD2	5.11	122.90	118.30
1	A	3969	ILE	CG1-CB-CG2	-5.11	100.16	111.40
1	G	2458	ARG	NE-CZ-NH2	-5.10	117.75	120.30
1	C	4837	LEU	CB-CG-CD2	-5.09	102.35	111.00
1	E	4163	PHE	CB-CG-CD1	-5.08	117.24	120.80
1	C	4920	PHE	CB-CG-CD2	-5.08	117.24	120.80
1	G	3885	PHE	CB-CG-CD2	-5.08	117.24	120.80
1	C	4180	ARG	NE-CZ-NH1	5.07	122.84	120.30
1	G	4173	TYR	CB-CG-CD1	-5.07	117.96	121.00
1	C	4181	ILE	CG1-CB-CG2	-5.07	100.25	111.40
1	E	4823	LEU	CB-CG-CD1	-5.07	102.39	111.00
1	G	3664	THR	N-CA-C	5.07	124.67	111.00
1	C	4237	PHE	CB-CG-CD1	-5.05	117.26	120.80
1	G	4026	MET	CG-SD-CE	-5.05	92.12	100.20
1	E	4181	ILE	CG1-CB-CG2	-5.04	100.30	111.40
1	C	4967	TYR	CB-CG-CD1	-5.04	117.97	121.00
1	E	2458	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	A	4880	MET	CG-SD-CE	5.03	108.25	100.20
1	A	4920	PHE	CB-CG-CD2	-5.03	117.28	120.80
1	E	4967	TYR	CB-CG-CD1	-5.03	117.98	121.00
1	G	4653	VAL	CG1-CB-CG2	-5.02	102.86	110.90
1	E	3904	ARG	NE-CZ-NH2	-5.02	117.79	120.30
1	G	5019	TRP	N-CA-C	5.01	124.53	111.00
1	C	4177	TYR	N-CA-C	5.01	124.52	111.00
1	A	2458	ARG	NE-CZ-NH2	-5.01	117.80	120.30
1	C	3721	LEU	CB-CG-CD2	-5.00	102.50	111.00
1	A	4629	TYR	CB-CG-CD1	5.00	124.00	121.00

There are no chirality outliers.

All (80) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1464	PHE	Mainchain,Peptide
1	A	1465	ASP	Peptide
1	A	1588	ALA	Mainchain,Peptide
1	A	1744	ALA	Mainchain,Peptide
1	A	1828	ASP	Mainchain,Peptide
1	A	1867	GLU	Peptide
1	A	2361	PRO	Mainchain,Peptide
1	A	3663	LEU	Mainchain,Peptide
1	A	697	GLY	Mainchain,Peptide
1	A	807	GLY	Mainchain,Peptide
1	A	841	GLY	Mainchain,Peptide
1	C	1464	PHE	Mainchain,Peptide
1	C	1465	ASP	Peptide
1	C	1588	ALA	Mainchain,Peptide
1	C	1744	ALA	Mainchain,Peptide
1	C	1828	ASP	Mainchain,Peptide
1	C	1867	GLU	Peptide
1	C	2361	PRO	Mainchain,Peptide
1	C	3663	LEU	Mainchain,Peptide
1	C	697	GLY	Mainchain,Peptide
1	C	807	GLY	Mainchain,Peptide
1	C	841	GLY	Mainchain,Peptide
1	E	1464	PHE	Mainchain,Peptide
1	E	1465	ASP	Peptide
1	E	1588	ALA	Mainchain,Peptide
1	E	1744	ALA	Mainchain,Peptide
1	E	1828	ASP	Mainchain,Peptide
1	E	1867	GLU	Peptide
1	E	2361	PRO	Mainchain,Peptide
1	E	3663	LEU	Mainchain,Peptide
1	E	697	GLY	Mainchain,Peptide
1	E	807	GLY	Mainchain,Peptide
1	E	841	GLY	Mainchain,Peptide
1	G	1464	PHE	Mainchain,Peptide
1	G	1465	ASP	Peptide
1	G	1588	ALA	Mainchain,Peptide
1	G	1744	ALA	Mainchain,Peptide
1	G	1828	ASP	Mainchain,Peptide
1	G	1867	GLU	Peptide
1	G	2361	PRO	Mainchain,Peptide
1	G	3663	LEU	Mainchain,Peptide
1	G	697	GLY	Mainchain,Peptide

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Mol	Chain	Res	Type	Group
1	G	807	GLY	Mainchain,Peptide
1	G	841	GLY	Mainchain,Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	26917	0	24461	801	0
1	C	26917	0	24461	789	0
1	E	26917	0	24461	787	0
1	G	26917	0	24461	770	0
2	B	832	0	831	34	0
2	D	832	0	831	35	0
2	F	832	0	831	33	0
2	H	832	0	831	28	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
All	All	111000	0	101168	3132	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 15.

All (3132) 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:G:1782:PHE:O	2:H:82:TYR:OH	1.75	1.03
1:A:1782:PHE:O	2:B:82:TYR:OH	1.76	1.03
1:A:4888:TYR:CD1	1:G:4914:VAL:HG23	1.95	1.02
1:C:1782:PHE:O	2:D:82:TYR:OH	1.78	1.01
1:E:1782:PHE:O	2:F:82:TYR:OH	1.77	1.00
1:E:4934:GLY:HA3	1:G:4937:ILE:HG12	1.44	1.00
1:G:3936:TYR:O	1:G:3940:LYS:NZ	1.99	0.95
1:A:4914:VAL:HG23	1:C:4888:TYR:CD1	2.02	0.95
1:C:4914:VAL:HG23	1:E:4888:TYR:CD1	2.03	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3936:TYR:O	1:A:3940:LYS:NZ	2.03	0.92
1:C:3936:TYR:O	1:C:3940:LYS:NZ	2.03	0.92
1:C:4865:LYS:NZ	1:C:4876:CYS:SG	2.44	0.91
1:E:3936:TYR:O	1:E:3940:LYS:NZ	2.03	0.91
1:A:4865:LYS:NZ	1:A:4876:CYS:SG	2.45	0.90
1:E:4914:VAL:HG23	1:G:4888:TYR:CD1	2.07	0.89
1:A:2452:ARG:NH1	1:G:174:VAL:O	2.05	0.89
1:E:174:VAL:O	1:G:2452:ARG:NH1	2.06	0.88
1:E:4865:LYS:NZ	1:E:4876:CYS:SG	2.45	0.88
1:A:174:VAL:O	1:C:2452:ARG:NH1	2.07	0.87
1:C:174:VAL:O	1:E:2452:ARG:NH1	2.07	0.87
1:A:1708:ARG:NH1	1:A:1836:PHE:O	2.08	0.87
1:G:1708:ARG:NH1	1:G:1836:PHE:O	2.08	0.87
1:A:2347:GLU:OE2	1:A:3852:LYS:HE3	1.74	0.87
1:E:1243:PRO:HD2	1:E:1458:HIS:HB3	1.56	0.87
1:E:1708:ARG:NH1	1:E:1836:PHE:O	2.07	0.86
1:C:1708:ARG:NH1	1:C:1836:PHE:O	2.08	0.86
1:C:683:ARG:NH1	1:C:705:ASN:O	2.09	0.86
1:A:4938:ASP:OD2	1:C:4940:PHE:HB3	1.76	0.86
1:A:277:GLY:HA2	1:A:317:ARG:HH12	1.40	0.85
1:A:683:ARG:NH1	1:A:705:ASN:O	2.10	0.85
1:C:277:GLY:HA2	1:C:317:ARG:HH12	1.40	0.85
1:E:277:GLY:HA2	1:E:317:ARG:HH12	1.40	0.85
1:E:683:ARG:NH1	1:E:705:ASN:O	2.09	0.85
1:C:4938:ASP:OD2	1:E:4940:PHE:HB3	1.76	0.85
1:A:2347:GLU:OE2	1:A:3852:LYS:CE	2.25	0.85
1:G:1610:ASN:ND2	1:G:1652:GLU:OE2	2.09	0.85
1:G:277:GLY:HA2	1:G:317:ARG:HH12	1.40	0.84
1:G:683:ARG:NH1	1:G:705:ASN:O	2.09	0.84
1:E:1727:ARG:NH1	1:E:1851:MET:O	2.11	0.84
1:C:1610:ASN:ND2	1:C:1652:GLU:OE2	2.09	0.84
1:G:1727:ARG:NH1	1:G:1851:MET:O	2.10	0.84
1:A:1727:ARG:NH1	1:A:1851:MET:O	2.11	0.84
1:E:495:ASN:HB3	1:E:553:ARG:HH22	1.43	0.83
1:E:1610:ASN:ND2	1:E:1652:GLU:OE2	2.11	0.83
1:G:495:ASN:HB3	1:G:553:ARG:HH22	1.43	0.83
1:G:4865:LYS:NZ	1:G:4876:CYS:SG	2.52	0.83
1:C:1727:ARG:NH1	1:C:1851:MET:O	2.11	0.83
1:E:4049:VAL:HG21	1:E:4159:ARG:HD3	1.61	0.83
1:A:4934:GLY:HA3	1:C:4937:ILE:HG12	1.58	0.82
1:A:2341:VAL:HG13	1:A:2342:ASN:H	1.45	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2341:VAL:HG13	1:C:2342:ASN:H	1.45	0.82
1:A:1610:ASN:ND2	1:A:1652:GLU:OE2	2.12	0.82
1:A:4049:VAL:HG21	1:A:4159:ARG:HD3	1.62	0.82
1:A:3969:ILE:HD11	1:A:3980:LEU:HD13	1.62	0.82
1:A:495:ASN:HB3	1:A:553:ARG:HH22	1.43	0.82
1:C:4049:VAL:HG21	1:C:4159:ARG:HD3	1.61	0.82
1:C:3969:ILE:HD11	1:C:3980:LEU:HD13	1.63	0.81
1:C:495:ASN:HB3	1:C:553:ARG:HH22	1.43	0.81
1:C:622:THR:HG23	1:C:626:LEU:HD12	1.61	0.81
1:A:622:THR:HG23	1:A:626:LEU:HD12	1.61	0.81
1:C:1243:PRO:HD2	1:C:1458:HIS:HB3	1.62	0.80
1:E:2341:VAL:HG13	1:E:2342:ASN:H	1.45	0.80
1:C:595:ARG:NE	1:C:1643:GLU:OE2	2.14	0.80
1:E:3969:ILE:HD11	1:E:3980:LEU:HD13	1.63	0.80
1:G:595:ARG:NE	1:G:1643:GLU:OE2	2.14	0.80
1:G:2341:VAL:HG13	1:G:2342:ASN:H	1.46	0.80
1:C:1206:GLN:H	1:C:1227:ALA:HB3	1.47	0.80
1:E:622:THR:HG23	1:E:626:LEU:HD12	1.61	0.80
1:E:4938:ASP:OD2	1:G:4940:PHE:HB3	1.81	0.80
1:G:622:THR:HG23	1:G:626:LEU:HD12	1.62	0.80
1:G:35:LEU:HD13	1:G:49:LEU:HD22	1.65	0.79
1:A:2770:LYS:HB3	1:A:2775:TRP:HB2	1.65	0.79
1:E:595:ARG:NE	1:E:1643:GLU:OE2	2.14	0.79
1:E:35:LEU:HD13	1:E:49:LEU:HD22	1.65	0.79
1:A:595:ARG:NE	1:A:1643:GLU:OE2	2.14	0.79
1:C:2770:LYS:HB3	1:C:2775:TRP:HB2	1.65	0.79
1:E:2770:LYS:HB3	1:E:2775:TRP:HB2	1.65	0.79
1:C:35:LEU:HD13	1:C:49:LEU:HD22	1.65	0.78
1:E:1125:ASN:HD22	1:E:1130:GLN:HG3	1.47	0.78
1:G:1206:GLN:H	1:G:1227:ALA:HB3	1.47	0.78
1:A:1125:ASN:HD22	1:A:1130:GLN:HG3	1.47	0.78
1:A:1206:GLN:H	1:A:1227:ALA:HB3	1.47	0.78
1:G:3927:GLN:HE21	1:G:3991:GLY:HA3	1.47	0.78
1:A:4658:ILE:HG22	1:A:4792:LEU:HB3	1.66	0.78
1:C:4658:ILE:HG22	1:C:4792:LEU:HB3	1.66	0.78
1:A:157:ARG:NH1	1:A:167:ASP:OD2	2.17	0.78
1:E:72:SER:O	1:E:99:ARG:NH1	2.17	0.78
1:E:157:ARG:NH1	1:E:167:ASP:OD2	2.17	0.78
1:G:2124:LEU:HD21	1:G:3677:LEU:HD21	1.66	0.78
1:G:2770:LYS:HB3	1:G:2775:TRP:HB2	1.64	0.77
1:A:35:LEU:HD13	1:A:49:LEU:HD22	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4934:GLY:HA3	1:E:4937:ILE:HG12	1.67	0.77
1:A:1623:ARG:HH11	1:A:1626:TRP:HE1	1.33	0.77
1:C:157:ARG:NH1	1:C:167:ASP:OD2	2.18	0.77
1:G:157:ARG:NH1	1:G:167:ASP:OD2	2.17	0.77
1:C:579:GLN:H	1:C:582:HIS:HD2	1.33	0.76
1:E:4658:ILE:HG22	1:E:4792:LEU:HB3	1.66	0.76
2:H:24:VAL:HG12	2:H:103:LEU:HA	1.66	0.76
1:A:3927:GLN:HE21	1:A:3991:GLY:HA3	1.50	0.76
1:A:674:PHE:HB3	2:B:40:ARG:HH12	1.51	0.76
1:C:674:PHE:HB3	2:D:40:ARG:HH12	1.50	0.76
1:C:76:ARG:HE	1:E:3844:LEU:HD21	1.51	0.76
1:E:674:PHE:HB3	2:F:40:ARG:HH12	1.50	0.76
1:A:579:GLN:H	1:A:582:HIS:HD2	1.33	0.75
1:A:72:SER:O	1:A:99:ARG:NH1	2.20	0.75
1:E:138:GLN:NE2	1:E:146:CYS:SG	2.58	0.75
1:G:3948:LYS:HG3	1:G:4012:LEU:HD12	1.66	0.75
1:C:138:GLN:NE2	1:C:146:CYS:SG	2.59	0.75
1:E:3927:GLN:HE21	1:E:3991:GLY:HA3	1.50	0.75
1:C:1623:ARG:HH11	1:C:1626:TRP:HE1	1.33	0.75
1:E:1206:GLN:H	1:E:1227:ALA:HB3	1.51	0.75
1:E:1623:ARG:HH11	1:E:1626:TRP:HE1	1.33	0.75
1:C:72:SER:O	1:C:99:ARG:NH1	2.20	0.75
1:A:138:GLN:NE2	1:A:146:CYS:SG	2.59	0.74
1:G:4984:ASN:O	1:G:4986:ALA:N	2.20	0.74
1:C:3927:GLN:HE21	1:C:3991:GLY:HA3	1.50	0.74
1:E:579:GLN:H	1:E:582:HIS:HD2	1.33	0.74
1:A:732:SER:HB3	1:A:764:VAL:HG13	1.70	0.74
1:A:76:ARG:HE	1:C:3844:LEU:HD21	1.51	0.74
1:E:674:PHE:HB3	2:F:40:ARG:NH1	2.02	0.74
1:G:1623:ARG:HH11	1:G:1626:TRP:HE1	1.32	0.74
1:C:408:ALA:O	1:C:412:ASN:ND2	2.21	0.74
1:A:408:ALA:O	1:A:412:ASN:ND2	2.21	0.74
1:C:2124:LEU:HD21	1:C:3677:LEU:HD21	1.70	0.74
1:G:72:SER:O	1:G:99:ARG:NH1	2.20	0.74
1:C:674:PHE:HB3	2:D:40:ARG:NH1	2.02	0.74
1:E:408:ALA:O	1:E:412:ASN:ND2	2.21	0.74
1:E:732:SER:HB3	1:E:764:VAL:HG13	1.70	0.74
1:E:2124:LEU:HD21	1:E:3677:LEU:HD21	1.70	0.73
1:A:674:PHE:HB3	2:B:40:ARG:NH1	2.02	0.73
1:G:579:GLN:H	1:G:582:HIS:HD2	1.33	0.73
1:G:138:GLN:NE2	1:G:146:CYS:SG	2.59	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3844:LEU:HD21	1:G:76:ARG:HE	1.52	0.73
1:C:4192:ARG:NH1	1:C:4982:GLU:OE1	2.22	0.73
1:E:663:TYR:OH	1:E:665:GLU:OE2	2.04	0.73
1:A:2124:LEU:HD21	1:A:3677:LEU:HD21	1.70	0.73
1:C:732:SER:HB3	1:C:764:VAL:HG13	1.70	0.73
1:E:1731:LEU:HA	1:E:1772:ARG:HE	1.53	0.73
1:E:3836:MET:HA	1:E:3839:CYS:SG	2.28	0.73
1:G:1731:LEU:HA	1:G:1772:ARG:HE	1.53	0.73
1:E:4192:ARG:NH1	1:E:4982:GLU:OE1	2.21	0.73
1:A:4192:ARG:NH1	1:A:4982:GLU:OE1	2.22	0.73
1:G:732:SER:HB3	1:G:764:VAL:HG13	1.70	0.73
1:G:1703:LEU:HD12	1:G:1704:PRO:HD2	1.70	0.73
1:G:2198:MET:HE3	1:G:2203:MET:SD	2.28	0.73
1:A:1105:ALA:HB3	1:A:1191:VAL:HG21	1.71	0.73
1:C:1703:LEU:HD12	1:C:1704:PRO:HD2	1.70	0.73
1:C:1731:LEU:HA	1:C:1772:ARG:HE	1.53	0.73
1:E:2198:MET:HE3	1:E:2203:MET:SD	2.28	0.73
1:C:663:TYR:OH	1:C:665:GLU:OE2	2.04	0.72
1:A:1731:LEU:HA	1:A:1772:ARG:HE	1.53	0.72
1:A:3836:MET:HA	1:A:3839:CYS:SG	2.29	0.72
1:A:215:THR:HG22	1:A:273:HIS:HA	1.72	0.72
1:E:1105:ALA:HB3	1:E:1191:VAL:HG21	1.70	0.72
1:E:1676:LEU:HD12	1:E:1725:ARG:HD3	1.72	0.72
1:A:3781:GLN:NE2	1:A:3819:TYR:OH	2.23	0.72
1:E:1766:GLY:HA2	1:E:1856:ASP:OD2	1.90	0.72
1:E:1703:LEU:HD12	1:E:1704:PRO:HD2	1.70	0.72
1:C:1676:LEU:HD12	1:C:1725:ARG:HD3	1.72	0.72
1:A:1703:LEU:HD12	1:A:1704:PRO:HD2	1.70	0.72
1:C:1766:GLY:HA2	1:C:1856:ASP:OD2	1.90	0.72
1:C:3836:MET:HA	1:C:3839:CYS:SG	2.29	0.72
1:G:215:THR:HG22	1:G:273:HIS:HA	1.72	0.72
1:A:1766:GLY:HA2	1:A:1856:ASP:OD2	1.90	0.71
1:C:215:THR:HG22	1:C:273:HIS:HA	1.71	0.71
1:E:706:GLY:H	1:E:711:LEU:HD13	1.55	0.71
1:A:706:GLY:H	1:A:711:LEU:HD13	1.55	0.71
1:G:1076:ARG:HD3	1:G:1109:LEU:HD11	1.72	0.71
1:C:1105:ALA:HB3	1:C:1191:VAL:HG21	1.72	0.71
1:G:1766:GLY:HA2	1:G:1856:ASP:OD2	1.90	0.71
1:A:745:SER:HB3	1:A:758:ARG:HB2	1.72	0.71
1:C:706:GLY:H	1:C:711:LEU:HD13	1.56	0.71
1:G:1676:LEU:HD12	1:G:1725:ARG:HD3	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:745:SER:HB3	1:G:758:ARG:HB2	1.72	0.71
1:A:1676:LEU:HD12	1:A:1725:ARG:HD3	1.71	0.71
2:B:24:VAL:HG12	2:B:103:LEU:HA	1.72	0.71
1:A:2198:MET:HE3	1:A:2203:MET:SD	2.29	0.71
1:G:408:ALA:O	1:G:412:ASN:ND2	2.21	0.71
1:G:674:PHE:HB3	2:H:40:ARG:NH1	2.06	0.71
1:C:1253:PRO:O	1:C:1281:ASN:ND2	2.24	0.70
1:E:3767:GLN:NE2	1:E:3805:LEU:O	2.25	0.70
1:G:706:GLY:H	1:G:711:LEU:HD13	1.56	0.70
1:A:1253:PRO:O	1:A:1281:ASN:ND2	2.24	0.70
1:E:215:THR:HG22	1:E:273:HIS:HA	1.72	0.70
1:C:3767:GLN:NE2	1:C:3805:LEU:O	2.25	0.70
2:D:24:VAL:HG12	2:D:103:LEU:HA	1.72	0.70
1:G:1808:ARG:NH1	1:G:1858:ASP:OD2	2.25	0.70
1:E:745:SER:HB3	1:E:758:ARG:HB2	1.73	0.70
1:A:1076:ARG:HD3	1:A:1109:LEU:HD11	1.73	0.70
1:E:3781:GLN:NE2	1:E:3819:TYR:OH	2.24	0.70
1:G:1105:ALA:HB3	1:G:1191:VAL:HG21	1.72	0.70
1:C:745:SER:HB3	1:C:758:ARG:HB2	1.72	0.70
1:C:2198:MET:HE3	1:C:2203:MET:SD	2.30	0.70
1:C:3842:LEU:HB3	1:C:3929:SER:OG	1.92	0.70
1:G:3836:MET:HA	1:G:3839:CYS:SG	2.32	0.70
1:A:1808:ARG:NH1	1:A:1858:ASP:OD2	2.25	0.70
1:A:3842:LEU:HB3	1:A:3929:SER:OG	1.92	0.70
1:G:4005:GLN:OE1	1:G:4113:SER:OG	2.09	0.70
1:C:1808:ARG:NH1	1:C:1858:ASP:OD2	2.24	0.70
1:C:3948:LYS:HG3	1:C:4012:LEU:HD12	1.73	0.70
1:G:4027:LEU:HA	1:G:4030:LEU:HB3	1.72	0.70
1:A:3920:VAL:HG22	1:A:3985:LEU:HD12	1.75	0.69
1:G:1253:PRO:O	1:G:1281:ASN:ND2	2.24	0.69
1:A:3948:LYS:HG3	1:A:4012:LEU:HD12	1.74	0.69
2:F:24:VAL:HG12	2:F:103:LEU:HA	1.72	0.69
1:G:1243:PRO:HD2	1:G:1458:HIS:HB3	1.72	0.69
1:C:76:ARG:NE	1:E:3844:LEU:HD21	2.07	0.69
1:E:1253:PRO:O	1:E:1281:ASN:ND2	2.24	0.69
1:C:1780:PRO:HG2	2:D:42:ARG:HE	1.58	0.69
1:E:1808:ARG:NH1	1:E:1858:ASP:OD2	2.25	0.69
1:C:1690:ASP:OD1	1:C:1691:GLN:N	2.26	0.69
1:E:3948:LYS:HG3	1:E:4012:LEU:HD12	1.74	0.69
1:G:1762:LEU:HD12	1:G:1763:PRO:HD2	1.73	0.69
1:A:2870:GLU:OE2	1:A:2939:ARG:NE	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3844:LEU:HD21	1:G:76:ARG:NE	2.07	0.69
1:C:607:CYS:SG	1:C:618:GLN:NE2	2.66	0.69
1:C:1719:HIS:HB3	1:C:1802:ILE:HD11	1.75	0.69
1:A:1719:HIS:HB3	1:A:1802:ILE:HD11	1.75	0.69
1:C:3781:GLN:NE2	1:C:3819:TYR:OH	2.24	0.69
1:E:3842:LEU:HB3	1:E:3929:SER:OG	1.92	0.69
1:G:1690:ASP:OD1	1:G:1691:GLN:N	2.26	0.69
1:A:3767:GLN:NE2	1:A:3805:LEU:O	2.25	0.69
1:E:110:ARG:HH21	1:E:115:ARG:HD2	1.59	0.69
1:A:475:GLN:NE2	1:A:528:SER:O	2.27	0.68
1:E:607:CYS:SG	1:E:618:GLN:NE2	2.66	0.68
1:G:475:GLN:NE2	1:G:528:SER:O	2.27	0.68
1:E:1719:HIS:HB3	1:E:1802:ILE:HD11	1.74	0.68
1:A:1690:ASP:OD1	1:A:1691:GLN:N	2.26	0.68
1:A:1762:LEU:HD12	1:A:1763:PRO:HD2	1.74	0.68
1:E:2870:GLU:OE2	1:E:2939:ARG:NE	2.26	0.68
1:A:607:CYS:SG	1:A:618:GLN:NE2	2.66	0.68
1:E:475:GLN:NE2	1:E:528:SER:O	2.27	0.68
1:E:1762:LEU:HD12	1:E:1763:PRO:HD2	1.74	0.68
2:B:23:VAL:HG22	2:B:47:LYS:HG2	1.75	0.68
1:C:1076:ARG:HD3	1:C:1109:LEU:HD11	1.73	0.68
1:C:1596:GLU:HB2	1:C:1599:MET:HG3	1.76	0.68
1:C:1762:LEU:HD12	1:C:1763:PRO:HD2	1.75	0.68
1:C:3920:VAL:HG22	1:C:3985:LEU:HD12	1.75	0.68
1:G:4573:ILE:HG21	1:G:4809:PHE:HE2	1.58	0.68
1:A:569:ILE:HG23	1:A:570:GLU:HG3	1.75	0.68
1:E:3920:VAL:HG22	1:E:3985:LEU:HD12	1.75	0.68
1:E:4030:LEU:HG	1:E:4040:ILE:HD11	1.76	0.68
1:G:1596:GLU:HB2	1:G:1599:MET:HG3	1.76	0.68
1:E:3780:LEU:HD12	1:E:3828:PHE:CE1	2.29	0.68
2:F:23:VAL:HG22	2:F:47:LYS:HG2	1.75	0.68
1:G:4236:SER:O	1:G:4675:LYS:NZ	2.26	0.68
1:C:475:GLN:NE2	1:C:528:SER:O	2.27	0.68
1:C:2876:GLU:OE2	1:C:2916:LYS:HD3	1.94	0.68
1:E:1076:ARG:HD3	1:E:1109:LEU:HD11	1.75	0.68
1:E:1596:GLU:HB2	1:E:1599:MET:HG3	1.76	0.68
1:G:607:CYS:SG	1:G:618:GLN:NE2	2.66	0.68
1:G:755:ILE:HB	1:G:768:PHE:HB2	1.76	0.68
1:A:76:ARG:NE	1:C:3844:LEU:HD21	2.07	0.68
1:E:1780:PRO:HG2	2:F:42:ARG:HE	1.59	0.67
1:A:755:ILE:HB	1:A:768:PHE:HB2	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1596:GLU:HB2	1:A:1599:MET:HG3	1.76	0.67
1:C:1432:THR:N	1:C:1518:CYS:SG	2.68	0.67
1:E:569:ILE:HG23	1:E:570:GLU:HG3	1.75	0.67
1:E:1432:THR:N	1:E:1518:CYS:SG	2.68	0.67
1:A:4030:LEU:HG	1:A:4040:ILE:HD11	1.76	0.67
1:C:2870:GLU:OE2	1:C:2939:ARG:NE	2.26	0.67
1:E:4971:THR:OG1	1:E:5029:ARG:NH2	2.27	0.67
1:G:569:ILE:HG23	1:G:570:GLU:HG3	1.75	0.67
1:G:1719:HIS:HB3	1:G:1802:ILE:HD11	1.75	0.67
1:A:1780:PRO:HG2	2:B:42:ARG:HE	1.57	0.67
1:C:4971:THR:OG1	1:C:5029:ARG:NH2	2.28	0.67
1:A:23:GLN:HE21	1:A:34:LYS:HB3	1.60	0.67
1:A:4934:GLY:CA	1:C:4937:ILE:HG12	2.23	0.67
1:C:3780:LEU:HD12	1:C:3828:PHE:CE1	2.29	0.67
1:A:1432:THR:N	1:A:1518:CYS:SG	2.68	0.67
1:A:1667:LEU:HG	1:A:1714:LEU:HD11	1.77	0.67
1:A:2876:GLU:OE2	1:A:2916:LYS:HD3	1.94	0.67
1:A:2917:ALA:HA	1:A:2920:ARG:HB3	1.77	0.67
1:C:569:ILE:HG23	1:C:570:GLU:HG3	1.75	0.67
1:E:1690:ASP:OD1	1:E:1691:GLN:N	2.27	0.67
1:C:1667:LEU:HG	1:C:1714:LEU:HD11	1.77	0.67
1:C:3966:THR:HG22	1:C:4026:MET:HA	1.77	0.67
1:E:755:ILE:HB	1:E:768:PHE:HB2	1.76	0.67
1:E:3966:THR:HG22	1:E:4026:MET:HA	1.77	0.67
1:G:2876:GLU:OE2	1:G:2916:LYS:HD3	1.93	0.67
1:C:2917:ALA:HA	1:C:2920:ARG:HB3	1.77	0.67
1:E:2917:ALA:HA	1:E:2920:ARG:HB3	1.77	0.67
1:C:110:ARG:HH21	1:C:115:ARG:HD2	1.59	0.67
1:C:3817:LEU:HD11	1:C:3821:LYS:HE2	1.77	0.67
2:D:23:VAL:HG22	2:D:47:LYS:HG2	1.75	0.67
1:G:1432:THR:N	1:G:1518:CYS:SG	2.68	0.67
1:A:110:ARG:HH21	1:A:115:ARG:HD2	1.59	0.67
1:C:755:ILE:HB	1:C:768:PHE:HB2	1.77	0.67
1:E:2876:GLU:OE2	1:E:2916:LYS:HD3	1.95	0.67
1:E:4934:GLY:CA	1:G:4937:ILE:HG12	2.21	0.67
1:A:3780:LEU:HD12	1:A:3828:PHE:CE1	2.29	0.66
1:A:3817:LEU:HD11	1:A:3821:LYS:HE2	1.78	0.66
1:G:110:ARG:HH21	1:G:115:ARG:HD2	1.60	0.66
1:G:2865:VAL:O	1:G:2928:LYS:NZ	2.28	0.66
1:A:4940:PHE:HB3	1:G:4938:ASP:OD2	1.95	0.66
1:C:35:LEU:HD22	1:C:49:LEU:HD13	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:35:LEU:HD22	1:E:49:LEU:HD13	1.77	0.66
1:E:1667:LEU:HG	1:E:1714:LEU:HD11	1.77	0.66
1:G:35:LEU:HD22	1:G:49:LEU:HD13	1.77	0.66
1:G:1735:ILE:HD11	1:G:2156:LEU:HD11	1.77	0.66
1:A:4937:ILE:HG12	1:G:4934:GLY:HA3	1.78	0.66
1:A:4971:THR:OG1	1:A:5029:ARG:NH2	2.29	0.66
1:G:3948:LYS:HE3	1:G:4012:LEU:HB2	1.77	0.66
1:A:2547:ALA:O	1:A:2551:ASN:ND2	2.28	0.66
1:C:665:GLU:HB2	1:C:792:LEU:HB2	1.78	0.66
1:E:34:LYS:O	1:E:52:THR:OG1	2.14	0.66
1:E:176:SER:HB2	1:E:178:ARG:HH21	1.60	0.66
1:E:2547:ALA:O	1:E:2551:ASN:ND2	2.28	0.66
1:E:3958:ALA:HA	1:E:3961:VAL:HG12	1.78	0.66
1:G:176:SER:HB2	1:G:178:ARG:HH21	1.60	0.66
1:G:618:GLN:OE1	1:G:1678:ASN:ND2	2.29	0.66
1:A:34:LYS:O	1:A:52:THR:OG1	2.14	0.66
1:A:3966:THR:HG22	1:A:4026:MET:HA	1.77	0.66
1:C:176:SER:HB2	1:C:178:ARG:HH21	1.60	0.66
1:E:23:GLN:HE21	1:E:34:LYS:HB3	1.60	0.66
1:C:2547:ALA:O	1:C:2551:ASN:ND2	2.28	0.66
1:A:3958:ALA:HA	1:A:3961:VAL:HG12	1.78	0.66
1:A:4917:ASP:OD2	1:C:4892:ARG:CZ	2.43	0.66
1:C:4027:LEU:HD11	1:C:4146:LEU:HD11	1.77	0.66
1:G:2547:ALA:O	1:G:2551:ASN:ND2	2.28	0.66
1:C:3958:ALA:HA	1:C:3961:VAL:HG12	1.78	0.66
1:E:1783:VAL:O	2:F:56:ILE:HG23	1.96	0.66
1:E:4573:ILE:HD11	1:E:4646:LEU:HB3	1.78	0.66
1:C:23:GLN:HE21	1:C:34:LYS:HB3	1.60	0.65
1:E:4037:ASN:HB3	1:E:4042:ARG:HH21	1.61	0.65
1:C:4030:LEU:HG	1:C:4040:ILE:HD11	1.76	0.65
1:E:3817:LEU:HD11	1:E:3821:LYS:HE2	1.78	0.65
1:G:34:LYS:O	1:G:52:THR:OG1	2.14	0.65
1:A:2822:THR:HG1	1:A:2938:THR:HG1	1.42	0.65
1:C:4901:ILE:HG21	1:C:4913:ARG:HH21	1.60	0.65
1:C:4917:ASP:OD2	1:E:4892:ARG:CZ	2.44	0.65
1:C:404:ILE:HD13	1:C:481:GLU:HG3	1.78	0.65
1:E:3754:GLU:OE2	1:E:4718:LYS:HE3	1.97	0.65
1:G:665:GLU:HB2	1:G:792:LEU:HB2	1.78	0.65
1:A:176:SER:HB2	1:A:178:ARG:HH21	1.60	0.65
1:A:2227:LYS:O	1:A:2230:THR:OG1	2.13	0.65
1:E:404:ILE:HD13	1:E:481:GLU:HG3	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:78:LEU:HD11	1:G:147:TRP:CG	2.32	0.65
1:G:1667:LEU:HG	1:G:1714:LEU:HD11	1.77	0.65
1:G:1783:VAL:O	2:H:56:ILE:HG23	1.96	0.65
1:G:23:GLN:HE21	1:G:34:LYS:HB3	1.60	0.65
1:A:206:CYS:HB3	1:A:271:GLY:HA3	1.78	0.65
1:A:4901:ILE:HG21	1:A:4913:ARG:HH21	1.61	0.65
1:E:627:PRO:HG3	2:F:89:GLY:HA2	1.79	0.65
1:E:2227:LYS:O	1:E:2230:THR:OG1	2.13	0.65
1:G:206:CYS:HB3	1:G:271:GLY:HA3	1.77	0.65
1:G:1438:ARG:HB3	1:G:1563:GLN:HB3	1.79	0.65
1:A:78:LEU:HD11	1:A:147:TRP:CG	2.32	0.65
1:E:4027:LEU:HD11	1:E:4146:LEU:HD11	1.78	0.65
1:G:404:ILE:HD13	1:G:481:GLU:HG3	1.78	0.65
1:C:34:LYS:O	1:C:52:THR:OG1	2.14	0.65
1:G:2227:LYS:O	1:G:2230:THR:OG1	2.13	0.65
1:A:663:TYR:OH	1:A:665:GLU:OE2	2.04	0.64
1:A:4027:LEU:HD11	1:A:4146:LEU:HD11	1.78	0.64
1:A:4573:ILE:HD11	1:A:4646:LEU:HB3	1.79	0.64
1:C:1735:ILE:HD11	1:C:2156:LEU:HD11	1.78	0.64
1:G:3966:THR:O	1:G:3970:GLN:N	2.29	0.64
1:A:665:GLU:HB2	1:A:792:LEU:HB2	1.78	0.64
1:A:1438:ARG:HB3	1:A:1563:GLN:HB3	1.79	0.64
1:G:865:PRO:HA	1:G:868:GLU:HB2	1.79	0.64
1:C:4037:ASN:HB3	1:C:4042:ARG:HH21	1.61	0.64
1:E:1611:HIS:HB2	1:E:1652:GLU:HB2	1.77	0.64
1:G:588:SER:O	1:G:592:LYS:HG2	1.98	0.64
1:G:674:PHE:O	2:H:40:ARG:NH1	2.29	0.64
1:G:3754:GLU:OE2	1:G:4718:LYS:HE3	1.97	0.64
1:A:35:LEU:HD22	1:A:49:LEU:HD13	1.78	0.64
1:A:1735:ILE:HD11	1:A:2156:LEU:HD11	1.77	0.64
1:C:277:GLY:HA2	1:C:317:ARG:NH1	2.13	0.64
1:C:865:PRO:HA	1:C:868:GLU:HB2	1.79	0.64
1:C:4573:ILE:HD11	1:C:4646:LEU:HB3	1.78	0.64
1:E:4185:GLY:O	1:E:4187:SER:N	2.30	0.64
1:G:1744:ALA:HB3	1:G:1745:ILE:HA	1.80	0.64
1:G:4185:GLY:O	1:G:4187:SER:N	2.31	0.64
1:A:491:ILE:O	1:A:495:ASN:ND2	2.31	0.64
1:A:4185:GLY:O	1:A:4187:SER:N	2.31	0.64
1:C:1115:LEU:HD13	1:C:1193:SER:HB2	1.80	0.64
1:E:618:GLN:OE1	1:E:1678:ASN:ND2	2.31	0.64
1:A:683:ARG:HD2	1:A:705:ASN:HB3	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1438:ARG:HB3	1:C:1563:GLN:HB3	1.80	0.64
1:C:3754:GLU:OE2	1:C:4718:LYS:HE3	1.96	0.64
1:E:206:CYS:HB3	1:E:271:GLY:HA3	1.79	0.64
1:E:665:GLU:HB2	1:E:792:LEU:HB2	1.78	0.64
1:E:683:ARG:HD2	1:E:705:ASN:HB3	1.80	0.64
1:A:1611:HIS:HB2	1:A:1652:GLU:HB2	1.79	0.64
1:C:206:CYS:HB3	1:C:271:GLY:HA3	1.78	0.64
1:C:588:SER:O	1:C:592:LYS:HG2	1.98	0.64
1:C:1611:HIS:HB2	1:C:1652:GLU:HB2	1.80	0.64
1:C:1716:ILE:HD11	1:C:1844:LEU:HA	1.80	0.64
2:D:14:THR:HG22	2:D:106:LEU:HD12	1.80	0.64
1:E:1438:ARG:HB3	1:E:1563:GLN:HB3	1.79	0.64
1:A:865:PRO:HA	1:A:868:GLU:HB2	1.79	0.64
1:A:1744:ALA:HB3	1:A:1745:ILE:HA	1.80	0.64
1:A:3754:GLU:OE2	1:A:4718:LYS:HE3	1.97	0.64
1:A:4037:ASN:HB3	1:A:4042:ARG:HH21	1.61	0.64
1:C:78:LEU:HD11	1:C:147:TRP:CG	2.32	0.64
1:C:618:GLN:OE1	1:C:1678:ASN:ND2	2.31	0.64
1:E:1716:ILE:HD11	1:E:1844:LEU:HA	1.80	0.64
1:G:683:ARG:HD2	1:G:705:ASN:HB3	1.80	0.64
1:C:491:ILE:O	1:C:495:ASN:ND2	2.31	0.64
1:E:1744:ALA:HB3	1:E:1745:ILE:HA	1.80	0.64
1:C:1744:ALA:HB3	1:C:1745:ILE:HA	1.80	0.64
1:E:1735:ILE:HD11	1:E:2156:LEU:HD11	1.78	0.64
1:G:674:PHE:HB3	2:H:40:ARG:HH12	1.61	0.64
1:G:1737:PRO:HG2	1:G:1742:THR:HG21	1.80	0.64
1:A:588:SER:O	1:A:592:LYS:HG2	1.98	0.63
1:G:1611:HIS:HB2	1:G:1652:GLU:HB2	1.79	0.63
1:A:627:PRO:HG3	2:B:89:GLY:HA2	1.80	0.63
1:A:1783:VAL:O	2:B:56:ILE:HG23	1.98	0.63
1:E:4914:VAL:CG2	1:G:4888:TYR:HB2	2.28	0.63
2:F:14:THR:HG22	2:F:106:LEU:HD12	1.80	0.63
1:A:1716:ILE:HD11	1:A:1844:LEU:HA	1.80	0.63
1:A:4034:ASN:OD1	1:A:4035:VAL:N	2.32	0.63
1:C:627:PRO:HG3	2:D:89:GLY:HA2	1.79	0.63
1:C:1783:VAL:O	2:D:56:ILE:HG23	1.97	0.63
1:E:546:TRP:HE1	1:E:550:LYS:HZ1	1.47	0.63
1:G:1716:ILE:HD11	1:G:1844:LEU:HA	1.80	0.63
1:G:2166:LEU:HD12	1:G:2206:THR:HG23	1.80	0.63
1:A:404:ILE:HD13	1:A:481:GLU:HG3	1.78	0.63
1:E:1115:LEU:HD13	1:E:1193:SER:HB2	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:491:ILE:O	1:G:495:ASN:ND2	2.31	0.63
1:A:1115:LEU:HD13	1:A:1193:SER:HB2	1.81	0.63
1:A:2166:LEU:HD12	1:A:2206:THR:HG23	1.80	0.63
2:B:71:ARG:NH2	2:B:100:ASP:OD2	2.32	0.63
1:E:491:ILE:O	1:E:495:ASN:ND2	2.31	0.63
1:E:588:SER:O	1:E:592:LYS:HG2	1.98	0.63
1:C:683:ARG:HD2	1:C:705:ASN:HB3	1.79	0.63
1:E:4917:ASP:OD2	1:G:4892:ARG:CZ	2.46	0.63
1:A:618:GLN:OE1	1:A:1678:ASN:ND2	2.31	0.63
2:B:14:THR:HG22	2:B:106:LEU:HD12	1.80	0.63
1:C:4984:ASN:O	1:C:4986:ALA:N	2.31	0.63
1:E:4034:ASN:OD1	1:E:4035:VAL:N	2.32	0.63
1:E:4984:ASN:O	1:E:4986:ALA:N	2.32	0.63
1:G:623:GLU:OE2	2:H:89:GLY:N	2.32	0.63
1:C:3813:GLN:NE2	1:C:3890:LEU:O	2.32	0.63
1:C:4034:ASN:OD1	1:C:4035:VAL:N	2.32	0.63
1:E:3958:ALA:HB3	1:E:4019:LEU:HD11	1.81	0.63
2:F:74:LEU:HB2	2:F:99:PHE:HB2	1.81	0.63
1:C:3958:ALA:HB3	1:C:4019:LEU:HD11	1.81	0.63
1:E:2166:LEU:HD12	1:E:2206:THR:HG23	1.81	0.63
1:G:1115:LEU:HD13	1:G:1193:SER:HB2	1.81	0.63
1:A:2149:VAL:O	1:A:2152:THR:OG1	2.15	0.62
1:C:687:ALA:HB2	1:C:711:LEU:HD23	1.81	0.62
1:C:1115:LEU:HD21	1:C:1123:VAL:HG11	1.81	0.62
1:E:3786:CYS:SG	1:E:3794:VAL:HG22	2.39	0.62
1:G:707:VAL:HA	1:G:725:HIS:HB2	1.82	0.62
1:G:4962:GLY:O	1:G:4964:GLY:N	2.32	0.62
1:A:1243:PRO:HD2	1:A:1458:HIS:HB3	1.82	0.62
1:C:3786:CYS:SG	1:C:3794:VAL:HG22	2.38	0.62
1:E:687:ALA:HB2	1:E:711:LEU:HD23	1.81	0.62
1:G:4049:VAL:HG21	1:G:4159:ARG:HD3	1.81	0.62
1:A:4962:GLY:O	1:A:4964:GLY:N	2.32	0.62
1:C:4934:GLY:CA	1:E:4937:ILE:HG12	2.30	0.62
1:G:4034:ASN:OD1	1:G:4035:VAL:N	2.32	0.62
1:C:4185:GLY:O	1:C:4187:SER:N	2.31	0.62
1:A:1115:LEU:HD21	1:A:1123:VAL:HG11	1.81	0.62
1:A:3813:GLN:NE2	1:A:3890:LEU:O	2.33	0.62
1:G:1115:LEU:HD21	1:G:1123:VAL:HG11	1.81	0.62
1:G:3781:GLN:NE2	1:G:3819:TYR:OH	2.28	0.62
1:A:276:TRP:NE1	1:A:338:GLU:OE2	2.28	0.62
1:A:3958:ALA:HB3	1:A:4019:LEU:HD11	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:38:ALA:HB1	1:C:64:ILE:HD12	1.81	0.62
1:C:790:ARG:HA	1:C:1627:ALA:HA	1.82	0.62
1:E:1737:PRO:HG2	1:E:1742:THR:HG21	1.81	0.62
1:G:4037:ASN:HB3	1:G:4042:ARG:HH21	1.63	0.62
1:C:1098:GLY:HA3	1:C:1198:GLN:HE21	1.65	0.62
1:C:3843:ASP:OD1	1:C:3844:LEU:N	2.32	0.62
1:C:4962:GLY:O	1:C:4964:GLY:N	2.32	0.62
1:E:76:ARG:NH1	1:E:79:GLN:OE1	2.32	0.62
1:E:78:LEU:HD11	1:E:147:TRP:CG	2.35	0.62
1:E:707:VAL:HA	1:E:725:HIS:HB2	1.82	0.62
1:E:739:ALA:O	1:E:741:GLU:N	2.30	0.62
1:E:3992:PHE:O	1:E:3996:PHE:N	2.29	0.62
1:A:707:VAL:HA	1:A:725:HIS:HB2	1.82	0.62
1:A:1125:ASN:ND2	1:A:1130:GLN:O	2.33	0.62
1:A:4888:TYR:HD1	1:G:4914:VAL:HG23	1.57	0.62
2:D:74:LEU:HB2	2:D:99:PHE:HB2	1.80	0.62
1:E:3919:THR:HG21	1:E:3968:TYR:HE2	1.65	0.62
1:C:2166:LEU:HD12	1:C:2206:THR:HG23	1.81	0.62
1:E:865:PRO:HA	1:E:868:GLU:HB2	1.80	0.62
1:E:4962:GLY:O	1:E:4964:GLY:N	2.32	0.62
1:G:3969:ILE:HG23	1:G:3977:GLN:HG2	1.80	0.62
1:C:276:TRP:NE1	1:C:338:GLU:OE2	2.28	0.61
1:C:2227:LYS:O	1:C:2230:THR:OG1	2.14	0.61
1:E:3813:GLN:NE2	1:E:3890:LEU:O	2.33	0.61
1:G:276:TRP:NE1	1:G:338:GLU:OE2	2.28	0.61
1:C:707:VAL:HA	1:C:725:HIS:HB2	1.82	0.61
1:E:1125:ASN:ND2	1:E:1130:GLN:O	2.33	0.61
1:G:627:PRO:HG3	2:H:89:GLY:HA2	1.81	0.61
1:A:38:ALA:HB1	1:A:64:ILE:HD12	1.81	0.61
1:A:76:ARG:HH21	1:C:3844:LEU:HD21	1.65	0.61
1:A:687:ALA:HB2	1:A:711:LEU:HD23	1.81	0.61
1:A:2107:GLN:NE2	1:A:3679:LYS:O	2.33	0.61
1:A:4984:ASN:O	1:A:4986:ALA:N	2.32	0.61
2:B:74:LEU:HB2	2:B:99:PHE:HB2	1.81	0.61
1:C:34:LYS:N	1:C:53:SER:OG	2.33	0.61
1:E:465:GLN:NE2	1:E:3712:GLU:OE1	2.33	0.61
1:G:38:ALA:HB1	1:G:64:ILE:HD12	1.81	0.61
1:C:2107:GLN:NE2	1:C:3679:LYS:O	2.33	0.61
1:E:3843:ASP:OD1	1:E:3844:LEU:N	2.32	0.61
1:G:3813:GLN:NE2	1:G:3890:LEU:O	2.33	0.61
1:A:33:LEU:HD11	1:A:51:PRO:HB3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:465:GLN:NE2	1:A:3712:GLU:OE1	2.33	0.61
1:A:790:ARG:HA	1:A:1627:ALA:HA	1.82	0.61
1:C:465:GLN:NE2	1:C:3712:GLU:OE1	2.34	0.61
1:C:4027:LEU:HD11	1:C:4146:LEU:CD1	2.31	0.61
1:C:4828:SER:HA	1:C:4831:THR:HG22	1.83	0.61
1:E:2107:GLN:NE2	1:E:3679:LYS:O	2.33	0.61
1:G:687:ALA:HB2	1:G:711:LEU:HD23	1.81	0.61
1:G:3423:TRP:O	1:G:3428:ASN:N	2.32	0.61
1:A:3844:LEU:HD21	1:G:76:ARG:HH21	1.65	0.61
1:A:4005:GLN:OE1	1:A:4113:SER:OG	2.19	0.61
1:C:1737:PRO:HG2	1:C:1742:THR:HG21	1.81	0.61
1:C:3919:THR:HG21	1:C:3968:TYR:HE2	1.65	0.61
1:E:38:ALA:HB1	1:E:64:ILE:HD12	1.82	0.61
1:E:4828:SER:HA	1:E:4831:THR:HG22	1.82	0.61
1:G:4837:LEU:HD11	1:G:4932:ILE:HG23	1.81	0.61
1:C:1970:GLN:NE2	1:C:3645:PRO:O	2.29	0.61
1:A:1098:GLY:HA3	1:A:1198:GLN:HE21	1.65	0.61
1:E:34:LYS:N	1:E:53:SER:OG	2.33	0.61
1:E:276:TRP:NE1	1:E:338:GLU:OE2	2.28	0.61
2:F:71:ARG:NH2	2:F:100:ASP:OD2	2.32	0.61
1:G:2149:VAL:O	1:G:2152:THR:OG1	2.14	0.61
1:G:2917:ALA:HA	1:G:2920:ARG:HB3	1.83	0.61
1:A:34:LYS:N	1:A:53:SER:OG	2.33	0.61
1:C:76:ARG:HH21	1:E:3844:LEU:HD21	1.66	0.61
2:D:71:ARG:NH2	2:D:100:ASP:OD2	2.31	0.61
1:E:4901:ILE:HG21	1:E:4913:ARG:HH21	1.65	0.61
1:G:790:ARG:HA	1:G:1627:ALA:HA	1.82	0.61
1:G:4573:ILE:HG21	1:G:4809:PHE:CE2	2.36	0.61
1:A:277:GLY:HA2	1:A:317:ARG:NH1	2.13	0.60
1:A:489:ASN:HB3	1:A:493:ARG:NH1	2.16	0.60
1:A:2865:VAL:O	1:A:2928:LYS:NZ	2.33	0.60
1:A:3919:THR:HG21	1:A:3968:TYR:HE2	1.65	0.60
1:A:4828:SER:HA	1:A:4831:THR:HG22	1.81	0.60
1:C:3805:LEU:O	1:C:3807:GLY:N	2.34	0.60
1:G:3969:ILE:HD11	1:G:3980:LEU:HD13	1.83	0.60
1:A:1737:PRO:HG2	1:A:1742:THR:HG21	1.82	0.60
1:E:4027:LEU:HD11	1:E:4146:LEU:CD1	2.31	0.60
1:G:3969:ILE:HD13	1:G:4030:LEU:HD13	1.83	0.60
1:A:4963:ILE:HD12	1:A:5030:LYS:NZ	2.16	0.60
1:C:1252:HIS:C	1:C:1254:HIS:H	2.05	0.60
1:G:33:LEU:HD11	1:G:51:PRO:HB3	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:699:GLY:O	1:A:1647:CYS:N	2.35	0.60
1:A:1252:HIS:C	1:A:1254:HIS:H	2.05	0.60
1:A:3844:LEU:HD21	1:G:76:ARG:NH2	2.16	0.60
1:E:790:ARG:HA	1:E:1627:ALA:HA	1.82	0.60
1:E:2822:THR:OG1	1:E:2938:THR:OG1	2.19	0.60
1:E:1115:LEU:HD21	1:E:1123:VAL:HG11	1.81	0.60
1:C:1125:ASN:HD22	1:C:1130:GLN:HG3	1.66	0.60
1:G:489:ASN:HB3	1:G:493:ARG:NH1	2.16	0.60
1:G:1098:GLY:HA3	1:G:1198:GLN:HE21	1.65	0.60
1:C:681:HIS:HA	1:C:716:PHE:CD1	2.37	0.60
1:C:4963:ILE:HD12	1:C:5030:LYS:NZ	2.16	0.60
1:E:3805:LEU:O	1:E:3807:GLY:N	2.33	0.60
1:C:33:LEU:HD11	1:C:51:PRO:HB3	1.83	0.60
1:E:1252:HIS:C	1:E:1254:HIS:H	2.05	0.60
1:G:681:HIS:HA	1:G:716:PHE:CD1	2.37	0.60
1:A:4027:LEU:HD11	1:A:4146:LEU:CD1	2.31	0.60
1:C:714:TYR:HB3	1:C:757:PHE:HD2	1.66	0.60
1:G:34:LYS:N	1:G:53:SER:OG	2.33	0.60
1:G:739:ALA:O	1:G:741:GLU:N	2.31	0.60
1:G:3920:VAL:HG22	1:G:3985:LEU:HD12	1.84	0.60
1:A:714:TYR:HB3	1:A:757:PHE:HD2	1.66	0.60
1:C:489:ASN:HB3	1:C:493:ARG:NH1	2.16	0.60
1:C:2149:VAL:O	1:C:2152:THR:OG1	2.15	0.60
1:E:1098:GLY:HA3	1:E:1198:GLN:HE21	1.65	0.60
1:E:2149:VAL:O	1:E:2152:THR:OG1	2.15	0.60
1:A:1927:LEU:HD21	1:A:2101:MET:HG2	1.83	0.59
1:A:4228:ALA:HB2	1:C:4976:GLU:OE1	2.01	0.59
1:E:674:PHE:O	2:F:40:ARG:NH1	2.35	0.59
1:E:4836:GLN:HB3	1:G:4826:ILE:HD11	1.83	0.59
1:A:1237:TRP:HD1	1:A:1611:HIS:HA	1.68	0.59
1:C:4005:GLN:OE1	1:C:4113:SER:OG	2.19	0.59
1:E:714:TYR:HB3	1:E:757:PHE:HD2	1.66	0.59
1:E:3891:LEU:HB3	1:E:3899:PHE:CE2	2.37	0.59
1:G:714:TYR:HB3	1:G:757:PHE:HD2	1.67	0.59
1:E:106:ALA:HA	1:E:149:THR:HA	1.83	0.59
1:E:4005:GLN:OE1	1:E:4113:SER:OG	2.18	0.59
1:G:1780:PRO:HG2	2:H:42:ARG:HE	1.67	0.59
1:A:2336:ARG:HG3	1:A:2435:ARG:HG3	1.85	0.59
1:C:2159:LEU:O	1:C:2162:ILE:HG22	2.02	0.59
1:C:4228:ALA:HB2	1:E:4976:GLU:OE1	2.02	0.59
1:E:1552:VAL:HG12	1:E:1554:VAL:HG23	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1927:LEU:HD21	1:E:2101:MET:HG2	1.84	0.59
1:E:4963:ILE:HD12	1:E:5030:LYS:NZ	2.17	0.59
1:G:2333:ASP:OD1	1:G:2336:ARG:NH2	2.36	0.59
1:A:1552:VAL:HG12	1:A:1554:VAL:HG23	1.84	0.59
1:A:2159:LEU:O	1:A:2162:ILE:HG22	2.02	0.59
1:C:1101:ARG:HG3	1:C:1193:SER:HB3	1.85	0.59
1:C:2336:ARG:HG3	1:C:2435:ARG:HG3	1.85	0.59
1:E:1243:PRO:HD2	1:E:1458:HIS:CB	2.29	0.59
1:E:3878:ASP:OD2	1:E:3953:LYS:HG3	2.03	0.59
1:C:76:ARG:NH2	1:E:3844:LEU:HD21	2.17	0.59
1:C:106:ALA:HA	1:C:149:THR:HA	1.83	0.59
1:C:402:ARG:NH1	1:C:405:HIS:HD2	2.01	0.59
1:C:3878:ASP:OD2	1:C:3953:LYS:HG3	2.03	0.59
1:E:2159:LEU:O	1:E:2162:ILE:HG22	2.02	0.59
1:G:277:GLY:HA2	1:G:317:ARG:NH1	2.13	0.59
1:G:1252:HIS:C	1:G:1254:HIS:H	2.05	0.59
1:G:1288:PHE:HE2	1:G:1460:HIS:HA	1.68	0.59
1:G:1552:VAL:HG12	1:G:1554:VAL:HG23	1.85	0.59
1:G:1648:MET:SD	1:G:1656:ARG:NH2	2.76	0.59
1:A:4928:LEU:O	1:A:4932:ILE:HD12	2.03	0.59
1:C:1637:MET:HG3	1:C:1650:ILE:HD13	1.85	0.59
1:C:3891:LEU:HB3	1:C:3899:PHE:CE2	2.37	0.59
1:C:4928:LEU:O	1:C:4932:ILE:HD12	2.03	0.59
1:E:699:GLY:O	1:E:1647:CYS:N	2.36	0.59
1:G:1637:MET:HG3	1:G:1650:ILE:HD13	1.84	0.59
1:A:3805:LEU:O	1:A:3807:GLY:N	2.33	0.59
1:A:3878:ASP:OD2	1:A:3953:LYS:HG3	2.03	0.59
1:C:674:PHE:O	2:D:40:ARG:NH1	2.36	0.59
1:G:1101:ARG:HG3	1:G:1193:SER:HB3	1.84	0.59
1:G:2336:ARG:HG3	1:G:2435:ARG:HG3	1.85	0.59
1:G:2756:ASN:OD1	1:G:2806:ARG:NH2	2.35	0.59
1:G:2875:ALA:HB2	1:G:2927:LEU:HD12	1.84	0.59
1:G:3891:LEU:HB3	1:G:3899:PHE:CE2	2.37	0.59
1:A:106:ALA:HA	1:A:149:THR:HA	1.83	0.59
1:A:674:PHE:O	2:B:40:ARG:NH1	2.35	0.59
1:A:1637:MET:HG3	1:A:1650:ILE:HD13	1.85	0.59
1:C:1648:MET:SD	1:C:1656:ARG:NH2	2.76	0.59
1:E:33:LEU:HD11	1:E:51:PRO:HB3	1.83	0.59
1:E:2333:ASP:OD1	1:E:2336:ARG:NH2	2.36	0.59
1:G:2107:GLN:NE2	1:G:3679:LYS:O	2.35	0.59
1:A:2333:ASP:OD1	1:A:2336:ARG:NH2	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4059:LEU:HD13	1:A:4167:ALA:HB2	1.85	0.59
1:A:4963:ILE:HD11	1:A:5025:GLY:O	2.03	0.59
1:C:530:ILE:HG23	1:C:537:CYS:HB3	1.85	0.59
1:C:2248:ARG:HG2	1:C:2286:LEU:HD11	1.85	0.59
1:E:489:ASN:HB3	1:E:493:ARG:NH1	2.16	0.59
1:G:106:ALA:HA	1:G:149:THR:HA	1.83	0.59
1:G:3805:LEU:O	1:G:3807:GLY:N	2.32	0.59
1:G:4963:ILE:HD11	1:G:5025:GLY:O	2.03	0.59
1:G:4971:THR:OG1	1:G:5029:ARG:NH2	2.36	0.59
1:A:76:ARG:NH2	1:C:3844:LEU:HD21	2.16	0.58
1:A:402:ARG:NH1	1:A:405:HIS:HD2	2.01	0.58
1:A:822:ARG:HA	1:A:1623:ARG:HH12	1.68	0.58
1:C:1927:LEU:HD21	1:C:2101:MET:HG2	1.84	0.58
1:C:3879:GLU:OE2	1:C:3883:ASP:OD2	2.21	0.58
1:E:1648:MET:SD	1:E:1656:ARG:NH2	2.76	0.58
1:E:2248:ARG:HG2	1:E:2286:LEU:HD11	1.85	0.58
1:G:530:ILE:HG23	1:G:537:CYS:HB3	1.85	0.58
1:C:4963:ILE:HD11	1:C:5025:GLY:O	2.03	0.58
1:E:880:GLU:HG2	1:E:967:PRO:HG2	1.85	0.58
1:E:1091:GLU:HB2	1:E:1203:ASN:HB2	1.86	0.58
1:E:1970:GLN:NE2	1:E:3645:PRO:O	2.29	0.58
1:C:1079:LYS:HA	1:C:1082:THR:HG23	1.85	0.58
1:E:1637:MET:HG3	1:E:1650:ILE:HD13	1.84	0.58
1:E:3727:ASP:HB3	1:E:3731:LYS:NZ	2.18	0.58
1:G:402:ARG:NH1	1:G:405:HIS:HD2	2.01	0.58
1:G:1657:LEU:HA	1:G:1660:GLN:HG2	1.85	0.58
1:A:681:HIS:HA	1:A:716:PHE:CD1	2.37	0.58
1:A:3843:ASP:OD1	1:A:3844:LEU:N	2.31	0.58
1:A:3992:PHE:O	1:A:3996:PHE:N	2.29	0.58
1:C:880:GLU:HG2	1:C:967:PRO:HG2	1.85	0.58
1:C:1552:VAL:HG12	1:C:1554:VAL:HG23	1.85	0.58
1:E:4214:LYS:HD2	1:E:4985:LEU:HD23	1.84	0.58
1:A:1648:MET:SD	1:A:1656:ARG:NH2	2.76	0.58
1:A:3879:GLU:OE2	1:A:3883:ASP:OD2	2.21	0.58
1:C:3992:PHE:O	1:C:3996:PHE:N	2.29	0.58
1:E:2336:ARG:HG3	1:E:2435:ARG:HG3	1.86	0.58
1:G:2159:LEU:O	1:G:2162:ILE:HG22	2.02	0.58
1:G:4818:MET:HA	1:G:4824:ARG:HG2	1.84	0.58
1:A:489:ASN:HB3	1:A:493:ARG:HH12	1.69	0.58
1:A:1091:GLU:HB2	1:A:1203:ASN:HB2	1.86	0.58
1:A:3891:LEU:HB3	1:A:3899:PHE:CE2	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:739:ALA:O	1:C:741:GLU:N	2.31	0.58
1:C:2865:VAL:O	1:C:2928:LYS:NZ	2.34	0.58
1:G:717:ASP:O	1:G:720:HIS:NE2	2.35	0.58
1:G:1125:ASN:HD22	1:G:1130:GLN:HG3	1.67	0.58
1:A:1970:GLN:NE2	1:A:3645:PRO:O	2.29	0.58
1:A:2248:ARG:HG2	1:A:2286:LEU:HD11	1.85	0.58
1:A:2875:ALA:HB2	1:A:2927:LEU:HD12	1.86	0.58
1:A:3727:ASP:HB3	1:A:3731:LYS:NZ	2.18	0.58
1:C:990:GLU:HG3	1:C:1024:TYR:HB3	1.86	0.58
1:E:277:GLY:HA2	1:E:317:ARG:NH1	2.13	0.58
1:G:465:GLN:HE21	1:G:3711:THR:HA	1.68	0.58
1:G:537:CYS:HB2	1:G:567:VAL:HG13	1.86	0.58
1:G:1091:GLU:HB2	1:G:1203:ASN:HB2	1.86	0.58
1:A:1101:ARG:HG3	1:A:1193:SER:HB3	1.86	0.58
1:A:1657:LEU:HA	1:A:1660:GLN:HG2	1.85	0.58
1:C:37:LEU:HD13	1:C:191:VAL:HG21	1.86	0.58
1:C:537:CYS:HB2	1:C:567:VAL:HG13	1.85	0.58
1:C:822:ARG:HA	1:C:1623:ARG:HH12	1.69	0.58
1:E:465:GLN:HE21	1:E:3711:THR:HA	1.69	0.58
1:E:530:ILE:HG23	1:E:537:CYS:HB3	1.85	0.58
1:E:1944:GLU:HG3	1:E:2123:LEU:HD21	1.86	0.58
1:G:489:ASN:HB3	1:G:493:ARG:HH12	1.69	0.58
1:G:3813:GLN:OE1	1:G:3896:ASN:ND2	2.37	0.58
1:G:3817:LEU:HD11	1:G:3821:LYS:HE2	1.84	0.58
1:A:3701:LEU:HD11	1:A:3725:TYR:CD1	2.39	0.58
1:C:465:GLN:HE21	1:C:3711:THR:HA	1.69	0.58
1:C:699:GLY:O	1:C:1647:CYS:N	2.36	0.58
1:C:1091:GLU:HB2	1:C:1203:ASN:HB2	1.86	0.58
1:C:1657:LEU:HA	1:C:1660:GLN:HG2	1.85	0.58
1:G:603:LEU:HA	1:G:606:LEU:HD12	1.86	0.58
1:G:699:GLY:O	1:G:1647:CYS:N	2.36	0.58
1:A:2347:GLU:OE2	1:A:3852:LYS:CD	2.52	0.58
1:A:2347:GLU:OE2	1:A:3852:LYS:HD3	2.04	0.58
1:C:546:TRP:HE1	1:C:550:LYS:HZ1	1.52	0.58
1:C:1802:ILE:HB	1:C:1804:LEU:HD12	1.86	0.58
1:C:2875:ALA:HB2	1:C:2927:LEU:HD12	1.86	0.58
1:C:4054:ASN:OD1	1:C:4055:VAL:N	2.37	0.58
1:E:402:ARG:NH1	1:E:405:HIS:HD2	2.01	0.58
1:E:537:CYS:HB2	1:E:567:VAL:HG13	1.85	0.58
1:E:681:HIS:HA	1:E:716:PHE:CD1	2.38	0.58
1:E:1657:LEU:HA	1:E:1660:GLN:HG2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:822:ARG:HA	1:G:1623:ARG:HH12	1.68	0.58
1:G:880:GLU:HG2	1:G:967:PRO:HG2	1.85	0.58
1:G:1079:LYS:HA	1:G:1082:THR:HG23	1.86	0.58
1:G:1927:LEU:HD21	1:G:2101:MET:HG2	1.84	0.58
1:A:37:LEU:HD13	1:A:191:VAL:HG21	1.86	0.57
1:A:465:GLN:HE21	1:A:3711:THR:HA	1.69	0.57
1:A:603:LEU:HA	1:A:606:LEU:HD12	1.86	0.57
1:A:880:GLU:HG2	1:A:967:PRO:HG2	1.85	0.57
1:E:1101:ARG:HG3	1:E:1193:SER:HB3	1.86	0.57
1:G:2870:GLU:OE2	1:G:2939:ARG:NE	2.37	0.57
1:C:1944:GLU:HG3	1:C:2123:LEU:HD21	1.86	0.57
1:C:3701:LEU:HD11	1:C:3725:TYR:CD1	2.39	0.57
1:E:1288:PHE:HE2	1:E:1460:HIS:HA	1.68	0.57
1:A:546:TRP:HE1	1:A:550:LYS:HZ1	1.51	0.57
1:A:1079:LYS:HA	1:A:1082:THR:HG23	1.85	0.57
1:C:3727:ASP:HB3	1:C:3731:LYS:NZ	2.18	0.57
1:E:1077:ALA:HA	1:E:1236:THR:HG22	1.87	0.57
1:E:2875:ALA:HB2	1:E:2927:LEU:HD12	1.86	0.57
1:G:1093:GLU:HB2	1:G:1201:HIS:HB3	1.87	0.57
1:G:1819:VAL:HG22	1:G:1926:LEU:HD13	1.87	0.57
1:A:990:GLU:HG3	1:A:1024:TYR:HB3	1.86	0.57
1:C:1819:VAL:HG22	1:C:1926:LEU:HD13	1.87	0.57
1:C:4059:LEU:HD13	1:C:4167:ALA:HB2	1.86	0.57
1:E:37:LEU:HD11	1:E:47:CYS:HB3	1.87	0.57
1:E:3879:GLU:OE2	1:E:3883:ASP:OD2	2.22	0.57
2:H:14:THR:HG22	2:H:106:LEU:HD12	1.86	0.57
1:C:489:ASN:HB3	1:C:493:ARG:HH12	1.69	0.57
1:E:37:LEU:HD13	1:E:191:VAL:HG21	1.86	0.57
1:E:1078:GLU:HA	1:E:1237:TRP:CZ3	2.40	0.57
1:E:4059:LEU:HD13	1:E:4167:ALA:HB2	1.85	0.57
1:E:4934:GLY:HA3	1:G:4937:ILE:CG1	2.29	0.57
1:G:1078:GLU:HA	1:G:1237:TRP:CZ3	2.40	0.57
1:A:1671:ARG:HD2	1:A:1713:ASP:HB3	1.87	0.57
1:C:1638:ALA:HA	1:C:1649:ASP:HA	1.87	0.57
1:E:990:GLU:HG3	1:E:1024:TYR:HB3	1.86	0.57
1:E:1638:ALA:HA	1:E:1649:ASP:HA	1.87	0.57
1:E:4054:ASN:OD1	1:E:4055:VAL:N	2.37	0.57
1:E:4849:TYR:O	1:E:4852:THR:HG22	2.05	0.57
1:G:990:GLU:HG3	1:G:1024:TYR:HB3	1.86	0.57
1:A:530:ILE:HG23	1:A:537:CYS:HB3	1.85	0.57
1:A:551:LEU:HG	1:A:589:LEU:HD22	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3937:TYR:HA	1:A:3940:LYS:HZ3	1.70	0.57
1:A:4054:ASN:OD1	1:A:4055:VAL:N	2.37	0.57
1:E:489:ASN:HB3	1:E:493:ARG:HH12	1.69	0.57
1:E:603:LEU:HA	1:E:606:LEU:HD12	1.86	0.57
1:E:717:ASP:O	1:E:720:HIS:NE2	2.38	0.57
1:E:1093:GLU:HB2	1:E:1201:HIS:HB3	1.87	0.57
1:E:4963:ILE:HD11	1:E:5025:GLY:O	2.04	0.57
1:A:717:ASP:O	1:A:720:HIS:NE2	2.38	0.57
1:A:1802:ILE:HB	1:A:1804:LEU:HD12	1.86	0.57
1:A:4214:LYS:HD2	1:A:4985:LEU:HD23	1.86	0.57
1:C:110:ARG:HH21	1:C:115:ARG:HH21	1.53	0.57
1:A:1638:ALA:HA	1:A:1649:ASP:HA	1.87	0.57
1:C:603:LEU:HA	1:C:606:LEU:HD12	1.86	0.57
1:C:717:ASP:O	1:C:720:HIS:NE2	2.38	0.57
1:C:2333:ASP:OD1	1:C:2336:ARG:NH2	2.36	0.57
1:G:37:LEU:HD13	1:G:191:VAL:HG21	1.86	0.57
1:G:37:LEU:HD11	1:G:47:CYS:HB3	1.86	0.57
1:G:1237:TRP:HD1	1:G:1611:HIS:HA	1.69	0.57
1:A:108:LEU:HB2	1:A:147:TRP:CZ3	2.40	0.57
1:A:1093:GLU:HB2	1:A:1201:HIS:HB3	1.86	0.57
1:A:1819:VAL:HG22	1:A:1926:LEU:HD13	1.87	0.57
1:C:1078:GLU:HA	1:C:1237:TRP:CZ3	2.40	0.57
1:E:110:ARG:HH21	1:E:115:ARG:HH21	1.53	0.57
1:E:1819:VAL:HG22	1:E:1926:LEU:HD13	1.87	0.57
1:G:108:LEU:HB2	1:G:147:TRP:CZ3	2.40	0.57
1:G:3780:LEU:HD12	1:G:3828:PHE:CE1	2.39	0.57
1:C:37:LEU:HD11	1:C:47:CYS:HB3	1.86	0.56
1:C:1514:LEU:O	1:C:1532:ASN:N	2.36	0.56
1:C:2829:GLY:HA3	1:C:2933:ASN:HA	1.86	0.56
1:E:3701:LEU:HD11	1:E:3725:TYR:CD1	2.39	0.56
1:G:2248:ARG:HG2	1:G:2286:LEU:HD11	1.87	0.56
1:C:1237:TRP:HD1	1:C:1611:HIS:HA	1.70	0.56
1:C:1671:ARG:HD2	1:C:1713:ASP:HB3	1.87	0.56
1:E:822:ARG:HA	1:E:1623:ARG:HH12	1.69	0.56
1:G:1944:GLU:HG3	1:G:2123:LEU:HD21	1.86	0.56
1:G:4000:MET:HA	1:G:4003:LEU:HB2	1.85	0.56
1:A:37:LEU:HD11	1:A:47:CYS:HB3	1.86	0.56
1:A:110:ARG:HH21	1:A:115:ARG:HH21	1.53	0.56
1:A:537:CYS:HB2	1:A:567:VAL:HG13	1.86	0.56
1:C:551:LEU:HG	1:C:589:LEU:HD22	1.87	0.56
1:C:705:ASN:OD1	1:C:706:GLY:N	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1093:GLU:HB2	1:C:1201:HIS:HB3	1.86	0.56
1:C:4214:LYS:HD2	1:C:4985:LEU:HD23	1.85	0.56
1:E:1237:TRP:HD1	1:E:1611:HIS:HA	1.69	0.56
1:E:4917:ASP:OD2	1:G:4892:ARG:NH2	2.37	0.56
1:G:110:ARG:HH21	1:G:115:ARG:HH21	1.52	0.56
1:G:1638:ALA:HA	1:G:1649:ASP:HA	1.87	0.56
1:G:1970:GLN:NE2	1:G:3645:PRO:O	2.33	0.56
1:C:4721:LYS:HG3	1:C:4741:LEU:HB3	1.88	0.56
1:E:1211:LEU:HG	1:E:1212:ARG:H	1.70	0.56
1:E:4928:LEU:O	1:E:4932:ILE:HD12	2.04	0.56
1:G:46:LEU:HD22	1:G:134:ASP:OD2	2.06	0.56
1:G:1211:LEU:HG	1:G:1212:ARG:H	1.71	0.56
1:G:2829:GLY:HA3	1:G:2933:ASN:HA	1.87	0.56
1:A:739:ALA:O	1:A:741:GLU:N	2.30	0.56
1:C:684:VAL:HG22	1:C:781:VAL:HA	1.87	0.56
1:E:551:LEU:HG	1:E:589:LEU:HD22	1.87	0.56
1:E:1802:ILE:HB	1:E:1804:LEU:HD12	1.86	0.56
1:G:4214:LYS:HD2	1:G:4985:LEU:HD23	1.86	0.56
1:A:1944:GLU:HG3	1:A:2123:LEU:HD21	1.86	0.56
1:A:3786:CYS:SG	1:A:3794:VAL:HG22	2.46	0.56
1:A:3993:LEU:HD13	1:A:4055:VAL:HG22	1.88	0.56
2:D:25:HIS:CG	2:D:40:ARG:HE	2.24	0.56
1:E:1561:VAL:HG13	1:E:1562:ILE:HG22	1.88	0.56
1:G:548:VAL:HG11	1:G:582:HIS:HA	1.88	0.56
1:G:705:ASN:OD1	1:G:706:GLY:N	2.39	0.56
1:G:1802:ILE:HB	1:G:1804:LEU:HD12	1.86	0.56
1:G:3989:VAL:HG13	1:G:4023:MET:SD	2.45	0.56
1:A:46:LEU:HD22	1:A:134:ASP:OD2	2.05	0.56
1:A:768:PHE:HB3	1:A:771:PHE:HE2	1.71	0.56
1:A:1211:LEU:HG	1:A:1212:ARG:H	1.70	0.56
1:C:3993:LEU:HD13	1:C:4055:VAL:HG22	1.88	0.56
1:C:4849:TYR:O	1:C:4852:THR:HG22	2.06	0.56
1:E:3993:LEU:HD13	1:E:4055:VAL:HG22	1.87	0.56
1:G:1104:TRP:HH2	1:G:1226:PHE:HZ	1.54	0.56
1:G:3886:ARG:O	1:G:3890:LEU:HD13	2.06	0.56
1:A:2829:GLY:HA3	1:A:2933:ASN:HA	1.87	0.56
1:A:3841:VAL:HG12	1:A:3843:ASP:H	1.71	0.56
1:C:1211:LEU:HG	1:C:1212:ARG:H	1.71	0.56
1:E:548:VAL:HG11	1:E:582:HIS:HA	1.88	0.56
1:G:551:LEU:HG	1:G:589:LEU:HD22	1.87	0.56
1:G:1109:LEU:HA	1:G:1120:LEU:HD13	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:684:VAL:HG22	1:A:781:VAL:HA	1.87	0.56
1:A:705:ASN:OD1	1:A:706:GLY:N	2.39	0.56
1:C:4664:LEU:O	1:C:4667:PRO:HD2	2.06	0.56
1:E:2756:ASN:OD1	1:E:2806:ARG:NH2	2.39	0.56
1:E:4721:LYS:HG3	1:E:4741:LEU:HB3	1.88	0.56
1:G:1077:ALA:HA	1:G:1236:THR:HG22	1.88	0.56
1:A:1078:GLU:HA	1:A:1237:TRP:CZ3	2.40	0.56
1:A:2756:ASN:OD1	1:A:2806:ARG:NH2	2.39	0.56
1:C:768:PHE:HB3	1:C:771:PHE:HE2	1.71	0.56
1:E:46:LEU:HD22	1:E:134:ASP:OD2	2.06	0.56
1:E:684:VAL:HG22	1:E:781:VAL:HA	1.87	0.56
1:E:2854:GLY:O	1:E:2856:ASN:ND2	2.39	0.56
2:F:25:HIS:CG	2:F:40:ARG:HE	2.24	0.56
1:A:1077:ALA:HA	1:A:1236:THR:HG22	1.87	0.55
1:A:1561:VAL:HG13	1:A:1562:ILE:HG22	1.88	0.55
1:C:46:LEU:HD22	1:C:134:ASP:OD2	2.05	0.55
1:C:108:LEU:HB2	1:C:147:TRP:CZ3	2.40	0.55
1:E:705:ASN:OD1	1:E:706:GLY:N	2.39	0.55
1:G:3990:VAL:HG13	1:G:4051:SER:HB2	1.88	0.55
1:A:3923:LEU:HD12	1:A:3961:VAL:HG13	1.89	0.55
1:A:3965:LEU:HD23	1:A:3968:TYR:HD2	1.71	0.55
1:A:4721:LYS:HG3	1:A:4741:LEU:HB3	1.88	0.55
1:C:2756:ASN:OD1	1:C:2806:ARG:NH2	2.39	0.55
1:E:636:ASN:OD1	1:E:637:LEU:N	2.39	0.55
1:G:1207:ASP:O	1:G:1210:SER:OG	2.19	0.55
1:G:2927:LEU:HD23	1:G:2930:LEU:HD12	1.87	0.55
1:A:768:PHE:HB3	1:A:771:PHE:CE2	2.41	0.55
1:A:2854:GLY:O	1:A:2856:ASN:ND2	2.39	0.55
1:C:113:HIS:CE1	1:C:402:ARG:HB3	2.42	0.55
1:C:2277:ALA:O	1:C:2281:ILE:HG13	2.07	0.55
1:E:4228:ALA:HB2	1:G:4976:GLU:OE1	2.06	0.55
1:G:636:ASN:OD1	1:G:637:LEU:N	2.39	0.55
1:G:768:PHE:HB3	1:G:771:PHE:HE2	1.71	0.55
1:C:636:ASN:OD1	1:C:637:LEU:N	2.39	0.55
1:C:768:PHE:HB3	1:C:771:PHE:CE2	2.41	0.55
1:C:1561:VAL:HG13	1:C:1562:ILE:HG22	1.89	0.55
1:C:2287:ALA:O	1:C:2349:ASN:ND2	2.31	0.55
1:C:2465:ASP:O	1:C:2467:VAL:N	2.40	0.55
1:C:3841:VAL:HG12	1:C:3843:ASP:H	1.71	0.55
1:C:3923:LEU:HD12	1:C:3961:VAL:HG13	1.89	0.55
1:E:42:PHE:HA	1:E:447:ASP:OD2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:768:PHE:HB3	1:E:771:PHE:CE2	2.41	0.55
1:E:1079:LYS:HA	1:E:1082:THR:HG23	1.86	0.55
1:E:1671:ARG:HD2	1:E:1713:ASP:HB3	1.87	0.55
1:G:42:PHE:HA	1:G:447:ASP:OD2	2.06	0.55
1:G:3767:GLN:NE2	1:G:3805:LEU:O	2.37	0.55
1:A:627:PRO:HG3	2:B:89:GLY:CA	2.37	0.55
1:A:4807:PHE:CZ	1:G:4856:PHE:CE2	2.94	0.55
1:C:627:PRO:HG3	2:D:89:GLY:CA	2.36	0.55
1:E:627:PRO:HG3	2:F:89:GLY:CA	2.36	0.55
1:E:2277:ALA:O	1:E:2281:ILE:HG13	2.07	0.55
1:G:2907:PRO:O	1:G:2910:THR:OG1	2.19	0.55
2:H:23:VAL:HG12	2:H:104:LEU:HD12	1.88	0.55
1:A:636:ASN:OD1	1:A:637:LEU:N	2.39	0.55
1:A:2287:ALA:O	1:A:2349:ASN:ND2	2.31	0.55
1:A:2465:ASP:O	1:A:2467:VAL:N	2.40	0.55
1:A:4892:ARG:CZ	1:G:4917:ASP:OD2	2.55	0.55
2:B:25:HIS:CG	2:B:40:ARG:HE	2.24	0.55
1:C:274:LEU:HD12	1:C:278:GLN:HE21	1.71	0.55
1:G:3825:GLU:O	1:G:3827:GLY:N	2.37	0.55
1:A:42:PHE:HA	1:A:447:ASP:OD2	2.07	0.55
1:A:4664:LEU:O	1:A:4667:PRO:HD2	2.07	0.55
1:E:108:LEU:HB2	1:E:147:TRP:CZ3	2.42	0.55
1:E:572:PRO:HB3	1:E:609:CYS:HB3	1.89	0.55
1:E:768:PHE:HB3	1:E:771:PHE:HE2	1.71	0.55
1:E:1684:ALA:O	1:E:1687:SER:HB3	2.06	0.55
1:E:2865:VAL:O	1:E:2928:LYS:NZ	2.34	0.55
1:G:684:VAL:HG22	1:G:781:VAL:HA	1.87	0.55
1:G:4712:PRO:O	1:G:4718:LYS:NZ	2.29	0.55
1:A:606:LEU:O	1:A:617:ASN:ND2	2.40	0.55
1:C:1745:ILE:O	1:C:1746:THR:OG1	2.25	0.55
1:C:2854:GLY:O	1:C:2856:ASN:ND2	2.39	0.55
1:E:113:HIS:CE1	1:E:402:ARG:HB3	2.42	0.55
1:E:2287:ALA:O	1:E:2349:ASN:ND2	2.31	0.55
1:E:2465:ASP:O	1:E:2467:VAL:N	2.40	0.55
1:E:3825:GLU:O	1:E:3827:GLY:N	2.34	0.55
1:E:3841:VAL:HG12	1:E:3843:ASP:H	1.72	0.55
1:G:103:TYR:CD1	1:G:152:PRO:HG3	2.41	0.55
1:G:1684:ALA:O	1:G:1687:SER:HB3	2.06	0.55
1:G:2431:ASP:O	1:G:2435:ARG:HG2	2.07	0.55
1:G:2854:GLY:O	1:G:2856:ASN:ND2	2.39	0.55
1:A:548:VAL:HG11	1:A:582:HIS:HA	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2277:ALA:O	1:A:2281:ILE:HG13	2.06	0.55
1:A:4849:TYR:O	1:A:4852:THR:HG22	2.06	0.55
1:C:606:LEU:O	1:C:617:ASN:ND2	2.40	0.55
1:C:1077:ALA:HA	1:C:1236:THR:HG22	1.88	0.55
1:E:590:LEU:HB2	1:E:599:VAL:HG11	1.89	0.55
1:E:3965:LEU:HD23	1:E:3968:TYR:HD2	1.71	0.55
1:A:572:PRO:HB3	1:A:609:CYS:HB3	1.89	0.55
1:A:1109:LEU:HA	1:A:1120:LEU:HD13	1.89	0.55
1:A:4051:SER:OG	1:A:4054:ASN:OD1	2.25	0.55
1:C:548:VAL:HG11	1:C:582:HIS:HA	1.88	0.55
1:C:1684:ALA:O	1:C:1687:SER:HB3	2.07	0.55
1:G:606:LEU:O	1:G:617:ASN:ND2	2.40	0.55
1:A:76:ARG:CZ	1:C:3844:LEU:HD21	2.37	0.54
1:C:42:PHE:HA	1:C:447:ASP:OD2	2.07	0.54
1:C:1243:PRO:HD2	1:C:1458:HIS:CB	2.34	0.54
1:G:2465:ASP:O	1:G:2467:VAL:N	2.40	0.54
1:G:4029:SER:HA	1:G:4032:GLU:HG3	1.89	0.54
1:A:274:LEU:HD12	1:A:278:GLN:HE21	1.71	0.54
1:C:572:PRO:HB3	1:C:609:CYS:HB3	1.90	0.54
1:C:590:LEU:HB2	1:C:599:VAL:HG11	1.89	0.54
1:E:919:ASN:HA	1:E:922:LEU:HB2	1.88	0.54
1:E:3937:TYR:HA	1:E:3940:LYS:NZ	2.22	0.54
1:E:3999:MET:O	1:E:4003:LEU:N	2.37	0.54
1:G:1671:ARG:HD2	1:G:1713:ASP:HB3	1.87	0.54
1:E:274:LEU:HD12	1:E:278:GLN:HE21	1.71	0.54
1:E:606:LEU:O	1:E:617:ASN:ND2	2.39	0.54
1:E:4664:LEU:O	1:E:4667:PRO:HD2	2.07	0.54
1:G:590:LEU:HB2	1:G:599:VAL:HG11	1.89	0.54
1:G:768:PHE:HB3	1:G:771:PHE:CE2	2.41	0.54
1:G:1514:LEU:O	1:G:1532:ASN:N	2.36	0.54
1:G:3889:GLN:HE22	1:G:3963:ASN:HB3	1.71	0.54
1:A:4055:VAL:HA	1:A:4058:ILE:HG12	1.89	0.54
1:C:2431:ASP:O	1:C:2435:ARG:HG2	2.07	0.54
1:C:4051:SER:OG	1:C:4054:ASN:OD1	2.25	0.54
1:C:4917:ASP:OD2	1:E:4892:ARG:NH2	2.41	0.54
1:E:2829:GLY:HA3	1:E:2933:ASN:HA	1.87	0.54
1:E:3989:VAL:HG13	1:E:4023:MET:SD	2.48	0.54
1:G:1561:VAL:HG13	1:G:1562:ILE:HG22	1.89	0.54
1:C:4055:VAL:HA	1:C:4058:ILE:HG12	1.89	0.54
1:G:33:LEU:HD12	1:G:53:SER:HB2	1.89	0.54
1:A:103:TYR:CD1	1:A:152:PRO:HG3	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1684:ALA:O	1:A:1687:SER:HB3	2.06	0.54
1:A:2431:ASP:O	1:A:2435:ARG:HG2	2.07	0.54
1:A:3932:ASP:OD1	1:G:76:ARG:HG2	2.08	0.54
1:E:103:TYR:CD1	1:E:152:PRO:HG3	2.43	0.54
1:G:111:HIS:HD2	1:G:114:SER:H	1.55	0.54
1:G:572:PRO:HB3	1:G:609:CYS:HB3	1.90	0.54
1:G:627:PRO:HG3	2:H:89:GLY:CA	2.38	0.54
1:G:2277:ALA:O	1:G:2281:ILE:HG13	2.07	0.54
1:G:4677:LEU:HD22	1:G:4711:PHE:CE1	2.42	0.54
1:G:4980:LEU:HA	1:G:4984:ASN:HB3	1.89	0.54
2:H:11:ASP:OD2	2:H:68:VAL:HB	2.06	0.54
2:H:71:ARG:NH2	2:H:100:ASP:OD2	2.40	0.54
1:A:157:ARG:HH22	1:A:164:ARG:HD2	1.73	0.54
1:A:1663:HIS:O	1:A:1666:THR:OG1	2.19	0.54
1:A:3999:MET:O	1:A:4003:LEU:N	2.37	0.54
1:A:4917:ASP:OD2	1:C:4892:ARG:NH2	2.41	0.54
1:C:103:TYR:CD1	1:C:152:PRO:HG3	2.42	0.54
1:C:3423:TRP:O	1:C:3428:ASN:N	2.41	0.54
1:E:33:LEU:HD12	1:E:53:SER:HB2	1.89	0.54
1:E:157:ARG:HH22	1:E:164:ARG:HD2	1.73	0.54
1:E:4901:ILE:HG21	1:E:4913:ARG:NH2	2.23	0.54
1:G:4030:LEU:HG	1:G:4040:ILE:HD11	1.89	0.54
1:A:113:HIS:CE1	1:A:402:ARG:HB3	2.42	0.54
1:A:4683:PHE:HE2	1:A:5017:ARG:HD2	1.73	0.54
1:C:76:ARG:CZ	1:E:3844:LEU:HD21	2.38	0.54
1:C:2827:ARG:HB2	1:C:2934:GLY:HA3	1.90	0.54
1:G:274:LEU:HD12	1:G:278:GLN:HE21	1.71	0.54
1:G:1243:PRO:HD2	1:G:1458:HIS:CB	2.38	0.54
1:A:2902:HIS:CG	1:A:2903:PRO:HD2	2.43	0.54
1:A:3423:TRP:O	1:A:3428:ASN:N	2.41	0.54
1:C:3965:LEU:HD23	1:C:3968:TYR:HD2	1.72	0.54
1:E:4051:SER:OG	1:E:4054:ASN:OD1	2.25	0.54
1:G:113:HIS:CE1	1:G:402:ARG:HB3	2.42	0.54
1:G:4240:ASP:CG	1:G:4675:LYS:HZ3	2.10	0.54
1:A:33:LEU:HD12	1:A:53:SER:HB2	1.90	0.54
1:C:157:ARG:HH22	1:C:164:ARG:HD2	1.73	0.54
1:C:2822:THR:OG1	1:C:2938:THR:OG1	2.19	0.54
1:C:4735:GLU:HA	1:C:4738:ALA:HB3	1.90	0.54
1:E:537:CYS:SG	1:E:571:SER:HB3	2.48	0.54
1:E:1104:TRP:HH2	1:E:1226:PHE:HZ	1.54	0.54
1:E:2431:ASP:O	1:E:2435:ARG:HG2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:3923:LEU:HD12	1:E:3961:VAL:HG13	1.89	0.54
1:G:965:TYR:CZ	1:G:967:PRO:HG3	2.43	0.54
1:A:965:TYR:CZ	1:A:967:PRO:HG3	2.43	0.53
1:E:111:HIS:HD2	1:E:114:SER:H	1.56	0.53
1:G:699:GLY:H	1:G:1647:CYS:HB3	1.72	0.53
1:G:3826:VAL:HA	1:G:3906:GLN:HE22	1.72	0.53
1:G:4901:ILE:HG21	1:G:4913:ARG:NH2	2.22	0.53
1:A:634:GLN:HB3	1:A:1640:HIS:CE1	2.44	0.53
1:A:4026:MET:O	1:A:4029:SER:OG	2.21	0.53
1:C:2927:LEU:HD23	1:C:2930:LEU:HD12	1.90	0.53
1:E:1109:LEU:HA	1:E:1120:LEU:HD13	1.89	0.53
1:G:2244:ARG:HB2	1:G:2283:ASN:HD21	1.72	0.53
1:A:590:LEU:HB2	1:A:599:VAL:HG11	1.89	0.53
1:A:1104:TRP:HH2	1:A:1226:PHE:HZ	1.56	0.53
1:A:3989:VAL:HG13	1:A:4023:MET:SD	2.48	0.53
1:C:965:TYR:CZ	1:C:967:PRO:HG3	2.43	0.53
1:E:2244:ARG:HB2	1:E:2283:ASN:HD21	1.73	0.53
1:E:2902:HIS:CG	1:E:2903:PRO:HD2	2.43	0.53
1:G:294:THR:HG22	1:G:296:ASP:H	1.74	0.53
1:A:3937:TYR:HA	1:A:3940:LYS:NZ	2.22	0.53
1:A:3969:ILE:HD13	1:A:4030:LEU:HD13	1.90	0.53
1:A:4712:PRO:O	1:A:4718:LYS:NZ	2.32	0.53
1:C:634:GLN:HB3	1:C:1640:HIS:CE1	2.43	0.53
1:C:3969:ILE:HD13	1:C:4030:LEU:HD13	1.91	0.53
1:G:4677:LEU:HD22	1:G:4711:PHE:CZ	2.43	0.53
1:A:76:ARG:HG2	1:C:3932:ASP:OD1	2.08	0.53
1:C:537:CYS:SG	1:C:571:SER:HB3	2.48	0.53
1:C:699:GLY:H	1:C:1647:CYS:HB3	1.73	0.53
1:G:1237:TRP:CD1	1:G:1611:HIS:HA	2.44	0.53
1:G:2902:HIS:CG	1:G:2903:PRO:HD2	2.44	0.53
1:A:3844:LEU:HD21	1:G:76:ARG:CZ	2.38	0.53
1:C:1104:TRP:HH2	1:C:1226:PHE:HZ	1.56	0.53
1:E:1745:ILE:O	1:E:1746:THR:OG1	2.25	0.53
1:E:3423:TRP:O	1:E:3428:ASN:N	2.41	0.53
1:E:3969:ILE:HD13	1:E:4030:LEU:HD13	1.91	0.53
1:E:4712:PRO:O	1:E:4718:LYS:NZ	2.32	0.53
1:G:1947:CYS:SG	1:G:2127:GLN:NE2	2.82	0.53
1:A:294:THR:HG22	1:A:296:ASP:H	1.74	0.53
1:A:2907:PRO:O	1:A:2910:THR:OG1	2.18	0.53
1:A:2927:LEU:HD23	1:A:2930:LEU:HD12	1.90	0.53
1:C:1109:LEU:HA	1:C:1120:LEU:HD13	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3825:GLU:O	1:C:3827:GLY:N	2.34	0.53
1:E:2827:ARG:HB2	1:E:2934:GLY:HA3	1.90	0.53
1:E:3937:TYR:HA	1:E:3940:LYS:HZ3	1.73	0.53
1:A:111:HIS:HD2	1:A:114:SER:H	1.56	0.53
1:A:537:CYS:SG	1:A:571:SER:HB3	2.48	0.53
1:A:1100:MET:O	1:A:1126:GLY:N	2.38	0.53
1:A:3955:MET:SD	1:A:4019:LEU:HD13	2.49	0.53
1:C:76:ARG:HG2	1:E:3932:ASP:OD1	2.08	0.53
1:E:3959:LYS:HG3	1:E:4022:ASP:OD2	2.09	0.53
1:G:102:LEU:HB2	1:G:105:HIS:CE1	2.44	0.53
1:G:537:CYS:SG	1:G:571:SER:HB3	2.49	0.53
1:G:634:GLN:HB3	1:G:1640:HIS:CE1	2.44	0.53
1:A:495:ASN:HA	1:A:553:ARG:HH12	1.74	0.53
1:C:70:GLU:HB2	1:C:108:LEU:HD23	1.91	0.53
1:C:3937:TYR:HA	1:C:3940:LYS:NZ	2.23	0.53
1:C:3989:VAL:HG13	1:C:4023:MET:SD	2.48	0.53
1:E:1240:LYS:HD3	1:E:1610:ASN:OD1	2.08	0.53
1:E:2927:LEU:HD23	1:E:2930:LEU:HD12	1.90	0.53
1:E:3962:PHE:O	1:E:3966:THR:HG23	2.09	0.53
1:G:663:TYR:OH	1:G:665:GLU:OE2	2.04	0.53
1:A:4731:ILE:HG23	1:A:4732:PHE:CD2	2.44	0.53
1:C:445:LEU:O	1:C:449:ILE:HG13	2.09	0.53
1:C:3955:MET:SD	1:C:4019:LEU:HD13	2.49	0.53
1:E:965:TYR:CZ	1:E:967:PRO:HG3	2.44	0.53
1:G:157:ARG:HH22	1:G:164:ARG:HD2	1.73	0.53
1:A:445:LEU:O	1:A:449:ILE:HG13	2.09	0.52
1:A:622:THR:O	1:A:627:PRO:HD3	2.09	0.52
1:C:33:LEU:HD12	1:C:53:SER:HB2	1.90	0.52
1:C:3959:LYS:HG3	1:C:4022:ASP:OD2	2.09	0.52
1:C:3962:PHE:O	1:C:3966:THR:HG23	2.09	0.52
1:E:699:GLY:H	1:E:1647:CYS:HB3	1.74	0.52
1:E:1610:ASN:HA	1:E:1652:GLU:OE2	2.09	0.52
1:A:1229:ASN:HB3	1:A:1827:ARG:HH11	1.74	0.52
1:A:1237:TRP:CD1	1:A:1611:HIS:HA	2.44	0.52
1:A:1514:LEU:O	1:A:1532:ASN:N	2.36	0.52
1:C:1229:ASN:HB3	1:C:1827:ARG:HH11	1.74	0.52
1:C:2855:TYR:CD2	1:C:2857:PRO:HD3	2.44	0.52
1:C:4026:MET:O	1:C:4029:SER:OG	2.21	0.52
1:E:284:HIS:HE2	1:E:286:THR:HG1	1.56	0.52
1:E:4055:VAL:HA	1:E:4058:ILE:HG12	1.89	0.52
1:E:4779:LYS:O	1:E:4783:ILE:HG12	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:LEU:HB2	1:A:105:HIS:CE1	2.45	0.52
1:C:102:LEU:HB2	1:C:105:HIS:CE1	2.45	0.52
1:C:111:HIS:HD2	1:C:114:SER:H	1.55	0.52
1:C:2902:HIS:CG	1:C:2903:PRO:HD2	2.43	0.52
1:E:445:LEU:O	1:E:449:ILE:HG13	2.09	0.52
1:G:4658:ILE:HG22	1:G:4792:LEU:HB3	1.91	0.52
1:G:4856:PHE:O	1:G:4860:ARG:NH1	2.42	0.52
1:A:2827:ARG:HB2	1:A:2934:GLY:HA3	1.90	0.52
1:C:750:LEU:O	1:C:752:VAL:N	2.43	0.52
1:C:4731:ILE:HG23	1:C:4732:PHE:CD2	2.44	0.52
1:E:705:ASN:ND2	1:E:782:SER:OG	2.43	0.52
1:G:647:ASN:HB2	1:G:822:ARG:O	2.10	0.52
1:G:1101:ARG:NH1	1:G:1115:LEU:O	2.43	0.52
1:A:600:LEU:HD21	1:A:1666:THR:HG22	1.92	0.52
1:A:623:GLU:OE2	2:B:89:GLY:N	2.42	0.52
1:C:2244:ARG:HB2	1:C:2283:ASN:HD21	1.74	0.52
1:E:70:GLU:HB2	1:E:108:LEU:HD23	1.91	0.52
1:E:495:ASN:HA	1:E:553:ARG:HH12	1.74	0.52
1:E:1101:ARG:NH1	1:E:1115:LEU:O	2.42	0.52
1:E:1237:TRP:CD1	1:E:1611:HIS:HA	2.45	0.52
1:E:3955:MET:SD	1:E:4019:LEU:HD13	2.49	0.52
1:E:4683:PHE:HE2	1:E:5017:ARG:HD2	1.73	0.52
1:E:4934:GLY:HA2	1:E:4937:ILE:HD12	1.90	0.52
1:C:622:THR:O	1:C:627:PRO:HD3	2.09	0.52
1:C:705:ASN:ND2	1:C:782:SER:OG	2.43	0.52
1:C:1237:TRP:CD1	1:C:1611:HIS:HA	2.44	0.52
1:E:1961:PHE:CE2	1:E:2066:LEU:HD22	2.45	0.52
1:E:4937:ILE:HD12	1:G:4937:ILE:HD13	1.91	0.52
1:E:4961:CYS:HB3	1:E:4963:ILE:HG12	1.92	0.52
1:G:445:LEU:O	1:G:449:ILE:HG13	2.09	0.52
1:A:1101:ARG:NH1	1:A:1115:LEU:O	2.42	0.52
1:A:1240:LYS:HD3	1:A:1610:ASN:OD1	2.10	0.52
1:A:3962:PHE:O	1:A:3966:THR:HG23	2.09	0.52
1:C:3836:MET:O	1:C:3925:ARG:NH2	2.43	0.52
1:C:4683:PHE:HE2	1:C:5017:ARG:HD2	1.73	0.52
1:E:623:GLU:OE2	2:F:89:GLY:N	2.43	0.52
1:E:4914:VAL:HG23	1:G:4888:TYR:CG	2.42	0.52
1:G:70:GLU:HB2	1:G:108:LEU:HD23	1.91	0.52
1:G:465:GLN:NE2	1:G:3712:GLU:OE1	2.43	0.52
1:A:35:LEU:HA	1:A:51:PRO:HA	1.92	0.52
1:A:750:LEU:O	1:A:752:VAL:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3496:LYS:O	1:A:3513:THR:N	2.43	0.52
1:C:623:GLU:OE2	2:D:89:GLY:N	2.43	0.52
1:C:1130:GLN:HA	1:C:1138:PRO:HA	1.92	0.52
1:E:634:GLN:HB3	1:E:1640:HIS:CE1	2.44	0.52
1:G:695:TYR:CD2	1:G:1240:LYS:HE3	2.45	0.52
1:G:750:LEU:O	1:G:752:VAL:N	2.43	0.52
1:G:2855:TYR:CD2	1:G:2857:PRO:HD3	2.45	0.52
1:G:3966:THR:HG22	1:G:4026:MET:HA	1.92	0.52
1:A:647:ASN:HB2	1:A:822:ARG:O	2.09	0.52
1:E:294:THR:HG22	1:E:296:ASP:H	1.75	0.52
1:E:750:LEU:O	1:E:752:VAL:N	2.43	0.52
1:E:4731:ILE:HG23	1:E:4732:PHE:CD2	2.44	0.52
1:E:4735:GLU:HA	1:E:4738:ALA:HB3	1.92	0.52
1:G:2745:VAL:HG21	1:G:2818:ALA:HB2	1.92	0.52
1:G:3804:ILE:HG22	1:G:3812:VAL:HG11	1.92	0.52
1:G:4731:ILE:HG23	1:G:4732:PHE:CD2	2.44	0.52
1:A:2855:TYR:CD2	1:A:2857:PRO:HD3	2.45	0.52
1:A:3825:GLU:O	1:A:3827:GLY:N	2.35	0.52
1:C:495:ASN:HA	1:C:553:ARG:HH12	1.74	0.52
1:C:3496:LYS:O	1:C:3513:THR:N	2.43	0.52
1:G:495:ASN:HA	1:G:553:ARG:HH12	1.74	0.52
1:G:1100:MET:O	1:G:1126:GLY:N	2.39	0.52
1:A:76:ARG:HE	1:C:3844:LEU:CD2	2.23	0.51
1:A:284:HIS:HE2	1:A:286:THR:HG1	1.53	0.51
1:A:1207:ASP:O	1:A:1210:SER:OG	2.19	0.51
1:A:1961:PHE:CE2	1:A:2066:LEU:HD22	2.45	0.51
1:A:3959:LYS:HG3	1:A:4022:ASP:OD2	2.09	0.51
1:C:35:LEU:HA	1:C:51:PRO:HA	1.93	0.51
1:C:1291:LEU:HB3	1:C:1550:PRO:HG2	1.92	0.51
1:E:1623:ARG:NH1	1:E:1626:TRP:HE1	2.06	0.51
1:G:4909:TYR:O	1:G:4913:ARG:N	2.43	0.51
1:A:699:GLY:H	1:A:1647:CYS:HB3	1.74	0.51
1:A:3836:MET:O	1:A:3925:ARG:NH2	2.43	0.51
1:C:600:LEU:HD21	1:C:1666:THR:HG22	1.92	0.51
1:E:1491:ASN:H	1:E:1493:TYR:HA	1.76	0.51
1:E:3496:LYS:O	1:E:3513:THR:N	2.43	0.51
1:G:2158:CYS:SG	1:G:2184:ASN:ND2	2.80	0.51
1:A:1598:GLN:O	1:A:1600:LEU:N	2.44	0.51
1:A:2341:VAL:HG13	1:A:2342:ASN:N	2.22	0.51
2:B:23:VAL:HG12	2:B:104:LEU:HD12	1.93	0.51
1:C:294:THR:HG22	1:C:296:ASP:H	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1663:HIS:O	1:C:1666:THR:OG1	2.19	0.51
1:G:158:SER:H	1:G:161:GLU:HG3	1.75	0.51
1:G:583:ILE:HD12	1:G:620:LEU:HD22	1.92	0.51
1:G:622:THR:O	1:G:627:PRO:HD3	2.09	0.51
1:G:3971:GLY:HA2	1:G:5005:GLY:HA3	1.92	0.51
1:G:4928:LEU:O	1:G:4932:ILE:HD12	2.08	0.51
1:A:70:GLU:HB2	1:A:108:LEU:HD23	1.91	0.51
1:A:4239:GLU:OE2	1:A:5014:TYR:OH	2.18	0.51
1:A:4779:LYS:O	1:A:4783:ILE:HG12	2.10	0.51
1:C:647:ASN:HB2	1:C:822:ARG:O	2.10	0.51
1:E:33:LEU:HD23	1:E:35:LEU:HD23	1.93	0.51
1:E:35:LEU:HA	1:E:51:PRO:HA	1.92	0.51
1:E:622:THR:O	1:E:627:PRO:HD3	2.09	0.51
1:E:647:ASN:HB2	1:E:822:ARG:O	2.10	0.51
1:E:1100:MET:O	1:E:1126:GLY:N	2.39	0.51
1:A:583:ILE:HD12	1:A:620:LEU:HD22	1.92	0.51
1:A:1291:LEU:HB3	1:A:1550:PRO:HG2	1.92	0.51
1:A:1453:VAL:HG12	1:A:1454:THR:O	2.11	0.51
1:C:78:LEU:HD11	1:C:147:TRP:CD2	2.45	0.51
1:E:1111:PRO:HG3	1:E:1609:PRO:HD3	1.92	0.51
1:E:2158:CYS:SG	1:E:2184:ASN:ND2	2.80	0.51
1:G:3826:VAL:HA	1:G:3906:GLN:NE2	2.25	0.51
1:G:3980:LEU:HD21	1:G:3985:LEU:HD13	1.91	0.51
1:A:1808:ARG:HA	1:A:1848:LEU:HD21	1.93	0.51
1:A:4217:PHE:CZ	1:A:4234:PHE:HA	2.46	0.51
1:A:4888:TYR:HB2	1:G:4914:VAL:CG2	2.41	0.51
1:C:33:LEU:HD23	1:C:35:LEU:HD23	1.93	0.51
1:C:1132:TRP:CD1	1:C:1136:SER:HA	2.46	0.51
1:C:1598:GLN:O	1:C:1600:LEU:N	2.44	0.51
1:C:3999:MET:O	1:C:4003:LEU:N	2.37	0.51
1:E:583:ILE:HD12	1:E:620:LEU:HD22	1.93	0.51
1:E:668:VAL:HA	1:E:789:VAL:HG12	1.93	0.51
2:F:23:VAL:HG12	2:F:104:LEU:HD12	1.93	0.51
1:G:233:ILE:O	1:G:257:ARG:NH1	2.44	0.51
1:G:705:ASN:ND2	1:G:782:SER:OG	2.42	0.51
1:G:721:LEU:HD11	1:G:728:ARG:HB2	1.93	0.51
1:G:1291:LEU:HB3	1:G:1550:PRO:HG2	1.92	0.51
1:G:1293:LEU:HD23	1:G:1584:ARG:HG2	1.93	0.51
2:H:25:HIS:CD2	2:H:104:LEU:HD11	2.46	0.51
1:A:705:ASN:ND2	1:A:782:SER:OG	2.43	0.51
1:A:1937:LEU:HD12	1:A:2116:LEU:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4222:VAL:HG11	1:A:4950:VAL:HA	1.93	0.51
1:C:919:ASN:HA	1:C:922:LEU:HB2	1.93	0.51
1:C:1111:PRO:HG3	1:C:1609:PRO:HD3	1.93	0.51
1:C:4712:PRO:O	1:C:4718:LYS:NZ	2.31	0.51
1:E:1204:LEU:HD22	1:E:1226:PHE:CD2	2.46	0.51
1:E:3836:MET:O	1:E:3925:ARG:NH2	2.44	0.51
1:G:1132:TRP:CD1	1:G:1136:SER:HA	2.45	0.51
1:G:1229:ASN:HB3	1:G:1827:ARG:HH11	1.74	0.51
1:G:2883:HIS:CE1	1:G:2911:LEU:HD11	2.45	0.51
1:A:4735:GLU:HA	1:A:4738:ALA:HB3	1.92	0.51
1:C:20:VAL:O	1:C:67:PHE:N	2.42	0.51
1:C:695:TYR:CD2	1:C:1240:LYS:HE3	2.45	0.51
1:E:1207:ASP:O	1:E:1210:SER:OG	2.18	0.51
1:E:1293:LEU:HD23	1:E:1584:ARG:HG2	1.93	0.51
1:E:3769:ARG:O	1:E:3773:ARG:NH1	2.41	0.51
1:E:4222:VAL:HG11	1:E:4950:VAL:HA	1.92	0.51
1:G:14:LEU:HD21	1:G:204:PRO:HG3	1.92	0.51
1:G:668:VAL:HA	1:G:789:VAL:HG12	1.92	0.51
1:G:2142:TYR:CD2	1:G:2197:LEU:HD12	2.46	0.51
1:G:3919:THR:HG21	1:G:3968:TYR:HE2	1.76	0.51
1:G:4956:THR:O	1:G:4965:SER:N	2.41	0.51
1:A:78:LEU:HD11	1:A:147:TRP:CD2	2.46	0.51
1:A:158:SER:H	1:A:161:GLU:HG3	1.76	0.51
1:C:400:ALA:O	1:C:404:ILE:HG13	2.11	0.51
1:C:1101:ARG:NH1	1:C:1115:LEU:O	2.43	0.51
1:C:1579:MET:O	1:C:1582:SER:OG	2.17	0.51
1:C:1937:LEU:HD12	1:C:2116:LEU:HB2	1.93	0.51
1:C:4222:VAL:HG11	1:C:4950:VAL:HA	1.93	0.51
1:C:4779:LYS:O	1:C:4783:ILE:HG12	2.09	0.51
1:C:4961:CYS:HB3	1:C:4963:ILE:HG12	1.92	0.51
1:E:600:LEU:HD21	1:E:1666:THR:HG22	1.92	0.51
1:E:2855:TYR:CD2	1:E:2857:PRO:HD3	2.45	0.51
1:G:2287:ALA:O	1:G:2349:ASN:ND2	2.30	0.51
1:A:2244:ARG:HB2	1:A:2283:ASN:HD21	1.74	0.51
1:A:4934:GLY:HA3	1:C:4937:ILE:CG1	2.34	0.51
2:B:74:LEU:HD23	2:B:76:ILE:HD11	1.93	0.51
1:C:1100:MET:O	1:C:1126:GLY:N	2.39	0.51
1:C:1961:PHE:CE2	1:C:2066:LEU:HD22	2.46	0.51
1:C:4217:PHE:CZ	1:C:4234:PHE:HA	2.46	0.51
1:E:1033:ARG:HA	1:E:1036:ARG:HG2	1.94	0.51
1:E:1078:GLU:HG3	1:E:1237:TRP:CH2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1141:ARG:NH2	1:E:1167:GLU:OE1	2.44	0.51
1:E:1291:LEU:HB3	1:E:1550:PRO:HG2	1.92	0.51
1:E:1514:LEU:O	1:E:1532:ASN:N	2.36	0.51
1:E:1663:HIS:O	1:E:1666:THR:OG1	2.19	0.51
1:E:1961:PHE:CD2	1:E:2066:LEU:HD22	2.46	0.51
1:E:4217:PHE:CZ	1:E:4234:PHE:HA	2.47	0.51
1:G:78:LEU:HD11	1:G:147:TRP:CD2	2.46	0.51
1:G:1453:VAL:HG12	1:G:1454:THR:O	2.11	0.51
1:G:1775:HIS:ND1	1:G:1775:HIS:O	2.44	0.51
1:G:1866:ILE:HG23	1:G:1927:LEU:HB2	1.93	0.51
1:A:1033:ARG:HA	1:A:1036:ARG:HG2	1.93	0.50
1:A:2340:PHE:HB2	1:A:2435:ARG:HB3	1.94	0.50
1:A:4055:VAL:HG11	1:A:4163:PHE:HZ	1.77	0.50
1:A:4914:VAL:CG2	1:C:4888:TYR:HB2	2.41	0.50
1:C:1190:PRO:HG2	1:C:1226:PHE:HE2	1.76	0.50
1:C:1853:ILE:O	1:C:1854:PHE:HB2	2.11	0.50
1:C:3674:ILE:HD13	1:C:3677:LEU:HD12	1.94	0.50
1:C:4735:GLU:O	1:C:4739:GLU:N	2.42	0.50
1:E:1775:HIS:ND1	1:E:1775:HIS:O	2.44	0.50
1:E:1853:ILE:O	1:E:1854:PHE:HB2	2.12	0.50
1:E:3992:PHE:HB3	1:E:3996:PHE:CE2	2.47	0.50
1:G:35:LEU:HA	1:G:51:PRO:HA	1.93	0.50
1:G:1130:GLN:HA	1:G:1138:PRO:HA	1.93	0.50
1:G:4963:ILE:HD12	1:G:5030:LYS:NZ	2.26	0.50
1:A:4961:CYS:HB3	1:A:4963:ILE:HG12	1.92	0.50
1:E:721:LEU:HD11	1:E:728:ARG:HB2	1.92	0.50
1:E:1453:VAL:HG12	1:E:1454:THR:O	2.11	0.50
1:E:1937:LEU:HD12	1:E:2116:LEU:HB2	1.93	0.50
1:G:600:LEU:HD21	1:G:1666:THR:HG22	1.92	0.50
1:G:1033:ARG:HA	1:G:1036:ARG:HG2	1.93	0.50
1:G:4683:PHE:HE2	1:G:5017:ARG:HD2	1.76	0.50
1:A:646:PRO:HA	1:A:823:LEU:HA	1.94	0.50
1:A:3850:GLN:HG3	1:A:3850:GLN:O	2.10	0.50
1:C:668:VAL:HA	1:C:789:VAL:HG12	1.93	0.50
1:C:2191:PHE:HD1	1:C:2198:MET:HE1	1.76	0.50
1:C:4055:VAL:HG11	1:C:4163:PHE:HZ	1.76	0.50
2:D:23:VAL:HG12	2:D:104:LEU:HD12	1.93	0.50
1:E:400:ALA:O	1:E:404:ILE:HG13	2.11	0.50
1:E:4055:VAL:HG11	1:E:4163:PHE:HZ	1.76	0.50
1:G:580:GLU:HB3	1:G:620:LEU:HD11	1.94	0.50
1:G:1623:ARG:NH1	1:G:1626:TRP:HE1	2.07	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1808:ARG:HA	1:G:1848:LEU:HD21	1.93	0.50
1:A:721:LEU:HD11	1:A:728:ARG:HB2	1.93	0.50
1:A:1078:GLU:HG3	1:A:1237:TRP:CH2	2.46	0.50
1:A:1436:SER:HA	1:A:1516:ILE:HA	1.93	0.50
1:A:2158:CYS:SG	1:A:2184:ASN:ND2	2.80	0.50
1:A:4677:LEU:HD22	1:A:4711:PHE:CE1	2.46	0.50
1:A:4930:ALA:HB2	1:C:4933:GLN:HG2	1.93	0.50
1:C:1288:PHE:HE2	1:C:1460:HIS:HA	1.77	0.50
1:E:2803:GLU:HA	1:E:2806:ARG:HB2	1.94	0.50
1:E:3674:ILE:HD13	1:E:3677:LEU:HD12	1.93	0.50
1:G:516:LYS:HG3	1:G:555:GLU:OE2	2.11	0.50
1:G:1111:PRO:HG3	1:G:1609:PRO:HD3	1.92	0.50
1:G:1141:ARG:NH2	1:G:1167:GLU:OE1	2.44	0.50
1:G:3806:ASN:H	1:G:3890:LEU:HD23	1.76	0.50
1:A:1141:ARG:NH2	1:A:1167:GLU:OE1	2.45	0.50
1:A:1961:PHE:CD2	1:A:2066:LEU:HD22	2.46	0.50
1:A:4837:LEU:HD11	1:A:4932:ILE:HG23	1.93	0.50
1:C:1207:ASP:O	1:C:1210:SER:OG	2.19	0.50
1:C:1453:VAL:HG12	1:C:1454:THR:O	2.11	0.50
1:C:1623:ARG:NH1	1:C:1626:TRP:HE1	2.06	0.50
1:C:3992:PHE:HB3	1:C:3996:PHE:CE2	2.47	0.50
1:C:4806:ASN:O	1:C:4809:PHE:HB3	2.12	0.50
1:C:4914:VAL:CG2	1:E:4888:TYR:HB2	2.42	0.50
1:E:516:LYS:HG3	1:E:555:GLU:OE2	2.11	0.50
1:E:638:ILE:HD12	1:E:678:GLN:NE2	2.27	0.50
1:E:1744:ALA:CB	1:E:1745:ILE:HA	2.41	0.50
1:E:4677:LEU:HD22	1:E:4711:PHE:CE1	2.47	0.50
1:G:401:ALA:HA	1:G:404:ILE:HD12	1.93	0.50
1:G:716:PHE:O	1:G:737:LEU:HG	2.12	0.50
1:G:1598:GLN:O	1:G:1600:LEU:N	2.44	0.50
1:A:179:TYR:OH	1:C:2359:ARG:NE	2.45	0.50
1:A:1491:ASN:H	1:A:1493:TYR:HA	1.76	0.50
1:C:516:LYS:HG3	1:C:555:GLU:OE2	2.11	0.50
1:C:583:ILE:HD12	1:C:620:LEU:HD22	1.93	0.50
1:C:646:PRO:HA	1:C:823:LEU:HA	1.94	0.50
1:C:1240:LYS:HD3	1:C:1610:ASN:OD1	2.12	0.50
1:C:1491:ASN:H	1:C:1493:TYR:HA	1.77	0.50
1:C:1808:ARG:HA	1:C:1848:LEU:HD21	1.93	0.50
1:E:14:LEU:HD21	1:E:204:PRO:HG3	1.92	0.50
1:E:4002:LYS:HA	1:E:4005:GLN:HG2	1.93	0.50
1:E:4806:ASN:O	1:E:4809:PHE:HB3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:4857:ASN:HD21	1:G:4807:PHE:HD2	1.60	0.50
1:G:214:VAL:HG22	1:G:341:TYR:CE1	2.47	0.50
1:G:1579:MET:O	1:G:1582:SER:OG	2.17	0.50
1:G:2299:VAL:HA	1:G:2302:LEU:HD12	1.94	0.50
1:G:4680:LYS:O	1:G:4685:GLY:N	2.37	0.50
1:A:595:ARG:HH12	1:A:632:LEU:HA	1.77	0.50
1:A:891:TRP:CH2	1:A:899:ASP:HA	2.47	0.50
1:A:1853:ILE:O	1:A:1854:PHE:HB2	2.11	0.50
1:C:473:ASN:O	1:C:477:LEU:HG	2.12	0.50
1:C:1141:ARG:NH2	1:C:1167:GLU:OE1	2.45	0.50
1:C:1866:ILE:HG23	1:C:1927:LEU:HB2	1.93	0.50
1:E:580:GLU:HB3	1:E:620:LEU:HD11	1.94	0.50
1:E:891:TRP:CH2	1:E:899:ASP:HA	2.47	0.50
1:G:732:SER:N	1:G:735:GLN:OE1	2.45	0.50
1:G:1853:ILE:O	1:G:1854:PHE:HB2	2.11	0.50
1:G:2124:LEU:HG	1:G:3673:MET:HE3	1.94	0.50
1:G:4961:CYS:HB3	1:G:4963:ILE:HG12	1.93	0.50
1:A:2347:GLU:CD	1:A:3852:LYS:HE3	2.32	0.50
1:A:2359:ARG:NE	1:G:179:TYR:OH	2.45	0.50
1:A:3674:ILE:HD13	1:A:3677:LEU:HD12	1.93	0.50
1:A:3992:PHE:HB3	1:A:3996:PHE:CE2	2.47	0.50
1:A:4937:ILE:HG12	1:G:4934:GLY:CA	2.40	0.50
1:C:233:ILE:O	1:C:257:ARG:NH1	2.45	0.50
1:C:1033:ARG:HA	1:C:1036:ARG:HG2	1.93	0.50
1:C:1436:SER:HA	1:C:1516:ILE:HA	1.93	0.50
1:C:2340:PHE:HB2	1:C:2435:ARG:HB3	1.94	0.50
1:C:4934:GLY:HA3	1:E:4937:ILE:CG1	2.40	0.50
1:E:20:VAL:O	1:E:67:PHE:N	2.42	0.50
1:E:214:VAL:HG22	1:E:341:TYR:CE1	2.47	0.50
1:E:401:ALA:HA	1:E:404:ILE:HD12	1.93	0.50
1:C:1000:ARG:HB3	1:C:1021:LEU:HD21	1.94	0.50
1:C:1293:LEU:HD23	1:C:1584:ARG:HG2	1.93	0.50
2:D:74:LEU:HD23	2:D:76:ILE:HD11	1.93	0.50
1:E:473:ASN:O	1:E:477:LEU:HG	2.12	0.50
1:E:1436:SER:HA	1:E:1516:ILE:HA	1.93	0.50
1:E:1866:ILE:HG23	1:E:1927:LEU:HB2	1.93	0.50
1:E:2907:PRO:O	1:E:2910:THR:OG1	2.18	0.50
1:E:4837:LEU:HD11	1:E:4932:ILE:HG23	1.94	0.50
1:G:400:ALA:O	1:G:404:ILE:HG13	2.11	0.50
1:G:473:ASN:O	1:G:477:LEU:HG	2.12	0.50
1:G:919:ASN:HA	1:G:922:LEU:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1744:ALA:CB	1:G:1745:ILE:HA	2.41	0.50
1:A:1111:PRO:HG3	1:A:1609:PRO:HD3	1.94	0.49
1:A:1775:HIS:ND1	1:A:1775:HIS:O	2.45	0.49
1:A:2299:VAL:HA	1:A:2302:LEU:HD12	1.94	0.49
1:A:3769:ARG:O	1:A:3773:ARG:NH1	2.41	0.49
1:A:3965:LEU:HD13	1:A:4026:MET:HE1	1.94	0.49
1:C:721:LEU:HD11	1:C:728:ARG:HB2	1.93	0.49
1:C:2158:CYS:SG	1:C:2184:ASN:ND2	2.80	0.49
1:C:2803:GLU:HA	1:C:2806:ARG:HB2	1.94	0.49
1:C:4002:LYS:HA	1:C:4005:GLN:HG2	1.93	0.49
1:E:1808:ARG:HA	1:E:1848:LEU:HD21	1.93	0.49
1:E:2340:PHE:HB2	1:E:2435:ARG:HB3	1.93	0.49
2:F:74:LEU:HD23	2:F:76:ILE:HD11	1.93	0.49
1:G:646:PRO:HA	1:G:823:LEU:HA	1.94	0.49
1:G:1190:PRO:HG2	1:G:1226:PHE:HE2	1.77	0.49
1:G:2340:PHE:HB2	1:G:2435:ARG:HB3	1.94	0.49
1:G:3891:LEU:HD23	1:G:3899:PHE:CZ	2.47	0.49
1:A:214:VAL:HG22	1:A:341:TYR:CE1	2.47	0.49
1:A:1293:LEU:HD23	1:A:1584:ARG:HG2	1.93	0.49
1:A:2242:ILE:HD11	1:A:2246:ASN:ND2	2.27	0.49
1:A:4677:LEU:HD22	1:A:4711:PHE:CZ	2.47	0.49
1:C:401:ALA:HA	1:C:404:ILE:HD12	1.93	0.49
1:C:580:GLU:HB3	1:C:620:LEU:HD11	1.94	0.49
1:C:1738:LEU:HD11	1:C:2143:THR:HB	1.94	0.49
1:C:1762:LEU:HG	1:C:1764:GLY:H	1.76	0.49
1:C:3769:ARG:O	1:C:3773:ARG:NH1	2.40	0.49
1:E:233:ILE:O	1:E:257:ARG:NH1	2.45	0.49
1:E:526:LEU:HD11	1:E:540:PHE:HZ	1.77	0.49
1:E:595:ARG:HH12	1:E:632:LEU:HA	1.78	0.49
1:E:1671:ARG:NH1	1:E:1713:ASP:OD2	2.46	0.49
1:G:891:TRP:CH2	1:G:899:ASP:HA	2.47	0.49
1:G:4799:SER:OG	1:G:4812:HIS:NE2	2.36	0.49
1:A:233:ILE:O	1:A:257:ARG:NH1	2.45	0.49
1:A:244:LEU:HD22	1:A:375:LYS:NZ	2.27	0.49
1:A:291:LEU:O	1:A:312:THR:OG1	2.23	0.49
1:A:516:LYS:HG3	1:A:555:GLU:OE2	2.11	0.49
1:A:668:VAL:HA	1:A:789:VAL:HG12	1.93	0.49
1:A:716:PHE:O	1:A:737:LEU:HG	2.13	0.49
1:A:919:ASN:HA	1:A:922:LEU:HB2	1.93	0.49
1:C:732:SER:N	1:C:735:GLN:OE1	2.46	0.49
1:C:2907:PRO:O	1:C:2910:THR:OG1	2.18	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4239:GLU:OE2	1:C:5014:TYR:OH	2.18	0.49
1:E:695:TYR:O	1:E:697:GLY:N	2.42	0.49
1:E:732:SER:N	1:E:735:GLN:OE1	2.45	0.49
1:E:1103:GLY:HA3	1:E:1123:VAL:HA	1.94	0.49
1:E:1190:PRO:HG2	1:E:1226:PHE:HE2	1.77	0.49
1:E:1738:LEU:HD11	1:E:2143:THR:HB	1.94	0.49
1:E:3965:LEU:HD13	1:E:4026:MET:HE1	1.94	0.49
1:G:559:GLY:O	1:G:563:VAL:HG23	2.12	0.49
1:G:1240:LYS:HD3	1:G:1610:ASN:OD1	2.12	0.49
1:G:1609:PRO:O	1:G:1610:ASN:ND2	2.45	0.49
1:G:4024:VAL:O	1:G:4028:LEU:N	2.41	0.49
1:A:14:LEU:HD21	1:A:204:PRO:HG3	1.93	0.49
1:A:559:GLY:O	1:A:563:VAL:HG23	2.12	0.49
1:A:575:LEU:HD12	1:A:609:CYS:SG	2.53	0.49
1:A:1103:GLY:HA3	1:A:1123:VAL:HA	1.94	0.49
1:A:2142:TYR:CD2	1:A:2197:LEU:HD12	2.47	0.49
1:C:1775:HIS:ND1	1:C:1775:HIS:O	2.45	0.49
1:C:4677:LEU:HD22	1:C:4711:PHE:CE1	2.46	0.49
1:C:4677:LEU:HD22	1:C:4711:PHE:CZ	2.47	0.49
1:E:1076:ARG:HH22	1:E:1609:PRO:HB3	1.77	0.49
1:E:4217:PHE:HZ	1:E:4234:PHE:HA	1.78	0.49
1:G:20:VAL:O	1:G:67:PHE:N	2.42	0.49
1:G:33:LEU:HD23	1:G:35:LEU:HD23	1.93	0.49
1:G:42:PHE:HD1	1:G:447:ASP:OD2	1.95	0.49
1:G:526:LEU:HD11	1:G:540:PHE:HZ	1.78	0.49
1:G:1436:SER:HA	1:G:1516:ILE:HA	1.93	0.49
1:G:1491:ASN:H	1:G:1493:TYR:HA	1.76	0.49
1:G:2499:LYS:HB3	1:G:2553:TYR:OH	2.13	0.49
1:A:1762:LEU:HG	1:A:1764:GLY:H	1.77	0.49
1:A:1952:GLN:NE2	1:A:1956:GLU:OE2	2.45	0.49
1:C:158:SER:H	1:C:161:GLU:HG3	1.76	0.49
1:C:221:ARG:NE	1:C:253:CYS:O	2.45	0.49
1:C:244:LEU:HD22	1:C:375:LYS:NZ	2.27	0.49
1:C:575:LEU:HD12	1:C:609:CYS:SG	2.53	0.49
1:C:2142:TYR:CD2	1:C:2197:LEU:HD12	2.47	0.49
1:E:42:PHE:HD1	1:E:447:ASP:OD2	1.95	0.49
1:E:575:LEU:HD12	1:E:609:CYS:SG	2.53	0.49
1:E:826:ILE:O	1:E:828:GLU:N	2.46	0.49
1:E:2142:TYR:CD2	1:E:2197:LEU:HD12	2.47	0.49
1:E:3889:GLN:HE22	1:E:3963:ASN:HB3	1.78	0.49
1:G:638:ILE:HD12	1:G:678:GLN:NE2	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1937:LEU:HD12	1:G:2116:LEU:HB2	1.95	0.49
1:G:3934:TYR:OH	1:G:3998:HIS:HB3	2.11	0.49
1:A:400:ALA:O	1:A:404:ILE:HG13	2.11	0.49
1:A:473:ASN:O	1:A:477:LEU:HG	2.12	0.49
1:A:826:ILE:O	1:A:828:GLU:N	2.46	0.49
1:A:2499:LYS:HB3	1:A:2553:TYR:OH	2.12	0.49
1:A:3799:LYS:HE3	1:A:3879:GLU:OE2	2.12	0.49
1:A:3844:LEU:CD2	1:G:76:ARG:HE	2.23	0.49
1:C:825:PRO:HG2	1:C:828:GLU:HG3	1.95	0.49
1:C:891:TRP:CH2	1:C:899:ASP:HA	2.47	0.49
1:C:2299:VAL:HA	1:C:2302:LEU:HD12	1.94	0.49
1:C:3727:ASP:O	1:C:3731:LYS:NZ	2.42	0.49
1:C:3937:TYR:HA	1:C:3940:LYS:HZ3	1.77	0.49
1:E:716:PHE:O	1:E:737:LEU:HG	2.13	0.49
1:E:1952:GLN:NE2	1:E:1956:GLU:OE2	2.45	0.49
1:E:2161:GLN:HE21	1:E:2177:LEU:HB3	1.77	0.49
1:G:615:ARG:NH1	1:G:1678:ASN:OD1	2.46	0.49
1:G:2242:ILE:HD11	1:G:2246:ASN:ND2	2.27	0.49
1:G:3825:GLU:C	1:G:3827:GLY:H	2.16	0.49
1:A:33:LEU:HD23	1:A:35:LEU:HD23	1.93	0.49
1:A:1671:ARG:NH1	1:A:1713:ASP:OD2	2.46	0.49
1:A:1738:LEU:HD11	1:A:2143:THR:HB	1.95	0.49
1:C:595:ARG:HH12	1:C:632:LEU:HA	1.78	0.49
1:C:1078:GLU:HG3	1:C:1237:TRP:CH2	2.47	0.49
1:C:1671:ARG:NH1	1:C:1713:ASP:OD2	2.46	0.49
1:C:4217:PHE:HZ	1:C:4234:PHE:HA	1.78	0.49
1:C:4702:ASP:O	1:C:4705:VAL:HG12	2.13	0.49
1:E:4702:ASP:O	1:E:4705:VAL:HG12	2.12	0.49
1:G:1078:GLU:HG3	1:G:1237:TRP:CH2	2.48	0.49
1:G:4205:TRP:HB2	1:G:4245:MET:HE1	1.95	0.49
1:A:20:VAL:O	1:A:67:PHE:N	2.42	0.49
1:A:732:SER:N	1:A:735:GLN:OE1	2.46	0.49
1:A:825:PRO:HG2	1:A:828:GLU:HG3	1.95	0.49
1:C:14:LEU:HD21	1:C:204:PRO:HG3	1.93	0.49
1:C:767:VAL:O	1:C:1475:THR:OG1	2.23	0.49
1:C:826:ILE:O	1:C:828:GLU:N	2.46	0.49
1:C:1952:GLN:NE2	1:C:1956:GLU:OE2	2.45	0.49
1:C:2242:ILE:HD11	1:C:2246:ASN:ND2	2.28	0.49
1:C:4139:ILE:O	1:C:4143:VAL:HG23	2.13	0.49
1:E:244:LEU:HD22	1:E:375:LYS:NZ	2.27	0.49
1:E:646:PRO:HA	1:E:823:LEU:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:2299:VAL:HA	1:E:2302:LEU:HD12	1.95	0.49
1:G:244:LEU:HD22	1:G:375:LYS:NZ	2.27	0.49
1:G:583:ILE:HD11	1:G:617:ASN:OD1	2.13	0.49
1:G:1000:ARG:HB3	1:G:1021:LEU:HD21	1.94	0.49
1:G:4183:ILE:HD12	1:G:4185:GLY:H	1.78	0.49
1:G:4820:VAL:O	1:G:4824:ARG:HG3	2.12	0.49
1:A:526:LEU:HD11	1:A:540:PHE:HZ	1.77	0.49
1:A:692:TYR:CE1	1:A:711:LEU:HD21	2.48	0.49
1:A:2505:PHE:CE1	1:A:2509:VAL:HG21	2.48	0.49
1:A:3727:ASP:HB3	1:A:3731:LYS:HZ1	1.76	0.49
1:A:4002:LYS:HA	1:A:4005:GLN:HG2	1.94	0.49
1:C:214:VAL:HG22	1:C:341:TYR:CE1	2.47	0.49
1:C:2142:TYR:HD2	1:C:2197:LEU:HD12	1.78	0.49
1:E:158:SER:OG	1:E:159:GLU:N	2.45	0.49
1:E:350:HIS:HD2	1:E:353:SER:H	1.61	0.49
1:A:109:LEU:HB2	1:A:118:LEU:HB3	1.95	0.49
1:A:1091:GLU:HA	1:A:1150:GLY:HA2	1.95	0.49
1:A:1744:ALA:CB	1:A:1745:ILE:HA	2.41	0.49
1:A:2142:TYR:HD2	1:A:2197:LEU:HD12	1.78	0.49
1:A:2803:GLU:HA	1:A:2806:ARG:HB2	1.95	0.49
1:A:4247:ILE:HD11	1:A:4667:PRO:HB2	1.95	0.49
1:A:4976:GLU:OE1	1:G:4228:ALA:HB2	2.13	0.49
1:C:526:LEU:HD11	1:C:540:PHE:HZ	1.77	0.49
1:C:1744:ALA:CB	1:C:1745:ILE:HA	2.41	0.49
1:E:4677:LEU:HD22	1:E:4711:PHE:CZ	2.48	0.49
1:G:1762:LEU:HG	1:G:1764:GLY:H	1.78	0.49
1:G:3842:LEU:HB3	1:G:3929:SER:OG	2.13	0.49
1:A:401:ALA:HA	1:A:404:ILE:HD12	1.94	0.48
1:A:402:ARG:NH1	1:A:405:HIS:CD2	2.81	0.48
1:A:583:ILE:HD11	1:A:617:ASN:OD1	2.13	0.48
1:A:1000:ARG:HB3	1:A:1021:LEU:HD21	1.94	0.48
1:A:1190:PRO:HG2	1:A:1226:PHE:HE2	1.77	0.48
1:A:1623:ARG:NH1	1:A:1626:TRP:HE1	2.06	0.48
1:A:1866:ILE:HG23	1:A:1927:LEU:HB2	1.93	0.48
1:A:2450:ALA:O	1:A:2453:ILE:HG12	2.13	0.48
1:C:638:ILE:HD12	1:C:678:GLN:NE2	2.27	0.48
1:C:695:TYR:O	1:C:697:GLY:N	2.42	0.48
1:C:1961:PHE:CD2	1:C:2066:LEU:HD22	2.47	0.48
1:C:2867:LEU:HG	1:C:2928:LYS:HZ3	1.77	0.48
1:C:3727:ASP:HB3	1:C:3731:LYS:HZ1	1.77	0.48
1:E:2242:ILE:HD11	1:E:2246:ASN:ND2	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:484:LEU:HD11	1:G:530:ILE:HD11	1.95	0.48
1:G:1663:HIS:O	1:G:1666:THR:OG1	2.19	0.48
1:G:1671:ARG:NH1	1:G:1713:ASP:OD2	2.46	0.48
1:G:1961:PHE:CE2	1:G:2066:LEU:HD22	2.48	0.48
1:A:42:PHE:HD1	1:A:447:ASP:OD2	1.95	0.48
1:A:4192:ARG:NH1	1:A:5028:PHE:CD2	2.81	0.48
1:C:1091:GLU:HA	1:C:1150:GLY:HA2	1.95	0.48
1:C:2161:GLN:HE21	1:C:2177:LEU:HB3	1.77	0.48
1:C:2499:LYS:HB3	1:C:2553:TYR:OH	2.13	0.48
1:C:2505:PHE:CE1	1:C:2509:VAL:HG21	2.48	0.48
1:C:3965:LEU:HD13	1:C:4026:MET:HE1	1.94	0.48
1:E:2499:LYS:HB3	1:E:2553:TYR:OH	2.13	0.48
1:E:4162:ASN:HA	1:E:4165:GLU:HG2	1.95	0.48
1:E:4923:PHE:O	1:E:4928:LEU:HD13	2.13	0.48
1:G:4664:LEU:O	1:G:4667:PRO:HD2	2.13	0.48
1:A:580:GLU:HB3	1:A:620:LEU:HD11	1.94	0.48
1:A:4162:ASN:HA	1:A:4165:GLU:HG2	1.95	0.48
1:A:4702:ASP:O	1:A:4705:VAL:HG12	2.12	0.48
1:A:4735:GLU:O	1:A:4739:GLU:N	2.44	0.48
1:C:158:SER:OG	1:C:159:GLU:N	2.46	0.48
1:E:583:ILE:HD11	1:E:617:ASN:OD1	2.13	0.48
1:E:692:TYR:CE1	1:E:711:LEU:HD21	2.48	0.48
1:E:4856:PHE:O	1:E:4860:ARG:NH1	2.46	0.48
1:G:825:PRO:HG2	1:G:828:GLU:HG3	1.95	0.48
1:G:826:ILE:O	1:G:828:GLU:N	2.46	0.48
1:G:1077:ALA:HB3	1:G:1190:PRO:HD2	1.96	0.48
1:G:2505:PHE:CE1	1:G:2509:VAL:HG21	2.48	0.48
1:G:2775:TRP:HH2	1:G:2783:GLU:HA	1.78	0.48
1:G:2803:GLU:HA	1:G:2806:ARG:HB2	1.95	0.48
1:A:1579:MET:O	1:A:1582:SER:OG	2.17	0.48
1:A:2191:PHE:HD1	1:A:2198:MET:HE1	1.78	0.48
1:A:2775:TRP:HH2	1:A:2783:GLU:HA	1.79	0.48
1:C:42:PHE:HD1	1:C:447:ASP:OD2	1.96	0.48
1:C:559:GLY:O	1:C:563:VAL:HG23	2.12	0.48
1:C:1609:PRO:O	1:C:1610:ASN:ND2	2.46	0.48
1:C:1815:LEU:HB3	1:C:1865:MET:HE3	1.94	0.48
1:C:3799:LYS:HE3	1:C:3879:GLU:OE2	2.12	0.48
1:E:102:LEU:HB2	1:E:105:HIS:CE1	2.47	0.48
1:E:825:PRO:HG2	1:E:828:GLU:HG3	1.95	0.48
1:E:1000:ARG:HB3	1:E:1021:LEU:HD21	1.94	0.48
1:E:1598:GLN:O	1:E:1600:LEU:N	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1849:LEU:HG	1:E:1945:TYR:CE2	2.49	0.48
1:E:2341:VAL:HG13	1:E:2342:ASN:N	2.22	0.48
1:E:3799:LYS:HE3	1:E:3879:GLU:OE2	2.12	0.48
1:E:4139:ILE:O	1:E:4143:VAL:HG23	2.13	0.48
1:G:63:ALA:HA	1:G:261:ARG:NH2	2.29	0.48
1:G:350:HIS:HD2	1:G:353:SER:H	1.61	0.48
1:G:603:LEU:HD22	1:G:621:ILE:HD12	1.96	0.48
1:A:590:LEU:HD23	1:A:631:LEU:HD21	1.95	0.48
1:A:4806:ASN:O	1:A:4809:PHE:HB3	2.13	0.48
1:E:484:LEU:HD11	1:E:530:ILE:HD11	1.96	0.48
1:E:559:GLY:O	1:E:563:VAL:HG23	2.12	0.48
1:E:1077:ALA:HB3	1:E:1190:PRO:HD2	1.96	0.48
1:E:4192:ARG:NH1	1:E:5028:PHE:CD2	2.82	0.48
1:G:1091:GLU:HA	1:G:1150:GLY:HA2	1.96	0.48
1:G:1849:LEU:HG	1:G:1945:TYR:CE2	2.48	0.48
1:G:3959:LYS:HG3	1:G:4022:ASP:OD2	2.14	0.48
1:G:3993:LEU:HD13	1:G:4055:VAL:HG22	1.96	0.48
1:G:4175:ARG:N	1:G:4176:PRO:HD2	2.29	0.48
1:A:158:SER:OG	1:A:159:GLU:N	2.46	0.48
1:A:683:ARG:HB3	1:A:713:SER:HB2	1.96	0.48
1:A:2161:GLN:HE21	1:A:2177:LEU:HB3	1.78	0.48
1:A:4807:PHE:CE2	1:G:4856:PHE:CD2	3.01	0.48
1:A:4901:ILE:HG21	1:A:4913:ARG:NH2	2.27	0.48
1:C:484:LEU:HD11	1:C:530:ILE:HD11	1.96	0.48
1:C:1077:ALA:HB3	1:C:1190:PRO:HD2	1.95	0.48
1:C:2341:VAL:HG13	1:C:2342:ASN:N	2.22	0.48
1:C:4835:LYS:HG2	1:E:4822:THR:HG21	1.94	0.48
1:G:109:LEU:HB2	1:G:118:LEU:HB3	1.95	0.48
1:G:692:TYR:CE1	1:G:711:LEU:HD21	2.48	0.48
1:G:2161:GLN:HE21	1:G:2177:LEU:HB3	1.78	0.48
1:G:2450:ALA:O	1:G:2453:ILE:HG12	2.14	0.48
1:G:4002:LYS:HA	1:G:4005:GLN:HG2	1.96	0.48
1:G:4031:LEU:HD12	1:G:4034:ASN:HD22	1.79	0.48
1:G:4677:LEU:CD1	1:G:4702:ASP:HB3	2.44	0.48
1:A:1088:TRP:HB2	1:A:1153:ILE:CG2	2.44	0.48
1:A:1849:LEU:HG	1:A:1945:TYR:CE2	2.48	0.48
1:C:583:ILE:HD11	1:C:617:ASN:OD1	2.13	0.48
1:C:1849:LEU:HG	1:C:1945:TYR:CE2	2.48	0.48
1:C:2450:ALA:O	1:C:2453:ILE:HG12	2.13	0.48
1:C:2793:PRO:O	1:C:2796:THR:OG1	2.24	0.48
1:C:4162:ASN:HA	1:C:4165:GLU:HG2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:109:LEU:HB2	1:E:118:LEU:HB3	1.95	0.48
1:E:603:LEU:HD22	1:E:621:ILE:HD12	1.95	0.48
1:E:1205:GLY:HA2	1:E:1225:PRO:HB3	1.96	0.48
1:E:4914:VAL:HG21	1:G:4888:TYR:HB2	1.94	0.48
1:C:1088:TRP:HB2	1:C:1153:ILE:CG2	2.44	0.48
1:C:4192:ARG:NH1	1:C:5028:PHE:CD2	2.82	0.48
1:E:22:LEU:HB3	1:E:200:TRP:CZ3	2.49	0.48
1:E:3727:ASP:HB3	1:E:3731:LYS:HZ1	1.77	0.48
1:E:4984:ASN:OD1	1:E:4987:ASN:ND2	2.47	0.48
1:G:3836:MET:O	1:G:3925:ARG:NH2	2.47	0.48
1:A:2142:TYR:CD2	1:A:2197:LEU:HB2	2.49	0.48
1:A:4139:ILE:O	1:A:4143:VAL:HG23	2.13	0.48
1:A:4984:ASN:OD1	1:A:4987:ASN:ND2	2.47	0.48
1:C:350:HIS:HD2	1:C:353:SER:H	1.61	0.48
1:C:615:ARG:NH1	1:C:1678:ASN:OD1	2.47	0.48
1:C:692:TYR:CE1	1:C:711:LEU:HD21	2.48	0.48
1:C:4552:LEU:HD11	1:C:4663:CYS:SG	2.54	0.48
1:E:709:ASP:OD2	1:E:1491:ASN:HA	2.14	0.48
1:E:1088:TRP:HB2	1:E:1153:ILE:CG2	2.44	0.48
1:E:2505:PHE:CE1	1:E:2509:VAL:HG21	2.48	0.48
1:G:1961:PHE:CD2	1:G:2066:LEU:HD22	2.49	0.48
1:G:3962:PHE:O	1:G:3966:THR:HG23	2.13	0.48
1:A:1687:SER:HB2	1:A:1782:PHE:CZ	2.49	0.48
1:A:2454:ARG:O	1:A:2458:ARG:HG3	2.14	0.48
1:C:590:LEU:HD23	1:C:631:LEU:HD21	1.95	0.48
1:C:602:VAL:O	1:C:605:SER:OG	2.22	0.48
1:C:2066:LEU:O	1:C:2070:VAL:HG23	2.14	0.48
1:C:4901:ILE:HG21	1:C:4913:ARG:NH2	2.27	0.48
1:C:4904:PRO:HB2	1:C:4910:GLU:HG3	1.96	0.48
1:E:3804:ILE:HG22	1:E:3812:VAL:HG11	1.96	0.48
1:G:1018:ASN:H	1:G:1021:LEU:HD12	1.79	0.48
1:G:2454:ARG:O	1:G:2458:ARG:HG3	2.14	0.48
1:A:229:GLU:HA	1:A:249:GLY:HA2	1.96	0.47
1:A:615:ARG:NH1	1:A:1678:ASN:OD1	2.46	0.47
1:A:638:ILE:HD12	1:A:678:GLN:NE2	2.27	0.47
1:A:3805:LEU:HB2	1:A:3890:LEU:HD23	1.95	0.47
1:A:3889:GLN:HE22	1:A:3963:ASN:HB3	1.78	0.47
1:A:4076:ALA:HA	1:A:4079:ASP:HB3	1.96	0.47
1:A:4914:VAL:HG23	1:C:4888:TYR:CG	2.48	0.47
1:E:646:PRO:O	1:E:648:ILE:N	2.41	0.47
1:E:855:PRO:HG2	1:E:998:ARG:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:2142:TYR:HD2	1:E:2197:LEU:HD12	1.78	0.47
1:E:2771:ILE:HD11	1:E:2857:PRO:HD2	1.96	0.47
1:E:3768:SER:HA	1:E:3771:HIS:CE1	2.49	0.47
1:E:3980:LEU:HD21	1:E:3985:LEU:HD13	1.96	0.47
2:F:37:ASP:OD1	2:F:38:SER:N	2.47	0.47
2:F:76:ILE:O	2:F:96:THR:HG23	2.14	0.47
1:G:546:TRP:HE1	1:G:550:LYS:HZ1	1.61	0.47
1:G:595:ARG:HH12	1:G:632:LEU:HA	1.79	0.47
1:A:1077:ALA:HB3	1:A:1190:PRO:HD2	1.96	0.47
1:C:3768:SER:HA	1:C:3771:HIS:CE1	2.49	0.47
1:C:4984:ASN:OD1	1:C:4987:ASN:ND2	2.47	0.47
1:E:158:SER:H	1:E:161:GLU:HG3	1.79	0.47
1:E:683:ARG:HB3	1:E:713:SER:HB2	1.96	0.47
1:E:2142:TYR:CD2	1:E:2197:LEU:HB2	2.48	0.47
1:E:2450:ALA:O	1:E:2453:ILE:HG12	2.14	0.47
1:G:575:LEU:HD12	1:G:609:CYS:SG	2.53	0.47
1:G:1676:LEU:HD23	1:G:1676:LEU:O	2.15	0.47
1:G:1952:GLN:NE2	1:G:1956:GLU:OE2	2.47	0.47
1:A:63:ALA:HA	1:A:261:ARG:NH2	2.30	0.47
1:A:484:LEU:HD11	1:A:530:ILE:HD11	1.96	0.47
1:A:4552:LEU:HD11	1:A:4663:CYS:SG	2.54	0.47
1:C:2775:TRP:HH2	1:C:2783:GLU:HA	1.79	0.47
2:D:37:ASP:OD1	2:D:38:SER:N	2.47	0.47
1:E:590:LEU:HD23	1:E:631:LEU:HD21	1.95	0.47
1:E:615:ARG:NH1	1:E:1678:ASN:OD1	2.46	0.47
1:E:4247:ILE:HD11	1:E:4667:PRO:HB2	1.95	0.47
1:G:402:ARG:NH1	1:G:405:HIS:CD2	2.81	0.47
1:G:1746:THR:O	1:G:1748:PHE:N	2.48	0.47
1:G:2827:ARG:HB2	1:G:2934:GLY:HA3	1.96	0.47
1:A:2066:LEU:O	1:A:2070:VAL:HG23	2.15	0.47
1:A:4217:PHE:HZ	1:A:4234:PHE:HA	1.78	0.47
1:C:830:ARG:HD3	1:C:1612:PHE:CZ	2.50	0.47
1:C:2142:TYR:CD2	1:C:2197:LEU:HB2	2.49	0.47
1:E:402:ARG:NH1	1:E:405:HIS:CD2	2.81	0.47
1:E:1687:SER:HB2	1:E:1782:PHE:CZ	2.49	0.47
1:E:2775:TRP:HH2	1:E:2783:GLU:HA	1.79	0.47
1:G:1081:TYR:CD2	1:G:1234:VAL:HG13	2.49	0.47
1:G:1088:TRP:HB2	1:G:1153:ILE:CG2	2.44	0.47
1:G:1662:PHE:O	1:G:1666:THR:HG23	2.15	0.47
1:G:3826:VAL:HG23	1:G:3909:ASN:HB3	1.96	0.47
1:G:4573:ILE:HD11	1:G:4646:LEU:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:LEU:HB3	1:A:200:TRP:CZ3	2.50	0.47
1:A:350:HIS:HD2	1:A:353:SER:H	1.61	0.47
1:A:603:LEU:HD22	1:A:621:ILE:HD12	1.96	0.47
1:A:4963:ILE:HD12	1:A:5030:LYS:HZ1	1.78	0.47
1:C:1729:SER:O	1:C:1733:GLU:HG2	2.15	0.47
1:C:2454:ARG:O	1:C:2458:ARG:HG3	2.14	0.47
1:E:1132:TRP:CD1	1:E:1136:SER:HA	2.50	0.47
1:E:1662:PHE:O	1:E:1666:THR:HG23	2.15	0.47
1:E:1746:THR:O	1:E:1748:PHE:N	2.47	0.47
1:E:4175:ARG:N	1:E:4176:PRO:HD2	2.30	0.47
1:E:4552:LEU:HD11	1:E:4663:CYS:SG	2.54	0.47
1:G:2136:ARG:HH11	1:G:3720:TYR:HE2	1.62	0.47
2:H:38:SER:HB3	2:H:41:ASP:OD2	2.15	0.47
2:B:76:ILE:O	2:B:96:THR:HG23	2.15	0.47
1:C:109:LEU:HB2	1:C:118:LEU:HB3	1.96	0.47
1:C:709:ASP:OD2	1:C:1491:ASN:HA	2.14	0.47
1:C:716:PHE:O	1:C:737:LEU:HG	2.13	0.47
1:C:3805:LEU:HB2	1:C:3890:LEU:HD23	1.96	0.47
1:C:4205:TRP:HB2	1:C:4245:MET:HE1	1.95	0.47
1:E:221:ARG:NE	1:E:253:CYS:O	2.44	0.47
1:E:695:TYR:CD2	1:E:1240:LYS:HE3	2.50	0.47
1:E:1815:LEU:HB3	1:E:1865:MET:HE3	1.96	0.47
1:E:4221:VAL:HG11	1:E:4230:LYS:HG3	1.96	0.47
1:E:4818:MET:HA	1:E:4824:ARG:HG2	1.96	0.47
1:E:4904:PRO:HB2	1:E:4910:GLU:HG3	1.97	0.47
1:G:675:LEU:CD2	1:G:1633:PRO:HG3	2.45	0.47
1:G:1091:GLU:HG2	1:G:1213:PHE:CD1	2.50	0.47
1:G:3780:LEU:HD23	1:G:3819:TYR:CD2	2.49	0.47
1:A:714:TYR:CB	1:A:757:PHE:HD2	2.28	0.47
1:A:843:SER:OG	1:A:844:ARG:N	2.48	0.47
1:A:1018:ASN:H	1:A:1021:LEU:HD12	1.80	0.47
1:A:1130:GLN:HA	1:A:1138:PRO:HA	1.97	0.47
1:A:1662:PHE:O	1:A:1666:THR:HG23	2.15	0.47
1:A:4030:LEU:CG	1:A:4040:ILE:HD11	2.44	0.47
1:A:4205:TRP:HB2	1:A:4245:MET:HE1	1.97	0.47
1:A:4818:MET:HA	1:A:4824:ARG:HG2	1.95	0.47
1:A:4892:ARG:NH2	1:G:4917:ASP:OD2	2.48	0.47
2:B:37:ASP:OD1	2:B:38:SER:N	2.47	0.47
1:C:111:HIS:CD2	1:C:113:HIS:HB3	2.50	0.47
1:C:402:ARG:NH1	1:C:405:HIS:CD2	2.81	0.47
1:C:1018:ASN:H	1:C:1021:LEU:HD12	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1091:GLU:HG2	1:C:1213:PHE:CD1	2.49	0.47
1:C:1662:PHE:O	1:C:1666:THR:HG23	2.15	0.47
1:C:1687:SER:HB2	1:C:1782:PHE:CZ	2.49	0.47
1:C:3889:GLN:HE22	1:C:3963:ASN:HB3	1.78	0.47
1:C:4247:ILE:HD11	1:C:4667:PRO:HB2	1.96	0.47
1:C:4791:TYR:HD2	1:C:4792:LEU:HD12	1.80	0.47
1:E:1091:GLU:HG2	1:E:1213:PHE:CD1	2.50	0.47
1:E:1609:PRO:O	1:E:1610:ASN:ND2	2.48	0.47
1:E:1748:PHE:HZ	1:E:2072:LEU:HB2	1.79	0.47
1:E:3805:LEU:HB2	1:E:3890:LEU:HD23	1.96	0.47
1:E:3962:PHE:HD1	1:E:4026:MET:SD	2.38	0.47
1:E:4677:LEU:HD11	1:E:4702:ASP:HB3	1.97	0.47
1:E:4791:TYR:HD2	1:E:4792:LEU:HD12	1.79	0.47
1:G:709:ASP:OD2	1:G:1491:ASN:HA	2.14	0.47
1:G:1676:LEU:HD21	1:G:2164:SER:O	2.15	0.47
1:G:1940:CYS:SG	1:G:2123:LEU:HD12	2.55	0.47
1:G:2066:LEU:O	1:G:2070:VAL:HG23	2.14	0.47
1:G:2771:ILE:HD11	1:G:2857:PRO:HD2	1.96	0.47
1:G:3889:GLN:NE2	1:G:3963:ASN:HB3	2.29	0.47
1:G:4646:LEU:HA	1:G:4649:LEU:HB3	1.97	0.47
1:G:4855:ALA:HB1	1:G:4863:TYR:HE2	1.80	0.47
1:G:4984:ASN:OD1	1:G:4987:ASN:ND2	2.48	0.47
2:H:25:HIS:CG	2:H:40:ARG:HE	2.33	0.47
1:A:1132:TRP:CD1	1:A:1136:SER:HA	2.50	0.47
1:A:3768:SER:HA	1:A:3771:HIS:CE1	2.49	0.47
1:A:4183:ILE:HD12	1:A:4185:GLY:H	1.80	0.47
1:A:4791:TYR:HD2	1:A:4792:LEU:HD12	1.80	0.47
1:C:22:LEU:HB3	1:C:200:TRP:CZ3	2.49	0.47
1:C:603:LEU:HD22	1:C:621:ILE:HD12	1.96	0.47
1:C:2206:THR:O	1:C:2210:VAL:HG23	2.15	0.47
1:C:4030:LEU:CG	1:C:4040:ILE:HD11	2.44	0.47
1:C:4837:LEU:HD11	1:C:4932:ILE:HG23	1.97	0.47
1:E:2454:ARG:O	1:E:2458:ARG:HG3	2.14	0.47
1:G:2819:TRP:CZ3	1:G:2877:GLN:HG2	2.50	0.47
1:G:3981:ALA:HA	1:G:3986:TRP:HE1	1.80	0.47
1:G:4141:PHE:O	1:G:4145:VAL:HG23	2.15	0.47
2:H:37:ASP:OD1	2:H:38:SER:N	2.48	0.47
1:A:646:PRO:O	1:A:648:ILE:N	2.41	0.47
1:A:1476:MET:H	1:A:1485:SER:HA	1.80	0.47
1:A:1610:ASN:HA	1:A:1652:GLU:OE2	2.15	0.47
1:A:1850:VAL:HA	1:A:1945:TYR:CE1	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3980:LEU:HD21	1:A:3985:LEU:HD13	1.95	0.47
1:A:4087:LEU:HD23	1:A:4122:MET:HB3	1.97	0.47
1:A:4904:PRO:HB2	1:A:4910:GLU:HG3	1.97	0.47
1:C:411:TYR:HB2	1:C:486:LEU:HD21	1.97	0.47
1:C:3980:LEU:HD21	1:C:3985:LEU:HD13	1.96	0.47
1:C:4175:ARG:N	1:C:4176:PRO:HD2	2.29	0.47
1:E:495:ASN:CA	1:E:553:ARG:HH12	2.28	0.47
1:E:2206:THR:O	1:E:2210:VAL:HG23	2.15	0.47
1:E:4087:LEU:HD23	1:E:4122:MET:HB3	1.97	0.47
1:G:843:SER:OG	1:G:844:ARG:N	2.48	0.47
1:G:1679:ASN:HA	1:G:1682:ALA:HB3	1.97	0.47
1:G:1850:VAL:HA	1:G:1945:TYR:CE1	2.50	0.47
1:A:695:TYR:CD2	1:A:1240:LYS:HE3	2.50	0.47
1:A:3962:PHE:HD1	1:A:4026:MET:SD	2.38	0.47
2:D:76:ILE:O	2:D:96:THR:HG23	2.15	0.47
1:E:418:LEU:HA	1:E:421:PHE:CE2	2.50	0.47
1:E:1812:LEU:HA	1:E:1815:LEU:HD12	1.97	0.47
1:G:22:LEU:HB3	1:G:200:TRP:CZ3	2.50	0.47
1:G:683:ARG:HB3	1:G:713:SER:HB2	1.96	0.47
1:G:2100:HIS:O	1:G:2104:ARG:HG2	2.15	0.47
2:H:23:VAL:HG22	2:H:47:LYS:HG2	1.96	0.47
1:A:495:ASN:CA	1:A:553:ARG:HH12	2.28	0.46
1:A:709:ASP:OD2	1:A:1491:ASN:HA	2.14	0.46
1:A:2100:HIS:O	1:A:2104:ARG:HG2	2.16	0.46
1:A:2206:THR:O	1:A:2210:VAL:HG23	2.15	0.46
1:A:2771:ILE:HD11	1:A:2857:PRO:HD2	1.96	0.46
1:C:229:GLU:HA	1:C:249:GLY:HA2	1.97	0.46
1:C:663:TYR:OH	1:C:804:PRO:HD2	2.16	0.46
1:C:1676:LEU:O	1:C:1676:LEU:HD23	2.15	0.46
2:F:55:VAL:HG21	2:F:59:TRP:HD1	1.81	0.46
1:G:158:SER:OG	1:G:159:GLU:N	2.46	0.46
1:G:495:ASN:CA	1:G:553:ARG:HH12	2.28	0.46
1:G:590:LEU:HD23	1:G:631:LEU:HD21	1.95	0.46
1:G:855:PRO:HG2	1:G:998:ARG:HD2	1.96	0.46
1:G:1685:LEU:O	1:G:1689:VAL:HG12	2.15	0.46
1:G:3955:MET:SD	1:G:4019:LEU:HD13	2.55	0.46
1:A:221:ARG:NE	1:A:253:CYS:O	2.45	0.46
1:A:284:HIS:NE2	1:A:286:THR:OG1	2.47	0.46
1:A:4175:ARG:N	1:A:4176:PRO:HD2	2.30	0.46
2:B:87:HIS:HD2	2:B:88:PRO:HD2	1.81	0.46
1:C:63:ALA:HA	1:C:261:ARG:NH2	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1746:THR:O	1:C:1748:PHE:N	2.47	0.46
1:C:2771:ILE:HD11	1:C:2857:PRO:HD2	1.96	0.46
1:C:2927:LEU:HD22	1:C:2937:VAL:HG11	1.97	0.46
1:C:4076:ALA:HA	1:C:4079:ASP:HB3	1.96	0.46
2:D:55:VAL:HG21	2:D:59:TRP:HD1	1.81	0.46
1:E:411:TYR:HB2	1:E:486:LEU:HD21	1.97	0.46
1:E:843:SER:OG	1:E:844:ARG:N	2.48	0.46
1:E:1018:ASN:H	1:E:1021:LEU:HD12	1.80	0.46
1:E:1091:GLU:HA	1:E:1150:GLY:HA2	1.97	0.46
1:E:1762:LEU:HG	1:E:1764:GLY:H	1.79	0.46
1:G:229:GLU:HA	1:G:249:GLY:HA2	1.97	0.46
1:A:418:LEU:HA	1:A:421:PHE:CE2	2.50	0.46
1:A:663:TYR:OH	1:A:804:PRO:HD2	2.16	0.46
1:A:1091:GLU:HG2	1:A:1213:PHE:CD1	2.49	0.46
1:A:1204:LEU:HD22	1:A:1226:PHE:CD2	2.51	0.46
1:A:1748:PHE:HZ	1:A:2072:LEU:HB2	1.80	0.46
1:A:4835:LYS:HG2	1:C:4822:THR:HG21	1.96	0.46
1:C:909:ASN:HA	1:C:965:TYR:CE1	2.51	0.46
1:C:1093:GLU:HG2	1:C:1148:VAL:HG22	1.97	0.46
1:C:1476:MET:H	1:C:1485:SER:HA	1.80	0.46
1:C:1676:LEU:HD21	1:C:2164:SER:O	2.16	0.46
1:E:229:GLU:HA	1:E:249:GLY:HA2	1.96	0.46
2:F:87:HIS:HD2	2:F:88:PRO:HD2	1.80	0.46
1:G:714:TYR:CB	1:G:757:PHE:HD2	2.28	0.46
1:G:1204:LEU:HD22	1:G:1226:PHE:CD2	2.51	0.46
1:G:1476:MET:H	1:G:1485:SER:HA	1.81	0.46
1:A:110:ARG:NH2	1:A:115:ARG:HD2	2.29	0.46
1:A:651:GLY:HA2	1:A:776:LEU:HG	1.98	0.46
1:A:1746:THR:O	1:A:1748:PHE:N	2.48	0.46
1:A:4677:LEU:HD11	1:A:4702:ASP:HB3	1.97	0.46
2:B:73:LYS:HA	2:B:99:PHE:O	2.16	0.46
1:C:843:SER:OG	1:C:844:ARG:N	2.48	0.46
1:C:3934:TYR:OH	1:C:3998:HIS:HB3	2.15	0.46
1:C:4053:SER:O	1:C:4056:GLU:HB3	2.15	0.46
1:C:4183:ILE:HD12	1:C:4185:GLY:H	1.80	0.46
1:E:63:ALA:HA	1:E:261:ARG:NH2	2.29	0.46
1:E:1081:TYR:CD2	1:E:1234:VAL:HG13	2.51	0.46
1:E:1476:MET:H	1:E:1485:SER:HA	1.80	0.46
1:E:4053:SER:O	1:E:4056:GLU:HB3	2.15	0.46
1:G:418:LEU:HA	1:G:421:PHE:CE2	2.50	0.46
1:G:2341:VAL:HG13	1:G:2342:ASN:N	2.22	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:3703:LEU:HD23	1:G:3703:LEU:O	2.16	0.46
1:G:3727:ASP:HB3	1:G:3731:LYS:NZ	2.31	0.46
1:G:3927:GLN:HE21	1:G:3991:GLY:CA	2.22	0.46
1:A:4053:SER:O	1:A:4056:GLU:HB3	2.15	0.46
1:C:418:LEU:HA	1:C:421:PHE:CE2	2.50	0.46
1:C:855:PRO:HG2	1:C:998:ARG:HD2	1.96	0.46
1:C:3962:PHE:HD1	1:C:4026:MET:SD	2.38	0.46
1:E:111:HIS:CD2	1:E:113:HIS:HB3	2.50	0.46
1:E:1130:GLN:HA	1:E:1138:PRO:HA	1.97	0.46
1:E:1685:LEU:O	1:E:1689:VAL:HG12	2.15	0.46
1:E:2066:LEU:O	1:E:2070:VAL:HG23	2.15	0.46
1:E:4076:ALA:HA	1:E:4079:ASP:HB3	1.97	0.46
1:G:221:ARG:NE	1:G:253:CYS:O	2.44	0.46
1:G:4904:PRO:HB2	1:G:4910:GLU:HG3	1.97	0.46
1:A:1093:GLU:HG2	1:A:1148:VAL:HG22	1.97	0.46
1:A:1685:LEU:O	1:A:1689:VAL:HG12	2.15	0.46
1:A:3804:ILE:HG22	1:A:3812:VAL:HG11	1.96	0.46
1:A:4807:PHE:HZ	1:G:4856:PHE:CE2	2.32	0.46
1:C:1204:LEU:HD22	1:C:1226:PHE:CD2	2.51	0.46
1:C:1685:LEU:O	1:C:1689:VAL:HG12	2.15	0.46
1:C:4677:LEU:HD11	1:C:4702:ASP:HB3	1.97	0.46
1:C:4914:VAL:HG23	1:E:4888:TYR:CG	2.49	0.46
1:E:1076:ARG:HH22	1:E:1609:PRO:CB	2.29	0.46
1:E:1729:SER:O	1:E:1733:GLU:HG2	2.15	0.46
1:E:1770:SER:OG	1:E:1771:LEU:N	2.49	0.46
1:E:3934:TYR:OH	1:E:3998:HIS:HB3	2.16	0.46
1:G:284:HIS:NE2	1:G:286:THR:OG1	2.48	0.46
1:G:646:PRO:O	1:G:648:ILE:N	2.40	0.46
1:G:1748:PHE:HZ	1:G:2072:LEU:HB2	1.80	0.46
1:G:3352:GLU:O	1:G:3356:SER:N	2.46	0.46
1:A:111:HIS:CD2	1:A:113:HIS:HB3	2.50	0.46
1:A:1676:LEU:HD21	1:A:2164:SER:O	2.15	0.46
1:A:1679:ASN:HA	1:A:1682:ALA:HB3	1.98	0.46
1:A:1812:LEU:HA	1:A:1815:LEU:HD12	1.97	0.46
2:B:55:VAL:HG21	2:B:59:TRP:HD1	1.81	0.46
1:C:282:ILE:HD12	1:C:314:PHE:HD2	1.81	0.46
1:C:651:GLY:HA2	1:C:776:LEU:HG	1.98	0.46
1:C:1081:TYR:CD2	1:C:1234:VAL:HG13	2.50	0.46
1:C:1586:ASN:O	1:C:1588:ALA:N	2.47	0.46
1:C:4783:ILE:HG22	1:C:4789:PHE:CD2	2.51	0.46
1:E:179:TYR:OH	1:G:2359:ARG:NE	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:207:SER:HB3	1:E:334:MET:SD	2.56	0.46
1:E:404:ILE:HG21	1:E:481:GLU:HG3	1.97	0.46
1:E:651:GLY:HA2	1:E:776:LEU:HG	1.98	0.46
1:E:1229:ASN:CG	1:E:1827:ARG:HH11	2.19	0.46
1:E:1679:ASN:HA	1:E:1682:ALA:HB3	1.98	0.46
1:E:4205:TRP:HB2	1:E:4245:MET:HE1	1.96	0.46
1:G:111:HIS:CD2	1:G:113:HIS:HB3	2.50	0.46
1:G:1943:LEU:HD11	1:G:2098:VAL:HG22	1.98	0.46
1:G:3658:LYS:HA	1:G:3662:ILE:HG13	1.97	0.46
1:G:3768:SER:HA	1:G:3771:HIS:CE1	2.51	0.46
1:A:207:SER:HB3	1:A:334:MET:SD	2.56	0.46
1:A:350:HIS:HD2	1:A:353:SER:N	2.14	0.46
1:A:1586:ASN:O	1:A:1588:ALA:N	2.47	0.46
1:A:1676:LEU:O	1:A:1676:LEU:HD23	2.16	0.46
1:A:4783:ILE:HG22	1:A:4789:PHE:CD2	2.51	0.46
1:C:76:ARG:HE	1:E:3844:LEU:CD2	2.22	0.46
1:C:76:ARG:HH21	1:E:3844:LEU:CD2	2.29	0.46
1:C:1238:PHE:HE2	1:C:1612:PHE:HA	1.81	0.46
1:C:3804:ILE:HG22	1:C:3812:VAL:HG11	1.96	0.46
1:E:118:LEU:HA	1:E:137:LEU:HD23	1.98	0.46
1:E:1676:LEU:HD21	1:E:2164:SER:O	2.15	0.46
1:E:2100:HIS:O	1:E:2104:ARG:HG2	2.15	0.46
1:G:4192:ARG:NH1	1:G:4982:GLU:OE1	2.48	0.46
1:A:1609:PRO:O	1:A:1610:ASN:ND2	2.49	0.46
1:C:4818:MET:HA	1:C:4824:ARG:HG2	1.96	0.46
1:E:119:SER:HB3	1:E:146:CYS:HA	1.98	0.46
1:E:891:TRP:HB3	1:E:907:LEU:HD11	1.98	0.46
1:E:1087:ARG:HH12	1:E:1157:GLU:HB3	1.81	0.46
2:F:25:HIS:CD2	2:F:104:LEU:HD11	2.51	0.46
1:G:2206:THR:O	1:G:2210:VAL:HG23	2.15	0.46
1:G:4577:LEU:HG	1:G:4580:TYR:HE1	1.80	0.46
1:A:411:TYR:HB2	1:A:486:LEU:HD21	1.97	0.46
1:A:909:ASN:HA	1:A:965:TYR:CE1	2.51	0.46
1:A:1081:TYR:CD2	1:A:1234:VAL:HG13	2.50	0.46
1:A:1729:SER:O	1:A:1733:GLU:HG2	2.15	0.46
1:A:3844:LEU:CD2	1:G:76:ARG:HH21	2.29	0.46
1:C:118:LEU:HA	1:C:137:LEU:HD23	1.98	0.46
1:C:350:HIS:HD2	1:C:353:SER:N	2.14	0.46
1:C:739:ALA:C	1:C:741:GLU:H	2.18	0.46
1:C:1850:VAL:HA	1:C:1945:TYR:CE1	2.50	0.46
2:D:73:LYS:HA	2:D:99:PHE:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:909:ASN:HA	1:E:965:TYR:CE1	2.51	0.46
1:E:1676:LEU:HD23	1:E:1676:LEU:O	2.16	0.46
1:E:3658:LYS:HA	1:E:3662:ILE:HG13	1.98	0.46
1:E:4783:ILE:HG22	1:E:4789:PHE:CD2	2.51	0.46
1:E:4801:LEU:HB3	1:E:4808:PHE:HD2	1.81	0.46
1:E:4829:SER:HA	1:E:4832:HIS:CD2	2.51	0.46
1:G:118:LEU:HA	1:G:137:LEU:HD23	1.98	0.46
1:G:1688:HIS:HE1	2:H:89:GLY:O	1.99	0.46
1:A:3658:LYS:HA	1:A:3662:ILE:HG13	1.98	0.45
1:C:683:ARG:HB3	1:C:713:SER:HB2	1.97	0.45
1:C:1087:ARG:HH12	1:C:1157:GLU:HB3	1.81	0.45
1:C:1679:ASN:HA	1:C:1682:ALA:HB3	1.98	0.45
1:C:3919:THR:HG21	1:C:3968:TYR:CE2	2.50	0.45
1:C:4856:PHE:O	1:C:4860:ARG:NH1	2.49	0.45
1:E:111:HIS:NE2	1:E:113:HIS:HB3	2.31	0.45
1:E:675:LEU:CD2	1:E:1633:PRO:HG3	2.46	0.45
1:E:1862:ILE:O	1:E:1865:MET:HB3	2.16	0.45
1:E:3727:ASP:O	1:E:3731:LYS:NZ	2.42	0.45
1:E:3826:VAL:HG23	1:E:3909:ASN:HB3	1.98	0.45
1:E:4105:GLY:HA2	1:E:4108:ILE:HD12	1.98	0.45
2:F:38:SER:HB3	2:F:41:ASP:OD2	2.16	0.45
1:G:767:VAL:O	1:G:1475:THR:OG1	2.24	0.45
1:G:1687:SER:HB2	1:G:1782:PHE:CZ	2.51	0.45
1:A:830:ARG:HD3	1:A:1612:PHE:CZ	2.51	0.45
1:A:891:TRP:HB3	1:A:907:LEU:HD11	1.98	0.45
1:A:3826:VAL:HG23	1:A:3909:ASN:HB3	1.98	0.45
1:A:4888:TYR:HB2	1:G:4914:VAL:HG21	1.98	0.45
1:C:2099:SER:O	1:C:2103:VAL:HG23	2.17	0.45
1:C:2761:TYR:HE2	1:C:2925:GLU:OE2	2.00	0.45
1:C:3826:VAL:HG23	1:C:3909:ASN:HB3	1.98	0.45
1:C:4087:LEU:HD23	1:C:4122:MET:HB3	1.98	0.45
2:D:38:SER:HB3	2:D:41:ASP:OD2	2.16	0.45
1:E:2867:LEU:HG	1:E:2928:LYS:HZ3	1.82	0.45
1:G:110:ARG:NH2	1:G:115:ARG:HD2	2.28	0.45
1:G:207:SER:HB3	1:G:334:MET:SD	2.56	0.45
1:G:651:GLY:HA2	1:G:776:LEU:HG	1.98	0.45
1:G:1812:LEU:HA	1:G:1815:LEU:HD12	1.97	0.45
1:G:3102:ASP:O	1:G:3106:MET:N	2.49	0.45
1:A:111:HIS:NE2	1:A:113:HIS:HB3	2.32	0.45
1:A:739:ALA:C	1:A:741:GLU:H	2.18	0.45
1:A:855:PRO:HG2	1:A:998:ARG:HD2	1.96	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3663:LEU:HA	1:A:3664:THR:O	2.17	0.45
1:A:4856:PHE:O	1:A:4860:ARG:NH1	2.49	0.45
1:C:46:LEU:HD13	1:C:125:ARG:NH1	2.32	0.45
1:C:1812:LEU:HA	1:C:1815:LEU:HD12	1.97	0.45
1:E:110:ARG:NH2	1:E:115:ARG:HD2	2.28	0.45
1:E:767:VAL:O	1:E:1475:THR:OG1	2.24	0.45
1:E:2122:SER:O	1:E:2125:HIS:HB3	2.17	0.45
1:G:111:HIS:NE2	1:G:113:HIS:HB3	2.31	0.45
1:G:350:HIS:HD2	1:G:353:SER:N	2.14	0.45
1:G:663:TYR:OH	1:G:804:PRO:HD2	2.16	0.45
1:G:830:ARG:HD3	1:G:1612:PHE:CZ	2.50	0.45
1:G:1205:GLY:HA2	1:G:1225:PRO:HB3	1.99	0.45
1:G:1611:HIS:HB2	1:G:1652:GLU:CB	2.45	0.45
1:G:1862:ILE:O	1:G:1865:MET:HB3	2.16	0.45
1:G:3838:THR:OG1	1:G:3839:CYS:N	2.49	0.45
1:G:4192:ARG:NH1	1:G:5028:PHE:CD2	2.84	0.45
1:G:4640:GLU:HB3	1:G:4641:PRO:HD3	1.98	0.45
1:A:1862:ILE:O	1:A:1865:MET:HB3	2.16	0.45
1:C:1688:HIS:HE1	2:D:89:GLY:O	2.00	0.45
1:C:2711:PRO:HA	1:C:3016:TYR:HA	1.98	0.45
1:C:3971:GLY:HA2	1:C:5005:GLY:HA3	1.98	0.45
1:C:4047:MET:HG3	1:C:4048:LEU:N	2.32	0.45
1:G:842:PRO:HD2	1:G:1196:PRO:HA	1.99	0.45
1:G:909:ASN:HA	1:G:965:TYR:CE1	2.50	0.45
1:G:1238:PHE:HE2	1:G:1612:PHE:HA	1.81	0.45
1:G:1954:ARG:HG2	1:G:2134:LEU:HD12	1.98	0.45
1:G:4686:LEU:HA	1:G:4690:GLU:HB2	1.98	0.45
1:A:76:ARG:HH21	1:C:3844:LEU:CD2	2.29	0.45
1:A:1087:ARG:HH12	1:A:1157:GLU:HB3	1.81	0.45
1:A:1940:CYS:SG	1:A:2123:LEU:HD12	2.57	0.45
1:A:1947:CYS:SG	1:A:2127:GLN:NE2	2.89	0.45
1:A:3934:TYR:OH	1:A:3998:HIS:HB3	2.16	0.45
1:C:207:SER:HB3	1:C:334:MET:SD	2.56	0.45
1:C:891:TRP:HB3	1:C:907:LEU:HD11	1.98	0.45
1:C:1940:CYS:SG	1:C:2123:LEU:HD12	2.57	0.45
1:C:2100:HIS:O	1:C:2104:ARG:HG2	2.15	0.45
1:C:5022:PHE:HA	1:C:5023:PRO:HD3	1.71	0.45
1:E:1767:VAL:O	1:E:1769:THR:N	2.50	0.45
1:E:2761:TYR:HE2	1:E:2925:GLU:OE2	1.99	0.45
1:G:772:ASN:HD21	1:G:1467:SER:HA	1.82	0.45
1:A:282:ILE:HD12	1:A:314:PHE:HD2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1745:ILE:O	1:A:1746:THR:OG1	2.25	0.45
1:A:1770:SER:OG	1:A:1771:LEU:N	2.49	0.45
1:C:111:HIS:NE2	1:C:113:HIS:HB3	2.32	0.45
1:C:1748:PHE:HZ	1:C:2072:LEU:HB2	1.81	0.45
1:C:1770:SER:OG	1:C:1771:LEU:N	2.49	0.45
1:C:1862:ILE:O	1:C:1865:MET:HB3	2.16	0.45
1:C:3663:LEU:HA	1:C:3664:THR:O	2.16	0.45
1:E:739:ALA:C	1:E:741:GLU:H	2.18	0.45
1:E:1093:GLU:HG2	1:E:1148:VAL:HG22	1.97	0.45
1:E:1940:CYS:SG	1:E:2123:LEU:HD12	2.57	0.45
1:E:2283:ASN:HB2	1:E:2286:LEU:HB2	1.99	0.45
1:G:282:ILE:HD12	1:G:314:PHE:HD2	1.81	0.45
1:G:411:TYR:HB2	1:G:486:LEU:HD21	1.98	0.45
1:G:633:LEU:HB2	1:G:1663:HIS:HD2	1.82	0.45
1:G:2142:TYR:CD2	1:G:2197:LEU:HB2	2.52	0.45
1:G:2247:GLN:HE21	1:G:2279:SER:C	2.20	0.45
2:H:67:SER:N	2:H:70:GLN:OE1	2.38	0.45
1:A:527:ALA:O	1:A:531:ARG:HG3	2.17	0.45
1:A:635:THR:HG23	1:A:1693:GLN:HE22	1.82	0.45
1:A:1954:ARG:HG2	1:A:2134:LEU:HD12	1.99	0.45
1:C:262:LEU:HD23	1:C:282:ILE:HG12	1.99	0.45
1:C:4105:GLY:HA2	1:C:4108:ILE:HD12	1.98	0.45
1:E:154:SER:HB3	1:E:156:GLN:OE1	2.17	0.45
1:E:262:LEU:HD23	1:E:282:ILE:HG12	1.99	0.45
1:E:491:ILE:HG22	1:E:495:ASN:HD21	1.82	0.45
1:E:633:LEU:HB2	1:E:1663:HIS:HD2	1.82	0.45
1:E:772:ASN:HD21	1:E:1467:SER:HA	1.82	0.45
1:E:830:ARG:HD3	1:E:1612:PHE:CZ	2.52	0.45
1:E:1850:VAL:HA	1:E:1945:TYR:CE1	2.51	0.45
1:E:2060:SER:HA	1:E:2063:LEU:HD12	1.99	0.45
1:E:2247:GLN:HE21	1:E:2279:SER:C	2.20	0.45
1:G:1729:SER:O	1:G:1733:GLU:HG2	2.16	0.45
1:G:2122:SER:O	1:G:2125:HIS:HB3	2.17	0.45
1:G:2191:PHE:HD1	1:G:2198:MET:HE1	1.81	0.45
1:G:2283:ASN:HB2	1:G:2286:LEU:HB2	1.99	0.45
1:G:2497:ASP:OD1	1:G:2498:HIS:N	2.50	0.45
1:G:3768:SER:O	1:G:3772:THR:OG1	2.22	0.45
1:A:3838:THR:OG1	1:A:3839:CYS:N	2.50	0.45
1:A:4807:PHE:HD2	1:G:4857:ASN:HD21	1.60	0.45
1:C:404:ILE:HG21	1:C:481:GLU:HG3	1.98	0.45
1:C:491:ILE:HG22	1:C:495:ASN:HD21	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1767:VAL:O	1:C:1769:THR:N	2.50	0.45
1:C:2819:TRP:CZ3	1:C:2877:GLN:HG2	2.52	0.45
1:C:4930:ALA:HB2	1:E:4933:GLN:HG2	1.98	0.45
2:D:25:HIS:CD2	2:D:104:LEU:HD11	2.51	0.45
1:E:282:ILE:HD12	1:E:314:PHE:HD2	1.81	0.45
1:E:663:TYR:OH	1:E:804:PRO:HD2	2.15	0.45
1:E:1690:ASP:OD1	2:F:41:ASP:HB3	2.17	0.45
1:E:2497:ASP:OD1	1:E:2498:HIS:N	2.50	0.45
1:E:2773:ASN:HB3	1:E:2775:TRP:CD1	2.52	0.45
1:E:4047:MET:HG3	1:E:4048:LEU:N	2.32	0.45
1:G:1229:ASN:CB	1:G:1827:ARG:HH11	2.30	0.45
1:G:1770:SER:OG	1:G:1771:LEU:N	2.49	0.45
1:G:1815:LEU:HB3	1:G:1865:MET:HE3	1.98	0.45
1:A:401:ALA:O	1:A:404:ILE:HB	2.17	0.45
1:A:1943:LEU:HD11	1:A:2098:VAL:HG22	1.99	0.45
1:A:2099:SER:O	1:A:2103:VAL:HG23	2.17	0.45
1:A:2423:MET:HG3	1:A:2498:HIS:CE1	2.52	0.45
1:A:2773:ASN:HB3	1:A:2775:TRP:CD1	2.52	0.45
1:A:3891:LEU:HB3	1:A:3899:PHE:HE2	1.82	0.45
2:B:25:HIS:CD2	2:B:104:LEU:HD11	2.51	0.45
1:C:1229:ASN:CB	1:C:1827:ARG:HH11	2.30	0.45
1:C:1947:CYS:SG	1:C:2127:GLN:NE2	2.89	0.45
1:C:4555:LEU:HD11	1:C:4656:LEU:HG	1.98	0.45
1:C:4801:LEU:HB3	1:C:4808:PHE:HD2	1.81	0.45
1:E:2819:TRP:CZ3	1:E:2877:GLN:HG2	2.52	0.45
1:E:3663:LEU:HA	1:E:3664:THR:O	2.16	0.45
1:E:3971:GLY:HA2	1:E:5005:GLY:HA3	1.98	0.45
2:F:73:LYS:HA	2:F:99:PHE:O	2.16	0.45
1:G:527:ALA:O	1:G:531:ARG:HG3	2.17	0.45
1:G:1087:ARG:HH12	1:G:1157:GLU:HB3	1.81	0.45
1:G:1198:GLN:OE1	1:G:1198:GLN:N	2.49	0.45
1:G:1289:LEU:HD12	1:G:1562:ILE:HD13	1.99	0.45
1:G:2773:ASN:HB3	1:G:2775:TRP:CD1	2.52	0.45
1:G:4056:GLU:OE2	1:G:4166:LEU:HD11	2.17	0.45
1:A:118:LEU:HA	1:A:137:LEU:HD23	1.98	0.45
1:A:247:TYR:CE2	1:A:359:TYR:HB3	2.52	0.45
1:A:1076:ARG:HH22	1:A:1609:PRO:CB	2.30	0.45
1:A:2711:PRO:HA	1:A:3016:TYR:HA	1.98	0.45
1:C:284:HIS:NE2	1:C:286:THR:OG1	2.49	0.45
1:C:1205:GLY:HA2	1:C:1225:PRO:HB3	1.99	0.45
1:C:2122:SER:O	1:C:2125:HIS:HB3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4963:ILE:HD12	1:C:5030:LYS:HZ1	1.80	0.45
1:E:401:ALA:O	1:E:404:ILE:HB	2.17	0.45
1:E:2927:LEU:HD22	1:E:2937:VAL:HG11	1.98	0.45
1:E:3842:LEU:HD11	1:E:3950:ASN:O	2.17	0.45
1:E:4030:LEU:CG	1:E:4040:ILE:HD11	2.44	0.45
1:E:4183:ILE:HD12	1:E:4185:GLY:H	1.81	0.45
1:E:4555:LEU:HD11	1:E:4656:LEU:HG	1.98	0.45
1:E:4735:GLU:O	1:E:4739:GLU:N	2.45	0.45
1:G:1104:TRP:CD1	1:G:1153:ILE:HB	2.52	0.45
1:G:3105:LYS:O	1:G:3109:ASN:N	2.49	0.45
1:A:1280:GLN:NE2	1:A:1559:GLN:OE1	2.51	0.44
1:A:1288:PHE:HE2	1:A:1460:HIS:HA	1.82	0.44
1:A:2497:ASP:OD1	1:A:2498:HIS:N	2.50	0.44
1:A:2761:TYR:HE2	1:A:2925:GLU:OE2	1.99	0.44
1:A:2927:LEU:HD22	1:A:2937:VAL:HG11	1.98	0.44
1:A:4849:TYR:HA	1:A:4852:THR:HG22	1.98	0.44
1:C:119:SER:HB3	1:C:146:CYS:HA	2.00	0.44
1:C:247:TYR:CE2	1:C:359:TYR:HB3	2.52	0.44
1:C:1954:ARG:HG2	1:C:2134:LEU:HD12	1.99	0.44
1:C:3658:LYS:HA	1:C:3662:ILE:HG13	1.98	0.44
1:C:3842:LEU:HD11	1:C:3950:ASN:O	2.17	0.44
1:E:1947:CYS:SG	1:E:2127:GLN:NE2	2.89	0.44
1:E:3919:THR:HG21	1:E:3968:TYR:CE2	2.49	0.44
1:E:4023:MET:O	1:E:4026:MET:HB3	2.17	0.44
1:E:4677:LEU:CD1	1:E:4702:ASP:HB3	2.47	0.44
1:G:293:LEU:HD13	1:G:378:LEU:HD12	1.99	0.44
1:G:401:ALA:O	1:G:404:ILE:HB	2.17	0.44
1:G:491:ILE:HG22	1:G:495:ASN:HD21	1.82	0.44
1:G:3965:LEU:HD13	1:G:4026:MET:HE1	1.98	0.44
1:A:100:THR:HG21	1:A:162:LYS:NZ	2.33	0.44
1:A:675:LEU:CD2	1:A:1633:PRO:HG3	2.46	0.44
1:A:842:PRO:HD2	1:A:1196:PRO:HA	1.99	0.44
1:A:1243:PRO:HD2	1:A:1458:HIS:CB	2.47	0.44
1:A:2060:SER:HA	1:A:2063:LEU:HD12	1.98	0.44
1:A:2247:GLN:HE21	1:A:2279:SER:C	2.20	0.44
1:A:3842:LEU:HD11	1:A:3950:ASN:O	2.17	0.44
1:A:4573:ILE:HG21	1:A:4809:PHE:CE2	2.53	0.44
1:A:4801:LEU:HB3	1:A:4808:PHE:HD2	1.83	0.44
2:B:25:HIS:NE2	2:B:104:LEU:HD11	2.33	0.44
1:C:495:ASN:CA	1:C:553:ARG:HH12	2.28	0.44
1:C:635:THR:HG23	1:C:1693:GLN:HE22	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2497:ASP:OD1	1:C:2498:HIS:N	2.50	0.44
1:C:4638:TYR:O	1:C:4641:PRO:HD2	2.18	0.44
2:D:25:HIS:NE2	2:D:104:LEU:HD11	2.33	0.44
1:E:284:HIS:NE2	1:E:286:THR:OG1	2.49	0.44
1:E:2099:SER:O	1:E:2103:VAL:HG23	2.17	0.44
1:E:2816:MET:HG2	1:E:2878:LEU:HD21	1.99	0.44
1:G:247:TYR:CE2	1:G:359:TYR:HB3	2.53	0.44
1:G:404:ILE:HG21	1:G:481:GLU:HG3	1.98	0.44
1:G:3658:LYS:HA	1:G:3662:ILE:CG1	2.47	0.44
1:A:46:LEU:HD13	1:A:125:ARG:NH1	2.32	0.44
1:A:58:VAL:HG22	1:A:305:CYS:HA	1.99	0.44
1:A:771:PHE:HE1	1:A:1472:VAL:HG13	1.82	0.44
1:A:1727:ARG:HG2	1:A:1727:ARG:O	2.17	0.44
1:A:1773:PRO:HA	1:A:1774:PRO:HD3	1.90	0.44
1:A:2242:ILE:HD11	1:A:2246:ASN:HD22	1.83	0.44
1:A:3886:ARG:O	1:A:3890:LEU:HD13	2.17	0.44
1:A:3940:LYS:O	1:A:3942:VAL:N	2.50	0.44
1:A:4047:MET:HG3	1:A:4048:LEU:N	2.32	0.44
2:B:38:SER:HB3	2:B:41:ASP:OD2	2.16	0.44
1:C:134:ASP:OD1	1:C:135:VAL:N	2.51	0.44
1:C:1969:LEU:O	1:C:1973:GLN:HG3	2.18	0.44
1:C:3706:SER:O	1:C:3710:LEU:HG	2.17	0.44
1:C:4680:LYS:HE2	1:C:4686:LEU:HD21	2.00	0.44
1:E:350:HIS:HD2	1:E:353:SER:N	2.15	0.44
1:E:842:PRO:HD2	1:E:1196:PRO:HA	1.99	0.44
1:E:1280:GLN:NE2	1:E:1559:GLN:OE1	2.51	0.44
1:E:1579:MET:O	1:E:1582:SER:OG	2.17	0.44
1:E:4922:PHE:HA	1:E:4926:VAL:HB	1.97	0.44
1:G:673:PRO:O	1:G:679:ALA:HA	2.17	0.44
1:G:3674:ILE:HG22	1:G:3769:ARG:HD3	2.00	0.44
1:A:119:SER:HB3	1:A:146:CYS:HA	2.00	0.44
1:A:495:ASN:HB3	1:A:553:ARG:NH2	2.23	0.44
1:A:1205:GLY:HA2	1:A:1225:PRO:HB3	1.99	0.44
1:A:1690:ASP:OD1	2:B:41:ASP:HB3	2.17	0.44
1:A:1767:VAL:O	1:A:1769:THR:N	2.50	0.44
1:A:4640:GLU:HB3	1:A:4641:PRO:HD3	2.00	0.44
1:C:527:ALA:O	1:C:531:ARG:HG3	2.17	0.44
1:C:1629:GLN:HE21	1:C:1631:GLN:HE21	1.65	0.44
1:C:1704:PRO:HG2	1:C:1707:LEU:HD12	1.99	0.44
1:E:402:ARG:CZ	1:E:405:HIS:HD2	2.31	0.44
1:E:1727:ARG:O	1:E:1727:ARG:HG2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1765:VAL:HG21	1:E:1953:HIS:CE1	2.53	0.44
1:E:1936:LYS:HA	1:E:1939:MET:HB3	2.00	0.44
1:E:4239:GLU:OE2	1:E:5014:TYR:OH	2.18	0.44
1:G:771:PHE:HE1	1:G:1472:VAL:HG13	1.82	0.44
1:G:1093:GLU:HG2	1:G:1148:VAL:HG22	1.98	0.44
1:G:1765:VAL:HG21	1:G:1953:HIS:CE1	2.52	0.44
1:G:2060:SER:HA	1:G:2063:LEU:HD12	1.98	0.44
1:G:2336:ARG:HD2	1:G:2435:ARG:NH1	2.33	0.44
1:G:2754:PHE:CZ	1:G:2930:LEU:HD23	2.53	0.44
1:G:3992:PHE:O	1:G:3996:PHE:N	2.37	0.44
1:A:404:ILE:HG21	1:A:481:GLU:HG3	1.98	0.44
1:A:1238:PHE:HE1	1:A:1612:PHE:HA	1.82	0.44
1:A:1765:VAL:HG21	1:A:1953:HIS:CE1	2.52	0.44
1:A:2283:ASN:HB2	1:A:2286:LEU:HB2	1.99	0.44
1:A:2819:TRP:CZ3	1:A:2877:GLN:HG2	2.52	0.44
1:A:3971:GLY:HA2	1:A:5005:GLY:HA3	1.98	0.44
1:A:4105:GLY:HA2	1:A:4108:ILE:HD12	1.98	0.44
1:A:4555:LEU:HD11	1:A:4656:LEU:HG	1.98	0.44
1:A:4577:LEU:HG	1:A:4580:TYR:HE1	1.82	0.44
1:C:100:THR:HG21	1:C:162:LYS:NZ	2.33	0.44
1:C:359:TYR:CD1	1:C:374:LYS:HD3	2.53	0.44
1:C:1690:ASP:OD1	2:D:41:ASP:HB3	2.17	0.44
1:C:1833:SER:HB3	1:C:1836:PHE:HD2	1.83	0.44
1:C:2060:SER:HA	1:C:2063:LEU:HD12	1.98	0.44
1:C:2423:MET:HG3	1:C:2498:HIS:CE1	2.53	0.44
1:E:4088:ILE:O	1:E:4123:ILE:N	2.51	0.44
1:E:4642:ALA:HA	1:E:4645:CYS:SG	2.58	0.44
1:E:4786:ASP:OD1	1:E:4787:ASN:N	2.51	0.44
2:F:25:HIS:NE2	2:F:104:LEU:HD11	2.33	0.44
1:G:402:ARG:CZ	1:G:405:HIS:HD2	2.31	0.44
1:G:1745:ILE:O	1:G:1746:THR:OG1	2.25	0.44
1:G:1833:SER:HB3	1:G:1836:PHE:HD2	1.82	0.44
1:G:2747:ILE:HG12	1:G:2817:ILE:HD12	1.98	0.44
1:A:959:TYR:HE2	1:A:966:LYS:HB2	1.83	0.44
1:A:1629:GLN:HE21	1:A:1631:GLN:HE21	1.66	0.44
1:A:1688:HIS:HE1	2:B:89:GLY:O	2.00	0.44
1:A:4638:TYR:O	1:A:4641:PRO:HD2	2.18	0.44
1:C:402:ARG:CZ	1:C:405:HIS:HD2	2.30	0.44
1:C:2283:ASN:HB2	1:C:2286:LEU:HB2	1.99	0.44
1:C:4677:LEU:CD1	1:C:4702:ASP:HB3	2.48	0.44
1:C:4849:TYR:HA	1:C:4852:THR:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:134:ASP:OD1	1:E:135:VAL:N	2.51	0.44
1:E:247:TYR:CE2	1:E:359:TYR:HB3	2.53	0.44
1:E:527:ALA:O	1:E:531:ARG:HG3	2.17	0.44
1:E:1198:GLN:OE1	1:E:1198:GLN:N	2.49	0.44
1:E:1289:LEU:HD12	1:E:1562:ILE:HD13	1.99	0.44
1:E:3706:SER:O	1:E:3710:LEU:HG	2.17	0.44
1:E:4026:MET:O	1:E:4029:SER:OG	2.21	0.44
1:E:4879:MET:HG2	1:G:4577:LEU:O	2.18	0.44
2:F:78:PRO:O	2:F:83:GLY:N	2.51	0.44
1:G:746:CYS:HA	1:G:757:PHE:CD1	2.53	0.44
1:G:1610:ASN:HA	1:G:1652:GLU:OE2	2.18	0.44
1:G:1704:PRO:HG2	1:G:1707:LEU:HD12	1.99	0.44
1:G:2891:LYS:O	1:G:2895:GLU:HG3	2.18	0.44
1:G:3701:LEU:HD11	1:G:3725:TYR:CD1	2.52	0.44
1:G:4004:ALA:O	1:G:4114:CYS:HA	2.18	0.44
1:A:180:LEU:O	1:A:200:TRP:NE1	2.51	0.44
1:A:746:CYS:HA	1:A:757:PHE:CD1	2.53	0.44
1:A:1229:ASN:CB	1:A:1827:ARG:HH11	2.30	0.44
1:A:1833:SER:HB3	1:A:1836:PHE:HD2	1.83	0.44
1:A:2336:ARG:HD2	1:A:2435:ARG:NH1	2.33	0.44
1:A:3706:SER:O	1:A:3710:LEU:HG	2.18	0.44
1:A:3727:ASP:O	1:A:3731:LYS:NZ	2.42	0.44
1:A:4642:ALA:HA	1:A:4645:CYS:SG	2.58	0.44
1:C:772:ASN:HD21	1:C:1467:SER:HA	1.82	0.44
1:C:1289:LEU:HD12	1:C:1562:ILE:HD13	1.98	0.44
1:C:2242:ILE:HD11	1:C:2246:ASN:HD22	1.83	0.44
1:C:4023:MET:O	1:C:4026:MET:HB3	2.17	0.44
1:C:4974:GLY:O	1:C:4977:THR:OG1	2.25	0.44
1:E:771:PHE:HE1	1:E:1472:VAL:HG13	1.82	0.44
1:E:1238:PHE:HE1	1:E:1612:PHE:HA	1.83	0.44
1:E:3940:LYS:O	1:E:3942:VAL:N	2.50	0.44
1:E:4680:LYS:HE2	1:E:4686:LEU:HD21	1.99	0.44
1:G:119:SER:HB3	1:G:146:CYS:HA	2.00	0.44
1:G:635:THR:HG23	1:G:1693:GLN:HE22	1.83	0.44
1:G:1244:GLN:HE22	1:G:1646:ARG:HH21	1.66	0.44
1:G:1767:VAL:O	1:G:1769:THR:N	2.50	0.44
1:G:1936:LYS:HA	1:G:1939:MET:HB3	2.00	0.44
1:G:1969:LEU:O	1:G:1973:GLN:HG3	2.18	0.44
2:H:88:PRO:O	2:H:90:ILE:HD12	2.16	0.44
1:A:2336:ARG:HD2	1:A:2435:ARG:CZ	2.48	0.44
1:A:4677:LEU:CD1	1:A:4702:ASP:HB3	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4807:PHE:CZ	1:G:4856:PHE:CD2	3.06	0.44
1:C:401:ALA:O	1:C:404:ILE:HB	2.17	0.44
1:C:675:LEU:CD2	1:C:1633:PRO:HG3	2.47	0.44
1:C:1280:GLN:NE2	1:C:1559:GLN:OE1	2.51	0.44
1:C:2380:ILE:HG23	1:C:2423:MET:SD	2.58	0.44
1:C:2773:ASN:HB3	1:C:2775:TRP:CD1	2.52	0.44
1:E:21:VAL:HG13	1:E:205:ILE:HD11	2.00	0.44
1:E:293:LEU:HD13	1:E:378:LEU:HD12	2.00	0.44
1:E:1089:TYR:CE2	1:E:1214:PHE:HD1	2.36	0.44
1:E:2244:ARG:O	1:E:2247:GLN:HB3	2.18	0.44
1:E:4640:GLU:HB3	1:E:4641:PRO:HD3	2.00	0.44
1:G:1727:ARG:HG2	1:G:1727:ARG:O	2.18	0.44
1:A:402:ARG:CZ	1:A:405:HIS:HD2	2.30	0.44
1:A:633:LEU:HB2	1:A:1663:HIS:HD2	1.82	0.44
1:A:1839:VAL:HB	1:A:1840:PRO:HD3	2.00	0.44
1:A:2122:SER:O	1:A:2125:HIS:HB3	2.17	0.44
1:A:2142:TYR:CE2	1:A:2197:LEU:HB2	2.53	0.44
1:A:3895:HIS:HE1	1:A:3970:GLN:HG3	1.83	0.44
1:C:1244:GLN:HE22	1:C:1646:ARG:HH21	1.66	0.44
1:C:3940:LYS:O	1:C:3942:VAL:N	2.50	0.44
1:E:2336:ARG:HD2	1:E:2435:ARG:NH1	2.33	0.44
1:E:3886:ARG:O	1:E:3890:LEU:HD13	2.17	0.44
1:E:4926:VAL:HG12	1:G:4932:ILE:HG21	2.00	0.44
1:G:484:LEU:HD21	1:G:540:PHE:CE1	2.53	0.44
1:G:602:VAL:O	1:G:605:SER:OG	2.23	0.44
1:G:1254:HIS:HD2	1:G:1280:GLN:HB2	1.83	0.44
1:G:1629:GLN:HE21	1:G:1631:GLN:HE21	1.66	0.44
1:G:1738:LEU:HD11	1:G:2143:THR:HB	2.00	0.44
1:G:2242:ILE:HD11	1:G:2246:ASN:HD22	1.82	0.44
1:G:2423:MET:HG3	1:G:2498:HIS:CE1	2.52	0.44
1:G:2551:ASN:HA	1:G:2554:LEU:HG	2.00	0.44
1:G:3878:ASP:HB2	1:G:3957:VAL:HG21	2.00	0.44
1:A:293:LEU:HD13	1:A:378:LEU:HD12	1.99	0.43
1:A:468:LEU:O	1:A:472:ARG:HG2	2.18	0.43
1:A:491:ILE:HG22	1:A:495:ASN:HD21	1.82	0.43
1:A:1293:LEU:HD21	1:A:1585:LYS:NZ	2.33	0.43
2:B:7:ILE:HD11	2:B:73:LYS:HB2	1.99	0.43
1:C:484:LEU:HD21	1:C:540:PHE:CE1	2.53	0.43
1:C:1198:GLN:OE1	1:C:1198:GLN:N	2.49	0.43
1:C:1727:ARG:O	1:C:1727:ARG:HG2	2.17	0.43
1:C:1765:VAL:HG21	1:C:1953:HIS:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2247:GLN:HE21	1:C:2279:SER:C	2.20	0.43
1:C:2336:ARG:HD2	1:C:2435:ARG:CZ	2.48	0.43
1:C:3657:TYR:O	1:C:3662:ILE:HG12	2.18	0.43
1:E:359:TYR:CD1	1:E:374:LYS:HD3	2.53	0.43
1:E:764:VAL:O	1:E:764:VAL:HG12	2.18	0.43
1:E:1688:HIS:HE1	2:F:89:GLY:O	2.00	0.43
1:E:2134:LEU:O	1:E:2138:LEU:HG	2.18	0.43
1:E:2380:ILE:HG23	1:E:2423:MET:SD	2.58	0.43
1:G:222:LEU:HB3	1:G:388:LEU:HD13	2.00	0.43
1:G:891:TRP:HB3	1:G:907:LEU:HD11	1.99	0.43
1:G:1293:LEU:HD21	1:G:1585:LYS:NZ	2.33	0.43
1:G:4209:GLN:O	1:G:4213:SER:N	2.47	0.43
1:G:4849:TYR:HA	1:G:4852:THR:HG22	2.00	0.43
1:A:359:TYR:CD1	1:A:374:LYS:HD3	2.53	0.43
1:A:764:VAL:O	1:A:764:VAL:HG12	2.18	0.43
1:A:772:ASN:HD21	1:A:1467:SER:HA	1.82	0.43
1:A:1104:TRP:CD1	1:A:1153:ILE:HB	2.53	0.43
1:A:1254:HIS:HD2	1:A:1280:GLN:HB2	1.83	0.43
1:A:1611:HIS:HB2	1:A:1652:GLU:CB	2.47	0.43
1:A:1828:ASP:HB3	1:A:1830:VAL:H	1.83	0.43
1:A:1936:LYS:HA	1:A:1939:MET:HB3	2.01	0.43
1:A:2340:PHE:CD1	1:A:2435:ARG:HD2	2.54	0.43
1:A:2380:ILE:HG23	1:A:2423:MET:SD	2.58	0.43
1:A:2551:ASN:HA	1:A:2554:LEU:HG	2.00	0.43
1:A:4023:MET:O	1:A:4026:MET:HB3	2.17	0.43
1:C:633:LEU:HB2	1:C:1663:HIS:HD2	1.82	0.43
1:C:673:PRO:O	1:C:679:ALA:HA	2.18	0.43
1:C:771:PHE:HE1	1:C:1472:VAL:HG13	1.82	0.43
1:C:1710:GLY:O	1:C:1714:LEU:HG	2.19	0.43
1:C:2163:ARG:O	1:C:2166:LEU:HB3	2.18	0.43
1:C:2770:LYS:HB3	1:C:2775:TRP:CB	2.44	0.43
1:C:4640:GLU:HB3	1:C:4641:PRO:HD3	2.00	0.43
1:E:892:THR:O	1:E:903:LEU:HA	2.19	0.43
1:E:959:TYR:HE2	1:E:966:LYS:HB2	1.83	0.43
1:E:1954:ARG:HG2	1:E:2134:LEU:HD12	1.99	0.43
1:E:2191:PHE:HD1	1:E:2198:MET:HE1	1.83	0.43
1:E:2747:ILE:HG22	1:E:2748:PRO:O	2.18	0.43
1:E:4980:LEU:HA	1:E:4984:ASN:HB3	2.01	0.43
1:G:46:LEU:HD13	1:G:125:ARG:NH1	2.32	0.43
1:G:359:TYR:CD1	1:G:374:LYS:HD3	2.53	0.43
1:G:2145:SER:HB3	1:G:3647:HIS:CD2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:3923:LEU:HD12	1:G:3961:VAL:HG13	2.00	0.43
1:A:664:PHE:HE2	1:A:686:TRP:CZ2	2.36	0.43
1:A:4576:ILE:HG22	1:A:4643:LEU:HD12	2.01	0.43
1:A:4680:LYS:HE2	1:A:4686:LEU:HD21	2.00	0.43
1:C:714:TYR:CB	1:C:757:PHE:HD2	2.28	0.43
1:C:746:CYS:HA	1:C:757:PHE:CD1	2.53	0.43
1:C:892:THR:O	1:C:903:LEU:HA	2.19	0.43
1:C:1828:ASP:HB3	1:C:1830:VAL:H	1.83	0.43
1:C:2134:LEU:O	1:C:2138:LEU:HG	2.18	0.43
1:C:2551:ASN:HA	1:C:2554:LEU:HG	2.00	0.43
1:E:180:LEU:O	1:E:200:TRP:NE1	2.51	0.43
1:E:635:THR:HG23	1:E:1693:GLN:HE22	1.82	0.43
1:E:1232:ARG:HE	1:E:1701:ALA:HB3	1.83	0.43
1:E:1293:LEU:HD21	1:E:1585:LYS:NZ	2.33	0.43
1:E:2142:TYR:CE2	1:E:2197:LEU:HB2	2.54	0.43
1:E:2423:MET:HG3	1:E:2498:HIS:CE1	2.52	0.43
2:F:7:ILE:HD11	2:F:73:LYS:HB2	2.00	0.43
1:G:4661:TYR:HE2	1:G:4789:PHE:HB2	1.83	0.43
2:H:2:VAL:HG23	2:H:76:ILE:HA	1.99	0.43
1:A:222:LEU:HB3	1:A:388:LEU:HD13	2.01	0.43
1:A:484:LEU:HD21	1:A:540:PHE:CE1	2.54	0.43
1:A:1289:LEU:HD12	1:A:1562:ILE:HD13	1.99	0.43
1:A:1969:LEU:O	1:A:1973:GLN:HG3	2.18	0.43
1:A:2244:ARG:O	1:A:2247:GLN:HB3	2.18	0.43
1:A:2816:MET:HG2	1:A:2878:LEU:HD21	1.99	0.43
1:A:4922:PHE:HA	1:A:4926:VAL:HB	2.00	0.43
1:C:217:GLY:O	1:C:261:ARG:NH1	2.52	0.43
1:C:4829:SER:HA	1:C:4832:HIS:CD2	2.54	0.43
1:C:4980:LEU:HA	1:C:4984:ASN:HB3	2.00	0.43
1:E:46:LEU:HD13	1:E:125:ARG:NH1	2.33	0.43
1:E:468:LEU:O	1:E:472:ARG:HG2	2.18	0.43
1:E:746:CYS:HA	1:E:757:PHE:CD1	2.53	0.43
1:E:1969:LEU:O	1:E:1973:GLN:HG3	2.17	0.43
1:E:2242:ILE:HD11	1:E:2246:ASN:HD22	1.82	0.43
1:E:2336:ARG:HD2	1:E:2435:ARG:CZ	2.48	0.43
1:E:3657:TYR:O	1:E:3662:ILE:HG12	2.18	0.43
1:E:3985:LEU:HA	1:E:3988:ALA:HB3	2.00	0.43
1:G:764:VAL:O	1:G:764:VAL:HG12	2.18	0.43
1:G:1828:ASP:HB3	1:G:1830:VAL:H	1.83	0.43
1:A:765:GLN:HE21	1:A:1479:GLU:H	1.66	0.43
1:A:1252:HIS:C	1:A:1254:HIS:N	2.72	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1704:PRO:HG2	1:A:1707:LEU:HD12	1.99	0.43
1:A:4980:LEU:HA	1:A:4984:ASN:HB3	2.00	0.43
1:C:58:VAL:HG22	1:C:305:CYS:HA	2.01	0.43
1:C:308:HIS:CE1	1:C:311:ALA:HB2	2.54	0.43
1:C:764:VAL:O	1:C:764:VAL:HG12	2.19	0.43
1:C:959:TYR:HE2	1:C:966:LYS:HB2	1.83	0.43
1:C:1293:LEU:HD21	1:C:1585:LYS:NZ	2.33	0.43
1:C:1936:LYS:HA	1:C:1939:MET:HB3	2.00	0.43
1:C:1958:LEU:HD23	1:C:2138:LEU:HD21	2.01	0.43
1:C:2142:TYR:CE2	1:C:2197:LEU:HB2	2.54	0.43
1:C:4239:GLU:OE1	1:C:4675:LYS:HD2	2.18	0.43
1:C:4786:ASP:OD1	1:C:4787:ASN:N	2.51	0.43
1:C:4922:PHE:HA	1:C:4926:VAL:HB	2.00	0.43
1:E:484:LEU:HD21	1:E:540:PHE:CE1	2.54	0.43
1:E:673:PRO:O	1:E:679:ALA:HA	2.18	0.43
1:E:1018:ASN:HB3	1:E:1021:LEU:HG	2.00	0.43
1:E:1254:HIS:HD2	1:E:1280:GLN:HB2	1.83	0.43
1:E:2340:PHE:CD1	1:E:2435:ARG:HD2	2.53	0.43
1:E:2711:PRO:HA	1:E:3016:TYR:HA	1.98	0.43
1:G:1280:GLN:NE2	1:G:1559:GLN:OE1	2.51	0.43
1:G:4855:ALA:HB1	1:G:4863:TYR:CE2	2.54	0.43
2:H:99:PHE:HB3	2:H:101:VAL:HG23	2.00	0.43
1:A:134:ASP:OD1	1:A:135:VAL:N	2.51	0.43
1:A:2747:ILE:HG22	1:A:2748:PRO:O	2.19	0.43
1:A:4786:ASP:OD1	1:A:4787:ASN:N	2.51	0.43
1:C:20:VAL:HG12	1:C:204:PRO:HA	2.00	0.43
1:C:110:ARG:NH2	1:C:115:ARG:HD2	2.29	0.43
1:C:842:PRO:HD2	1:C:1196:PRO:HA	2.00	0.43
1:C:4088:ILE:O	1:C:4123:ILE:N	2.51	0.43
1:C:4235:VAL:HG21	1:C:5019:TRP:CZ3	2.53	0.43
2:D:87:HIS:HD2	2:D:88:PRO:HD2	1.84	0.43
2:D:88:PRO:O	2:D:90:ILE:HD12	2.18	0.43
1:E:1629:GLN:HE21	1:E:1631:GLN:HE21	1.66	0.43
1:E:1839:VAL:HB	1:E:1840:PRO:HD3	2.00	0.43
1:E:1943:LEU:HD11	1:E:2098:VAL:HG22	1.99	0.43
1:E:2551:ASN:HA	1:E:2554:LEU:HG	2.01	0.43
1:E:4840:THR:OG1	1:G:4826:ILE:HD13	2.19	0.43
1:G:20:VAL:HG12	1:G:204:PRO:HA	2.00	0.43
1:G:100:THR:HG21	1:G:162:LYS:NZ	2.33	0.43
1:G:176:SER:HB2	1:G:178:ARG:NH2	2.32	0.43
1:G:262:LEU:HD23	1:G:282:ILE:HG12	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1189:LEU:HA	1:G:1190:PRO:HD3	1.87	0.43
1:G:1710:GLY:O	1:G:1714:LEU:HG	2.18	0.43
1:G:2134:LEU:O	1:G:2138:LEU:HG	2.18	0.43
1:G:2163:ARG:O	1:G:2166:LEU:HB3	2.19	0.43
1:G:2380:ILE:HG23	1:G:2423:MET:SD	2.58	0.43
1:G:4682:GLU:OE2	1:G:4723:LYS:HD2	2.18	0.43
1:A:262:LEU:HD23	1:A:282:ILE:HG12	1.99	0.43
1:A:308:HIS:CE1	1:A:311:ALA:HB2	2.54	0.43
1:A:892:THR:O	1:A:903:LEU:HA	2.19	0.43
1:A:1695:LEU:O	1:A:1699:GLU:HG3	2.19	0.43
1:A:3924:LEU:O	1:A:3927:GLN:HB3	2.19	0.43
1:C:21:VAL:HG13	1:C:205:ILE:HD11	2.01	0.43
1:C:293:LEU:HD13	1:C:378:LEU:HD12	2.00	0.43
1:C:637:LEU:O	1:C:638:ILE:HD13	2.19	0.43
1:C:1101:ARG:CG	1:C:1193:SER:HB3	2.47	0.43
1:C:2747:ILE:HG22	1:C:2748:PRO:O	2.18	0.43
1:C:2816:MET:HG2	1:C:2878:LEU:HD21	1.99	0.43
1:C:3886:ARG:O	1:C:3890:LEU:HD13	2.17	0.43
1:C:3895:HIS:HE1	1:C:3970:GLN:HG3	1.83	0.43
1:C:4814:LEU:HD23	1:C:4814:LEU:HA	1.91	0.43
1:E:4239:GLU:OE1	1:E:4675:LYS:HD2	2.19	0.43
1:E:4849:TYR:HA	1:E:4852:THR:HG22	2.01	0.43
1:G:892:THR:O	1:G:903:LEU:HA	2.18	0.43
1:G:1022:VAL:HG23	1:G:1027:LEU:HB3	2.00	0.43
1:G:1252:HIS:C	1:G:1254:HIS:N	2.72	0.43
1:G:1586:ASN:O	1:G:1588:ALA:N	2.47	0.43
1:G:1715:LEU:HD13	1:G:1844:LEU:HD11	2.01	0.43
1:G:1958:LEU:HD22	1:G:2134:LEU:HD11	2.01	0.43
1:G:4705:VAL:HB	1:G:4778:TRP:CD2	2.54	0.43
1:A:21:VAL:HG13	1:A:205:ILE:HD11	2.01	0.43
1:A:889:GLN:HB3	1:A:891:TRP:HD1	1.84	0.43
1:A:3985:LEU:HA	1:A:3988:ALA:HB3	2.01	0.43
1:A:4856:PHE:CE2	1:C:4807:PHE:CZ	3.07	0.43
2:B:88:PRO:O	2:B:90:ILE:HD12	2.18	0.43
1:C:664:PHE:HE2	1:C:686:TRP:CZ2	2.36	0.43
1:C:889:GLN:HB3	1:C:891:TRP:HD1	1.84	0.43
1:C:2336:ARG:HD2	1:C:2435:ARG:NH1	2.33	0.43
1:C:4642:ALA:HA	1:C:4645:CYS:SG	2.58	0.43
1:E:214:VAL:HG22	1:E:341:TYR:CZ	2.54	0.43
1:E:889:GLN:HB3	1:E:891:TRP:HD1	1.84	0.43
1:E:1022:VAL:HG23	1:E:1027:LEU:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:3891:LEU:HB3	1:E:3899:PHE:HE2	1.82	0.43
1:E:4235:VAL:HG21	1:E:5019:TRP:CZ3	2.54	0.43
1:G:959:TYR:HE2	1:G:966:LYS:HB2	1.83	0.43
1:G:1018:ASN:HB3	1:G:1021:LEU:HG	2.01	0.43
1:G:2711:PRO:HA	1:G:3016:TYR:HA	2.00	0.43
1:G:2774:ASN:OD1	1:G:2852:ARG:NE	2.52	0.43
1:A:20:VAL:HG12	1:A:204:PRO:HA	2.00	0.43
1:A:214:VAL:HG22	1:A:341:TYR:CZ	2.54	0.43
1:A:673:PRO:O	1:A:679:ALA:HA	2.18	0.43
1:A:1124:PHE:HB2	1:A:1162:PHE:CE2	2.54	0.43
1:A:2063:LEU:O	1:A:2066:LEU:HB3	2.19	0.43
1:A:2163:ARG:O	1:A:2166:LEU:HB3	2.19	0.43
1:A:4235:VAL:HG21	1:A:5019:TRP:CZ3	2.53	0.43
1:C:252:VAL:HA	1:C:255:HIS:CE1	2.54	0.43
1:C:1076:ARG:HH22	1:C:1609:PRO:CB	2.32	0.43
1:C:1695:LEU:O	1:C:1699:GLU:HG3	2.19	0.43
1:C:1812:LEU:HD21	1:C:1861:GLN:HG2	2.01	0.43
1:C:1943:LEU:HD11	1:C:2098:VAL:HG22	1.99	0.43
1:E:222:LEU:HB3	1:E:388:LEU:HD13	2.00	0.43
1:E:252:VAL:HA	1:E:255:HIS:CE1	2.54	0.43
1:E:308:HIS:CE1	1:E:311:ALA:HB2	2.54	0.43
1:E:602:VAL:O	1:E:605:SER:OG	2.22	0.43
1:E:2063:LEU:O	1:E:2066:LEU:HB3	2.19	0.43
1:E:4638:TYR:O	1:E:4641:PRO:HD2	2.18	0.43
2:F:82:TYR:CE1	2:F:87:HIS:HB2	2.54	0.43
1:G:134:ASP:OD1	1:G:135:VAL:N	2.51	0.43
1:G:180:LEU:O	1:G:200:TRP:NE1	2.51	0.43
1:G:217:GLY:O	1:G:261:ARG:NH1	2.52	0.43
1:G:1780:PRO:HD3	1:G:1801:ALA:H	1.84	0.43
1:G:1958:LEU:HD23	1:G:2138:LEU:HD21	2.01	0.43
1:G:2244:ARG:O	1:G:2247:GLN:HB3	2.18	0.43
1:G:4806:ASN:O	1:G:4809:PHE:HB3	2.18	0.43
2:H:55:VAL:HG21	2:H:59:TRP:HD1	1.84	0.43
1:A:2770:LYS:HG3	1:A:2791:LEU:HD21	2.01	0.43
1:A:4888:TYR:O	1:A:4892:ARG:HD3	2.19	0.43
1:C:1715:LEU:HD13	1:C:1844:LEU:HD11	2.01	0.43
1:C:3971:GLY:O	1:C:3973:CYS:N	2.51	0.43
1:C:4856:PHE:CE2	1:E:4807:PHE:CZ	3.06	0.43
1:E:20:VAL:HG12	1:E:204:PRO:HA	2.00	0.43
1:E:217:GLY:O	1:E:261:ARG:NH1	2.52	0.43
1:E:495:ASN:HB3	1:E:553:ARG:NH2	2.23	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:664:PHE:HE2	1:E:686:TRP:CZ2	2.36	0.43
1:E:1089:TYR:HE2	1:E:1214:PHE:HD1	1.67	0.43
1:E:1715:LEU:HD13	1:E:1844:LEU:HD11	2.01	0.43
2:F:88:PRO:O	2:F:90:ILE:HD12	2.18	0.43
1:G:21:VAL:HG13	1:G:205:ILE:HD11	2.01	0.43
1:G:203:ASN:HA	1:G:204:PRO:HD3	1.89	0.43
1:G:291:LEU:O	1:G:312:THR:OG1	2.24	0.43
1:G:393:CYS:SG	1:G:397:GLU:HB2	2.59	0.43
1:G:664:PHE:HE2	1:G:686:TRP:CZ2	2.36	0.43
1:G:821:LEU:HD23	1:G:1626:TRP:CZ2	2.54	0.43
1:G:1839:VAL:HB	1:G:1840:PRO:HD3	2.00	0.43
1:G:4145:VAL:O	1:G:4149:ASN:N	2.49	0.43
1:A:181:HIS:CD2	1:A:196:MET:HB2	2.54	0.42
1:A:614:VAL:HG13	1:A:617:ASN:HB3	2.01	0.42
1:A:771:PHE:CE1	1:A:1472:VAL:HG13	2.54	0.42
1:A:3717:ASP:OD1	1:A:3717:ASP:N	2.52	0.42
1:A:4239:GLU:OE1	1:A:4675:LYS:HD2	2.19	0.42
1:A:4667:PRO:HA	1:A:4670:ILE:HG22	2.02	0.42
2:B:78:PRO:O	2:B:83:GLY:N	2.51	0.42
1:C:222:LEU:HB3	1:C:388:LEU:HD13	2.00	0.42
1:C:821:LEU:HD23	1:C:1626:TRP:CZ2	2.54	0.42
1:C:2340:PHE:CD1	1:C:2435:ARG:HD2	2.53	0.42
1:C:3981:ALA:O	1:C:3986:TRP:NE1	2.46	0.42
1:E:181:HIS:CD2	1:E:196:MET:HB2	2.54	0.42
1:E:637:LEU:O	1:E:638:ILE:HD13	2.19	0.42
1:E:1124:PHE:HB2	1:E:1162:PHE:CE2	2.54	0.42
1:E:1773:PRO:HA	1:E:1774:PRO:HD3	1.90	0.42
1:E:1833:SER:HB3	1:E:1836:PHE:HD2	1.84	0.42
1:E:2163:ARG:O	1:E:2166:LEU:HB3	2.19	0.42
1:G:43:GLY:HA2	1:G:444:SER:HA	2.01	0.42
1:G:637:LEU:O	1:G:638:ILE:HD13	2.19	0.42
1:G:765:GLN:HE21	1:G:1479:GLU:H	1.67	0.42
1:G:1101:ARG:CG	1:G:1193:SER:HB3	2.48	0.42
1:G:2336:ARG:HD2	1:G:2435:ARG:CZ	2.49	0.42
1:G:2340:PHE:CD1	1:G:2435:ARG:HD2	2.54	0.42
1:G:2747:ILE:HG22	1:G:2748:PRO:O	2.19	0.42
1:A:1652:GLU:O	1:A:1655:GLU:HG2	2.19	0.42
1:A:2134:LEU:O	1:A:2138:LEU:HG	2.18	0.42
1:A:2741:GLU:HB3	1:A:2744:ASN:HD22	1.84	0.42
1:C:59:PRO:HB3	1:C:281:ARG:CZ	2.49	0.42
1:C:468:LEU:O	1:C:472:ARG:HG2	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:771:PHE:CE1	1:C:1472:VAL:HG13	2.54	0.42
1:C:1103:GLY:HA3	1:C:1123:VAL:HA	2.00	0.42
1:C:1124:PHE:HB2	1:C:1162:PHE:CE2	2.54	0.42
1:C:1611:HIS:HB2	1:C:1652:GLU:CB	2.46	0.42
1:C:1767:VAL:C	1:C:1768:THR:HG1	2.23	0.42
1:C:2244:ARG:O	1:C:2247:GLN:HB3	2.18	0.42
1:E:43:GLY:HA2	1:E:444:SER:HA	2.01	0.42
1:E:771:PHE:CE1	1:E:1472:VAL:HG13	2.54	0.42
1:E:1279:SER:HB3	1:E:1558:HIS:HA	2.02	0.42
1:E:1586:ASN:O	1:E:1588:ALA:N	2.48	0.42
1:E:1652:GLU:O	1:E:1655:GLU:HG2	2.19	0.42
1:E:1958:LEU:HD23	1:E:2138:LEU:HD21	2.01	0.42
1:E:3924:LEU:O	1:E:3927:GLN:HB3	2.19	0.42
1:G:154:SER:HB3	1:G:156:GLN:OE1	2.19	0.42
1:G:468:LEU:O	1:G:472:ARG:HG2	2.19	0.42
1:G:580:GLU:HA	1:G:620:LEU:HD21	2.01	0.42
1:A:252:VAL:HA	1:A:255:HIS:CE1	2.54	0.42
1:A:1160:ILE:O	1:A:1178:ALA:N	2.53	0.42
1:A:1189:LEU:HA	1:A:1190:PRO:HD3	1.87	0.42
1:A:1198:GLN:OE1	1:A:1198:GLN:N	2.50	0.42
1:A:1649:ASP:OD1	1:A:1649:ASP:N	2.53	0.42
1:A:1958:LEU:HD23	1:A:2138:LEU:HD21	2.02	0.42
1:A:2761:TYR:CE2	1:A:2862:LEU:HD22	2.53	0.42
1:A:2774:ASN:OD1	1:A:2852:ARG:NE	2.52	0.42
1:A:2788:HIS:CG	1:A:2789:PRO:HD2	2.54	0.42
1:C:685:GLY:HA3	1:C:712:TYR:O	2.20	0.42
1:C:765:GLN:HE21	1:C:1479:GLU:H	1.66	0.42
1:C:868:GLU:O	1:C:871:ARG:HB2	2.20	0.42
1:C:1229:ASN:CG	1:C:1827:ARG:HH11	2.23	0.42
1:C:1290:ARG:HH21	1:C:1549:PHE:HE2	1.66	0.42
1:C:2788:HIS:CG	1:C:2789:PRO:HD2	2.54	0.42
2:D:7:ILE:HD11	2:D:73:LYS:HB2	2.00	0.42
1:E:176:SER:HB2	1:E:178:ARG:NH2	2.32	0.42
1:E:586:ILE:O	1:E:589:LEU:HB3	2.19	0.42
1:E:852:VAL:HG22	1:E:853:PRO:HD2	2.01	0.42
1:E:1231:GLN:OE1	1:E:1821:ASP:HB2	2.20	0.42
1:E:1586:ASN:N	1:E:1587:PRO:HD2	2.35	0.42
1:E:1695:LEU:O	1:E:1699:GLU:HG3	2.19	0.42
1:E:4667:PRO:HA	1:E:4670:ILE:HG22	2.01	0.42
1:G:58:VAL:HG22	1:G:305:CYS:HA	2.01	0.42
1:G:214:VAL:HG22	1:G:341:TYR:CZ	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:2182:ILE:O	1:G:2186:MET:HG2	2.20	0.42
1:G:4965:SER:HA	1:G:4975:PHE:CD1	2.54	0.42
1:A:821:LEU:HD23	1:A:1626:TRP:CZ2	2.54	0.42
1:A:868:GLU:O	1:A:871:ARG:HB2	2.19	0.42
1:A:1101:ARG:CG	1:A:1193:SER:HB3	2.48	0.42
1:A:1710:GLY:O	1:A:1714:LEU:HG	2.19	0.42
1:A:1747:LEU:HB2	1:A:1957:SER:OG	2.19	0.42
1:A:1767:VAL:C	1:A:1768:THR:HG1	2.23	0.42
1:A:2145:SER:HB3	1:A:3647:HIS:CD2	2.54	0.42
1:A:2767:ALA:HB3	1:A:2857:PRO:HG3	2.01	0.42
1:A:3657:TYR:O	1:A:3662:ILE:HG12	2.18	0.42
1:C:180:LEU:O	1:C:200:TRP:NE1	2.51	0.42
1:C:1279:SER:HB3	1:C:1558:HIS:HA	2.02	0.42
1:C:4667:PRO:HA	1:C:4670:ILE:HG22	2.01	0.42
2:D:78:PRO:O	2:D:83:GLY:N	2.52	0.42
1:E:393:CYS:SG	1:E:397:GLU:HB2	2.60	0.42
1:E:2182:ILE:O	1:E:2186:MET:HG2	2.20	0.42
1:E:2761:TYR:CE2	1:E:2862:LEU:HD22	2.54	0.42
1:E:3895:HIS:HE1	1:E:3970:GLN:HG3	1.83	0.42
1:G:23:GLN:NE2	1:G:34:LYS:HB3	2.32	0.42
1:G:59:PRO:HB3	1:G:281:ARG:CZ	2.50	0.42
1:G:495:ASN:HB3	1:G:553:ARG:NH2	2.23	0.42
1:G:586:ILE:O	1:G:589:LEU:HB3	2.20	0.42
1:G:638:ILE:HG23	1:G:678:GLN:HE22	1.84	0.42
1:G:889:GLN:HB3	1:G:891:TRP:HD1	1.85	0.42
1:G:3958:ALA:HA	1:G:3961:VAL:HG12	2.02	0.42
1:G:4090:LYS:N	1:G:4121:GLU:O	2.53	0.42
1:A:43:GLY:HA2	1:A:444:SER:HA	2.01	0.42
1:A:685:GLY:HA3	1:A:712:TYR:O	2.19	0.42
1:A:1022:VAL:HG23	1:A:1027:LEU:HB3	2.00	0.42
1:A:1673:VAL:HG11	1:A:1681:VAL:HG11	2.02	0.42
1:A:4809:PHE:O	1:A:4812:HIS:ND1	2.48	0.42
2:B:56:ILE:HB	2:B:80:TYR:O	2.19	0.42
1:C:1254:HIS:HD2	1:C:1280:GLN:HB2	1.83	0.42
1:C:1610:ASN:HA	1:C:1652:GLU:OE2	2.18	0.42
1:C:2182:ILE:O	1:C:2186:MET:HG2	2.20	0.42
1:E:184:THR:HA	1:E:189:LEU:HD23	2.01	0.42
1:E:685:GLY:HA3	1:E:712:TYR:O	2.19	0.42
1:E:714:TYR:CB	1:E:757:PHE:HD2	2.28	0.42
1:E:1673:VAL:HG11	1:E:1681:VAL:HG11	2.01	0.42
1:E:1704:PRO:HG2	1:E:1707:LEU:HD12	1.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1710:GLY:O	1:E:1714:LEU:HG	2.19	0.42
1:E:1747:LEU:HB2	1:E:1957:SER:OG	2.19	0.42
1:E:2741:GLU:HB3	1:E:2744:ASN:HD22	1.84	0.42
1:E:4963:ILE:HD12	1:E:5030:LYS:HZ1	1.83	0.42
1:G:695:TYR:O	1:G:697:GLY:N	2.42	0.42
1:G:1747:LEU:HB2	1:G:1957:SER:OG	2.19	0.42
1:G:2063:LEU:O	1:G:2066:LEU:HB3	2.18	0.42
1:G:2142:TYR:CE2	1:G:2197:LEU:HB2	2.54	0.42
1:G:3694:LYS:HA	1:G:3695:PRO:HD3	1.80	0.42
1:G:4028:LEU:HD23	1:G:4146:LEU:HD12	2.02	0.42
1:G:4786:ASP:OD1	1:G:4787:ASN:N	2.52	0.42
1:A:767:VAL:O	1:A:1475:THR:OG1	2.24	0.42
1:A:2867:LEU:HG	1:A:2928:LYS:HZ3	1.84	0.42
1:A:3958:ALA:CB	1:A:4019:LEU:HD11	2.47	0.42
1:A:4829:SER:HA	1:A:4832:HIS:CD2	2.54	0.42
1:A:4934:GLY:HA2	1:A:4937:ILE:HD12	2.02	0.42
1:A:5022:PHE:HA	1:A:5023:PRO:HD3	1.72	0.42
2:B:82:TYR:CE1	2:B:87:HIS:HB2	2.55	0.42
1:C:580:GLU:HA	1:C:620:LEU:HD21	2.02	0.42
1:C:2063:LEU:O	1:C:2066:LEU:HB3	2.19	0.42
1:C:2145:SER:HB3	1:C:3647:HIS:CD2	2.54	0.42
1:C:2770:LYS:HG3	1:C:2791:LEU:HD21	2.01	0.42
1:C:3713:LYS:O	1:C:3715:LYS:N	2.53	0.42
1:C:3985:LEU:HA	1:C:3988:ALA:HB3	2.02	0.42
1:C:4576:ILE:HG22	1:C:4643:LEU:HD12	2.02	0.42
1:E:588:SER:HB3	1:E:592:LYS:NZ	2.35	0.42
1:E:614:VAL:HG13	1:E:617:ASN:HB3	2.01	0.42
1:E:3775:ALA:O	1:E:3778:MET:HG2	2.20	0.42
1:E:4576:ILE:HG22	1:E:4643:LEU:HD12	2.01	0.42
1:E:4938:ASP:CG	1:G:4940:PHE:HB3	2.39	0.42
1:E:5026:ASP:O	1:E:5027:CYS:SG	2.75	0.42
1:G:118:LEU:HD12	1:G:136:GLY:O	2.20	0.42
1:G:739:ALA:C	1:G:741:GLU:H	2.18	0.42
1:G:1695:LEU:O	1:G:1699:GLU:HG3	2.19	0.42
1:G:2747:ILE:HD11	1:G:2814:LYS:HG3	2.02	0.42
1:G:2770:LYS:HB3	1:G:2775:TRP:CB	2.43	0.42
1:A:548:VAL:HG21	1:A:582:HIS:HB3	2.02	0.42
1:A:1279:SER:HB3	1:A:1558:HIS:HA	2.02	0.42
1:A:1715:LEU:HD13	1:A:1844:LEU:HD11	2.01	0.42
1:C:393:CYS:SG	1:C:397:GLU:HB2	2.60	0.42
1:C:548:VAL:HG21	1:C:582:HIS:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1530:THR:HG22	1:C:1535:GLU:HA	2.01	0.42
1:C:1839:VAL:HB	1:C:1840:PRO:HD3	2.01	0.42
1:C:2761:TYR:CE2	1:C:2862:LEU:HD22	2.54	0.42
1:C:4963:ILE:HD12	1:C:4963:ILE:HG23	1.86	0.42
1:E:821:LEU:HD23	1:E:1626:TRP:CZ2	2.54	0.42
1:E:1530:THR:HG22	1:E:1535:GLU:HA	2.02	0.42
1:E:1564:PHE:HB3	1:E:1565:GLU:H	1.70	0.42
1:E:2788:HIS:CG	1:E:2789:PRO:HD2	2.54	0.42
1:G:639:ASN:OD1	1:G:640:TYR:N	2.53	0.42
1:G:1652:GLU:O	1:G:1655:GLU:HG2	2.20	0.42
1:G:2121:PHE:CD1	1:G:3701:LEU:HD12	2.55	0.42
1:G:2161:GLN:NE2	1:G:2177:LEU:HB3	2.35	0.42
1:G:3825:GLU:O	1:G:3826:VAL:HG12	2.20	0.42
1:G:4054:ASN:OD1	1:G:4055:VAL:N	2.53	0.42
1:G:4217:PHE:CZ	1:G:4234:PHE:HA	2.55	0.42
1:G:4898:GLY:HA2	1:G:4901:ILE:HG22	2.02	0.42
1:A:410:LEU:HD21	1:A:441:VAL:HG22	2.02	0.42
1:A:580:GLU:HA	1:A:620:LEU:HD21	2.02	0.42
1:A:586:ILE:O	1:A:589:LEU:HB3	2.19	0.42
1:A:2272:PRO:O	1:A:2275:VAL:HB	2.20	0.42
1:A:3825:GLU:C	1:A:3827:GLY:H	2.22	0.42
1:A:3919:THR:HG21	1:A:3968:TYR:CE2	2.49	0.42
1:A:3971:GLY:O	1:A:3973:CYS:N	2.51	0.42
1:C:221:ARG:N	1:C:391:THR:O	2.44	0.42
1:C:588:SER:HB3	1:C:592:LYS:NZ	2.35	0.42
1:C:633:LEU:HD22	1:C:1641:ILE:HG22	2.02	0.42
1:C:1089:TYR:CE2	1:C:1214:PHE:HD1	2.38	0.42
1:C:3924:LEU:O	1:C:3927:GLN:HB3	2.19	0.42
1:C:4573:ILE:HG21	1:C:4809:PHE:CE2	2.54	0.42
1:E:118:LEU:HD12	1:E:136:GLY:O	2.20	0.42
1:E:410:LEU:HD21	1:E:441:VAL:HG22	2.02	0.42
1:E:580:GLU:HA	1:E:620:LEU:HD21	2.02	0.42
1:E:765:GLN:HE21	1:E:1479:GLU:H	1.66	0.42
1:E:2145:SER:HB3	1:E:3647:HIS:CD2	2.55	0.42
1:E:2203:MET:O	1:E:2207:VAL:HG23	2.20	0.42
2:F:56:ILE:HB	2:F:80:TYR:O	2.19	0.42
1:G:1279:SER:HB3	1:G:1558:HIS:HA	2.02	0.42
1:G:2770:LYS:HG3	1:G:2791:LEU:HD21	2.01	0.42
1:G:3775:ALA:O	1:G:3778:MET:HG2	2.19	0.42
1:G:4922:PHE:HA	1:G:4926:VAL:HB	2.01	0.42
1:A:738:LEU:HA	1:A:742:ASP:OD2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4088:ILE:O	1:A:4123:ILE:N	2.51	0.42
1:A:4886:HIS:CE1	1:A:4897:ILE:HD12	2.55	0.42
1:A:4930:ALA:HB1	1:C:4933:GLN:HA	2.02	0.42
1:C:43:GLY:HA2	1:C:444:SER:HA	2.00	0.42
1:C:118:LEU:HD12	1:C:136:GLY:O	2.20	0.42
1:C:154:SER:HB3	1:C:156:GLN:OE1	2.19	0.42
1:C:214:VAL:HG22	1:C:341:TYR:CZ	2.54	0.42
1:C:410:LEU:HD21	1:C:441:VAL:HG22	2.02	0.42
1:C:646:PRO:O	1:C:648:ILE:N	2.41	0.42
1:C:1747:LEU:HB2	1:C:1957:SER:OG	2.19	0.42
1:C:2203:MET:O	1:C:2207:VAL:HG23	2.20	0.42
1:C:2882:TYR:HD2	1:C:2919:ASP:HB3	1.85	0.42
1:C:3694:LYS:HA	1:C:3695:PRO:HD3	1.79	0.42
1:E:471:LEU:HA	1:E:474:ARG:HE	1.85	0.42
1:E:1160:ILE:O	1:E:1178:ALA:N	2.53	0.42
1:E:2770:LYS:HG3	1:E:2791:LEU:HD21	2.01	0.42
1:G:252:VAL:HA	1:G:255:HIS:CE1	2.54	0.42
1:G:548:VAL:HG21	1:G:582:HIS:HB3	2.01	0.42
1:G:771:PHE:CE1	1:G:1472:VAL:HG13	2.54	0.42
1:G:2561:LEU:HD11	1:G:2601:ASP:HA	2.02	0.42
1:G:4652:LEU:O	1:G:4656:LEU:N	2.51	0.42
1:A:154:SER:HB3	1:A:156:GLN:OE1	2.19	0.42
1:A:1018:ASN:HB3	1:A:1021:LEU:HG	2.01	0.42
1:A:1229:ASN:CG	1:A:1827:ARG:HH11	2.23	0.42
1:A:1655:GLU:HG3	1:A:1656:ARG:HG3	2.02	0.42
1:A:3713:LYS:O	1:A:3715:LYS:N	2.53	0.42
1:C:76:ARG:NH1	1:C:79:GLN:OE1	2.53	0.42
1:C:181:HIS:CD2	1:C:196:MET:HB2	2.55	0.42
1:C:3806:ASN:H	1:C:3890:LEU:HD23	1.85	0.42
1:E:868:GLU:O	1:E:871:ARG:HB2	2.20	0.42
1:E:2272:PRO:O	1:E:2275:VAL:HB	2.20	0.42
1:E:4020:GLN:O	1:E:4024:VAL:HG22	2.20	0.42
1:G:685:GLY:HA3	1:G:712:TYR:O	2.19	0.42
1:G:1767:VAL:C	1:G:1768:THR:HG1	2.23	0.42
1:A:3806:ASN:H	1:A:3890:LEU:HD23	1.85	0.41
2:B:54:GLU:HG3	2:B:55:VAL:HG13	2.02	0.41
1:C:184:THR:HA	1:C:189:LEU:HD23	2.01	0.41
1:C:586:ILE:O	1:C:589:LEU:HB3	2.20	0.41
1:C:662:TRP:CZ3	1:C:814:ALA:HB2	2.56	0.41
1:C:2161:GLN:NE2	1:C:2177:LEU:HB3	2.35	0.41
1:C:2741:GLU:HB3	1:C:2744:ASN:HD22	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4047:MET:O	1:C:4051:SER:N	2.51	0.41
1:E:1101:ARG:CG	1:E:1193:SER:HB3	2.48	0.41
1:E:2774:ASN:OD1	1:E:2852:ARG:NE	2.52	0.41
1:E:3713:LYS:O	1:E:3715:LYS:N	2.53	0.41
1:G:686:TRP:HD1	1:G:757:PHE:HZ	1.68	0.41
1:G:1290:ARG:HH21	1:G:1549:PHE:HE2	1.67	0.41
1:G:1673:VAL:HG11	1:G:1681:VAL:HG11	2.02	0.41
1:G:2131:LEU:HD21	1:G:3662:ILE:O	2.20	0.41
1:G:2788:HIS:CG	1:G:2789:PRO:HD2	2.54	0.41
1:G:3780:LEU:HD21	1:G:3820:LEU:HG	2.01	0.41
1:G:4677:LEU:HD11	1:G:4702:ASP:HB3	2.01	0.41
1:G:4913:ARG:O	1:G:4916:PHE:HB3	2.20	0.41
1:A:637:LEU:O	1:A:638:ILE:HD13	2.19	0.41
1:A:662:TRP:CZ3	1:A:814:ALA:HB2	2.56	0.41
1:A:1081:TYR:HD2	1:A:1234:VAL:HG13	1.85	0.41
1:A:2231:SER:HA	1:A:2234:ARG:HH11	1.85	0.41
1:A:4963:ILE:HD12	1:A:4963:ILE:HG23	1.85	0.41
1:C:471:LEU:HA	1:C:474:ARG:HE	1.85	0.41
1:C:852:VAL:HG22	1:C:853:PRO:HD2	2.01	0.41
1:C:1295:VAL:O	1:C:1547:LYS:HA	2.21	0.41
1:C:1652:GLU:O	1:C:1655:GLU:HG2	2.20	0.41
1:C:1685:LEU:HD23	1:C:1685:LEU:HA	1.92	0.41
1:C:3969:ILE:O	1:C:3969:ILE:HG22	2.20	0.41
1:E:58:VAL:HG22	1:E:305:CYS:HA	2.02	0.41
1:E:111:HIS:CD2	1:E:113:HIS:H	2.38	0.41
1:E:168:ASP:HB3	1:E:199:LEU:HD22	2.03	0.41
1:E:633:LEU:HD22	1:E:1641:ILE:HG22	2.03	0.41
1:E:2767:ALA:HB3	1:E:2857:PRO:HG3	2.01	0.41
1:E:4573:ILE:HG21	1:E:4809:PHE:CE2	2.54	0.41
1:G:308:HIS:CE1	1:G:311:ALA:HB2	2.55	0.41
1:G:359:TYR:HA	1:G:376:ALA:HA	2.03	0.41
1:G:410:LEU:HD21	1:G:441:VAL:HG22	2.02	0.41
1:G:1081:TYR:HD2	1:G:1234:VAL:HG13	1.84	0.41
1:G:1295:VAL:O	1:G:1547:LYS:HA	2.20	0.41
1:G:1655:GLU:HG3	1:G:1656:ARG:HG3	2.02	0.41
1:G:2133:GLU:HA	1:G:2136:ARG:HE	1.85	0.41
1:G:2211:MET:HE1	1:G:2272:PRO:HB3	2.02	0.41
1:A:221:ARG:N	1:A:391:THR:O	2.44	0.41
1:A:682:LEU:O	1:A:684:VAL:HG23	2.21	0.41
1:A:852:VAL:HG22	1:A:853:PRO:HD2	2.01	0.41
1:A:943:ASP:HB3	1:A:1050:GLY:HA3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1089:TYR:CE2	1:A:1214:PHE:HD1	2.38	0.41
1:A:1812:LEU:HD21	1:A:1861:GLN:HG2	2.02	0.41
1:A:3775:ALA:O	1:A:3778:MET:HG2	2.20	0.41
1:C:1081:TYR:HD2	1:C:1234:VAL:HG13	1.85	0.41
1:C:1586:ASN:N	1:C:1587:PRO:HD2	2.35	0.41
1:E:59:PRO:HB3	1:E:281:ARG:CZ	2.50	0.41
1:E:2145:SER:HB3	1:E:3647:HIS:HD2	1.85	0.41
1:E:4028:LEU:HD21	1:E:4146:LEU:HA	2.03	0.41
1:G:633:LEU:HD22	1:G:1641:ILE:HG22	2.02	0.41
1:G:943:ASP:HB3	1:G:1050:GLY:HA3	2.03	0.41
1:G:1530:THR:HG22	1:G:1535:GLU:HA	2.02	0.41
1:G:1586:ASN:N	1:G:1587:PRO:HD2	2.36	0.41
1:G:2231:SER:HA	1:G:2234:ARG:HH11	1.85	0.41
1:G:2821:TRP:HH2	1:G:2877:GLN:HB3	1.85	0.41
1:A:64:ILE:O	1:A:111:HIS:HE1	2.04	0.41
1:A:217:GLY:O	1:A:261:ARG:NH1	2.53	0.41
1:A:393:CYS:SG	1:A:397:GLU:HB2	2.60	0.41
1:A:588:SER:HB3	1:A:592:LYS:NZ	2.35	0.41
1:A:3965:LEU:HA	1:A:3968:TYR:CD2	2.55	0.41
1:C:179:TYR:OH	1:E:2359:ARG:NE	2.53	0.41
1:C:257:ARG:HB3	1:C:481:GLU:OE2	2.20	0.41
1:C:359:TYR:HA	1:C:376:ALA:HA	2.03	0.41
1:C:614:VAL:HG13	1:C:617:ASN:HB3	2.01	0.41
1:C:1116:GLY:O	1:C:1132:TRP:HB3	2.20	0.41
1:C:1673:VAL:HG11	1:C:1681:VAL:HG11	2.02	0.41
1:C:3717:ASP:OD1	1:C:3717:ASP:N	2.51	0.41
1:C:3775:ALA:O	1:C:3778:MET:HG2	2.20	0.41
1:C:4056:GLU:OE2	1:C:4166:LEU:HD11	2.20	0.41
1:E:548:VAL:HG21	1:E:582:HIS:HB3	2.02	0.41
1:E:2745:VAL:HG21	1:E:2818:ALA:HB2	2.03	0.41
1:E:3717:ASP:OD1	1:E:3717:ASP:N	2.51	0.41
1:E:4930:ALA:HB1	1:G:4933:GLN:HA	2.01	0.41
2:F:54:GLU:HG3	2:F:55:VAL:HG13	2.02	0.41
1:G:184:THR:HA	1:G:189:LEU:HD23	2.01	0.41
1:G:495:ASN:HB2	1:G:550:LYS:HZ3	1.85	0.41
1:G:662:TRP:CZ3	1:G:814:ALA:HB2	2.55	0.41
1:G:1089:TYR:HE2	1:G:1214:PHE:HD1	1.69	0.41
1:G:1783:VAL:HG11	2:H:46:PHE:CZ	2.55	0.41
1:G:2136:ARG:NH1	1:G:3720:TYR:HE2	2.19	0.41
1:G:2210:VAL:O	1:G:2214:VAL:HG23	2.21	0.41
1:G:4878:ASP:HB3	1:G:4881:THR:OG1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:471:LEU:HA	1:A:474:ARG:HE	1.85	0.41
1:A:639:ASN:OD1	1:A:640:TYR:N	2.54	0.41
1:A:1564:PHE:HB3	1:A:1565:GLU:H	1.70	0.41
1:A:1815:LEU:HB3	1:A:1865:MET:HE3	2.01	0.41
1:A:2161:GLN:NE2	1:A:2177:LEU:HB3	2.35	0.41
1:A:2182:ILE:O	1:A:2186:MET:HG2	2.20	0.41
1:A:3817:LEU:HD13	1:A:3899:PHE:HD1	1.86	0.41
1:A:5026:ASP:O	1:A:5027:CYS:SG	2.76	0.41
1:C:639:ASN:OD1	1:C:640:TYR:N	2.54	0.41
1:C:1018:ASN:HB3	1:C:1021:LEU:HG	2.01	0.41
1:C:1022:VAL:HG23	1:C:1027:LEU:HB3	2.00	0.41
1:C:1089:TYR:HE2	1:C:1214:PHE:HD1	1.68	0.41
1:C:2145:SER:HB3	1:C:3647:HIS:HD2	1.85	0.41
1:E:359:TYR:HA	1:E:376:ALA:HA	2.02	0.41
1:E:639:ASN:OD1	1:E:640:TYR:N	2.53	0.41
1:E:1092:PHE:CD2	1:E:1102:VAL:HG21	2.56	0.41
1:E:1295:VAL:O	1:E:1547:LYS:HA	2.21	0.41
1:E:3981:ALA:O	1:E:3986:TRP:NE1	2.46	0.41
1:E:4820:VAL:O	1:E:4824:ARG:HG3	2.20	0.41
1:G:181:HIS:CD2	1:G:196:MET:HB2	2.55	0.41
1:G:588:SER:HB3	1:G:592:LYS:NZ	2.35	0.41
1:G:1116:GLY:O	1:G:1132:TRP:HB3	2.20	0.41
1:G:1160:ILE:O	1:G:1178:ALA:N	2.53	0.41
1:G:1783:VAL:O	2:H:56:ILE:N	2.54	0.41
1:G:3972:PRO:HD3	1:G:5005:GLY:HA3	2.02	0.41
1:A:359:TYR:HA	1:A:376:ALA:HA	2.03	0.41
1:A:686:TRP:HD1	1:A:757:PHE:HZ	1.68	0.41
1:A:1290:ARG:HH21	1:A:1549:PHE:HE2	1.67	0.41
1:A:1295:VAL:O	1:A:1547:LYS:HA	2.20	0.41
1:A:1586:ASN:N	1:A:1587:PRO:HD2	2.35	0.41
1:A:2882:TYR:HD2	1:A:2919:ASP:HB3	1.85	0.41
1:A:4857:ASN:HD21	1:C:4807:PHE:HD2	1.64	0.41
1:C:111:HIS:CD2	1:C:113:HIS:H	2.38	0.41
1:C:3965:LEU:HA	1:C:3968:TYR:CD2	2.55	0.41
1:C:4020:GLN:O	1:C:4024:VAL:HG22	2.20	0.41
2:D:56:ILE:HB	2:D:80:TYR:O	2.20	0.41
1:E:1104:TRP:CD1	1:E:1153:ILE:HB	2.56	0.41
1:E:1293:LEU:HB3	1:E:1584:ARG:HG2	2.03	0.41
1:E:1685:LEU:HD23	1:E:1685:LEU:HA	1.92	0.41
1:E:2161:GLN:NE2	1:E:2177:LEU:HB3	2.35	0.41
1:E:2281:ILE:HG12	1:E:2337:PHE:CD1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:2882:TYR:HD2	1:E:2919:ASP:HB3	1.85	0.41
1:G:685:GLY:HA3	1:G:713:SER:HA	2.02	0.41
1:G:1812:LEU:HD21	1:G:1861:GLN:HG2	2.01	0.41
1:G:2203:MET:O	1:G:2207:VAL:HG23	2.20	0.41
1:A:596:ASN:HB2	1:A:599:VAL:HG23	2.02	0.41
1:A:3969:ILE:O	1:A:3969:ILE:HG22	2.20	0.41
1:A:4020:GLN:O	1:A:4024:VAL:HG22	2.21	0.41
1:A:4695:ASP:OD1	1:A:4696:ASP:N	2.54	0.41
1:C:4090:LYS:N	1:C:4121:GLU:O	2.54	0.41
1:C:4695:ASP:OD1	1:C:4696:ASP:N	2.54	0.41
1:E:76:ARG:NE	1:G:3844:LEU:HD23	2.36	0.41
1:E:121:LEU:HD11	1:E:136:GLY:HA3	2.03	0.41
1:E:274:LEU:HD12	1:E:278:GLN:NE2	2.36	0.41
1:E:682:LEU:O	1:E:684:VAL:HG23	2.21	0.41
1:E:4927:ILE:HG22	1:E:4928:LEU:HD12	2.03	0.41
1:G:111:HIS:CD2	1:G:113:HIS:H	2.38	0.41
1:G:596:ASN:HB2	1:G:599:VAL:HG23	2.03	0.41
1:G:614:VAL:HG13	1:G:617:ASN:HB3	2.01	0.41
1:G:1076:ARG:HH22	1:G:1609:PRO:CB	2.33	0.41
1:G:1649:ASP:OD1	1:G:1649:ASP:N	2.53	0.41
1:G:3717:ASP:N	1:G:3717:ASP:OD1	2.52	0.41
1:G:4685:GLY:O	1:G:4689:THR:N	2.54	0.41
1:A:236:ALA:HA	1:A:242:ARG:NH1	2.36	0.41
1:A:257:ARG:O	1:A:284:HIS:HE1	2.03	0.41
1:A:1089:TYR:HE2	1:A:1214:PHE:HD1	1.68	0.41
1:A:3793:MET:O	1:A:3797:THR:HG23	2.21	0.41
1:A:4090:LYS:N	1:A:4121:GLU:O	2.54	0.41
1:A:4936:ILE:HG21	1:G:4931:ILE:HG12	2.03	0.41
1:C:121:LEU:HD11	1:C:136:GLY:HA3	2.02	0.41
1:C:575:LEU:O	1:C:578:ILE:HG22	2.21	0.41
1:C:596:ASN:HB2	1:C:599:VAL:HG23	2.02	0.41
1:C:682:LEU:O	1:C:684:VAL:HG23	2.21	0.41
1:C:1655:GLU:HG3	1:C:1656:ARG:HG3	2.02	0.41
1:C:4686:LEU:HA	1:C:4690:GLU:HB2	2.03	0.41
1:C:4820:VAL:O	1:C:4824:ARG:HG3	2.21	0.41
1:C:4930:ALA:HB1	1:E:4933:GLN:HA	2.03	0.41
1:E:76:ARG:NE	1:G:3844:LEU:CD2	2.84	0.41
1:E:257:ARG:HB3	1:E:481:GLU:OE2	2.21	0.41
1:E:1736:VAL:HA	1:E:1737:PRO:HD2	1.90	0.41
1:E:2210:VAL:O	1:E:2214:VAL:HG23	2.21	0.41
1:E:3997:ALA:O	1:E:4001:MET:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:4047:MET:O	1:E:4051:SER:N	2.51	0.41
1:E:4056:GLU:OE2	1:E:4166:LEU:HD11	2.20	0.41
1:G:523:TYR:CD1	1:G:560:ILE:HG13	2.56	0.41
1:G:868:GLU:O	1:G:871:ARG:HB2	2.19	0.41
1:G:1124:PHE:HB2	1:G:1162:PHE:CE2	2.55	0.41
1:G:1229:ASN:CG	1:G:1827:ARG:HH11	2.23	0.41
1:G:2761:TYR:CE2	1:G:2862:LEU:HD22	2.55	0.41
1:G:3843:ASP:OD2	1:G:3846:ALA:HB2	2.21	0.41
1:G:5026:ASP:O	1:G:5027:CYS:SG	2.76	0.41
1:A:59:PRO:HB3	1:A:281:ARG:CZ	2.50	0.41
1:A:184:THR:HA	1:A:189:LEU:HD23	2.01	0.41
1:A:685:GLY:HA3	1:A:713:SER:HA	2.03	0.41
1:A:695:TYR:O	1:A:697:GLY:N	2.42	0.41
1:A:697:GLY:HA2	1:A:698:GLY:HA2	1.86	0.41
1:A:1530:THR:HG22	1:A:1535:GLU:HA	2.02	0.41
1:A:2203:MET:O	1:A:2207:VAL:HG23	2.20	0.41
1:A:2239:PHE:O	1:A:2242:ILE:HG12	2.20	0.41
1:A:2735:PHE:CD1	1:A:2907:PRO:HA	2.56	0.41
1:A:3969:ILE:HG23	1:A:3977:GLN:HG2	2.03	0.41
1:A:4056:GLU:OE2	1:A:4166:LEU:HD11	2.20	0.41
1:A:4722:ARG:HA	1:A:4725:LEU:HG	2.03	0.41
1:A:4807:PHE:CD2	1:G:4857:ASN:ND2	2.87	0.41
1:C:225:GLY:HA2	1:C:389:PHE:HE2	1.86	0.41
1:C:281:ARG:HG2	1:C:312:THR:HG23	2.03	0.41
1:C:638:ILE:HG23	1:C:678:GLN:HE22	1.86	0.41
1:C:738:LEU:HA	1:C:742:ASP:OD2	2.21	0.41
1:C:1104:TRP:CD1	1:C:1153:ILE:HB	2.55	0.41
1:C:1252:HIS:CG	1:C:1253:PRO:HD2	2.56	0.41
1:C:1632:ASP:HA	1:C:1633:PRO:HD2	1.77	0.41
1:C:2212:VAL:HG21	1:C:2256:TYR:CE2	2.56	0.41
1:C:2231:SER:HA	1:C:2234:ARG:HH11	1.85	0.41
1:C:2272:PRO:O	1:C:2275:VAL:HB	2.21	0.41
1:C:2774:ASN:OD1	1:C:2852:ARG:NE	2.52	0.41
1:C:3969:ILE:HG23	1:C:3977:GLN:HG2	2.03	0.41
1:C:4028:LEU:HD21	1:C:4146:LEU:HA	2.03	0.41
1:C:4722:ARG:HA	1:C:4725:LEU:HG	2.03	0.41
1:C:4886:HIS:CE1	1:C:4897:ILE:HD12	2.56	0.41
2:D:6:THR:HG23	2:D:70:GLN:HE21	1.85	0.41
1:E:221:ARG:N	1:E:391:THR:O	2.44	0.41
1:E:281:ARG:HG2	1:E:312:THR:HG23	2.03	0.41
1:E:596:ASN:HB2	1:E:599:VAL:HG23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:686:TRP:HD1	1:E:757:PHE:HZ	1.68	0.41
1:E:695:TYR:HA	1:E:696:PRO:HD3	1.84	0.41
1:E:1767:VAL:C	1:E:1768:THR:HG1	2.23	0.41
1:E:1846:SER:O	1:E:1850:VAL:HG23	2.21	0.41
1:E:2231:SER:HA	1:E:2234:ARG:HH11	1.85	0.41
1:E:2561:LEU:HD11	1:E:2601:ASP:HA	2.03	0.41
1:E:3841:VAL:HG12	1:E:3843:ASP:N	2.36	0.41
1:E:4708:THR:HA	1:E:4709:PRO:HD3	1.91	0.41
1:E:4722:ARG:HA	1:E:4725:LEU:HG	2.03	0.41
1:E:5022:PHE:HA	1:E:5023:PRO:HD3	1.72	0.41
1:G:149:THR:HG23	1:G:174:VAL:HG22	2.03	0.41
1:G:225:GLY:HA2	1:G:389:PHE:HE2	1.86	0.41
1:G:236:ALA:HA	1:G:242:ARG:NH1	2.36	0.41
1:G:682:LEU:O	1:G:684:VAL:HG23	2.21	0.41
1:G:1238:PHE:CE2	1:G:1612:PHE:HA	2.55	0.41
1:G:1439:VAL:HG11	1:G:1448:VAL:HG21	2.03	0.41
1:G:2239:PHE:O	1:G:2242:ILE:HG12	2.20	0.41
1:G:3759:GLU:O	1:G:3763:LEU:N	2.48	0.41
1:G:4648:LEU:O	1:G:4652:LEU:N	2.48	0.41
1:G:4667:PRO:O	1:G:4670:ILE:HG22	2.20	0.41
2:H:87:HIS:HD2	2:H:88:PRO:HD2	1.86	0.41
1:A:523:TYR:CD1	1:A:560:ILE:HG13	2.56	0.41
1:A:4184:MET:HG2	1:A:4190:ILE:HG12	2.03	0.41
2:B:49:MET:N	2:B:54:GLU:OE2	2.54	0.41
1:C:479:GLN:OE1	1:C:484:LEU:HD13	2.21	0.41
1:C:2767:ALA:HB3	1:C:2857:PRO:HG3	2.02	0.41
1:C:3666:ASP:O	1:C:3669:PHE:HD1	2.04	0.41
1:C:4037:ASN:HB3	1:C:4042:ARG:NH2	2.34	0.41
1:C:4809:PHE:HA	1:C:4812:HIS:CE1	2.56	0.41
1:E:523:TYR:CD1	1:E:560:ILE:HG13	2.56	0.41
1:E:638:ILE:HG23	1:E:678:GLN:HE22	1.86	0.41
1:E:662:TRP:CZ3	1:E:814:ALA:HB2	2.56	0.41
1:E:738:LEU:HA	1:E:742:ASP:OD2	2.20	0.41
1:E:1632:ASP:HA	1:E:1633:PRO:HD2	1.75	0.41
1:E:3965:LEU:HA	1:E:3968:TYR:CD2	2.56	0.41
1:E:3969:ILE:O	1:E:3969:ILE:HG22	2.20	0.41
1:E:4207:MET:N	1:E:4208:PRO:HD3	2.36	0.41
1:G:453:GLU:HA	1:G:454:PRO:HD3	1.91	0.41
1:G:575:LEU:O	1:G:578:ILE:HG22	2.21	0.41
1:G:2138:LEU:N	1:G:2139:PRO:HD2	2.36	0.41
1:G:2212:VAL:HG21	1:G:2256:TYR:CE2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:4638:TYR:O	1:G:4641:PRO:HD2	2.21	0.41
1:A:1231:GLN:OE1	1:A:1821:ASP:HB2	2.21	0.40
1:A:2210:VAL:O	1:A:2214:VAL:HG23	2.21	0.40
1:A:3969:ILE:HG21	1:A:4030:LEU:HA	2.03	0.40
1:A:4820:VAL:O	1:A:4824:ARG:HG3	2.21	0.40
1:A:4913:ARG:O	1:A:4916:PHE:HB3	2.22	0.40
1:A:4927:ILE:HG22	1:A:4928:LEU:HD12	2.01	0.40
1:C:283:ARG:HB2	1:C:290:TYR:CE2	2.57	0.40
1:C:1293:LEU:HB3	1:C:1584:ARG:HG2	2.04	0.40
1:C:3780:LEU:HD21	1:C:3820:LEU:HG	2.04	0.40
1:C:4927:ILE:HG22	1:C:4928:LEU:HD12	2.03	0.40
1:E:1290:ARG:HH21	1:E:1549:PHE:HE2	1.68	0.40
1:E:1780:PRO:HD3	1:E:1801:ALA:H	1.86	0.40
1:E:1843:LYS:O	1:E:1846:SER:OG	2.25	0.40
1:E:2212:VAL:HG21	1:E:2256:TYR:CE2	2.56	0.40
1:E:3943:ILE:HB	1:E:4009:GLN:NE2	2.36	0.40
1:E:4711:PHE:HB3	1:E:4712:PRO:HD3	2.03	0.40
1:G:257:ARG:HB3	1:G:481:GLU:OE2	2.21	0.40
1:G:1103:GLY:HA3	1:G:1123:VAL:HA	2.04	0.40
1:G:2272:PRO:O	1:G:2275:VAL:HB	2.21	0.40
1:G:2288:LEU:O	1:G:3849:ARG:HD3	2.21	0.40
1:G:4023:MET:O	1:G:4026:MET:HB3	2.21	0.40
1:A:111:HIS:CD2	1:A:113:HIS:H	2.38	0.40
1:A:274:LEU:HD12	1:A:278:GLN:NE2	2.36	0.40
1:A:575:LEU:O	1:A:578:ILE:HG22	2.21	0.40
1:A:1252:HIS:CG	1:A:1253:PRO:HD2	2.56	0.40
1:A:2062:ARG:O	1:A:2065:SER:OG	2.33	0.40
1:A:2103:VAL:HG21	1:A:3676:ASP:OD2	2.21	0.40
1:A:2145:SER:HB3	1:A:3647:HIS:HD2	1.85	0.40
1:A:2745:VAL:HG21	1:A:2818:ALA:HB2	2.02	0.40
1:A:2747:ILE:HG12	1:A:2817:ILE:HD12	2.03	0.40
1:A:3878:ASP:OD1	1:A:3879:GLU:N	2.55	0.40
1:A:4047:MET:O	1:A:4051:SER:N	2.51	0.40
1:A:4551:PHE:O	1:A:4555:LEU:HB2	2.21	0.40
1:A:4686:LEU:HA	1:A:4690:GLU:HB2	2.03	0.40
1:A:4823:LEU:HA	1:A:4826:ILE:HD12	2.03	0.40
1:C:64:ILE:O	1:C:111:HIS:HE1	2.04	0.40
1:C:1238:PHE:CE2	1:C:1612:PHE:HA	2.55	0.40
1:C:1780:PRO:HD3	1:C:1801:ALA:H	1.86	0.40
1:C:2561:LEU:HD11	1:C:2601:ASP:HA	2.03	0.40
1:C:2747:ILE:HG12	1:C:2817:ILE:HD12	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4551:PHE:O	1:C:4555:LEU:HB2	2.21	0.40
1:C:4878:ASP:HB3	1:C:4881:THR:OG1	2.21	0.40
1:E:545:ASP:HA	1:E:582:HIS:CE1	2.56	0.40
1:E:1439:VAL:HG11	1:E:1448:VAL:HG21	2.03	0.40
1:E:2211:MET:HG3	1:E:2229:VAL:HG13	2.03	0.40
1:E:4886:HIS:CE1	1:E:4897:ILE:HD12	2.56	0.40
1:E:4888:TYR:O	1:E:4892:ARG:HD3	2.21	0.40
1:G:471:LEU:HA	1:G:474:ARG:HE	1.85	0.40
1:G:852:VAL:HG22	1:G:853:PRO:HD2	2.02	0.40
1:G:2142:TYR:HD2	1:G:2197:LEU:HD12	1.86	0.40
1:G:3831:SER:O	1:G:3835:LEU:HG	2.21	0.40
1:G:3919:THR:HG21	1:G:3968:TYR:CE2	2.54	0.40
1:A:23:GLN:NE2	1:A:34:LYS:HB3	2.32	0.40
1:A:1293:LEU:HB3	1:A:1584:ARG:HG2	2.03	0.40
1:A:1778:SER:HA	1:A:1779:PRO:HD3	1.89	0.40
1:A:2821:TRP:HH2	1:A:2877:GLN:HB3	1.87	0.40
1:A:3981:ALA:O	1:A:3986:TRP:NE1	2.46	0.40
1:C:149:THR:HG23	1:C:174:VAL:HG22	2.03	0.40
1:C:1160:ILE:O	1:C:1178:ALA:N	2.55	0.40
1:C:1439:VAL:HG11	1:C:1448:VAL:HG21	2.03	0.40
1:C:2239:PHE:O	1:C:2242:ILE:HG12	2.20	0.40
1:C:2281:ILE:HG12	1:C:2337:PHE:CD1	2.56	0.40
1:C:2735:PHE:CD1	1:C:2907:PRO:HA	2.56	0.40
1:C:3817:LEU:HD13	1:C:3899:PHE:HD1	1.86	0.40
1:C:3958:ALA:CB	1:C:4019:LEU:HD11	2.47	0.40
1:C:3969:ILE:HG21	1:C:4030:LEU:HA	2.03	0.40
1:C:4207:MET:N	1:C:4208:PRO:HD3	2.36	0.40
1:C:4809:PHE:O	1:C:4812:HIS:ND1	2.49	0.40
2:D:82:TYR:CE1	2:D:87:HIS:HB2	2.57	0.40
1:E:64:ILE:O	1:E:111:HIS:HE1	2.03	0.40
1:E:575:LEU:O	1:E:578:ILE:HG22	2.21	0.40
1:E:4695:ASP:OD1	1:E:4696:ASP:N	2.54	0.40
1:E:4878:ASP:HB3	1:E:4881:THR:OG1	2.21	0.40
1:G:545:ASP:HA	1:G:582:HIS:CE1	2.57	0.40
1:G:1232:ARG:HE	1:G:1701:ALA:HB3	1.86	0.40
1:G:3706:SER:O	1:G:3710:LEU:HG	2.21	0.40
1:G:4002:LYS:HE2	1:G:4002:LYS:HB3	1.84	0.40
1:G:4150:LEU:O	1:G:4154:VAL:N	2.38	0.40
1:A:121:LEU:HD11	1:A:136:GLY:HA3	2.03	0.40
1:A:225:GLY:HA2	1:A:389:PHE:HE2	1.86	0.40
1:A:284:HIS:CD2	1:A:287:THR:H	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:633:LEU:HD22	1:A:1641:ILE:HG22	2.04	0.40
1:A:2281:ILE:HG12	1:A:2337:PHE:CD1	2.56	0.40
1:A:4711:PHE:HB3	1:A:4712:PRO:HD3	2.04	0.40
1:C:523:TYR:CD1	1:C:560:ILE:HG13	2.56	0.40
1:C:2238:TYR:O	1:C:2242:ILE:HG23	2.22	0.40
1:C:3844:LEU:HD22	1:C:3932:ASP:OD2	2.22	0.40
1:C:3997:ALA:O	1:C:4001:MET:HG2	2.21	0.40
2:D:49:MET:N	2:D:54:GLU:OE2	2.55	0.40
2:D:54:GLU:HG3	2:D:55:VAL:HG13	2.03	0.40
1:E:244:LEU:HD22	1:E:375:LYS:HZ3	1.86	0.40
1:E:283:ARG:HB2	1:E:290:TYR:CE2	2.56	0.40
1:E:453:GLU:HA	1:E:454:PRO:HD3	1.91	0.40
1:E:1076:ARG:HH11	1:E:1109:LEU:HD11	1.86	0.40
1:E:2239:PHE:O	1:E:2242:ILE:HG12	2.20	0.40
1:E:2821:TRP:HH2	1:E:2877:GLN:HB3	1.87	0.40
1:E:3878:ASP:OD1	1:E:3879:GLU:N	2.55	0.40
1:E:3958:ALA:CB	1:E:4019:LEU:HD11	2.48	0.40
1:E:4686:LEU:HA	1:E:4690:GLU:HB2	2.02	0.40
1:E:4829:SER:O	1:E:4939:ALA:HB1	2.21	0.40
1:G:675:LEU:HD23	1:G:676:THR:OG1	2.22	0.40
1:G:1089:TYR:CE2	1:G:1214:PHE:HD1	2.38	0.40
1:G:2099:SER:O	1:G:2103:VAL:HG23	2.20	0.40
1:G:2281:ILE:HG12	1:G:2337:PHE:CD1	2.56	0.40
1:G:4839:MET:O	1:G:4843:LEU:N	2.52	0.40
1:A:281:ARG:HG2	1:A:312:THR:HG23	2.03	0.40
1:A:626:LEU:HB3	1:A:1688:HIS:CE1	2.56	0.40
1:A:1092:PHE:CD2	1:A:1102:VAL:HG21	2.56	0.40
1:A:1238:PHE:CE1	1:A:1612:PHE:HA	2.57	0.40
1:C:943:ASP:HB3	1:C:1050:GLY:HA3	2.03	0.40
1:C:1092:PHE:CD2	1:C:1102:VAL:HG21	2.57	0.40
1:C:1131:ARG:NH1	1:C:1179:PHE:CD1	2.89	0.40
1:C:1612:PHE:O	1:C:1613:LEU:HB2	2.22	0.40
1:C:2211:MET:HG3	1:C:2229:VAL:HG13	2.04	0.40
1:C:4857:ASN:HD21	1:E:4807:PHE:HD2	1.64	0.40
1:E:225:GLY:HA2	1:E:389:PHE:HE2	1.86	0.40
1:E:2735:PHE:CD1	1:E:2907:PRO:HA	2.56	0.40
1:E:2803:GLU:OE2	1:E:2810:LYS:NZ	2.54	0.40
1:E:3793:MET:O	1:E:3797:THR:HG23	2.22	0.40
1:E:3971:GLY:O	1:E:3973:CYS:N	2.51	0.40
1:E:4823:LEU:HA	1:E:4826:ILE:HD12	2.03	0.40
1:G:281:ARG:HG2	1:G:312:THR:HG23	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:626:LEU:HB3	1:G:1688:HIS:CE1	2.56	0.40
1:G:1293:LEU:HB3	1:G:1584:ARG:HG2	2.03	0.40
1:G:1674:CYS:SG	1:G:1685:LEU:HD12	2.62	0.40
1:G:2062:ARG:O	1:G:2065:SER:OG	2.30	0.40
1:G:4574:ASN:HA	1:G:4577:LEU:HD13	2.03	0.40
1:G:4705:VAL:O	1:G:4708:THR:OG1	2.29	0.40
1:G:4779:LYS:O	1:G:4783:ILE:HG12	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	3496/5037 (69%)	3185 (91%)	227 (6%)	84 (2%)	6	36
1	C	3496/5037 (69%)	3185 (91%)	228 (6%)	83 (2%)	6	36
1	E	3496/5037 (69%)	3187 (91%)	226 (6%)	83 (2%)	6	36
1	G	3496/5037 (69%)	3192 (91%)	217 (6%)	87 (2%)	5	35
2	B	105/108 (97%)	96 (91%)	9 (9%)	0	100	100
2	D	105/108 (97%)	96 (91%)	9 (9%)	0	100	100
2	F	105/108 (97%)	96 (91%)	9 (9%)	0	100	100
2	H	105/108 (97%)	93 (89%)	12 (11%)	0	100	100
All	All	14404/20580 (70%)	13130 (91%)	937 (6%)	337 (2%)	9	37

All (337) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	701	GLY
1	A	915	GLU
1	A	916	PRO

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Mol	Chain	Res	Type
1	A	969	PRO
1	A	1589	PRO
1	A	2341	VAL
1	A	2466	LEU
1	A	3826	VAL
1	A	4084	PRO
1	A	4115	SER
1	A	4984	ASN
1	A	4985	LEU
1	C	701	GLY
1	C	808	TYR
1	C	915	GLU
1	C	916	PRO
1	C	969	PRO
1	C	1589	PRO
1	C	2341	VAL
1	C	2466	LEU
1	C	3826	VAL
1	C	4084	PRO
1	C	4115	SER
1	C	4984	ASN
1	C	4985	LEU
1	E	701	GLY
1	E	915	GLU
1	E	916	PRO
1	E	969	PRO
1	E	2341	VAL
1	E	2466	LEU
1	E	3826	VAL
1	E	4084	PRO
1	E	4115	SER
1	E	4984	ASN
1	E	4985	LEU
1	G	701	GLY
1	G	808	TYR
1	G	915	GLU
1	G	916	PRO
1	G	969	PRO
1	G	1589	PRO
1	G	2341	VAL
1	G	2466	LEU
1	G	3664	THR

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Mol	Chain	Res	Type
1	G	3826	VAL
1	G	4084	PRO
1	G	4115	SER
1	G	4984	ASN
1	G	4985	LEU
1	A	208	CYS
1	A	329	ARG
1	A	385	ASP
1	A	510	GLU
1	A	557	SER
1	A	609	CYS
1	A	808	TYR
1	A	865	PRO
1	A	1480	GLN
1	A	1768	THR
1	A	2281	ILE
1	A	2359	ARG
1	A	2465	ASP
1	A	3714	SER
1	A	3806	ASN
1	A	3941	ASP
1	A	4206	GLU
1	C	208	CYS
1	C	329	ARG
1	C	385	ASP
1	C	510	GLU
1	C	557	SER
1	C	609	CYS
1	C	865	PRO
1	C	1480	GLN
1	C	1768	THR
1	C	2281	ILE
1	C	2359	ARG
1	C	2465	ASP
1	C	3714	SER
1	C	3806	ASN
1	C	3941	ASP
1	C	4206	GLU
1	E	208	CYS
1	E	329	ARG
1	E	385	ASP
1	E	510	GLU

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Mol	Chain	Res	Type
1	E	557	SER
1	E	609	CYS
1	E	808	TYR
1	E	865	PRO
1	E	1480	GLN
1	E	1768	THR
1	E	2281	ILE
1	E	2359	ARG
1	E	2465	ASP
1	E	3714	SER
1	E	3806	ASN
1	E	3941	ASP
1	E	4206	GLU
1	G	208	CYS
1	G	329	ARG
1	G	385	ASP
1	G	510	GLU
1	G	557	SER
1	G	609	CYS
1	G	865	PRO
1	G	1480	GLN
1	G	1768	THR
1	G	2281	ILE
1	G	2359	ARG
1	G	2465	ASP
1	G	3714	SER
1	G	3806	ASN
1	G	3843	ASP
1	G	3941	ASP
1	G	4031	LEU
1	G	4036	VAL
1	A	692	TYR
1	A	698	GLY
1	A	720	HIS
1	A	770	ALA
1	A	817	PRO
1	A	827	LYS
1	A	1034	SER
1	A	1483	VAL
1	A	1545	ASN
1	A	1599	MET
1	A	1717	SER

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Mol	Chain	Res	Type
1	A	1747	LEU
1	A	1818	ALA
1	A	1854	PHE
1	A	2826	ALA
1	A	4036	VAL
1	A	4186	ALA
1	C	30	LYS
1	C	692	TYR
1	C	698	GLY
1	C	720	HIS
1	C	770	ALA
1	C	817	PRO
1	C	827	LYS
1	C	1034	SER
1	C	1483	VAL
1	C	1545	ASN
1	C	1599	MET
1	C	1717	SER
1	C	1747	LEU
1	C	1818	ALA
1	C	1854	PHE
1	C	2826	ALA
1	C	4036	VAL
1	C	4186	ALA
1	E	30	LYS
1	E	692	TYR
1	E	698	GLY
1	E	720	HIS
1	E	770	ALA
1	E	817	PRO
1	E	827	LYS
1	E	1034	SER
1	E	1483	VAL
1	E	1545	ASN
1	E	1599	MET
1	E	1717	SER
1	E	1747	LEU
1	E	1818	ALA
1	E	1854	PHE
1	E	2826	ALA
1	E	4186	ALA
1	G	692	TYR

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Mol	Chain	Res	Type
1	G	698	GLY
1	G	720	HIS
1	G	770	ALA
1	G	817	PRO
1	G	827	LYS
1	G	1034	SER
1	G	1483	VAL
1	G	1545	ASN
1	G	1599	MET
1	G	1717	SER
1	G	1747	LEU
1	G	1818	ALA
1	G	1854	PHE
1	G	4186	ALA
1	G	4691	GLN
1	G	5025	GLY
1	A	29	LEU
1	A	30	LYS
1	A	309	THR
1	A	676	THR
1	A	826	ILE
1	A	1134	LEU
1	A	1186	ASP
1	A	1206	GLN
1	A	1541	GLN
1	A	4032	GLU
1	A	4052	SER
1	A	4119	GLU
1	A	4691	GLN
1	A	4869	GLU
1	C	29	LEU
1	C	676	THR
1	C	826	ILE
1	C	1134	LEU
1	C	1186	ASP
1	C	1206	GLN
1	C	1541	GLN
1	C	1614	GLN
1	C	4032	GLU
1	C	4052	SER
1	C	4119	GLU
1	C	4691	GLN

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Mol	Chain	Res	Type
1	C	4869	GLU
1	E	29	LEU
1	E	676	THR
1	E	826	ILE
1	E	1134	LEU
1	E	1186	ASP
1	E	1206	GLN
1	E	1541	GLN
1	E	4032	GLU
1	E	4036	VAL
1	E	4052	SER
1	E	4119	GLU
1	E	4691	GLN
1	E	4869	GLU
1	E	5025	GLY
1	G	29	LEU
1	G	30	LYS
1	G	676	THR
1	G	826	ILE
1	G	1134	LEU
1	G	1186	ASP
1	G	1206	GLN
1	G	1541	GLN
1	G	2826	ALA
1	G	4119	GLU
1	G	4206	GLU
1	G	4869	GLU
1	G	5027	CYS
1	A	252	VAL
1	A	422	SER
1	A	751	SER
1	A	1017	ARG
1	A	1126	GLY
1	A	1614	GLN
1	A	1772	ARG
1	A	2191	PHE
1	A	3664	THR
1	A	4208	PRO
1	A	5025	GLY
1	A	5027	CYS
1	C	252	VAL
1	C	309	THR

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Mol	Chain	Res	Type
1	C	422	SER
1	C	751	SER
1	C	1017	ARG
1	C	1772	ARG
1	C	2191	PHE
1	C	3664	THR
1	C	4208	PRO
1	C	5025	GLY
1	C	5027	CYS
1	E	252	VAL
1	E	309	THR
1	E	422	SER
1	E	751	SER
1	E	1017	ARG
1	E	1126	GLY
1	E	1772	ARG
1	E	2191	PHE
1	E	3664	THR
1	E	4208	PRO
1	E	5027	CYS
1	G	252	VAL
1	G	309	THR
1	G	422	SER
1	G	751	SER
1	G	1017	ARG
1	G	1772	ARG
1	G	2191	PHE
1	G	3668	SER
1	G	4040	ILE
1	G	4208	PRO
1	G	4821	LYS
1	A	611	GLY
1	A	740	PRO
1	A	4712	PRO
1	A	4734	ARG
1	A	4872	PRO
1	C	611	GLY
1	C	740	PRO
1	C	1126	GLY
1	C	4712	PRO
1	C	4872	PRO
1	E	611	GLY

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Mol	Chain	Res	Type
1	E	740	PRO
1	E	4712	PRO
1	E	4734	ARG
1	E	4872	PRO
1	G	611	GLY
1	G	740	PRO
1	G	1126	GLY
1	G	4872	PRO
1	G	4963	ILE
1	A	781	VAL
1	A	1830	VAL
1	A	4040	ILE
1	A	4963	ILE
1	C	781	VAL
1	C	1830	VAL
1	C	4040	ILE
1	C	4963	ILE
1	E	781	VAL
1	E	1830	VAL
1	E	4040	ILE
1	E	4963	ILE
1	G	781	VAL
1	G	1830	VAL
1	G	3085	PRO
1	G	4712	PRO
1	C	842	PRO
1	G	842	PRO
1	G	2044	ILE
1	A	842	PRO
1	A	1544	PRO
1	E	842	PRO
1	E	1544	PRO
1	E	1589	PRO
1	G	4895	GLY
1	C	1544	PRO
1	G	1544	PRO
1	A	1253	PRO
1	C	1253	PRO
1	E	1253	PRO
1	G	1253	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	2503/4276 (58%)	2493 (100%)	10 (0%)	91	94
1	C	2502/4276 (58%)	2492 (100%)	10 (0%)	91	94
1	E	2500/4276 (58%)	2491 (100%)	9 (0%)	91	94
1	G	2501/4276 (58%)	2489 (100%)	12 (0%)	88	93
2	B	89/90 (99%)	88 (99%)	1 (1%)	73	85
2	D	89/90 (99%)	88 (99%)	1 (1%)	73	85
2	F	89/90 (99%)	88 (99%)	1 (1%)	73	85
2	H	89/90 (99%)	89 (100%)	0	100	100
All	All	10362/17464 (59%)	10318 (100%)	44 (0%)	91	94

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	806	PRO
1	A	865	PRO
1	A	914	PRO
1	A	916	PRO
1	A	979	PRO
1	A	1001	VAL
1	A	1055	PRO
1	A	4844	LEU
1	A	4850	LEU
1	A	4972	PRO
2	B	34	LYS
1	C	806	PRO
1	C	865	PRO
1	C	914	PRO
1	C	916	PRO
1	C	979	PRO
1	C	1001	VAL
1	C	1055	PRO
1	C	4844	LEU

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Mol	Chain	Res	Type
1	C	4850	LEU
1	C	4972	PRO
2	D	34	LYS
1	E	806	PRO
1	E	865	PRO
1	E	914	PRO
1	E	916	PRO
1	E	979	PRO
1	E	1001	VAL
1	E	1055	PRO
1	E	4850	LEU
1	E	4972	PRO
2	F	34	LYS
1	G	806	PRO
1	G	865	PRO
1	G	914	PRO
1	G	916	PRO
1	G	979	PRO
1	G	1001	VAL
1	G	1055	PRO
1	G	1455	PRO
1	G	4106	PRO
1	G	4166	LEU
1	G	4850	LEU
1	G	4972	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (208) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	ASN
1	A	105	HIS
1	A	111	HIS
1	A	113	HIS
1	A	138	GLN
1	A	218	HIS
1	A	278	GLN
1	A	379	HIS
1	A	405	HIS
1	A	460	GLN
1	A	465	GLN
1	A	582	HIS
1	A	596	ASN

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Mol	Chain	Res	Type
1	A	610	ASN
1	A	618	GLN
1	A	678	GLN
1	A	765	GLN
1	A	772	ASN
1	A	838	HIS
1	A	1125	ASN
1	A	1201	HIS
1	A	1254	HIS
1	A	1631	GLN
1	A	1663	HIS
1	A	1665	HIS
1	A	1678	ASN
1	A	2107	GLN
1	A	2127	GLN
1	A	2161	GLN
1	A	2184	ASN
1	A	2194	HIS
1	A	2260	ASN
1	A	2420	HIS
1	A	2744	ASN
1	A	3647	HIS
1	A	3651	ASN
1	A	3781	GLN
1	A	3895	HIS
1	A	3906	GLN
1	A	3960	GLN
1	A	3970	GLN
1	A	3998	HIS
1	A	4009	GLN
1	A	4162	ASN
1	A	4223	ASN
1	A	4691	GLN
1	A	4803	HIS
1	A	4836	GLN
1	A	4857	ASN
1	A	4886	HIS
1	A	4987	ASN
1	A	5003	HIS
2	B	25	HIS
2	B	87	HIS
1	C	57	ASN

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Mol	Chain	Res	Type
1	C	105	HIS
1	C	111	HIS
1	C	113	HIS
1	C	138	GLN
1	C	218	HIS
1	C	278	GLN
1	C	379	HIS
1	C	405	HIS
1	C	460	GLN
1	C	465	GLN
1	C	582	HIS
1	C	596	ASN
1	C	678	GLN
1	C	765	GLN
1	C	772	ASN
1	C	838	HIS
1	C	1201	HIS
1	C	1254	HIS
1	C	1631	GLN
1	C	1663	HIS
1	C	1665	HIS
1	C	2107	GLN
1	C	2127	GLN
1	C	2161	GLN
1	C	2184	ASN
1	C	2194	HIS
1	C	2260	ASN
1	C	2420	HIS
1	C	2744	ASN
1	C	3647	HIS
1	C	3651	ASN
1	C	3781	GLN
1	C	3895	HIS
1	C	3906	GLN
1	C	3960	GLN
1	C	3970	GLN
1	C	3998	HIS
1	C	4009	GLN
1	C	4162	ASN
1	C	4223	ASN
1	C	4691	GLN
1	C	4803	HIS

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Mol	Chain	Res	Type
1	C	4836	GLN
1	C	4857	ASN
1	C	4886	HIS
1	C	4987	ASN
1	C	5003	HIS
2	D	25	HIS
2	D	87	HIS
1	E	57	ASN
1	E	105	HIS
1	E	111	HIS
1	E	113	HIS
1	E	138	GLN
1	E	218	HIS
1	E	278	GLN
1	E	379	HIS
1	E	405	HIS
1	E	460	GLN
1	E	465	GLN
1	E	582	HIS
1	E	596	ASN
1	E	618	GLN
1	E	678	GLN
1	E	765	GLN
1	E	772	ASN
1	E	838	HIS
1	E	1125	ASN
1	E	1201	HIS
1	E	1254	HIS
1	E	1280	GLN
1	E	1559	GLN
1	E	1631	GLN
1	E	1663	HIS
1	E	1665	HIS
1	E	1678	ASN
1	E	2107	GLN
1	E	2127	GLN
1	E	2161	GLN
1	E	2184	ASN
1	E	2194	HIS
1	E	2260	ASN
1	E	2420	HIS
1	E	2744	ASN

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Mol	Chain	Res	Type
1	E	3647	HIS
1	E	3651	ASN
1	E	3781	GLN
1	E	3895	HIS
1	E	3906	GLN
1	E	3960	GLN
1	E	3970	GLN
1	E	3998	HIS
1	E	4009	GLN
1	E	4162	ASN
1	E	4691	GLN
1	E	4803	HIS
1	E	4836	GLN
1	E	4857	ASN
1	E	4886	HIS
1	E	4987	ASN
1	E	5003	HIS
2	F	25	HIS
2	F	87	HIS
1	G	57	ASN
1	G	105	HIS
1	G	111	HIS
1	G	113	HIS
1	G	138	GLN
1	G	218	HIS
1	G	278	GLN
1	G	379	HIS
1	G	405	HIS
1	G	460	GLN
1	G	465	GLN
1	G	582	HIS
1	G	596	ASN
1	G	610	ASN
1	G	678	GLN
1	G	765	GLN
1	G	772	ASN
1	G	838	HIS
1	G	1201	HIS
1	G	1254	HIS
1	G	1631	GLN
1	G	1663	HIS
1	G	2107	GLN

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Mol	Chain	Res	Type
1	G	2127	GLN
1	G	2161	GLN
1	G	2184	ASN
1	G	2194	HIS
1	G	2260	ASN
1	G	2420	HIS
1	G	2744	ASN
1	G	3651	ASN
1	G	3781	GLN
1	G	3895	HIS
1	G	3896	ASN
1	G	3906	GLN
1	G	3960	GLN
1	G	3998	HIS
1	G	4009	GLN
1	G	4020	GLN
1	G	4153	HIS
1	G	4162	ASN
1	G	4223	ASN
1	G	4650	HIS
1	G	4691	GLN
1	G	4836	GLN
1	G	4857	ASN
1	G	4886	HIS
1	G	4987	ASN
2	H	25	HIS
2	H	87	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

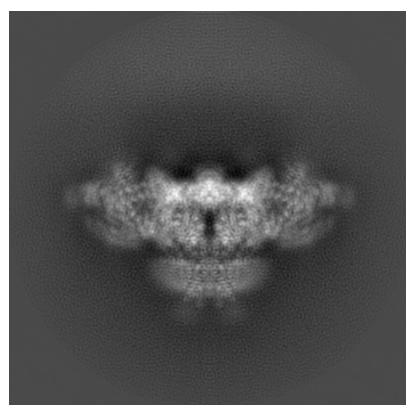
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9519. These allow visual inspection of the internal detail of the map and identification of artifacts.

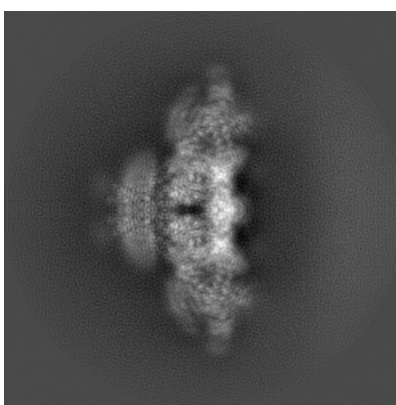
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

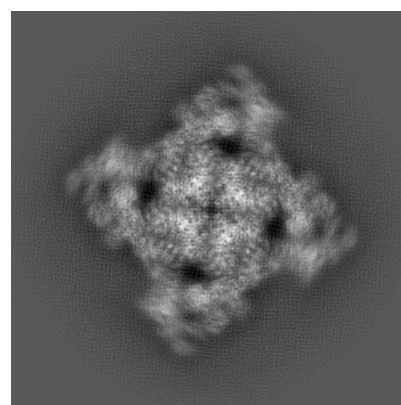
6.1.1 Primary map



X



Y

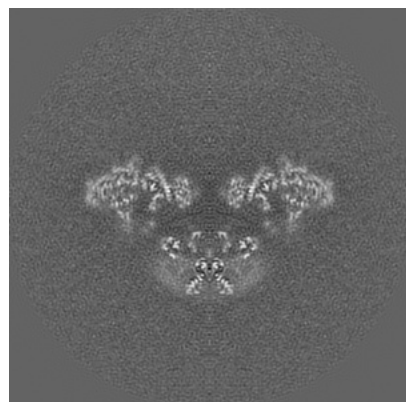


Z

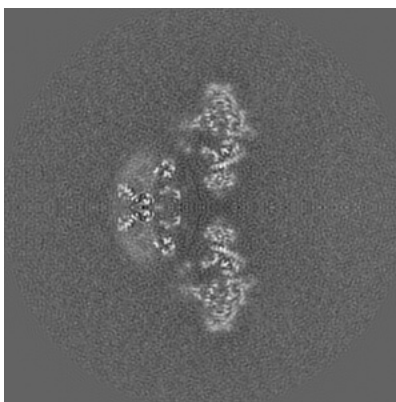
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

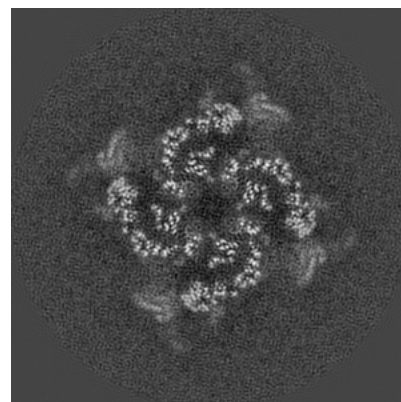
6.2.1 Primary map



X Index: 180



Y Index: 180

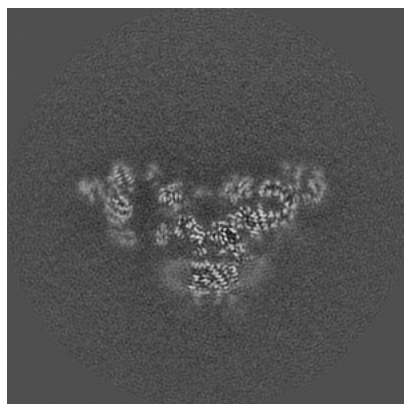


Z Index: 180

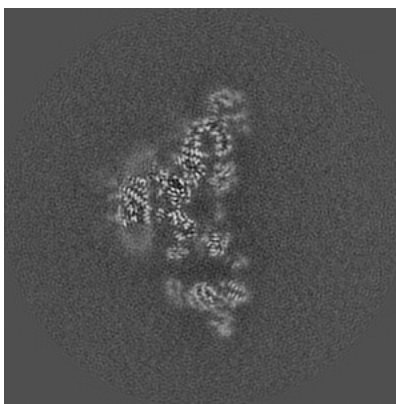
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

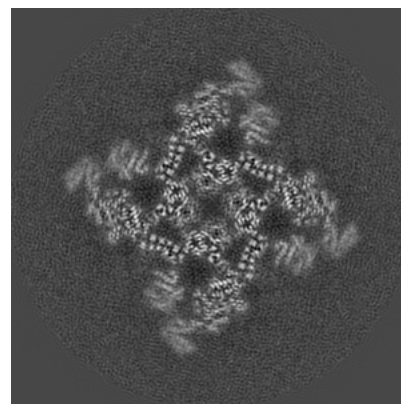
6.3.1 Primary map



X Index: 169



Y Index: 191

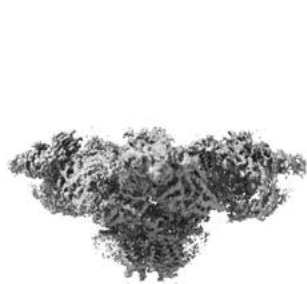


Z Index: 190

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

6.4 Orthogonal surface views [i](#)

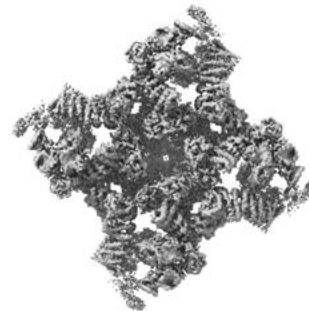
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.085. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

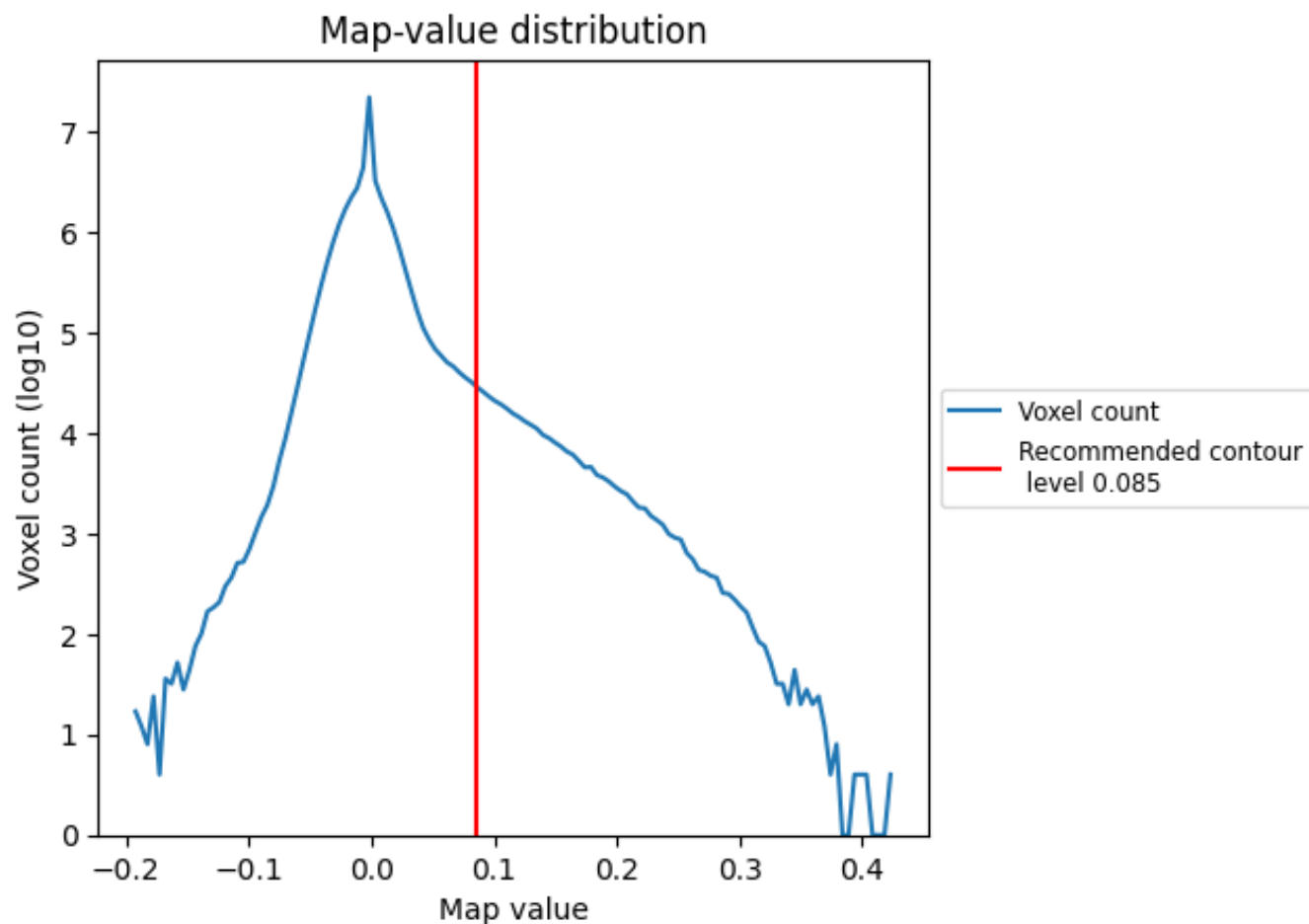
6.5 Mask visualisation

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

7 Map analysis [i](#)

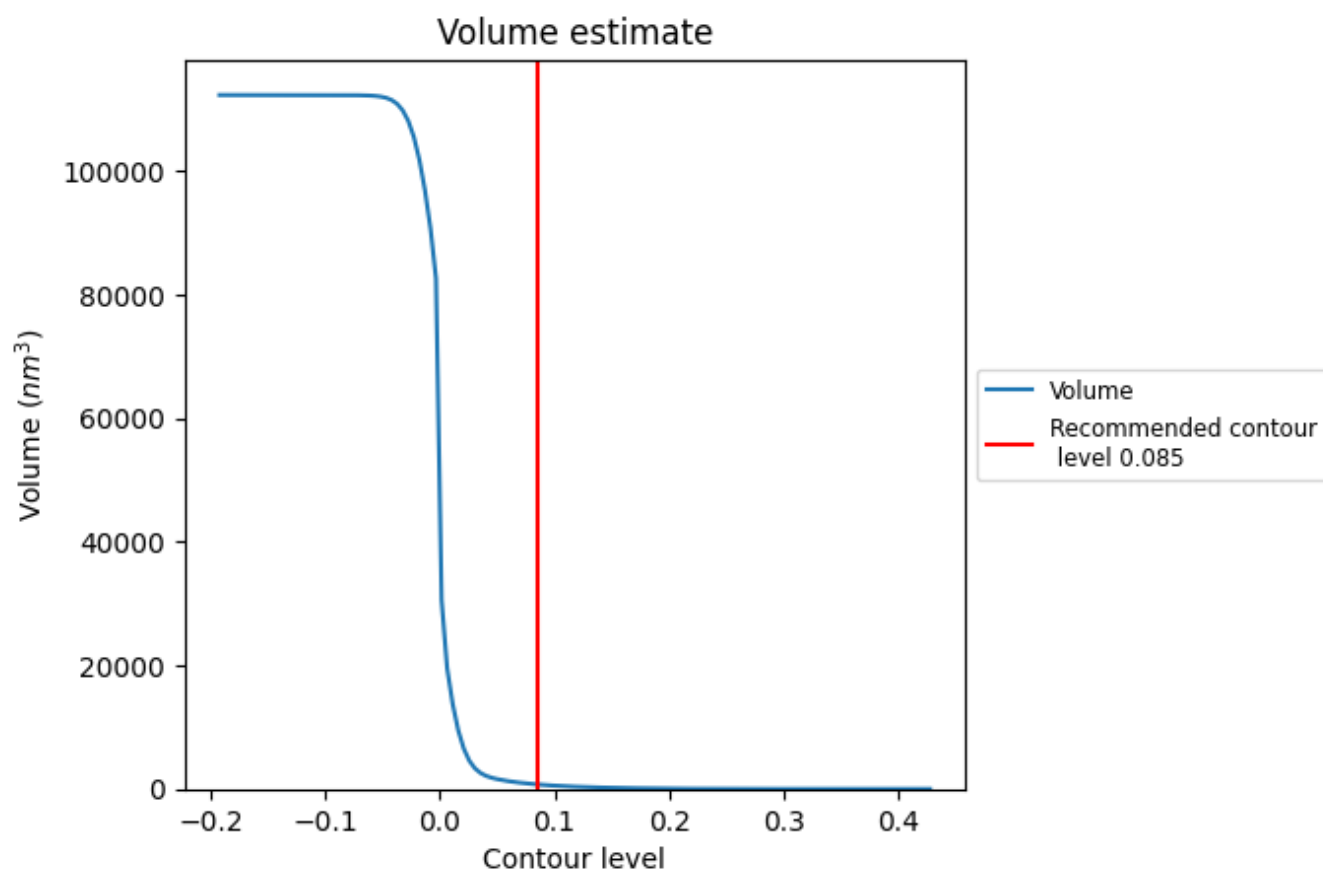
This section contains the results of statistical analysis of the map.

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.

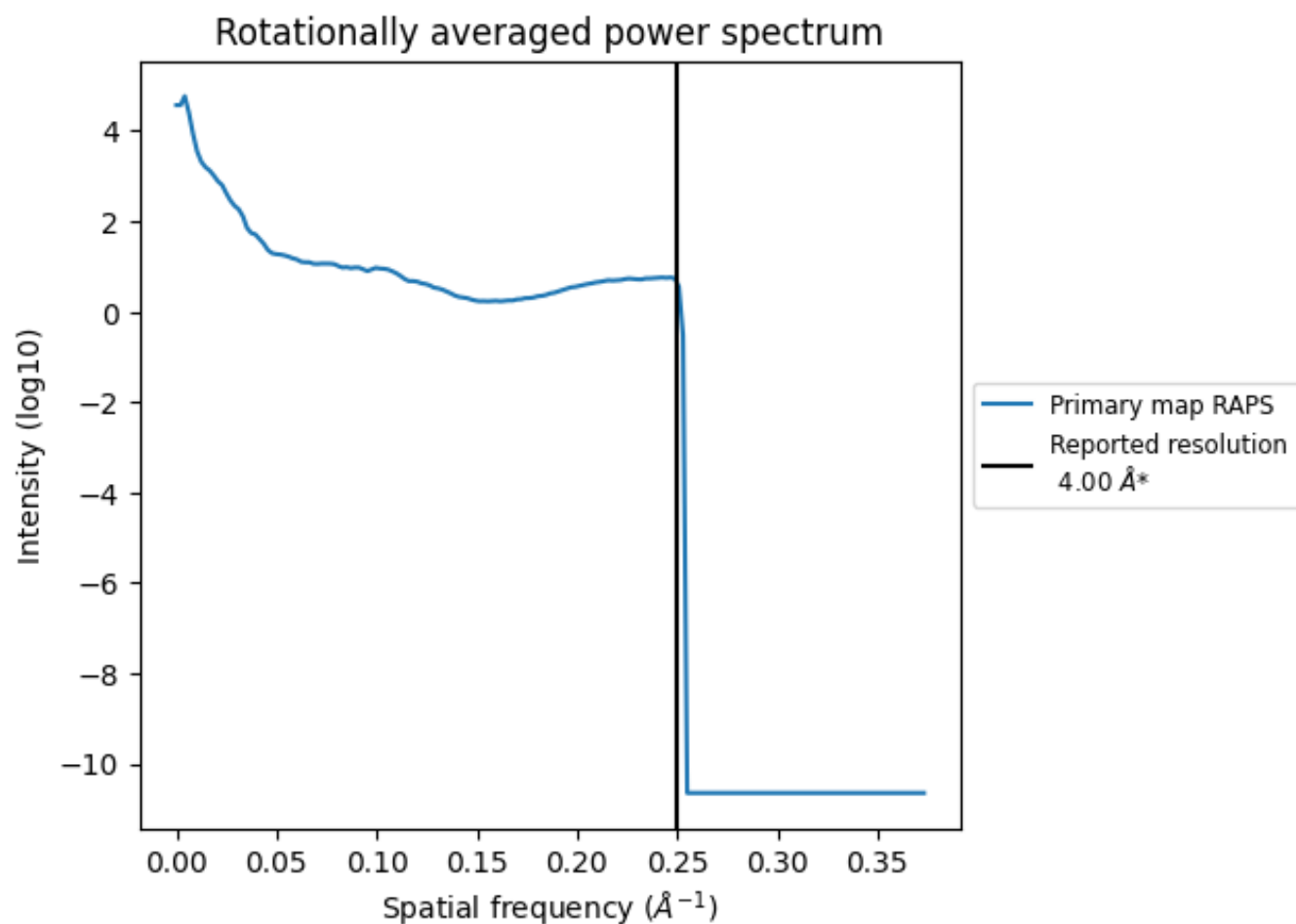
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 734 nm^3 ; this corresponds to an approximate mass of 663 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 0.250 \AA^{-1}

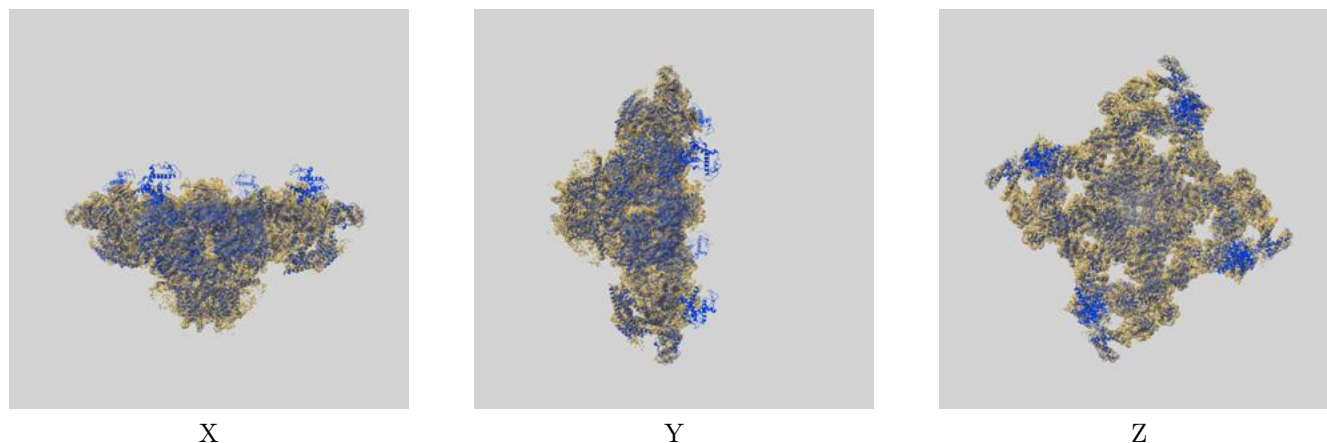
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

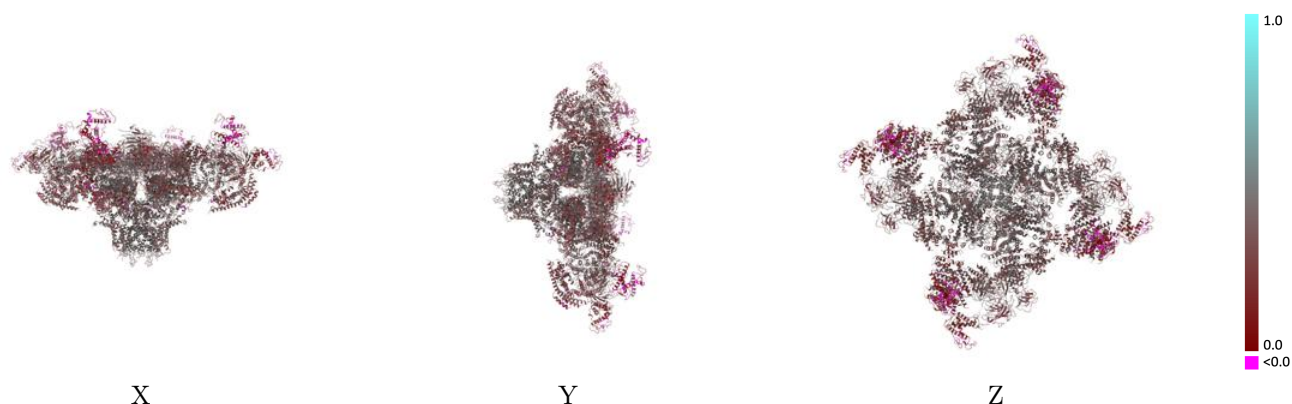
This section contains information regarding the fit between EMDB map EMD-9519 and PDB model 5GKZ. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



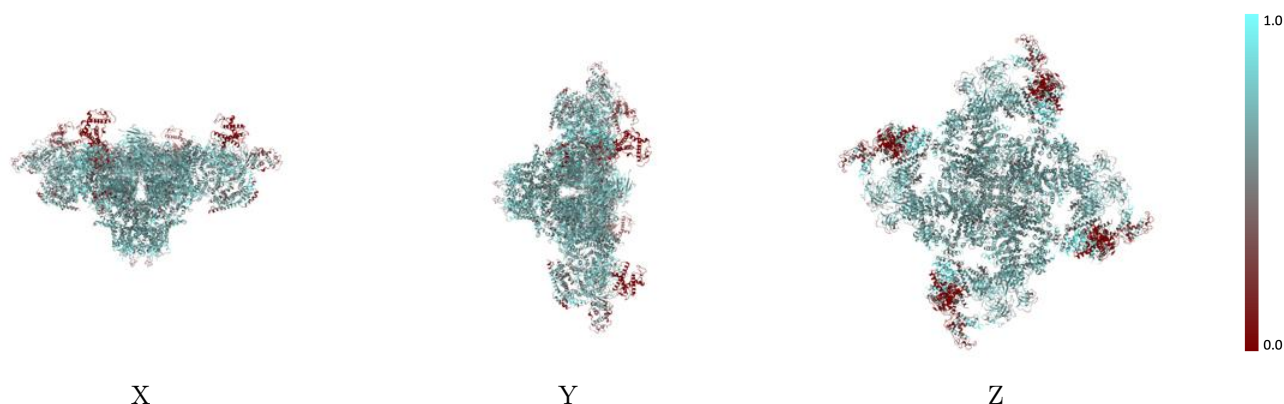
The images above show the 3D surface view of the map at the recommended contour level 0.085 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



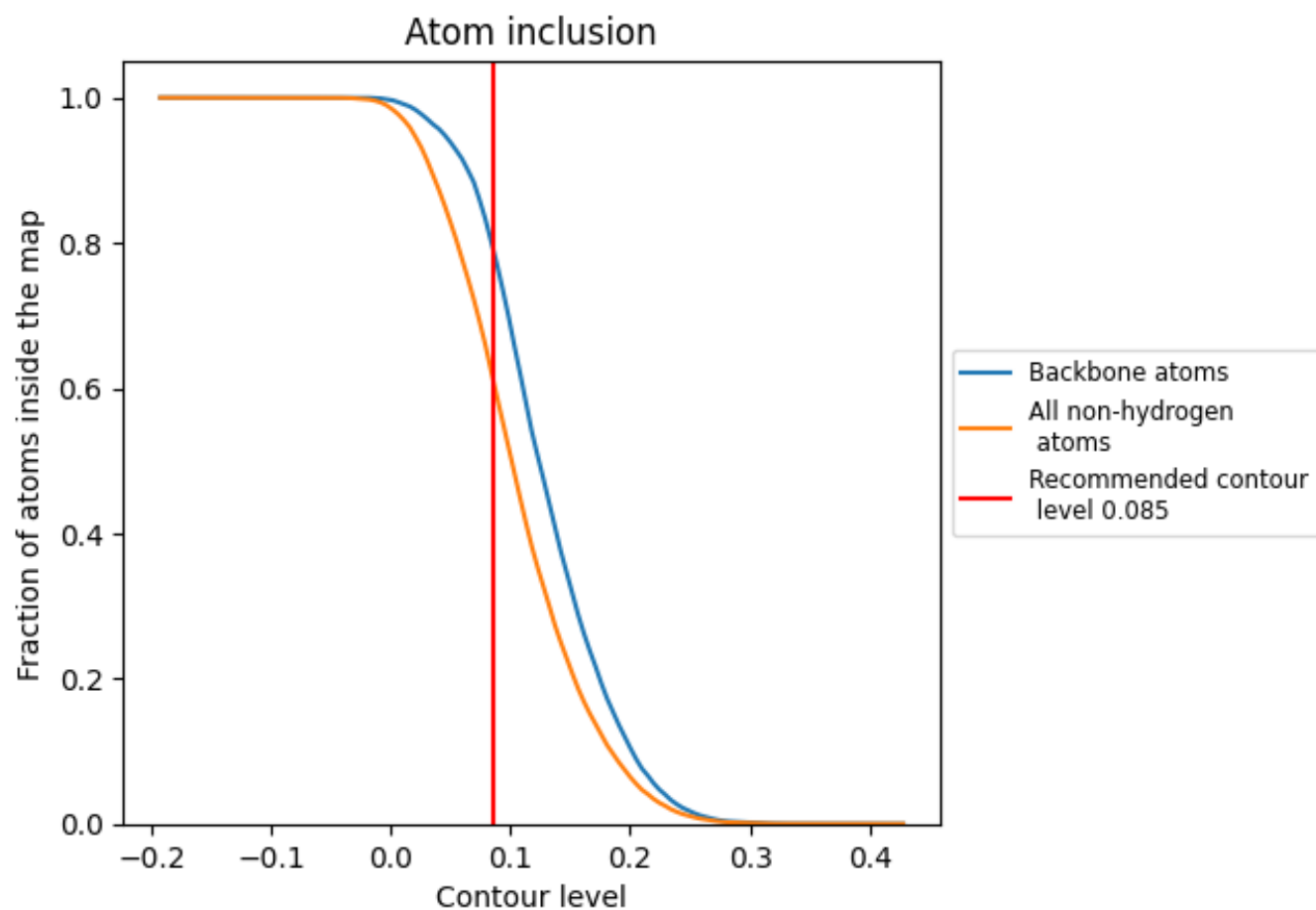
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.085).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 62% 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 (0.085) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.6153	<div><div></div></div> 0.3370
A	<div><div></div></div> 0.6164	<div><div></div></div> 0.3370
B	<div><div></div></div> 0.5723	<div><div></div></div> 0.3390
C	<div><div></div></div> 0.6168	<div><div></div></div> 0.3360
D	<div><div></div></div> 0.5699	<div><div></div></div> 0.3370
E	<div><div></div></div> 0.6165	<div><div></div></div> 0.3360
F	<div><div></div></div> 0.5699	<div><div></div></div> 0.3360
G	<div><div></div></div> 0.6168	<div><div></div></div> 0.3400
H	<div><div></div></div> 0.5711	<div><div></div></div> 0.3380

1.0

0.0

<0.0