



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 09:40 PM UTC

PDB ID : 7JMH / pdb_00007jmh
EMDB ID : EMD-22394
Title : Functional Pathways of Biomolecules Retrieved from Single-particle Snapshots
- Frame 35 - State 4 (S4)
Authors : Dashti, A.; des Georges, A.; Frank, J.; Ourmazd, A.
Deposited on : 2020-07-31
Resolution : 4.50 Å(reported)
Based on initial model : 5TB4

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

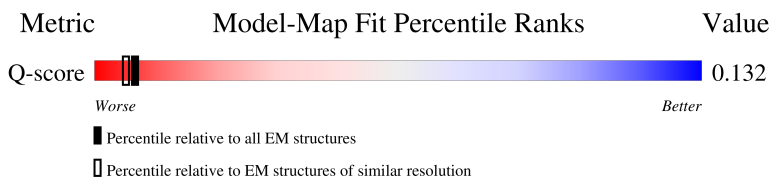
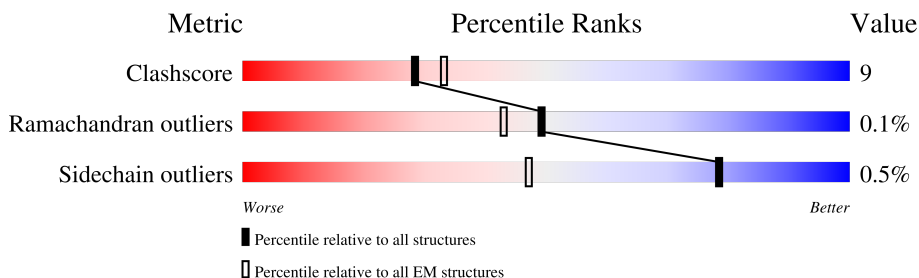
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2937 (4.00 - 5.00)

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	107	30% 68% 31% .
1	F	107	44% 67% 33%
1	H	107	46% 69% 31%
1	J	107	43% 66% 34%

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Mol	Chain	Length	Quality of chain
2	B	4687	34%70%18%11%
2	E	4687	38%70%18%11%
2	G	4687	44%70%19%11%
2	I	4687	43%71%18%11%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 120756 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 Peptidyl-prolyl cis-trans isomerase FKBP1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	F	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	H	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	J	107	Total	C	N	O	S	0	0
			818	516	144	154	4		

- Molecule 2 is a protein called ryanodine receptor type 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	4168	Total	C	N	O	S	0	0
			29369	18608	5202	5402	157		
2	E	4168	Total	C	N	O	S	0	0
			29369	18608	5202	5402	157		
2	G	4168	Total	C	N	O	S	0	0
			29369	18608	5202	5402	157		
2	I	4168	Total	C	N	O	S	0	0
			29369	18608	5202	5402	157		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	B	1	Total	Zn	0
			1	1	
3	E	1	Total	Zn	0
			1	1	
3	G	1	Total	Zn	0
			1	1	
3	I	1	Total	Zn	0
			1	1	

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest")

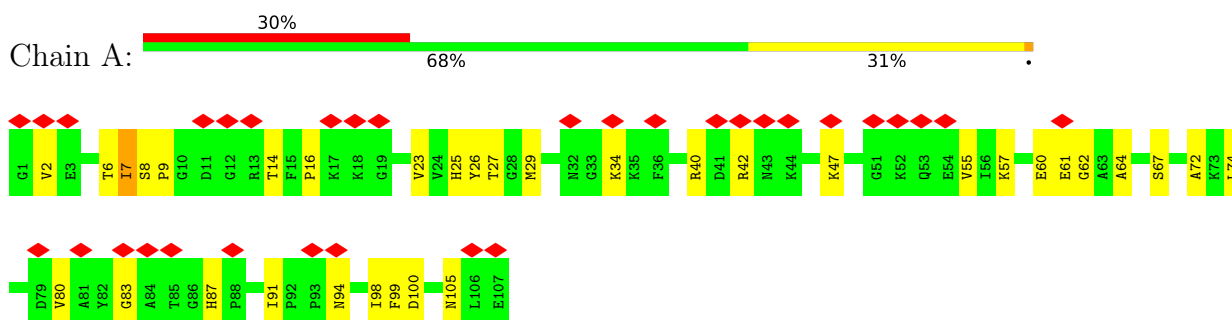
by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	B	1	Total 1	Ca 1	0
4	E	1	Total 1	Ca 1	0
4	G	1	Total 1	Ca 1	0
4	I	1	Total 1	Ca 1	0

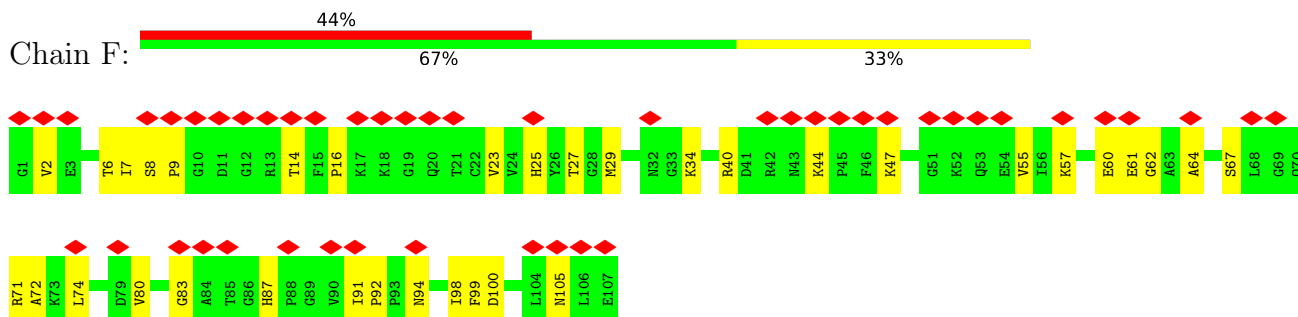
3 Residue-property plots [i](#)

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.

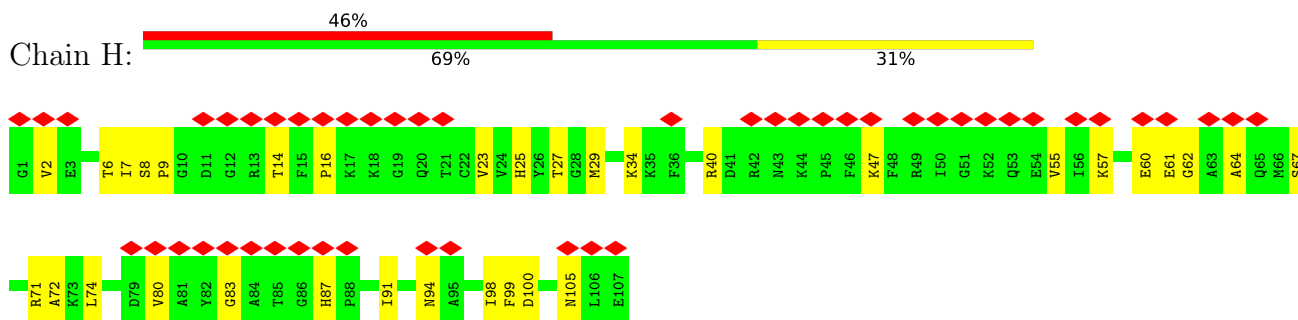
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



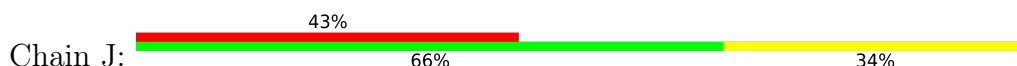
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

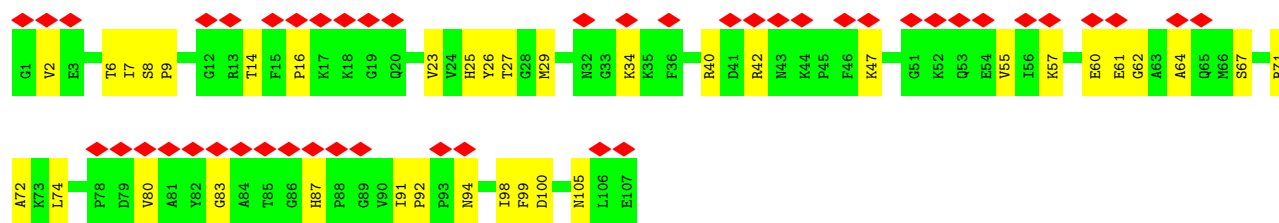


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B





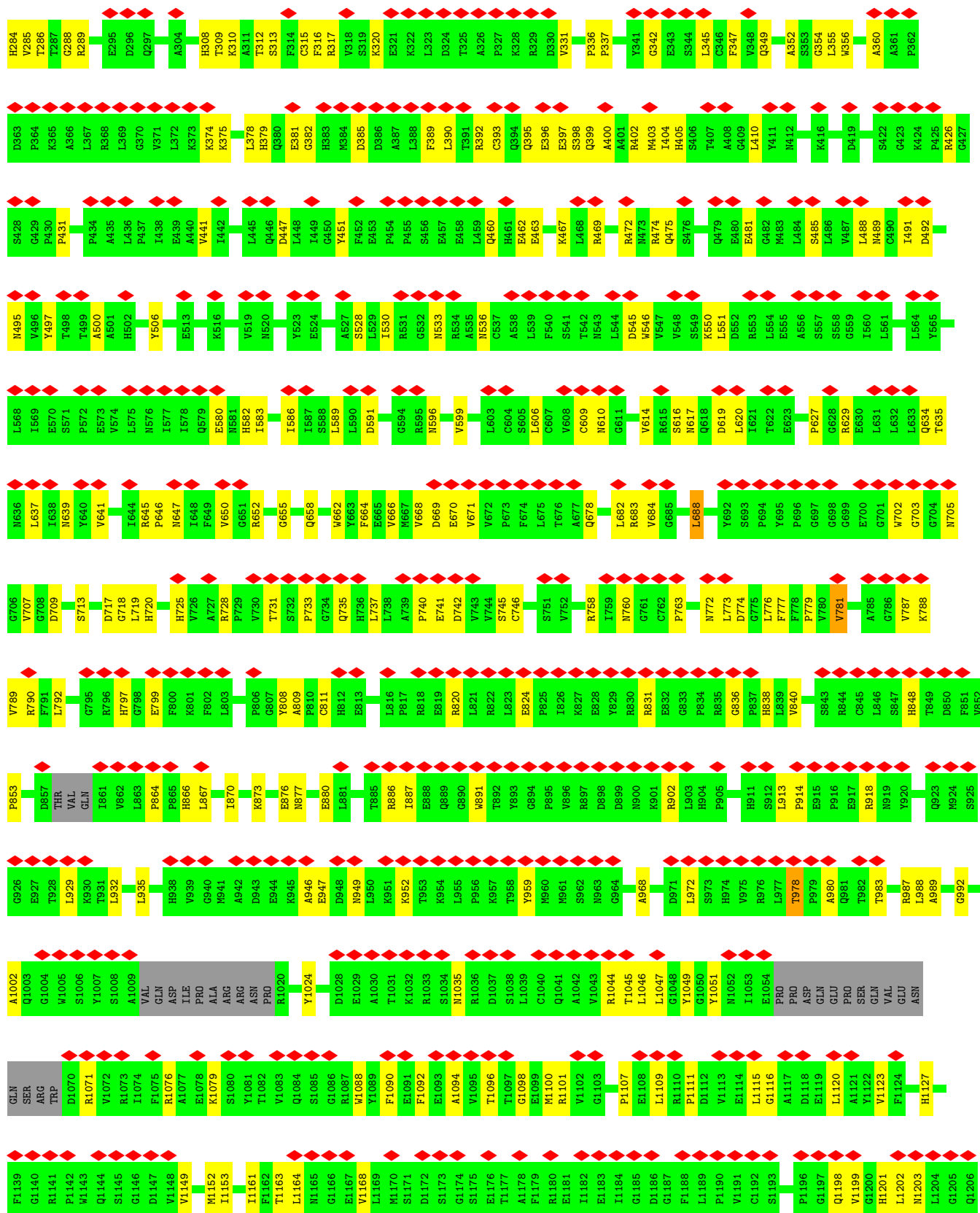
• Molecule 2: ryanodine receptor type 1

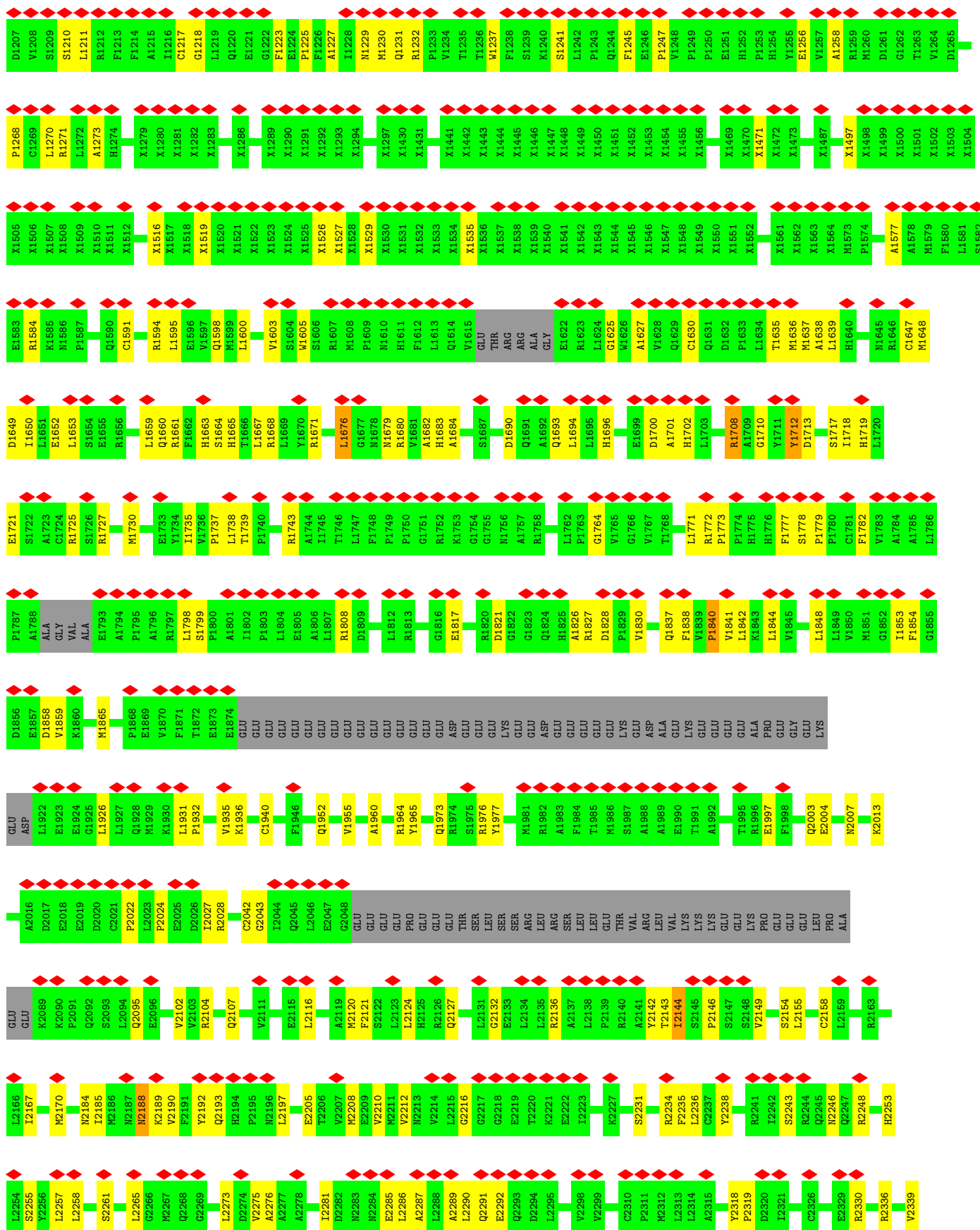






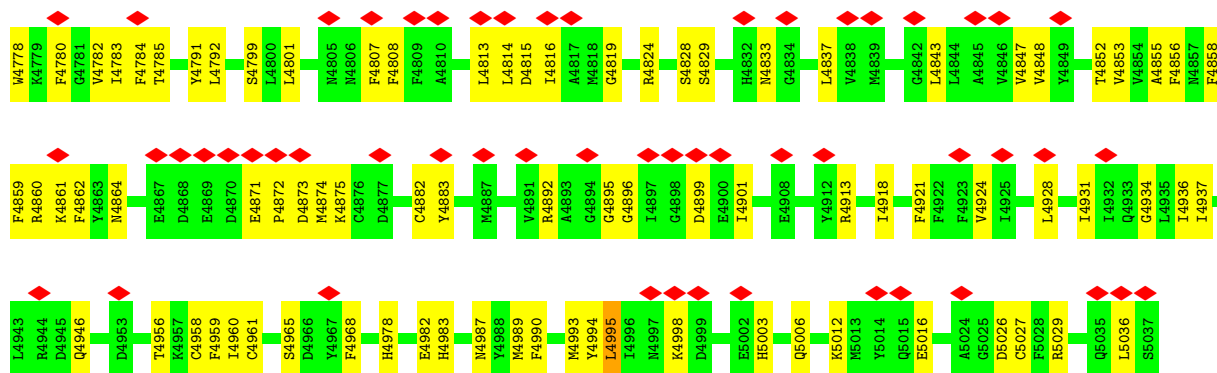
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LEU	LEU	GLU	H4156	Q4076	G3991	L3903	K3821	G3738	M3652	X3557	X3421	X3337	X3248
ALA	ARG	ALA	F3992	D4078	F3992	L3904	E3826	G3739	F3653	X3556	X3422	X3338	X3249
GLY	ARG	ASP	L3993	D4079	H3994	T3905	F3829	E3740	L3654	X3558	X3423	X3341	X3250
THR	THR	ASP	Q3906	T4082	V3996	T3907	Q3830	N3741	E3655	X3559	X3424	X3342	X3251
ALA	ALA	GLY	T3907	D4083	M4000	T3910	Q3831	GLU	A3659	X3560	X3425	X3343	X3252
GLY	GLY	MET	T3911	P4084	M4001	T3911	L3832	ALA	I3662	X3561	X3426	X3344	X3253
THR	ALA	GLY	T3912	R4085	M4002	T3912	Q3833	GLU	L3663	X3562	X3427	X3345	X3254
ALA	ALA	ALA	T3915	L4088	L4003	T3915	S3840	GLU	T3664	X3563	X3428	X3346	X3261
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GLY	ALA	GLY	L3924	Q4094	L4012	L3924	N3844	E3748	D3665	X3565	X3430	X3348	X3263
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ALA	ALA	GLY	W3935	Q4100	V4027	W3935	K3852	K3756	K3679	X3571	X3436	X3354	X3271
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ALA	ALA	THR	A3954	Q4109	I4040	A3954	E3861	H3771	E3688	X3580	X3470	X3363	X3280
ARG	ARG	ARG	M3955	S4113	A4041	M3955	D3862	T3772	E3689	X3581	X3471	X3364	X3281
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ALA	ALA	ALA	Q3960	D4118	M4047	Q3960	V3865	A3775	E3692	X3584	X3474	X3367	X3284
ALA	ALA	ALA	N3963	E4119	E4050	N3963	E3866	A3776	K3693	X3585	X3475	X3368	X3285
ALA	ALA	ARG	T3966	E4120	S4051	T3966	N3867	Q3781	E3712	X3586	X3476	X3369	X3286
ALA	GLY	ALA	G3971	E4121	E4056	G3971	R3868	S3784	K3713	X3587	X3477	X3370	X3287
LEU	GLY	ARG	P3972	M4122	M4057	P3972	Q3869	A3785	G3714	X3588	X3478	X3371	X3288
LEU	LEU	GLY	C3973	M4123	I4058	C3973	N3870	C3786	K3715	X3589	X3479	X3372	X3301
LEU	LEU	LEU	T3974	M4124	L4059	T3974	E3872	K3787	L3716	X3590	X3480	X3373	X3304
SER	GLY	SER	F4062	F4125	F4062	F4062	K3873	Q3788	D3717	X3591	X3481	X3374	X3307
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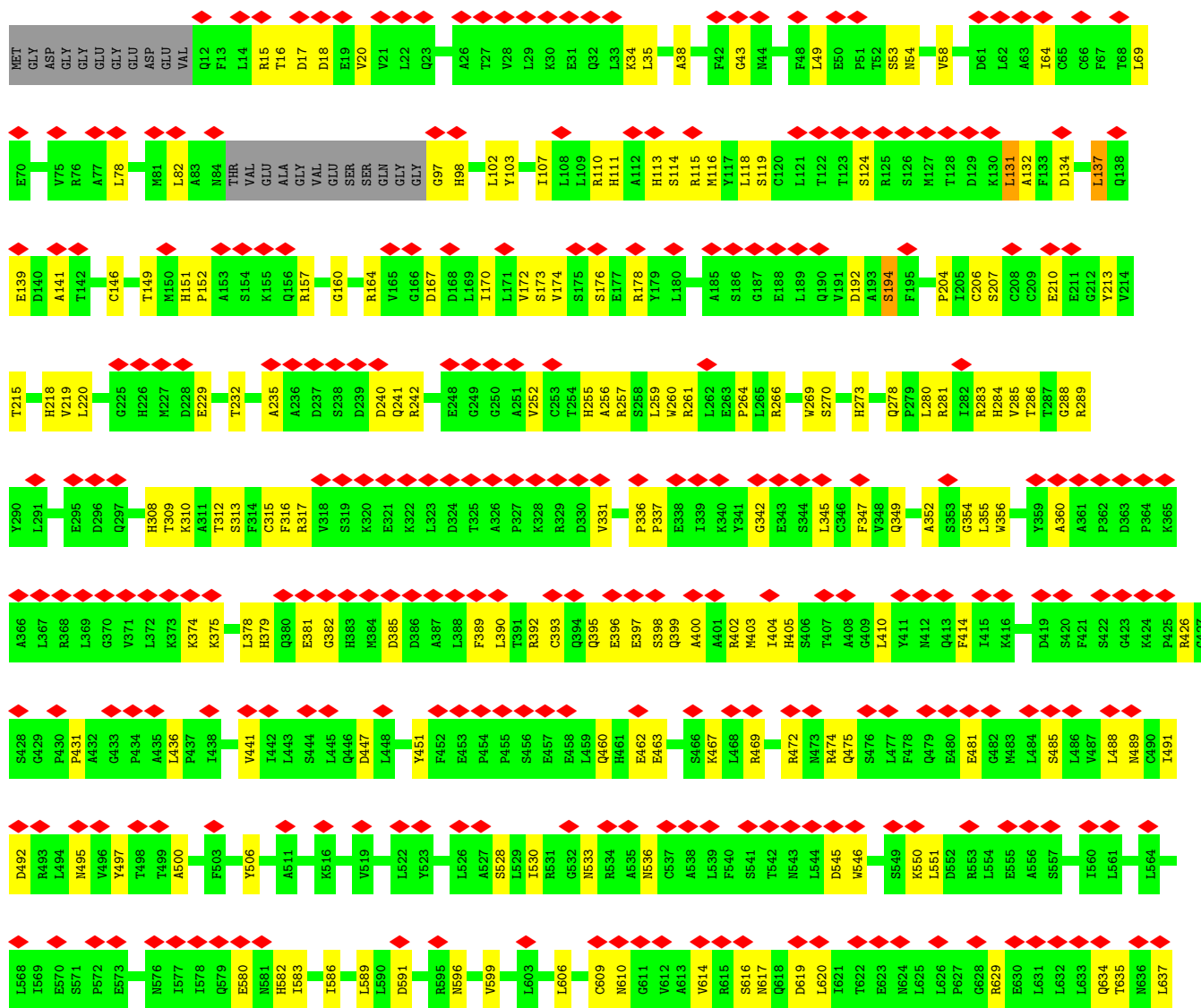
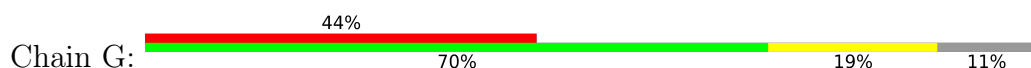


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X2561	X2562	X2563	X2564	X2565	X2568	X2582	X2583	X2584	X2585	X2586	X2591	X2603	X2604	X2605	X2610	X2611	X2612	X2613	X2614	X2615	X2616	X2617	X2618	X2619	X2620	X2621	X2622	X2623	X2624	X2625	X2626	X2629	X2641	X2644	X2645	X2646	X2647	X2648	X2649	X2650	X2651	X2652	X2653	X2654	X2655	X2658	X2672	X2673											
X2674	X2675	X2678	X2683	X2686	X2687	X2688	X2689	X2690	X2691	X2692	X2693	X2694	X2695	X2696	X2697	X2698	X2699	X2700	X2701	X2702	X2703	M2734	F2735	D2736	P2737	R2738	P2739	V2740	E2741	T2742	L2743	N2744	V2745	I2746	L2747	P2748	E2749	K2750	L2751	D2752	S2753	F2754	L2755	M2756	K2757	F2758	A2759	E2760	L2761	T2762	H2763	E2764	K2765	W2766	A2767	F2768			
D2769	K2770	I2771	Q2772	N2773	N2774	W2775	S2776	Y2777	G2778	E2779	L2780	N2781	D2782	E2783	E2784	L2785	K2786	T2787	H2788	P2789	M2790	L2791	R2792	P2793	Y2794	K2795	T2796	F2797	S2798	E2799	K2800	D2801	K2802	E2803	L2804	Y2805	R2806	W2807	P2808	L2809	K2810	E2811	S2812	L2813	K2814	A2815	M2816	L2817	A2818	W2819	E2820	W2821	T2822	L2823	K2824	K2825	A2826	R2827	E2828
G2829	E2830	GLU	GLU	ARG	THR	GLU	LYS	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	TTR	ASP	PRO	ARG	GLU	GLY	Y2855	W2856	P2857	Q2858	P2859	P2860	D2861	L2862	S2863	G2864	T2865	L2867	S2868	E2870	L2871	Q2872	A2873	W2874	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	L2911	T2912	A2913	K2914	E2915	K2916	A2917	R2918	D2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	M2932	N2933	G2934	Y2935	A2936	T2937	N2938	R2939	X2942	X2943	X2944	X2945	X2946	X2947	X2948	X2949	Y2950
X2951	X2952	X2953	X2954	X2955	X2956	X2964	X2971	X2975	X2976	X2995	X3009	X3013	X3014	X3015	X3016	X3017	X3018	X3019	X3020	X3021	X3022	X3023	X3024	X3025	X3045	X3046	X3047	X3048	X3049	X3050	X3051	X3052	X3057	X3060	X3061	X3062	X3063	X3134	X3135	X3136	X3137	X3138	X3139	X3143	X3158	X3161	X3162												
X3171	X3172	X3173	X3174	X3177	X3186	X3187	X3188	X3189	X3190	X3191	X3192	X3193	X3194	X3195	X3196	X3197	X3200	X3214	X3215	X3216	X3217	X3218	X3219	X3220	X3229	X3234	X3235	X3236	X3241	X3242	X3243	X3244	X3245	X3246	X3247	X3248	X3249	X3250	X3251	X3252	X3253	X3254	X3261	X3262	X3263	X3264	X3265	X3266	X3269	X3270	X3271	X3272							
X3273	X3274	X3275	X3276	X3277	X3278	X3279	X3280	X3281	X3282	X3283	X3284	X3285	X3286	X3287	X3288	X3289	X3292	X3302	X3311	X3312	X3313	X3314	X3315	X3316	X3317	X3318	X3319	X3320	X3321	X3331	X3332	X3336	X3337	X3338	X3344	X3345	X3346	X3347	X3348	X3349	X3350	X3351	X3352	X3353	X3354	X3355	X3356	X3357	X3358	X3359	X3360	X3361	X3362						
X3363	X3364	X3365	X3366	X3367	X3368	X3369	X3370	X3373	X3374	X3377	X3384	X3387	X3388	X3389	X3390	X3391	X3392	X3393	X3394	X3395	X3398	X3399	X3410	X3417	X3421	X3424	X3425	X3426	X3427	X3428	X3429	X3430	X3431	X3432	X3433	X3434	X3435	X3436	X3464	X3465	X3466	X3467	X3468	X3511	X3512	X3513	X3514	X3520											
X3521	X3524	X3529	X3530	X3531	X3532	X3533	X3534	X3535	X3539	X3540	X3546	X3547	X3548	X3549	X3552	X3556	X3559	X3560	X3561	X3562	X3563	X3564	X3565	X3566	X3567	X3568	X3569	X3572	X3575	X3576	X3577	X3578	X3579	X3580	X3581	X3582	X3583	X3584	X3585	X3586	X3587	X3588	X3589	X3590	X3591	X3606	X3609	X3610											
X3611	X3612	X3613	Y3642	N3643	L3644	P3645	R3648	A3649	C3650	N3651	N3652	F3653	K3658	A3659	A3660	W3661	L3662	L3663	T3664	F3665	D3666	H3667	S3668	D3671	R3672	K3673	L3674	D3675	D3676	K3679	A3680	G3681	E3682	Q3683	E3684	E3685	E3686	E3687	E3688	E3689	V3690	E3691	E3692	P3697	L3701	H3704	T3708	X3709	L3710	T3711									





• Molecule 2: ryanodine receptor type 1

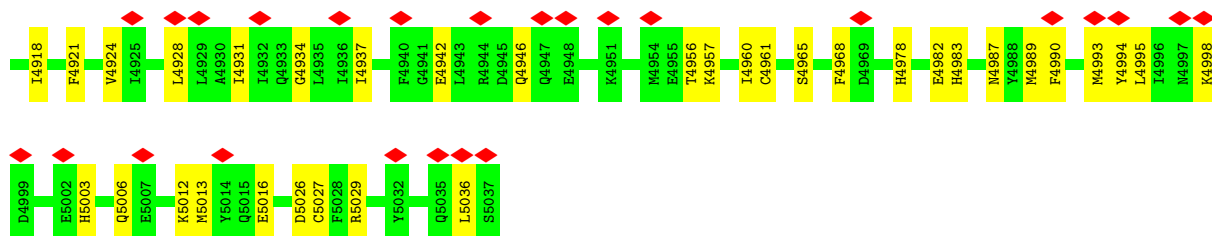




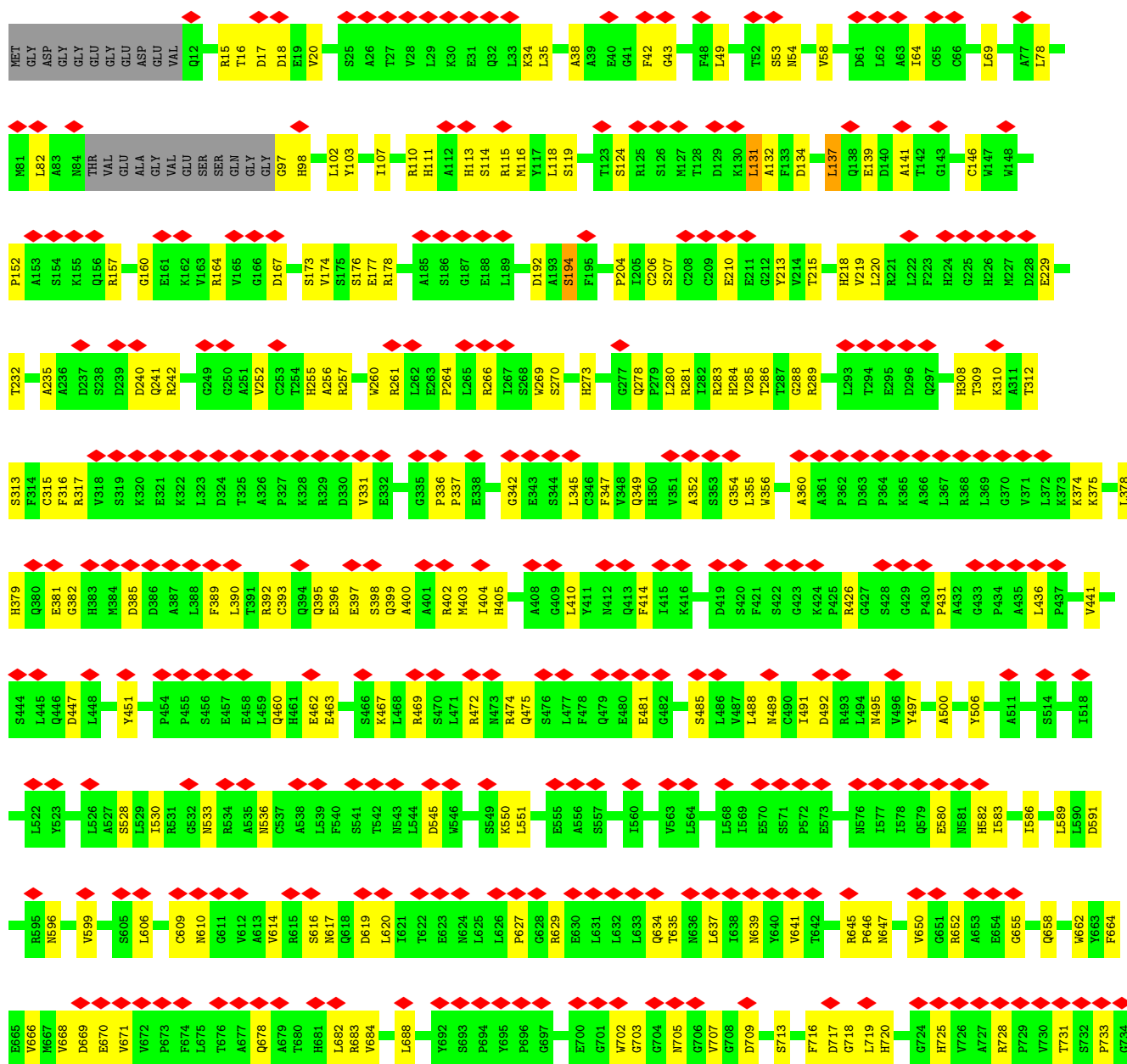
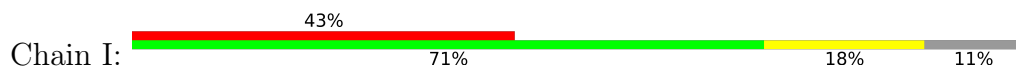








• Molecule 2: ryanodine receptor type 1







K3948	K3870	K3799	L3735	T3664	X3559	X3424	X3342	X3252	X3143	X2954	K2892	GLU
F3951	G3871	L3802	E3736	E3665	X3560	X3425	X3343	X3253	X3146	X2965	E2893	THR
A3954	E3872	S3803	E3737	D3666	X3561	X3426	X3344	X3254	X3145	X2985	L2894	GLU
K3955	K3873	L3805	G3738	H3667	X3562	X3427	X3345	X3261	X3172	X2968	E2896	LYS
S3956	K3874	L3806	G3739	S3668	X3563	X3428	X3346	X3262	X3173	X2975	K2897	LYS
V3957	M3875	N3806	E3740	F3669	X3564	X3429	X3347	X3263	X3183	X2976	G2898	THR
A3958	D3876	K3807	M3741	E3670	X3565	X3430	X3348	X3264	X3186	X2995	G2899	ARG
K3959	E3879	G3808	GLU	M3673	X3566	X3431	X3349	X3265	X3187	X2996	G2900	LYS
F3960	F3880	N3809	ALA	L3674	X3567	X3432	X3350	X3266	X3188	X2997	G2901	ILE
V3961	T3881	K3815	GLU	D3675	X3568	X3433	X3351	X3269	X3189	X2998	T2901	SER
Q3882	Q3882	M3816	GLU	D3676	X3569	X3434	X3352	X3270	X3190	X3004	H2902	GLN
L3883	L3884	L3817	E3747	A3680	X3570	X3435	X3353	X3271	X3191	X3010	P2903	ALA
F3885	F3885	L3820	V3749	G3681	X3571	X3436	X3354	X3272	X3192	X3011	L2904	THR
L3888	L3888	K3821	E3750	Q3682	X3572	X3437	X3355	X3273	X3193	X3012	V2906	ASP
Q3889	Q3889	F3824	V3751	E3684	X3573	X3444	X3356	X3274	X3194	X3013	P2907	PRO
E3893	E3893	E3825	S3752	E3685	X3574	X3462	X3357	X3275	X3195	X3014	D2909	ARG
N3897	N3897	F3829	F3753	E3686	X3575	X3463	X3358	X3276	X3196	X3015	T2910	GLY
D3898	D3898	Q3830	E3754	E3687	X3576	X3464	X3359	X3277	X3197	X3016	L2911	Y2855
F3899	F3899	S3831	E3755	E3688	X3577	X3465	X3360	X3278	X3198	X3017	T2912	M2856
L3903	L3903	L3832	K3756	E3689	X3578	X3466	X3361	X3279	X3199	X3018	A2913	P2857
R3904	R3904	Q3833	E3759	V3690	X3579	X3467	X3362	X3280	X3200	X3019	K2914	Q2858
T3905	T3905	M3836	X3760	X3691	X3580	X3468	X3363	X3281	X3201	X3020	E2915	P2859
Q3906	Q3906	Q3837	Q3761	E3692	X3581	X3469	X3364	X3282	X3202	X3021	L2916	P2860
T3907	T3907	S3840	L3763	K3693	X3582	X3470	X3365	X3283	X3203	X3022	A2917	T2861
T3910	T3910	V3841	L3764	L3698	X3583	X3471	X3366	X3284	X3204	X3023	R2918	L2862
T3911	T3911	L3842	V3765	V3702	X3584	X3472	X3367	X3285	X3205	X3024	D2919	S2863
I3913	I3913	D3843	Q3766	X3702	X3585	X3473	X3368	X3286	X3206	X3025	E2920	G2864
N3914	N3914	L3844	Q3767	X3703	X3586	X3474	X3369	X3287	X3207	X3026	R2921	V2865
I3915	I3915	N3845	Q3768	S3706	X3587	X3475	X3370	X3288	X3208	X3027	E2922	T2866
I3916	I3916	A3846	R3769	R3707	X3588	X3476	X3371	X3297	X3209	X3028	K2923	L2867
I3917	I3917	F3847	T3708	T3708	X3589	X3477	X3372	X3297	X3210	X3029	A2924	S2868
V3920	V3920	L3847	L3710	L3710	X3590	X3478	X3373	X3297	X3211	X3030	Q2925	E2870
D3921	D3921	R3848	L3711	L3711	X3591	X3479	X3374	X3297	X3212	X3031	L2926	L2871
L3924	L3924	E3848	L3712	L3712	X3602	X3480	X3375	X3297	X3213	X3032	L2927	Q2872
R3925	R3925	Q3849	E3712	E3712	X3605	X3481	X3376	X3297	X3214	X3033	Q2928	A2873
L3926	L3926	Q3850	K3713	K3713	X3606	X3482	X3377	X3297	X3215	X3034	F2929	M2874
Q3927	Q3927	N3851	S3714	S3714	X3607	X3483	X3378	X3297	X3216	X3035	L2930	A2875
E3928	E3928	K3852	L3715	L3715	X3608	X3484	X3379	X3297	X3217	X3036	Q2931	E2876
S3931	S3931	E3853	L3716	L3716	X3609	X3485	X3380	X3297	X3218	X3037	M2932	Q2877
D3932	D3932	F3854	D3717	D3717	X3610	X3486	X3381	X3297	X3219	X3038	N2933	L2878
M3935	M3935	G3782	E3718	E3718	X3611	X3487	X3382	X3297	X3220	X3039	G2934	A2879
Y3936	Y3936	S3784	E3719	E3719	X3612	X3488	X3383	X3297	X3221	X3040	Y2935	E2880
Y3937	Y3937	A3785	X3720	X3720	X3613	X3489	X3384	X3297	X3222	X3041	A2936	N2881
S3938	S3938	C3786	M3723	M3723	X3614	X3490	X3385	X3297	X3223	X3042	Z2937	M2882
Q3939	Q3939	G3787	A3724	A3724	X3615	X3491	X3386	X3297	X3224	X3043	V2938	H2883
K3940	K3940	G3788	Y3725	Y3725	X3616	X3492	X3387	X3297	X3225	X3044	R2939	N2884
D3941	D3941	E3789	D3726	D3726	X3617	X3493	X3388	X3297	X3226	X3045	X2942	T2885
		T3790	D3727	D3727	X3618	X3494	X3389	X3297	X3227	X3046	X2943	W2886
		G3791	N3651	N3651	X3619	X3495	X3390	X3297	X3228	X3047	X2944	Q2887
		A3792	M3652	M3652	X3620	X3496	X3391	X3297	X3229	X3048	X2945	R2888
		K3793	E3655	E3655	X3621	X3497	X3392	X3297	X3230	X3049	X2946	K2889
		V3794	K3731	K3731	X3622	X3498	X3393	X3297	X3231	X3050	X2947	L2890
		S3795	S3732	S3732	X3623	X3499	X3394	X3297	X3232	X3051	X2948	T2891
		L3798	C3733	C3733	X3624	X3500	X3395	X3297	X3233	X3052	X2949	
			H3734	H3734	X3625	X3501	X3396	X3297	X3234	X3053	X2950	
					X3626	X3502	X3397	X3297	X3235	X3054	X2951	
					X3627	X3503	X3398	X3297	X3236	X3055	X2952	
					X3628	X3504	X3399	X3297	X3237	X3056	X2953	
					X3629	X3505	X3400	X3297	X3238	X3057		
					X3630	X3506	X3401	X3297	X3239	X3058		
					X3631	X3507	X3402	X3297	X3240	X3059		
					X3632	X3508	X3403	X3297	X3241	X3060		
					X3633	X3509	X3404	X3297	X3242	X3061		
					X3634	X3510	X3405	X3297	X3243	X3062		
					X3635	X3511	X3406	X3297	X3244	X3063		
					X3636	X3512	X3407	X3297	X3245	X3064		
					X3637	X3513	X3408	X3297	X3246	X3065		
					X3638	X3514	X3409	X3297	X3247	X3066		
					X3639	X3515	X3410	X3297	X3248	X3067		
					X3640	X3516	X3411	X3297	X3249	X3068		
					X3641	X3517	X3412	X3297	X3250	X3069		
					X3642	X3518	X3413	X3297	X3251	X3070		
					X3643	X3519	X3414	X3297	X3252	X3071		
					X3644	X3520	X3415	X3297	X3253	X3072		
					X3645	X3521	X3416	X3297	X3254	X3073		
					X3646	X3522	X3417	X3297	X3255	X3074		
					X3647	X3523	X3418	X3297	X3256	X3075		
					X3648	X3524	X3419	X3297	X3257	X3076		
					X3649	X3525	X3420	X3297	X3258	X3077		
					X3650	X3526	X3421	X3297	X3259	X3078		
					X3651	X3527	X3422	X3297	X3260	X3079		
					X3652	X3528	X3423	X3297	X3261	X3080		
					X3653	X3529	X3424	X3297	X3262	X3081		
					X3654	X3530	X3425	X3297	X3263	X3082		
					X3655	X3531	X3426	X3297	X3264	X3083		
					X3656	X3532	X3427	X3297	X3265	X3084		
					X3657	X3533	X3428	X3297	X3266	X3085		
					X3658	X3534	X3429	X3297	X3267	X3086		
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					X3662	X3538	X3433	X3297	X3271	X3090		
					X3663	X3539	X3434	X3297	X3272	X3091		
					X3664	X3540	X3435	X3297	X3273	X3092		
					X3665	X3541	X3436	X3297	X3274	X3093		
					X3666	X3542	X3437	X3297	X3275	X3094		
					X3667	X3543	X3438	X3297	X3276	X3095		
					X3668	X3544	X3439	X3297	X3277	X3096		
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					X3671	X3547	X3442	X3297	X3280	X3099		
					X3672	X3548	X3443	X3297	X3281	X3100		
					X3673	X3549	X3444	X3297	X3282	X3101		
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					X3675	X3551	X3446	X3297	X3284	X3103		
					X3676	X3552	X3447	X3297	X3285	X3104		
					X3677	X3553	X3448	X3297	X3286	X3105		
					X3678	X3554	X3449	X3297	X3287	X3106		
					X3679	X3555	X3450	X3297	X3288	X3107		
					X3680	X3556	X3451	X3297	X3289	X3108		
					X3681	X3557	X3452	X3297	X3290	X3109		
					X3682	X3558	X3453	X3297	X3291	X3110		
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					X3684	X3560	X3455	X3297	X3293	X3112		
					X3685	X3561	X3456	X3297	X3294	X3113		
					X3686	X3562	X3457	X3297	X3295	X3114		
					X3687	X3563	X3458	X3297	X3296	X3115		
					X3688	X3564	X3459	X3297	X3297	X3116		
					X3689	X3565	X3460	X3297	X3298	X3117		
					X3690	X3566	X3461	X3297	X3299	X3118		
					X3691	X3567	X3462	X3297	X3300	X3119		



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	791956	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.486	Depositor
Minimum map value	-0.257	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.16	Depositor
Map size (Å)	502.0, 502.0, 502.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.255, 1.255, 1.255	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, 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	0.24	0/834	0.63	3/1123 (0.3%)
1	F	0.23	0/834	0.63	1/1123 (0.1%)
1	H	0.24	0/834	0.63	1/1123 (0.1%)
1	J	0.24	0/834	0.63	1/1123 (0.1%)
2	B	0.28	0/25428	0.64	6/34534 (0.0%)
2	E	0.29	0/25428	0.64	6/34534 (0.0%)
2	G	0.29	0/25428	0.64	6/34534 (0.0%)
2	I	0.28	0/25428	0.64	4/34534 (0.0%)
All	All	0.28	0/105048	0.64	28/142628 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	23
2	E	0	23
2	G	0	23
2	I	0	23
All	All	0	92

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	4872	PRO	N-CA-C	-7.30	103.38	113.53
2	E	4872	PRO	N-CA-C	-7.21	103.50	113.53
2	I	4872	PRO	N-CA-C	-7.21	103.51	113.53
2	B	4872	PRO	N-CA-C	-7.18	103.55	113.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	8	SER	N-CA-C	5.61	120.54	113.25
1	A	8	SER	N-CA-C	5.57	120.49	113.25
1	J	8	SER	N-CA-C	5.57	120.49	113.25
1	F	8	SER	N-CA-C	5.56	120.48	113.25
2	E	4639	MET	CA-C-N	5.33	134.82	121.80
2	E	4639	MET	C-N-CA	5.33	134.82	121.80
2	I	4639	MET	CA-C-N	5.33	134.81	121.80
2	I	4639	MET	C-N-CA	5.33	134.81	121.80
2	B	4639	MET	CA-C-N	5.32	134.77	121.80
2	B	4639	MET	C-N-CA	5.32	134.77	121.80
2	G	4639	MET	CA-C-N	5.31	134.75	121.80
2	G	4639	MET	C-N-CA	5.31	134.75	121.80
2	G	4073	GLY	N-CA-C	-5.19	100.87	113.18
2	B	4073	GLY	N-CA-C	-5.19	100.87	113.18
2	E	4073	GLY	N-CA-C	-5.19	100.88	113.18
2	I	4073	GLY	N-CA-C	-5.19	100.88	113.18
2	G	3642	TYR	CA-C-N	5.07	129.31	122.07
2	G	3642	TYR	C-N-CA	5.07	129.31	122.07
2	B	3642	TYR	CA-C-N	5.04	129.27	122.07
2	B	3642	TYR	C-N-CA	5.04	129.27	122.07
2	E	3642	TYR	CA-C-N	5.03	129.26	122.07
2	E	3642	TYR	C-N-CA	5.03	129.26	122.07
1	A	7	ILE	CA-C-N	5.03	128.41	120.97
1	A	7	ILE	C-N-CA	5.03	128.41	120.97

There are no chirality outliers.

All (92) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	137	LEU	Peptide
2	B	1676	LEU	Peptide
2	B	1690	ASP	Peptide
2	B	1712	TYR	Peptide
2	B	1828	ASP	Peptide
2	B	1840	PRO	Peptide
2	B	194	SER	Peptide
2	B	2188	ASN	Peptide
2	B	2291	GLN	Peptide
2	B	2292	GLU	Peptide
2	B	2342	ASN	Peptide
2	B	2343	GLY	Peptide
2	B	240	ASP	Peptide

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Mol	Chain	Res	Type	Group
2	B	2472	LEU	Peptide
2	B	2807	TRP	Peptide
2	B	3786	CYS	Peptide
2	B	3971	GLY	Peptide
2	B	4666	VAL	Peptide
2	B	4696	ASP	Peptide
2	B	4807	PHE	Peptide
2	B	4873	ASP	Peptide
2	B	4901	ILE	Peptide
2	B	808	TYR	Peptide
2	E	137	LEU	Peptide
2	E	1676	LEU	Peptide
2	E	1690	ASP	Peptide
2	E	1712	TYR	Peptide
2	E	1828	ASP	Peptide
2	E	1840	PRO	Peptide
2	E	194	SER	Peptide
2	E	2188	ASN	Peptide
2	E	2291	GLN	Peptide
2	E	2292	GLU	Peptide
2	E	2342	ASN	Peptide
2	E	2343	GLY	Peptide
2	E	240	ASP	Peptide
2	E	2472	LEU	Peptide
2	E	2807	TRP	Peptide
2	E	3786	CYS	Peptide
2	E	3971	GLY	Peptide
2	E	4666	VAL	Peptide
2	E	4696	ASP	Peptide
2	E	4807	PHE	Peptide
2	E	4873	ASP	Peptide
2	E	4901	ILE	Peptide
2	E	808	TYR	Peptide
2	G	137	LEU	Peptide
2	G	1676	LEU	Peptide
2	G	1690	ASP	Peptide
2	G	1712	TYR	Peptide
2	G	1828	ASP	Peptide
2	G	1840	PRO	Peptide
2	G	194	SER	Peptide
2	G	2188	ASN	Peptide
2	G	2291	GLN	Peptide

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Mol	Chain	Res	Type	Group
2	G	2292	GLU	Peptide
2	G	2342	ASN	Peptide
2	G	2343	GLY	Peptide
2	G	240	ASP	Peptide
2	G	2472	LEU	Peptide
2	G	2807	TRP	Peptide
2	G	3786	CYS	Peptide
2	G	3971	GLY	Peptide
2	G	4666	VAL	Peptide
2	G	4696	ASP	Peptide
2	G	4807	PHE	Peptide
2	G	4873	ASP	Peptide
2	G	4901	ILE	Peptide
2	G	808	TYR	Peptide
2	I	137	LEU	Peptide
2	I	1676	LEU	Peptide
2	I	1690	ASP	Peptide
2	I	1712	TYR	Peptide
2	I	1828	ASP	Peptide
2	I	1840	PRO	Peptide
2	I	194	SER	Peptide
2	I	2188	ASN	Peptide
2	I	2291	GLN	Peptide
2	I	2292	GLU	Peptide
2	I	2342	ASN	Peptide
2	I	2343	GLY	Peptide
2	I	240	ASP	Peptide
2	I	2472	LEU	Peptide
2	I	2807	TRP	Peptide
2	I	3786	CYS	Peptide
2	I	3971	GLY	Peptide
2	I	4666	VAL	Peptide
2	I	4696	ASP	Peptide
2	I	4807	PHE	Peptide
2	I	4873	ASP	Peptide
2	I	4901	ILE	Peptide
2	I	808	TYR	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	818	0	824	18	0
1	F	818	0	824	20	0
1	H	818	0	824	18	0
1	J	818	0	824	20	0
2	B	29369	0	24713	512	0
2	E	29369	0	24712	524	0
2	G	29369	0	24716	522	0
2	I	29369	0	24713	508	0
3	B	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
3	I	1	0	0	0	0
4	B	1	0	0	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
4	I	1	0	0	0	0
All	All	120756	0	102150	2114	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 9.

All (2114) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:4859:PHE:HA	2:G:4862:PHE:CD2	1.88	1.08
2:G:4859:PHE:HA	2:G:4862:PHE:HD2	1.28	0.97
2:E:4859:PHE:HA	2:E:4862:PHE:CD2	2.05	0.92
2:E:4859:PHE:HA	2:E:4862:PHE:HD2	1.43	0.83
2:G:4859:PHE:CA	2:G:4862:PHE:HD2	1.99	0.73
2:E:4855:ALA:HA	2:E:4859:PHE:HB2	1.71	0.72
2:I:853:PRO:HB3	2:I:1024:TYR:H	1.56	0.71
2:B:853:PRO:HB3	2:B:1024:TYR:H	1.56	0.71
2:B:2318:TYR:HH	2:B:2414:ASN:N	1.90	0.70
2:I:2318:TYR:HH	2:I:2414:ASN:N	1.90	0.70
2:E:853:PRO:HB3	2:E:1024:TYR:H	1.56	0.69
2:I:788:LYS:HG2	2:I:1630:CYS:H	1.58	0.69
2:G:788:LYS:HG2	2:G:1630:CYS:H	1.58	0.69
2:G:2318:TYR:HH	2:G:2414:ASN:N	1.91	0.69
2:E:788:LYS:HG2	2:E:1630:CYS:H	1.58	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:853:PRO:HB3	2:G:1024:TYR:H	1.56	0.69
2:E:2318:TYR:HH	2:E:2414:ASN:N	1.91	0.69
2:B:646:PRO:HD2	2:B:779:PRO:HB2	1.76	0.68
2:B:788:LYS:HG2	2:B:1630:CYS:H	1.58	0.68
2:B:1671:ARG:NH2	2:B:1710:GLY:O	2.26	0.68
2:E:1671:ARG:NH2	2:E:1710:GLY:O	2.26	0.68
2:G:1671:ARG:NH2	2:G:1710:GLY:O	2.26	0.68
2:I:1671:ARG:NH2	2:I:1710:GLY:O	2.26	0.68
2:E:646:PRO:HD2	2:E:779:PRO:HB2	1.76	0.68
2:I:646:PRO:HD2	2:I:779:PRO:HB2	1.76	0.68
2:G:379:HIS:HD2	2:G:382:GLY:H	1.40	0.68
2:E:379:HIS:HD2	2:E:382:GLY:H	1.40	0.67
2:G:646:PRO:HD2	2:G:779:PRO:HB2	1.76	0.67
2:B:745:SER:HB2	2:B:758:ARG:HB3	1.76	0.67
2:I:745:SER:HB2	2:I:758:ARG:HB3	1.76	0.67
2:B:379:HIS:HD2	2:B:382:GLY:H	1.40	0.66
2:G:4864:ASN:H	2:G:4874:MET:HE3	1.61	0.66
2:I:379:HIS:HD2	2:I:382:GLY:H	1.40	0.66
2:E:4864:ASN:H	2:E:4874:MET:HE3	1.61	0.66
2:G:745:SER:HB2	2:G:758:ARG:HB3	1.76	0.66
2:B:132:ALA:HA	2:B:194:SER:HB2	1.77	0.66
2:I:2764:GLU:HG3	2:I:2857:PRO:HB2	1.77	0.66
1:H:74:LEU:HB2	1:H:99:PHE:HB2	1.78	0.66
2:I:132:ALA:HA	2:I:194:SER:HB2	1.77	0.66
2:E:132:ALA:HA	2:E:194:SER:HB2	1.77	0.66
2:E:4673:ARG:HH22	2:E:4698:LYS:HB2	1.61	0.66
1:J:74:LEU:HB2	1:J:99:PHE:HB2	1.78	0.66
2:B:2764:GLU:HG3	2:B:2857:PRO:HB2	1.78	0.65
2:E:4934:GLY:HA3	2:G:4937:ILE:HD12	1.78	0.65
2:B:3937:TYR:O	2:B:4002:LYS:NZ	2.30	0.65
2:G:2764:GLU:HG3	2:G:2857:PRO:HB2	1.78	0.65
2:G:4177:TYR:HA	2:G:4202:ARG:HH22	1.61	0.65
2:I:4673:ARG:HH22	2:I:4698:LYS:HB2	1.61	0.65
2:E:745:SER:HB2	2:E:758:ARG:HB3	1.76	0.65
2:G:132:ALA:HA	2:G:194:SER:HB2	1.77	0.65
2:I:4177:TYR:HA	2:I:4202:ARG:HH22	1.61	0.65
1:F:74:LEU:HB2	1:F:99:PHE:HB2	1.78	0.65
2:I:1092:PHE:HB3	2:I:1149:VAL:HB	1.79	0.65
2:B:3990:VAL:HG13	2:B:4051:SER:HB2	1.78	0.65
1:A:74:LEU:HB2	1:A:99:PHE:HB2	1.78	0.65
2:B:3903:LEU:HG	2:B:3915:ILE:HD12	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:4177:TYR:HA	2:E:4202:ARG:HH22	1.61	0.65
2:B:1092:PHE:HB3	2:B:1149:VAL:HB	1.79	0.64
2:B:1247:PRO:HA	2:B:1598:GLN:HA	1.79	0.64
2:B:4177:TYR:HA	2:B:4202:ARG:HH22	1.61	0.64
2:E:1667:LEU:HD23	2:E:1671:ARG:HH12	1.61	0.64
2:E:2764:GLU:HG3	2:E:2857:PRO:HB2	1.77	0.64
2:G:1667:LEU:HD23	2:G:1671:ARG:HH12	1.61	0.64
2:G:4673:ARG:HH22	2:G:4698:LYS:HB2	1.61	0.64
2:G:3990:VAL:HG13	2:G:4051:SER:HB2	1.78	0.64
2:B:4864:ASN:H	2:B:4874:MET:HE3	1.61	0.64
2:E:3903:LEU:HG	2:E:3915:ILE:HD12	1.79	0.64
2:G:3903:LEU:HG	2:G:3915:ILE:HD12	1.79	0.64
2:G:3937:TYR:O	2:G:4002:LYS:NZ	2.30	0.64
2:I:1667:LEU:HD23	2:I:1671:ARG:HH12	1.61	0.64
2:I:4864:ASN:H	2:I:4874:MET:HE3	1.61	0.64
2:G:1232:ARG:HH21	2:G:1701:ALA:HB1	1.63	0.64
1:H:23:VAL:HG22	1:H:47:LYS:HG2	1.80	0.64
2:I:3937:TYR:O	2:I:4002:LYS:NZ	2.30	0.64
2:E:3937:TYR:O	2:E:4002:LYS:NZ	2.30	0.64
1:F:23:VAL:HG22	1:F:47:LYS:HG2	1.80	0.64
2:I:3903:LEU:HG	2:I:3915:ILE:HD12	1.79	0.64
2:B:4673:ARG:HH22	2:B:4698:LYS:HB2	1.61	0.64
1:J:23:VAL:HG22	1:J:47:LYS:HG2	1.80	0.64
2:B:1667:LEU:HD23	2:B:1671:ARG:HH12	1.61	0.64
2:G:1092:PHE:HB3	2:G:1149:VAL:HB	1.79	0.64
1:A:23:VAL:HG22	1:A:47:LYS:HG2	1.80	0.63
2:G:606:LEU:O	2:G:617:ASN:ND2	2.31	0.63
2:E:1232:ARG:HH21	2:E:1701:ALA:HB1	1.63	0.63
2:E:3990:VAL:HG13	2:E:4051:SER:HB2	1.79	0.63
2:B:606:LEU:O	2:B:617:ASN:ND2	2.31	0.63
2:B:2755:ILE:HD13	2:B:2810:LYS:HG2	1.81	0.63
2:E:4741:LEU:HB2	2:E:4743:MET:HE2	1.80	0.63
2:I:1232:ARG:HH21	2:I:1701:ALA:HB1	1.63	0.63
2:E:606:LEU:O	2:E:617:ASN:ND2	2.31	0.63
2:E:1092:PHE:HB3	2:E:1149:VAL:HB	1.79	0.63
2:B:111:HIS:HD2	2:B:114:SER:H	1.47	0.63
2:G:1247:PRO:HA	2:G:1598:GLN:HA	1.79	0.63
2:I:3990:VAL:HG13	2:I:4051:SER:HB2	1.78	0.63
2:E:1247:PRO:HA	2:E:1598:GLN:HA	1.79	0.63
2:I:111:HIS:HD2	2:I:114:SER:H	1.47	0.63
2:I:606:LEU:O	2:I:617:ASN:ND2	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1247:PRO:HA	2:I:1598:GLN:HA	1.79	0.63
2:B:1232:ARG:HH21	2:B:1701:ALA:HB1	1.63	0.63
2:G:111:HIS:HD2	2:G:114:SER:H	1.47	0.63
2:I:2755:ILE:HD13	2:I:2810:LYS:HG2	1.81	0.63
2:B:1743:ARG:O	2:B:1964:ARG:NH2	2.32	0.62
2:G:4741:LEU:HB2	2:G:4743:MET:HE2	1.80	0.62
2:B:4741:LEU:HB2	2:B:4743:MET:HE2	1.80	0.62
2:G:1700:ASP:OD2	2:G:1708:ARG:NH2	2.32	0.62
2:G:2755:ILE:HD13	2:G:2810:LYS:HG2	1.81	0.62
2:B:3767:GLN:HB3	2:B:3772:THR:HG22	1.82	0.62
2:E:261:ARG:HB3	2:E:283:ARG:HB3	1.82	0.62
2:G:1101:ARG:HE	2:G:1115:LEU:HB3	1.64	0.62
2:I:1700:ASP:OD2	2:I:1708:ARG:NH2	2.33	0.62
2:I:3767:GLN:HB3	2:I:3772:THR:HG22	1.82	0.62
2:B:1700:ASP:OD2	2:B:1708:ARG:NH2	2.33	0.61
2:E:1519:UNK:HA	2:E:1526:UNK:HA	1.82	0.61
2:E:1973:GLN:O	2:E:1977:TYR:N	2.33	0.61
2:E:1101:ARG:HE	2:E:1115:LEU:HB3	1.64	0.61
2:G:261:ARG:HB3	2:G:283:ARG:HB3	1.82	0.61
2:E:2755:ILE:HD13	2:E:2810:LYS:HG2	1.81	0.61
2:E:1700:ASP:OD2	2:E:1708:ARG:NH2	2.32	0.61
2:E:4581:LYS:HB2	2:E:4632:LEU:HB2	1.82	0.61
2:B:1973:GLN:O	2:B:1977:TYR:N	2.33	0.61
2:E:111:HIS:HD2	2:E:114:SER:H	1.47	0.61
2:E:1743:ARG:O	2:E:1964:ARG:NH2	2.32	0.61
2:G:1743:ARG:O	2:G:1964:ARG:NH2	2.32	0.61
2:I:4741:LEU:HB2	2:I:4743:MET:HE2	1.80	0.61
2:I:1743:ARG:O	2:I:1964:ARG:NH2	2.32	0.61
2:B:972:LEU:O	2:B:1044:ARG:NH2	2.33	0.61
2:E:972:LEU:O	2:E:1044:ARG:NH2	2.33	0.61
2:G:18:ASP:HB2	2:G:69:LEU:HD12	1.83	0.61
2:G:4581:LYS:HB2	2:G:4632:LEU:HB2	1.82	0.61
2:B:1101:ARG:HE	2:B:1115:LEU:HB3	1.64	0.60
2:G:1519:UNK:HA	2:G:1526:UNK:HA	1.83	0.60
2:B:261:ARG:HB3	2:B:283:ARG:HB3	1.82	0.60
2:B:1211:LEU:HD11	2:B:1225:PRO:HB3	1.84	0.60
2:E:18:ASP:HB2	2:E:69:LEU:HD12	1.83	0.60
2:G:3882:GLN:HB2	2:G:3957:VAL:HG22	1.82	0.60
2:I:261:ARG:HB3	2:I:283:ARG:HB3	1.82	0.60
2:B:20:VAL:HG12	2:B:204:PRO:HA	1.82	0.60
2:B:4581:LYS:HB2	2:B:4632:LEU:HB2	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:235:ALA:HA	2:G:257:ARG:HD3	1.83	0.60
2:G:4704:LEU:HD22	2:G:4778:TRP:HB2	1.83	0.60
2:B:4829:SER:O	2:B:4833:ASN:ND2	2.35	0.60
2:E:20:VAL:HG12	2:E:204:PRO:HA	1.82	0.60
2:E:3767:GLN:HB3	2:E:3772:THR:HG22	1.82	0.60
2:G:4961:CYS:SG	2:G:4978:HIS:NE2	2.75	0.60
2:I:972:LEU:O	2:I:1044:ARG:NH2	2.33	0.60
2:I:1101:ARG:HE	2:I:1115:LEU:HB3	1.64	0.60
2:B:664:PHE:HB2	2:B:746:CYS:HB2	1.83	0.60
2:I:235:ALA:HA	2:I:257:ARG:HD3	1.84	0.60
2:G:3767:GLN:HB3	2:G:3772:THR:HG22	1.82	0.60
2:I:1973:GLN:O	2:I:1977:TYR:N	2.33	0.60
2:I:4581:LYS:HB2	2:I:4632:LEU:HB2	1.82	0.60
2:I:4961:CYS:SG	2:I:4978:HIS:NE2	2.75	0.60
2:E:742:ASP:HA	2:E:760:ASN:HD21	1.67	0.60
2:E:1649:ASP:HB3	2:E:1652:GLU:HG2	1.84	0.60
2:E:4961:CYS:SG	2:E:4978:HIS:NE2	2.75	0.60
2:B:1649:ASP:HB3	2:B:1652:GLU:HG2	1.84	0.60
2:G:4829:SER:O	2:G:4833:ASN:ND2	2.35	0.60
2:I:635:THR:O	1:J:34:LYS:NZ	2.34	0.60
2:I:742:ASP:HA	2:I:760:ASN:HD21	1.67	0.60
2:E:1211:LEU:HD11	2:E:1225:PRO:HB3	1.84	0.60
2:I:1211:LEU:HD11	2:I:1225:PRO:HB3	1.84	0.60
2:E:4829:SER:O	2:E:4833:ASN:ND2	2.35	0.60
2:I:20:VAL:HG12	2:I:204:PRO:HA	1.82	0.60
2:B:3882:GLN:HB2	2:B:3957:VAL:HG22	1.82	0.59
2:B:4704:LEU:HD22	2:B:4778:TRP:HB2	1.83	0.59
2:G:664:PHE:HB2	2:G:746:CYS:HB2	1.83	0.59
2:I:18:ASP:HB2	2:I:69:LEU:HD12	1.83	0.59
2:B:235:ALA:HA	2:B:257:ARG:HD3	1.84	0.59
2:B:742:ASP:HA	2:B:760:ASN:HD21	1.67	0.59
2:E:4704:LEU:HD22	2:E:4778:TRP:HB2	1.83	0.59
2:I:4829:SER:O	2:I:4833:ASN:ND2	2.35	0.59
2:E:3882:GLN:HB2	2:E:3957:VAL:HG22	1.83	0.59
2:E:664:PHE:HB2	2:E:746:CYS:HB2	1.83	0.59
2:E:1271:ARG:HA	2:E:1471:UNK:HA	1.85	0.59
2:G:1649:ASP:HB3	2:G:1652:GLU:HG2	1.84	0.59
2:I:989:ALA:O	2:I:1035:ASN:ND2	2.36	0.59
2:I:3882:GLN:HB2	2:I:3957:VAL:HG22	1.82	0.59
2:B:989:ALA:O	2:B:1035:ASN:ND2	2.36	0.59
2:G:20:VAL:HG12	2:G:204:PRO:HA	1.82	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:1211:LEU:HD11	2:G:1225:PRO:HB3	1.83	0.59
2:I:1777:PHE:HA	2:I:1799:SER:HB2	1.85	0.59
2:B:18:ASP:HB2	2:B:69:LEU:HD12	1.83	0.59
2:G:742:ASP:HA	2:G:760:ASN:HD21	1.67	0.59
2:G:1777:PHE:HA	2:G:1799:SER:HB2	1.85	0.59
2:G:2205:GLU:HG2	2:G:2253:HIS:HE1	1.67	0.59
2:G:989:ALA:O	2:G:1035:ASN:ND2	2.36	0.59
2:G:1218:GLY:HA2	2:G:1223:PHE:HB2	1.85	0.59
2:E:4895:GLY:O	2:G:4892:ARG:NH2	2.34	0.59
2:I:664:PHE:HB2	2:I:746:CYS:HB2	1.83	0.59
2:I:4704:LEU:HD22	2:I:4778:TRP:HB2	1.83	0.59
2:B:1218:GLY:HA2	2:B:1223:PHE:HB2	1.85	0.59
2:E:235:ALA:HA	2:E:257:ARG:HD3	1.83	0.59
2:G:1808:ARG:NH1	2:G:1853:ILE:O	2.36	0.59
2:G:1973:GLN:O	2:G:1977:TYR:N	2.33	0.59
2:B:1777:PHE:HA	2:B:1799:SER:HB2	1.85	0.59
2:I:1218:GLY:HA2	2:I:1223:PHE:HB2	1.85	0.59
2:E:2205:GLU:HG2	2:E:2253:HIS:HE1	1.67	0.58
2:E:2751:LEU:HD11	2:E:2823:ILE:HG21	1.85	0.58
2:E:4155:PRO:HD2	2:E:5036:LEU:HD23	1.85	0.58
2:G:4860:ARG:HD2	2:I:4582:VAL:HG11	1.85	0.58
2:I:1649:ASP:HB3	2:I:1652:GLU:HG2	1.83	0.58
2:B:2205:GLU:HG2	2:B:2253:HIS:HE1	1.67	0.58
2:B:4155:PRO:HD2	2:B:5036:LEU:HD23	1.85	0.58
2:E:1777:PHE:HA	2:E:1799:SER:HB2	1.85	0.58
2:G:2748:PRO:HD2	2:G:2751:LEU:HD12	1.85	0.58
2:I:1808:ARG:NH1	2:I:1853:ILE:O	2.36	0.58
2:I:4000:MET:HE1	2:I:4058:ILE:HG23	1.85	0.58
2:G:972:LEU:O	2:G:1044:ARG:NH2	2.33	0.58
2:G:2751:LEU:HD11	2:G:2823:ILE:HG21	1.85	0.58
2:I:2205:GLU:HG2	2:I:2253:HIS:HE1	1.67	0.58
2:I:4749:GLU:HA	2:I:4752:ALA:HB3	1.86	0.58
2:G:426:ARG:HB2	2:G:506:TYR:HA	1.85	0.58
2:B:4000:MET:HE1	2:B:4058:ILE:HG23	1.85	0.58
1:A:6:THR:HA	1:A:72:ALA:HA	1.85	0.58
2:B:2042:CYS:SG	2:B:2043:GLY:N	2.76	0.58
2:B:3846:ALA:HB1	2:B:3873:LYS:HG2	1.86	0.58
2:E:989:ALA:O	2:E:1035:ASN:ND2	2.36	0.58
2:E:1808:ARG:NH1	2:E:1853:ILE:O	2.36	0.58
2:I:426:ARG:HB2	2:I:506:TYR:HA	1.85	0.58
2:I:627:PRO:HB2	1:J:92:PRO:HD3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:426:ARG:HB2	2:B:506:TYR:HA	1.85	0.58
2:B:1519:UNK:HA	2:B:1526:UNK:HA	1.85	0.58
1:F:6:THR:HA	1:F:72:ALA:HA	1.85	0.58
2:G:1079:LYS:NZ	2:G:1107:PRO:O	2.37	0.58
2:G:4000:MET:HE1	2:G:4058:ILE:HG23	1.85	0.58
2:B:1079:LYS:NZ	2:B:1107:PRO:O	2.36	0.58
2:B:2748:PRO:HD2	2:B:2751:LEU:HD12	1.85	0.58
2:B:4749:GLU:HA	2:B:4752:ALA:HB3	1.86	0.58
2:E:3846:ALA:HB1	2:E:3873:LYS:HG2	1.86	0.58
2:E:242:ARG:NH1	2:E:481:GLU:OE1	2.37	0.58
2:G:242:ARG:NH1	2:G:481:GLU:OE1	2.37	0.58
2:G:4749:GLU:HA	2:G:4752:ALA:HB3	1.86	0.58
2:I:2748:PRO:HD2	2:I:2751:LEU:HD12	1.85	0.58
1:J:27:THR:HB	1:J:100:ASP:HB3	1.86	0.58
2:B:1808:ARG:NH1	2:B:1853:ILE:O	2.36	0.57
2:E:426:ARG:HB2	2:E:506:TYR:HA	1.85	0.57
2:E:1218:GLY:HA2	2:E:1223:PHE:HB2	1.85	0.57
1:A:27:THR:HB	1:A:100:ASP:HB3	1.86	0.57
2:B:242:ARG:NH1	2:B:481:GLU:OE1	2.37	0.57
2:E:2440:MET:O	2:E:2444:GLN:N	2.36	0.57
1:H:27:THR:HB	1:H:100:ASP:HB3	1.86	0.57
2:I:242:ARG:NH1	2:I:481:GLU:OE1	2.37	0.57
2:I:4155:PRO:HD2	2:I:5036:LEU:HD23	1.85	0.57
2:B:887:ILE:HG21	2:B:959:TYR:HA	1.85	0.57
2:B:3780:LEU:HD11	2:B:3816:MET:HG3	1.86	0.57
2:E:887:ILE:HG21	2:E:959:TYR:HA	1.85	0.57
2:E:3780:LEU:HD11	2:E:3816:MET:HG3	1.87	0.57
2:E:4000:MET:HE1	2:E:4058:ILE:HG23	1.85	0.57
2:G:1830:VAL:HB	2:G:1837:GLN:HA	1.87	0.57
2:G:3780:LEU:HD11	2:G:3816:MET:HG3	1.87	0.57
1:F:27:THR:HB	1:F:100:ASP:HB3	1.86	0.57
2:G:887:ILE:HG21	2:G:959:TYR:HA	1.86	0.57
2:G:4155:PRO:HD2	2:G:5036:LEU:HD23	1.85	0.57
2:I:210:GLU:HG3	2:I:337:PRO:HG3	1.86	0.57
2:I:2440:MET:O	2:I:2444:GLN:N	2.36	0.57
2:I:3780:LEU:HD11	2:I:3816:MET:HG3	1.86	0.57
1:J:6:THR:HA	1:J:72:ALA:HA	1.85	0.57
2:B:1271:ARG:HA	2:B:1471:UNK:HA	1.86	0.57
2:B:4937:ILE:HD12	2:I:4934:GLY:HA3	1.86	0.57
2:G:210:GLU:HG3	2:G:337:PRO:HG3	1.86	0.57
2:I:1079:LYS:NZ	2:I:1107:PRO:O	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1271:ARG:HA	2:I:1471:UNK:HA	1.86	0.57
2:I:1519:UNK:HA	2:I:1526:UNK:HA	1.86	0.57
2:I:2042:CYS:SG	2:I:2043:GLY:N	2.76	0.57
2:I:3846:ALA:HB1	2:I:3873:LYS:HG2	1.86	0.57
2:E:4749:GLU:HA	2:E:4752:ALA:HB3	1.86	0.57
2:I:2287:ALA:HA	2:I:2290:LEU:HD13	1.87	0.57
2:I:2751:LEU:HD11	2:I:2823:ILE:HG21	1.85	0.57
2:B:669:ASP:OD2	2:B:790:ARG:NH2	2.38	0.57
2:E:2748:PRO:HD2	2:E:2751:LEU:HD12	1.85	0.57
2:G:645:ARG:N	2:G:824:GLU:O	2.38	0.57
2:I:887:ILE:HG21	2:I:959:TYR:HA	1.86	0.57
2:I:1830:VAL:HB	2:I:1837:GLN:HA	1.87	0.57
2:B:210:GLU:HG3	2:B:337:PRO:HG3	1.86	0.57
2:B:4177:TYR:HE1	2:B:4199:GLU:HB2	1.70	0.57
2:E:1079:LYS:NZ	2:E:1107:PRO:O	2.37	0.57
2:G:3846:ALA:HB1	2:G:3873:LYS:HG2	1.86	0.57
2:I:669:ASP:OD2	2:I:790:ARG:NH2	2.38	0.57
2:I:719:LEU:HD22	2:I:735:GLN:HG2	1.87	0.57
2:B:4151:SER:HA	2:B:4160:LEU:HD21	1.87	0.57
2:E:1830:VAL:HB	2:E:1837:GLN:HA	1.87	0.57
2:E:3843:ASP:H	2:E:3874:VAL:HG13	1.70	0.57
2:E:4201:ASN:O	2:E:4205:TRP:N	2.38	0.57
2:G:683:ARG:NH1	2:G:707:VAL:O	2.37	0.57
2:B:645:ARG:N	2:B:824:GLU:O	2.38	0.56
2:E:4859:PHE:CA	2:E:4862:PHE:HD2	2.18	0.56
2:G:669:ASP:OD2	2:G:790:ARG:NH2	2.38	0.56
2:G:2042:CYS:SG	2:G:2043:GLY:N	2.76	0.56
2:B:4126:GLU:O	2:B:4130:ASN:ND2	2.38	0.56
2:E:210:GLU:HG3	2:E:337:PRO:HG3	1.86	0.56
2:G:4151:SER:HA	2:G:4160:LEU:HD21	1.87	0.56
2:G:4177:TYR:HE1	2:G:4199:GLU:HB2	1.70	0.56
2:G:4815:ASP:O	2:G:4819:GLY:N	2.37	0.56
2:I:609:CYS:SG	2:I:610:ASN:N	2.78	0.56
2:I:4151:SER:HA	2:I:4160:LEU:HD21	1.87	0.56
2:E:315:CYS:SG	2:E:316:PHE:N	2.79	0.56
2:E:683:ARG:NH1	2:E:707:VAL:O	2.37	0.56
2:G:451:TYR:O	2:G:474:ARG:NH1	2.38	0.56
2:G:2281:ILE:HG23	2:G:2341:VAL:HG11	1.88	0.56
2:I:645:ARG:N	2:I:824:GLU:O	2.38	0.56
2:B:399:GLN:HG2	2:B:403:MET:HE3	1.88	0.56
2:B:2751:LEU:HD11	2:B:2823:ILE:HG21	1.85	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:609:CYS:SG	2:E:610:ASN:N	2.78	0.56
2:G:4126:GLU:O	2:G:4130:ASN:ND2	2.38	0.56
1:H:6:THR:HA	1:H:72:ALA:HA	1.85	0.56
2:I:4126:GLU:O	2:I:4130:ASN:ND2	2.38	0.56
2:B:719:LEU:HD22	2:B:735:GLN:HG2	1.87	0.56
2:B:1830:VAL:HB	2:B:1837:GLN:HA	1.86	0.56
2:E:4012:LEU:O	2:E:4016:LEU:N	2.39	0.56
2:E:4151:SER:HA	2:E:4160:LEU:HD21	1.87	0.56
2:E:4177:TYR:HE1	2:E:4199:GLU:HB2	1.70	0.56
2:I:683:ARG:NH1	2:I:707:VAL:O	2.37	0.56
2:E:399:GLN:HG2	2:E:403:MET:HE3	1.88	0.56
2:E:4126:GLU:O	2:E:4130:ASN:ND2	2.38	0.56
2:E:719:LEU:HD22	2:E:735:GLN:HG2	1.87	0.56
2:G:315:CYS:SG	2:G:316:PHE:N	2.79	0.56
2:G:682:LEU:HD13	2:G:787:VAL:HG11	1.88	0.56
2:G:719:LEU:HD22	2:G:735:GLN:HG2	1.87	0.56
2:B:315:CYS:SG	2:B:316:PHE:N	2.79	0.56
2:E:2287:ALA:HA	2:E:2290:LEU:HD13	1.87	0.56
2:I:4201:ASN:O	2:I:4205:TRP:N	2.38	0.56
2:B:609:CYS:SG	2:B:610:ASN:N	2.78	0.56
2:B:2287:ALA:HA	2:B:2290:LEU:HD13	1.87	0.56
2:E:451:TYR:O	2:E:474:ARG:NH1	2.38	0.56
2:E:669:ASP:OD2	2:E:790:ARG:NH2	2.38	0.56
2:G:2287:ALA:HA	2:G:2290:LEU:HD13	1.87	0.56
2:G:3765:TYR:O	2:G:3769:ARG:N	2.36	0.56
2:I:682:LEU:HD13	2:I:787:VAL:HG11	1.88	0.56
2:G:17:ASP:HB2	2:G:98:HIS:HE1	1.71	0.55
2:I:2281:ILE:HG23	2:I:2341:VAL:HG11	1.88	0.55
2:B:451:TYR:O	2:B:474:ARG:NH1	2.39	0.55
2:I:551:LEU:HD11	2:I:589:LEU:HD13	1.87	0.55
2:B:17:ASP:HB2	2:B:98:HIS:HE1	1.71	0.55
2:B:682:LEU:HD13	2:B:787:VAL:HG11	1.88	0.55
2:B:3843:ASP:H	2:B:3874:VAL:HG13	1.71	0.55
2:E:2281:ILE:HG23	2:E:2341:VAL:HG11	1.88	0.55
2:G:717:ASP:OD1	2:G:720:HIS:ND1	2.40	0.55
2:I:315:CYS:SG	2:I:316:PHE:N	2.79	0.55
2:I:4815:ASP:O	2:I:4819:GLY:N	2.37	0.55
2:B:4563:ARG:NH1	2:B:4815:ASP:OD2	2.36	0.55
2:E:682:LEU:HD13	2:E:787:VAL:HG11	1.88	0.55
2:E:4924:VAL:O	2:E:4928:LEU:N	2.35	0.55
2:G:157:ARG:NH2	2:G:167:ASP:OD1	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:3843:ASP:H	2:G:3874:VAL:HG13	1.70	0.55
2:G:4114:CYS:O	2:G:4131:ARG:NH2	2.40	0.55
2:G:4184:MET:HB3	2:G:4190:ILE:HD13	1.89	0.55
2:B:551:LEU:HD11	2:B:589:LEU:HD13	1.87	0.55
2:B:1090:PHE:HD2	2:B:1202:LEU:HD11	1.72	0.55
2:B:2440:MET:O	2:B:2444:GLN:N	2.36	0.55
2:G:399:GLN:HG2	2:G:403:MET:HE3	1.88	0.55
2:I:717:ASP:OD1	2:I:720:HIS:ND1	2.40	0.55
2:I:718:GLY:HA3	2:I:737:LEU:HA	1.88	0.55
2:B:718:GLY:HA3	2:B:737:LEU:HA	1.88	0.55
2:B:4697:VAL:O	2:B:4701:TRP:N	2.39	0.55
2:I:451:TYR:O	2:I:474:ARG:NH1	2.38	0.55
2:B:1667:LEU:O	2:B:1671:ARG:NH1	2.40	0.55
2:E:551:LEU:HD11	2:E:589:LEU:HD13	1.88	0.55
2:G:393:CYS:SG	2:G:395:GLN:NE2	2.80	0.55
2:G:609:CYS:SG	2:G:610:ASN:N	2.78	0.55
2:G:4201:ASN:O	2:G:4205:TRP:N	2.38	0.55
2:I:2189:LYS:HA	2:I:2192:TYR:HD2	1.72	0.55
2:I:4114:CYS:O	2:I:4131:ARG:NH2	2.40	0.55
2:I:4563:ARG:NH1	2:I:4815:ASP:OD2	2.36	0.55
2:B:717:ASP:OD1	2:B:720:HIS:ND1	2.40	0.55
2:B:2003:GLN:O	2:B:2007:ASN:ND2	2.40	0.55
2:B:4815:ASP:O	2:B:4819:GLY:N	2.37	0.55
2:E:331:VAL:HG11	2:E:336:PRO:HD2	1.89	0.55
2:E:717:ASP:OD1	2:E:720:HIS:ND1	2.40	0.55
2:G:551:LEU:HD11	2:G:589:LEU:HD13	1.88	0.55
2:G:1667:LEU:O	2:G:1671:ARG:NH1	2.40	0.55
2:I:399:GLN:HG2	2:I:403:MET:HE3	1.88	0.55
2:I:1090:PHE:HD2	2:I:1202:LEU:HD11	1.72	0.55
2:I:2003:GLN:O	2:I:2007:ASN:ND2	2.40	0.55
2:I:4177:TYR:HE1	2:I:4199:GLU:HB2	1.70	0.55
2:B:1679:ASN:HA	2:B:1682:ALA:HB3	1.89	0.55
2:B:2281:ILE:HG23	2:B:2341:VAL:HG11	1.88	0.55
2:B:2739:PRO:HB3	2:B:2884:ASN:HB3	1.89	0.55
2:B:4114:CYS:O	2:B:4131:ARG:NH2	2.40	0.55
2:E:4114:CYS:O	2:E:4131:ARG:NH2	2.40	0.55
2:I:17:ASP:HB2	2:I:98:HIS:HE1	1.71	0.55
2:I:219:VAL:HG13	2:I:285:VAL:HG21	1.89	0.55
2:I:1258:ALA:HB3	2:I:1271:ARG:HB3	1.89	0.55
2:B:219:VAL:HG13	2:B:285:VAL:HG21	1.89	0.54
2:B:2189:LYS:HA	2:B:2192:TYR:HD2	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:3767:GLN:NE2	2:E:3804:ILE:O	2.40	0.54
2:G:331:VAL:HG11	2:G:336:PRO:HD2	1.89	0.54
2:G:635:THR:O	1:H:34:LYS:NZ	2.40	0.54
2:G:1258:ALA:HB3	2:G:1271:ARG:HB3	1.89	0.54
2:I:393:CYS:SG	2:I:395:GLN:NE2	2.80	0.54
2:I:488:LEU:O	2:I:492:ASP:N	2.39	0.54
2:B:683:ARG:NH1	2:B:707:VAL:O	2.37	0.54
2:E:1667:LEU:O	2:E:1671:ARG:NH1	2.40	0.54
2:G:2803:GLU:OE2	2:G:2806:ARG:NH1	2.40	0.54
2:I:1721:GLU:OE2	2:I:1725:ARG:NH2	2.38	0.54
2:I:4184:MET:HB3	2:I:4190:ILE:HD13	1.89	0.54
2:E:393:CYS:SG	2:E:395:GLN:NE2	2.80	0.54
2:E:718:GLY:HA3	2:E:737:LEU:HA	1.88	0.54
2:E:1090:PHE:HD2	2:E:1202:LEU:HD11	1.72	0.54
2:G:219:VAL:HG13	2:G:285:VAL:HG21	1.90	0.54
2:G:2003:GLN:O	2:G:2007:ASN:ND2	2.40	0.54
2:I:1679:ASN:HA	2:I:1682:ALA:HB3	1.89	0.54
2:E:2803:GLU:OE2	2:E:2806:ARG:NH1	2.40	0.54
2:E:4184:MET:HB3	2:E:4190:ILE:HD13	1.89	0.54
2:G:718:GLY:HA3	2:G:737:LEU:HA	1.88	0.54
2:I:331:VAL:HG11	2:I:336:PRO:HD2	1.89	0.54
2:B:472:ARG:NH2	2:B:3712:GLU:OE2	2.40	0.54
2:B:1965:TYR:OH	2:B:2027:ILE:O	2.26	0.54
2:B:3992:PHE:O	2:B:3996:PHE:N	2.38	0.54
2:E:645:ARG:N	2:E:824:GLU:O	2.38	0.54
2:E:2003:GLN:O	2:E:2007:ASN:ND2	2.40	0.54
2:E:2189:LYS:HA	2:E:2192:TYR:HD2	1.72	0.54
2:E:4697:VAL:O	2:E:4701:TRP:N	2.39	0.54
2:G:3830:GLN:HA	2:G:3833:GLN:HG2	1.89	0.54
2:B:1258:ALA:HB3	2:B:1271:ARG:HB3	1.89	0.54
2:B:2803:GLU:OE2	2:B:2806:ARG:NH1	2.40	0.54
2:E:472:ARG:NH2	2:E:3712:GLU:OE2	2.40	0.54
2:G:731:THR:OG1	2:G:1519:UNK:O	2.25	0.54
2:G:2189:LYS:HA	2:G:2192:TYR:HD2	1.72	0.54
2:I:3767:GLN:NE2	2:I:3804:ILE:O	2.40	0.54
2:B:393:CYS:SG	2:B:395:GLN:NE2	2.80	0.54
2:E:219:VAL:HG13	2:E:285:VAL:HG21	1.89	0.54
2:G:2739:PRO:HB3	2:G:2884:ASN:HB3	1.89	0.54
2:I:1667:LEU:O	2:I:1671:ARG:NH1	2.40	0.54
2:I:3843:ASP:H	2:I:3874:VAL:HG13	1.71	0.54
2:B:3767:GLN:NE2	2:B:3804:ILE:O	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:3830:GLN:HA	2:B:3833:GLN:HG2	1.89	0.54
2:E:1258:ALA:HB3	2:E:1271:ARG:HB3	1.89	0.54
2:E:2739:PRO:HB3	2:E:2884:ASN:HB3	1.89	0.54
2:E:4815:ASP:O	2:E:4819:GLY:N	2.37	0.54
2:I:4012:LEU:O	2:I:4016:LEU:N	2.39	0.54
2:B:647:ASN:ND2	2:B:820:ARG:O	2.41	0.54
2:B:731:THR:OG1	2:B:1519:UNK:O	2.27	0.54
2:B:4012:LEU:O	2:B:4016:LEU:N	2.39	0.54
2:E:2042:CYS:SG	2:E:2043:GLY:N	2.76	0.54
2:E:3830:GLN:HA	2:E:3833:GLN:HG2	1.89	0.54
2:I:157:ARG:NH2	2:I:167:ASP:OD1	2.38	0.54
2:I:1713:ASP:O	2:I:1717:SER:N	2.41	0.54
2:I:4848:VAL:HG23	2:I:4883:TYR:HE1	1.73	0.54
1:J:62:GLY:HA3	1:J:74:LEU:HD21	1.90	0.54
2:E:17:ASP:HB2	2:E:98:HIS:HE1	1.71	0.53
2:E:1965:TYR:OH	2:E:2027:ILE:O	2.26	0.53
2:G:1090:PHE:HD2	2:G:1202:LEU:HD11	1.72	0.53
2:G:1271:ARG:HA	2:G:1471:UNK:HA	1.89	0.53
2:G:2022:PRO:HB2	2:G:2024:PRO:HD2	1.90	0.53
2:G:3767:GLN:NE2	2:G:3804:ILE:O	2.41	0.53
2:G:4012:LEU:O	2:G:4016:LEU:N	2.39	0.53
2:B:157:ARG:NH2	2:B:167:ASP:OD1	2.38	0.53
2:B:331:VAL:HG11	2:B:336:PRO:HD2	1.89	0.53
2:B:3932:ASP:HA	2:B:3935:TRP:HD1	1.73	0.53
2:B:4184:MET:HB3	2:B:4190:ILE:HD13	1.89	0.53
2:E:4848:VAL:HG23	2:E:4883:TYR:HE1	1.73	0.53
2:G:2336:ARG:HD3	2:G:2435:ARG:HD2	1.89	0.53
2:G:4848:VAL:HG23	2:G:4883:TYR:HE1	1.73	0.53
2:I:4024:VAL:HG23	2:I:4027:LEU:HD12	1.90	0.53
2:B:111:HIS:N	2:B:116:MET:O	2.36	0.53
2:E:2022:PRO:HB2	2:E:2024:PRO:HD2	1.91	0.53
2:E:4824:ARG:O	2:E:4828:SER:N	2.38	0.53
2:I:281:ARG:NH2	2:I:309:THR:OG1	2.41	0.53
2:I:2739:PRO:HB3	2:I:2884:ASN:HB3	1.89	0.53
2:I:2803:GLU:OE2	2:I:2806:ARG:NH1	2.40	0.53
2:B:891:TRP:HA	2:B:902:ARG:HB3	1.90	0.53
2:E:3992:PHE:O	2:E:3996:PHE:N	2.38	0.53
2:G:281:ARG:NH2	2:G:309:THR:OG1	2.41	0.53
2:G:2440:MET:O	2:G:2444:GLN:N	2.36	0.53
2:I:2022:PRO:HB2	2:I:2024:PRO:HD2	1.91	0.53
2:B:1679:ASN:ND2	2:B:1798:LEU:O	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1721:GLU:HG2	2:B:1725:ARG:HH12	1.73	0.53
2:B:4924:VAL:O	2:B:4928:LEU:N	2.35	0.53
2:E:1231:GLN:NE2	2:E:1821:ASP:O	2.42	0.53
2:G:1721:GLU:OE2	2:G:1725:ARG:NH2	2.38	0.53
2:I:3932:ASP:HA	2:I:3935:TRP:HD1	1.73	0.53
2:I:4088:ILE:HG23	2:I:4123:ILE:HB	1.90	0.53
2:B:2336:ARG:HD3	2:B:2435:ARG:HD2	1.89	0.53
2:E:256:ALA:HB1	2:E:286:THR:HG21	1.91	0.53
2:E:1679:ASN:HA	2:E:1682:ALA:HB3	1.89	0.53
1:F:62:GLY:HA3	1:F:74:LEU:HD21	1.90	0.53
2:G:4088:ILE:HG23	2:G:4123:ILE:HB	1.90	0.53
2:I:1231:GLN:NE2	2:I:1821:ASP:O	2.42	0.53
2:I:3830:GLN:HA	2:I:3833:GLN:HG2	1.89	0.53
1:A:62:GLY:HA3	1:A:74:LEU:HD21	1.90	0.53
2:B:2022:PRO:HB2	2:B:2024:PRO:HD2	1.90	0.53
2:E:1679:ASN:ND2	2:E:1798:LEU:O	2.42	0.53
2:G:3781:GLN:HA	2:G:3784:SER:HB3	1.91	0.53
2:I:1960:ALA:O	2:I:1964:ARG:NE	2.42	0.53
2:B:619:ASP:OD1	2:B:1680:ARG:NH1	2.42	0.53
2:E:731:THR:OG1	2:E:1519:UNK:O	2.27	0.53
2:E:891:TRP:HA	2:E:902:ARG:HB3	1.90	0.53
2:E:1721:GLU:OE2	2:E:1725:ARG:NH2	2.39	0.53
2:E:2336:ARG:HD3	2:E:2435:ARG:HD2	1.89	0.53
2:G:1679:ASN:HA	2:G:1682:ALA:HB3	1.89	0.53
2:G:2257:LEU:HD11	2:G:2276:ALA:HB2	1.91	0.53
2:I:647:ASN:ND2	2:I:820:ARG:O	2.41	0.53
2:I:2336:ARG:HD3	2:I:2435:ARG:HD2	1.89	0.53
2:B:1721:GLU:OE2	2:B:1725:ARG:NH2	2.38	0.53
2:B:4978:HIS:HA	2:B:4982:GLU:HB2	1.90	0.53
2:E:488:LEU:O	2:E:492:ASP:N	2.39	0.53
2:E:4978:HIS:HA	2:E:4982:GLU:HB2	1.90	0.53
2:I:1679:ASN:ND2	2:I:1798:LEU:O	2.42	0.53
2:E:157:ARG:NH2	2:E:167:ASP:OD1	2.38	0.53
2:E:1721:GLU:HG2	2:E:1725:ARG:HH12	1.73	0.53
2:G:15:ARG:HD3	2:G:98:HIS:HB3	1.91	0.53
2:G:472:ARG:NH2	2:G:3712:GLU:OE2	2.40	0.53
2:G:619:ASP:OD1	2:G:1680:ARG:NH1	2.42	0.53
2:G:891:TRP:HA	2:G:902:ARG:HB3	1.90	0.53
2:G:3932:ASP:HA	2:G:3935:TRP:HD1	1.73	0.53
2:G:4024:VAL:HG23	2:G:4027:LEU:HD12	1.90	0.53
2:G:4738:ALA:HA	2:G:4743:MET:HE3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:15:ARG:HD3	2:I:98:HIS:HB3	1.91	0.53
2:I:891:TRP:HA	2:I:902:ARG:HB3	1.90	0.53
2:I:3781:GLN:HA	2:I:3784:SER:HB3	1.91	0.53
2:I:4697:VAL:O	2:I:4701:TRP:N	2.39	0.53
2:B:641:VAL:HG21	2:B:705:ASN:HA	1.91	0.52
2:B:877:ASN:HD22	2:B:1045:THR:HG23	1.74	0.52
2:B:1838:PHE:HB3	2:B:1842:LEU:HD11	1.91	0.52
2:B:4201:ASN:O	2:B:4205:TRP:N	2.38	0.52
2:B:4892:ARG:NH2	2:I:4899:ASP:OD1	2.40	0.52
2:E:641:VAL:HG21	2:E:705:ASN:HA	1.91	0.52
2:G:488:LEU:O	2:G:492:ASP:N	2.39	0.52
2:G:1679:ASN:ND2	2:G:1798:LEU:O	2.42	0.52
2:B:281:ARG:NH2	2:B:309:THR:OG1	2.41	0.52
2:B:4780:PHE:O	2:B:4784:PHE:N	2.42	0.52
2:E:877:ASN:HD22	2:E:1045:THR:HG23	1.74	0.52
2:E:2257:LEU:HD11	2:E:2276:ALA:HB2	1.91	0.52
2:G:395:GLN:HG3	2:G:397:GLU:H	1.75	0.52
2:G:1231:GLN:NE2	2:G:1821:ASP:O	2.42	0.52
2:G:4782:VAL:O	2:G:4785:THR:OG1	2.26	0.52
2:I:641:VAL:HG21	2:I:705:ASN:HA	1.91	0.52
2:I:1838:PHE:HB3	2:I:1842:LEU:HD11	1.92	0.52
2:B:4738:ALA:HA	2:B:4743:MET:HE3	1.90	0.52
2:E:206:CYS:SG	2:E:207:SER:N	2.83	0.52
2:I:1865:MET:N	2:I:1865:MET:SD	2.83	0.52
2:B:1865:MET:N	2:B:1865:MET:SD	2.83	0.52
2:B:4024:VAL:HG23	2:B:4027:LEU:HD12	1.90	0.52
2:B:4782:VAL:O	2:B:4785:THR:OG1	2.26	0.52
2:B:4860:ARG:HD2	2:E:4582:VAL:HG11	1.91	0.52
2:E:281:ARG:NH2	2:E:309:THR:OG1	2.41	0.52
2:E:2265:LEU:HB3	2:E:2330:ARG:HG2	1.92	0.52
1:H:62:GLY:HA3	1:H:74:LEU:HD21	1.90	0.52
2:I:4978:HIS:HA	2:I:4982:GLU:HB2	1.90	0.52
1:A:57:LYS:HB2	1:A:80:VAL:HB	1.92	0.52
2:B:206:CYS:SG	2:B:207:SER:N	2.83	0.52
2:B:256:ALA:HB1	2:B:286:THR:HG21	1.91	0.52
2:B:1713:ASP:O	2:B:1717:SER:N	2.41	0.52
2:B:4892:ARG:NH2	2:I:4895:GLY:O	2.43	0.52
2:E:619:ASP:OD1	2:E:1680:ARG:NH1	2.42	0.52
2:E:3932:ASP:HA	2:E:3935:TRP:HD1	1.73	0.52
2:G:256:ALA:HB1	2:G:286:THR:HG21	1.91	0.52
2:G:1965:TYR:OH	2:G:2027:ILE:O	2.26	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:2737:PRO:O	2:I:2888:ARG:NH2	2.43	0.52
2:B:1231:GLN:NE2	2:B:1821:ASP:O	2.42	0.52
2:B:4848:VAL:HG23	2:B:4883:TYR:HE1	1.73	0.52
2:E:647:ASN:ND2	2:E:820:ARG:O	2.41	0.52
2:E:2737:PRO:O	2:E:2888:ARG:NH2	2.43	0.52
2:E:4024:VAL:HG23	2:E:4027:LEU:HD12	1.90	0.52
1:F:57:LYS:HB2	1:F:80:VAL:HB	1.92	0.52
2:G:1721:GLU:HG2	2:G:1725:ARG:HH12	1.74	0.52
2:G:2170:MET:HE1	2:G:2210:VAL:HG23	1.91	0.52
2:G:4697:VAL:O	2:G:4701:TRP:N	2.39	0.52
2:B:395:GLN:HG3	2:B:397:GLU:H	1.74	0.52
2:B:2737:PRO:O	2:B:2888:ARG:NH2	2.43	0.52
2:E:2170:MET:HE1	2:E:2210:VAL:HG23	1.92	0.52
2:E:4782:VAL:O	2:E:4785:THR:OG1	2.26	0.52
2:G:206:CYS:SG	2:G:207:SER:N	2.83	0.52
2:G:2265:LEU:HB3	2:G:2330:ARG:HG2	1.92	0.52
2:G:4824:ARG:O	2:G:4828:SER:N	2.38	0.52
2:G:4924:VAL:O	2:G:4928:LEU:N	2.35	0.52
2:I:317:ARG:HB2	2:I:347:PHE:HB2	1.92	0.52
2:I:4782:VAL:O	2:I:4785:THR:OG1	2.26	0.52
2:B:4040:ILE:O	2:B:4044:MET:N	2.41	0.52
2:E:395:GLN:HG3	2:E:397:GLU:H	1.75	0.52
2:E:1653:LEU:HB3	2:E:1660:GLN:HB2	1.92	0.52
2:E:4088:ILE:HG23	2:E:4123:ILE:HB	1.90	0.52
2:E:4563:ARG:NH1	2:E:4815:ASP:OD2	2.36	0.52
2:G:317:ARG:HB2	2:G:347:PHE:HB2	1.92	0.52
2:G:647:ASN:ND2	2:G:820:ARG:O	2.41	0.52
2:I:877:ASN:HD22	2:I:1045:THR:HG23	1.74	0.52
2:I:880:GLU:OE1	2:I:968:ALA:N	2.43	0.52
2:I:1653:LEU:HB3	2:I:1660:GLN:HB2	1.92	0.52
2:I:2457:LEU:HD23	2:I:2460:LEU:HD12	1.92	0.52
2:B:880:GLU:OE1	2:B:968:ALA:N	2.43	0.52
2:E:15:ARG:HD3	2:E:98:HIS:HB3	1.91	0.52
2:E:3781:GLN:HA	2:E:3784:SER:HB3	1.91	0.52
2:E:4738:ALA:HA	2:E:4743:MET:HE3	1.90	0.52
2:G:877:ASN:HD22	2:G:1045:THR:HG23	1.74	0.52
2:G:1653:LEU:HB3	2:G:1660:GLN:HB2	1.92	0.52
2:G:1838:PHE:HB3	2:G:1842:LEU:HD11	1.92	0.52
2:G:1865:MET:N	2:G:1865:MET:SD	2.83	0.52
2:G:3992:PHE:O	2:G:3996:PHE:N	2.38	0.52
2:I:1721:GLU:HG2	2:I:1725:ARG:HH12	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:4738:ALA:HA	2:I:4743:MET:HE3	1.90	0.52
2:B:2170:MET:HE1	2:B:2210:VAL:HG23	1.91	0.52
2:B:3781:GLN:HA	2:B:3784:SER:HB3	1.91	0.52
2:E:728:ARG:NH2	2:E:1527:UNK:O	2.43	0.52
2:E:2368:LEU:HD13	2:E:2376:LEU:HB2	1.91	0.52
2:G:111:HIS:CD2	2:G:114:SER:H	2.28	0.52
2:G:1636:MET:HE2	2:G:1638:ALA:HB2	1.92	0.52
2:G:2457:LEU:HD23	2:G:2460:LEU:HD12	1.92	0.52
2:I:619:ASP:OD1	2:I:1680:ARG:NH1	2.42	0.52
1:J:25:HIS:HB3	1:J:40:ARG:HD3	1.92	0.52
2:B:1653:LEU:HB3	2:B:1660:GLN:HB2	1.92	0.51
2:B:1960:ALA:O	2:B:1964:ARG:NE	2.42	0.51
2:B:2257:LEU:HD11	2:B:2276:ALA:HB2	1.91	0.51
2:B:2368:LEU:HD13	2:B:2376:LEU:HB2	1.91	0.51
2:B:4088:ILE:HG23	2:B:4123:ILE:HB	1.90	0.51
2:E:1838:PHE:HB3	2:E:1842:LEU:HD11	1.92	0.51
2:G:641:VAL:HG21	2:G:705:ASN:HA	1.91	0.51
2:G:792:LEU:HD22	2:G:799:GLU:H	1.75	0.51
2:G:2368:LEU:HD13	2:G:2376:LEU:HB2	1.91	0.51
2:I:472:ARG:NH2	2:I:3712:GLU:OE2	2.40	0.51
2:I:1684:ALA:HA	2:I:1782:PHE:HZ	1.75	0.51
2:I:4780:PHE:O	2:I:4784:PHE:N	2.42	0.51
2:I:4855:ALA:HA	2:I:4859:PHE:HB2	1.92	0.51
2:B:15:ARG:HD3	2:B:98:HIS:HB3	1.91	0.51
2:B:2457:LEU:HD23	2:B:2460:LEU:HD12	1.92	0.51
2:E:1865:MET:N	2:E:1865:MET:SD	2.83	0.51
2:G:2737:PRO:O	2:G:2888:ARG:NH2	2.43	0.51
2:G:4978:HIS:HA	2:G:4982:GLU:HB2	1.90	0.51
2:I:103:TYR:HB3	2:I:152:PRO:HD3	1.92	0.51
2:I:206:CYS:SG	2:I:207:SER:N	2.83	0.51
2:I:256:ALA:HB1	2:I:286:THR:HG21	1.91	0.51
2:I:1636:MET:HE2	2:I:1638:ALA:HB2	1.92	0.51
2:I:1727:ARG:HH12	2:I:1772:ARG:HB3	1.76	0.51
2:I:4571:PHE:O	2:I:4575:PHE:N	2.43	0.51
2:B:43:GLY:N	2:B:447:ASP:OD2	2.43	0.51
2:B:1659:LEU:O	2:B:1663:HIS:N	2.41	0.51
2:E:111:HIS:CD2	2:E:114:SER:H	2.28	0.51
2:G:1684:ALA:HA	2:G:1782:PHE:HZ	1.76	0.51
2:G:1713:ASP:O	2:G:1717:SER:N	2.41	0.51
2:I:111:HIS:N	2:I:116:MET:O	2.36	0.51
2:I:4824:ARG:O	2:I:4828:SER:N	2.38	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:111:HIS:CD2	2:B:114:SER:H	2.28	0.51
1:F:87:HIS:N	1:F:91:ILE:O	2.44	0.51
2:G:103:TYR:HB3	2:G:152:PRO:HD3	1.91	0.51
2:G:3955:MET:HG3	2:G:4019:LEU:HD22	1.93	0.51
2:G:4040:ILE:O	2:G:4044:MET:N	2.41	0.51
1:H:57:LYS:HB2	1:H:80:VAL:HB	1.92	0.51
1:H:87:HIS:N	1:H:91:ILE:O	2.44	0.51
2:I:2257:LEU:HD11	2:I:2276:ALA:HB2	1.91	0.51
2:I:4040:ILE:O	2:I:4044:MET:N	2.41	0.51
1:A:87:HIS:N	1:A:91:ILE:O	2.44	0.51
2:B:317:ARG:HB2	2:B:347:PHE:HB2	1.92	0.51
2:B:1727:ARG:HH12	2:B:1772:ARG:HB3	1.76	0.51
2:E:2190:VAL:HA	2:E:2193:GLN:HB2	1.93	0.51
2:E:4780:PHE:O	2:E:4784:PHE:N	2.42	0.51
2:E:4998:LYS:HB3	2:E:5003:HIS:HE1	1.76	0.51
2:I:792:LEU:HD22	2:I:799:GLU:H	1.76	0.51
2:I:2368:LEU:HD13	2:I:2376:LEU:HB2	1.91	0.51
1:J:57:LYS:HB2	1:J:80:VAL:HB	1.92	0.51
2:B:637:LEU:HD23	2:B:1637:MET:HB3	1.93	0.51
2:B:3955:MET:HG3	2:B:4019:LEU:HD22	1.93	0.51
2:E:1960:ALA:O	2:E:1964:ARG:NE	2.42	0.51
2:E:3552:UNK:O	2:E:3556:UNK:N	2.43	0.51
2:G:728:ARG:NH2	2:G:1527:UNK:O	2.44	0.51
2:I:111:HIS:CD2	2:I:114:SER:H	2.28	0.51
2:I:2170:MET:HE1	2:I:2210:VAL:HG23	1.91	0.51
2:B:792:LEU:HD22	2:B:799:GLU:H	1.76	0.51
2:B:2758:PHE:O	2:B:2762:THR:N	2.43	0.51
2:E:43:GLY:N	2:E:447:ASP:OD2	2.44	0.51
2:E:111:HIS:N	2:E:116:MET:O	2.36	0.51
2:E:792:LEU:HD22	2:E:799:GLU:H	1.76	0.51
2:E:4899:ASP:OD1	2:G:4892:ARG:NH2	2.37	0.51
2:G:671:VAL:HG22	2:G:740:PRO:HG3	1.93	0.51
2:G:3552:UNK:O	2:G:3556:UNK:N	2.44	0.51
2:G:4918:ILE:HD13	2:I:4892:ARG:HD3	1.92	0.51
2:I:3756:LYS:O	2:I:3760:LYS:NZ	2.37	0.51
2:B:103:TYR:HB3	2:B:152:PRO:HD3	1.92	0.51
2:B:1694:LEU:O	2:B:1712:TYR:OH	2.24	0.51
2:B:2265:LEU:HB3	2:B:2330:ARG:HG2	1.92	0.51
2:B:3552:UNK:O	2:B:3556:UNK:N	2.44	0.51
2:B:4934:GLY:HA3	2:E:4937:ILE:HD12	1.92	0.51
2:E:637:LEU:HD23	2:E:1637:MET:HB3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:639:ASN:H	2:G:678:GLN:HE22	1.59	0.51
2:G:1727:ARG:HH12	2:G:1772:ARG:HB3	1.76	0.51
2:G:2235:PHE:HA	2:G:2238:TYR:HD2	1.76	0.51
2:G:4859:PHE:CA	2:G:4862:PHE:CD2	2.75	0.51
2:I:2235:PHE:HA	2:I:2238:TYR:HD2	1.76	0.51
2:I:2265:LEU:HB3	2:I:2330:ARG:HG2	1.92	0.51
2:I:3955:MET:HG3	2:I:4019:LEU:HD22	1.93	0.51
1:J:29:MET:HB3	1:J:98:ILE:HB	1.93	0.51
2:B:1636:MET:HE2	2:B:1638:ALA:HB2	1.92	0.51
2:B:4855:ALA:HA	2:B:4859:PHE:HB2	1.92	0.51
2:E:103:TYR:HB3	2:E:152:PRO:HD3	1.92	0.51
2:E:880:GLU:OE1	2:E:968:ALA:N	2.43	0.51
2:E:1713:ASP:O	2:E:1717:SER:N	2.41	0.51
2:E:2248:ARG:NH2	2:E:2285:GLU:OE1	2.44	0.51
2:E:4843:LEU:HD22	2:E:4928:LEU:HD11	1.93	0.51
2:G:1778:SER:N	2:G:1799:SER:O	2.44	0.51
2:G:1960:ALA:O	2:G:1964:ARG:NE	2.42	0.51
2:B:709:ASP:O	2:B:725:HIS:ND1	2.44	0.51
2:B:1071:ARG:HD3	2:B:1241:SER:HB3	1.93	0.51
2:B:2248:ARG:NH2	2:B:2285:GLU:OE1	2.44	0.51
2:B:3904:ARG:NH2	2:B:3973:CYS:SG	2.84	0.51
2:E:317:ARG:HB2	2:E:347:PHE:HB2	1.92	0.51
2:E:2013:LYS:HA	2:E:2028:ARG:HB2	1.93	0.51
2:E:2770:LYS:HB3	2:E:2775:TRP:HB2	1.93	0.51
2:E:3955:MET:HG3	2:E:4019:LEU:HD22	1.93	0.51
2:E:4745:LEU:O	2:E:4749:GLU:N	2.43	0.51
2:I:43:GLY:N	2:I:447:ASP:OD2	2.43	0.51
2:I:671:VAL:HG22	2:I:740:PRO:HG3	1.93	0.51
2:I:731:THR:OG1	2:I:1519:UNK:O	2.29	0.51
2:I:1109:LEU:HA	2:I:1120:LEU:HD21	1.93	0.51
2:I:2190:VAL:HA	2:I:2193:GLN:HB2	1.93	0.51
2:I:4570:ALA:O	2:I:4574:ASN:ND2	2.44	0.51
2:B:639:ASN:H	2:B:678:GLN:HE22	1.59	0.50
2:B:1684:ALA:HA	2:B:1782:PHE:HZ	1.75	0.50
2:E:639:ASN:H	2:E:678:GLN:HE22	1.59	0.50
2:I:2248:ARG:NH2	2:I:2285:GLU:OE1	2.44	0.50
2:I:4998:LYS:HB3	2:I:5003:HIS:HE1	1.76	0.50
2:B:134:ASP:HA	2:B:192:ASP:HA	1.94	0.50
2:B:1865:MET:HB3	2:B:1926:LEU:HB2	1.94	0.50
2:B:2770:LYS:HB3	2:B:2775:TRP:HB2	1.94	0.50
2:E:1865:MET:HB3	2:E:1926:LEU:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:4570:ALA:O	2:E:4574:ASN:ND2	2.44	0.50
1:F:25:HIS:HB3	1:F:40:ARG:HD3	1.92	0.50
2:G:1071:ARG:HD3	2:G:1241:SER:HB3	1.92	0.50
2:G:4843:LEU:HD22	2:G:4928:LEU:HD11	1.93	0.50
2:I:396:GLU:O	2:I:400:ALA:N	2.40	0.50
2:I:1659:LEU:O	2:I:1663:HIS:N	2.41	0.50
2:B:932:LEU:HD23	2:B:935:LEU:HD12	1.94	0.50
2:B:4998:LYS:HB3	2:B:5003:HIS:HE1	1.76	0.50
2:E:54:ASN:O	2:E:58:VAL:N	2.43	0.50
2:E:1241:SER:HA	2:E:1603:VAL:HA	1.92	0.50
2:E:1636:MET:HE2	2:E:1638:ALA:HB2	1.92	0.50
2:E:3889:GLN:OE1	2:E:3960:GLN:NE2	2.45	0.50
2:G:637:LEU:HD23	2:G:1637:MET:HB3	1.92	0.50
2:G:709:ASP:O	2:G:725:HIS:ND1	2.44	0.50
2:I:395:GLN:HG3	2:I:397:GLU:H	1.74	0.50
2:I:932:LEU:HD23	2:I:935:LEU:HD12	1.94	0.50
2:B:2235:PHE:HA	2:B:2238:TYR:HD2	1.76	0.50
2:B:4570:ALA:O	2:B:4574:ASN:ND2	2.44	0.50
2:E:69:LEU:HD22	2:E:107:ILE:HD11	1.93	0.50
2:E:134:ASP:HA	2:E:192:ASP:HA	1.94	0.50
2:E:232:THR:HB	2:E:252:VAL:HG11	1.93	0.50
2:E:1727:ARG:HH12	2:E:1772:ARG:HB3	1.76	0.50
2:E:2235:PHE:HA	2:E:2238:TYR:HD2	1.76	0.50
2:G:2248:ARG:NH2	2:G:2285:GLU:OE1	2.44	0.50
2:G:2770:LYS:HB3	2:G:2775:TRP:HB2	1.93	0.50
2:I:3772:THR:OG1	2:I:3815:LYS:NZ	2.44	0.50
2:I:4109:GLN:O	2:I:4113:SER:N	2.43	0.50
2:I:4843:LEU:HD22	2:I:4928:LEU:HD11	1.93	0.50
2:B:1109:LEU:HA	2:B:1120:LEU:HD21	1.93	0.50
2:E:1684:ALA:HA	2:E:1782:PHE:HZ	1.76	0.50
2:E:1778:SER:N	2:E:1799:SER:O	2.44	0.50
2:E:2457:LEU:HD23	2:E:2460:LEU:HD12	1.92	0.50
2:G:880:GLU:OE1	2:G:968:ALA:N	2.43	0.50
2:G:2190:VAL:HA	2:G:2193:GLN:HB2	1.93	0.50
2:G:4855:ALA:HA	2:G:4859:PHE:HB2	1.92	0.50
1:H:29:MET:HB3	1:H:98:ILE:HB	1.93	0.50
2:I:2013:LYS:HA	2:I:2028:ARG:HB2	1.93	0.50
2:I:4184:MET:HE2	2:I:4188:ARG:HA	1.94	0.50
2:B:1241:SER:HA	2:B:1603:VAL:HA	1.92	0.50
2:B:3765:TYR:O	2:B:3769:ARG:N	2.36	0.50
2:E:2927:LEU:HD23	2:E:2930:LEU:HD12	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:932:LEU:HD23	2:G:935:LEU:HD12	1.94	0.50
2:G:1109:LEU:HA	2:G:1120:LEU:HD21	1.93	0.50
2:G:1931:LEU:HB3	2:G:1935:VAL:HB	1.94	0.50
2:G:2257:LEU:O	2:G:2261:SER:N	2.45	0.50
2:G:2466:LEU:HA	2:G:2469:ILE:HD12	1.94	0.50
2:G:3904:ARG:NH2	2:G:3973:CYS:SG	2.84	0.50
2:I:2758:PHE:O	2:I:2762:THR:N	2.43	0.50
2:B:1721:GLU:O	2:B:1725:ARG:NH2	2.45	0.50
2:B:1778:SER:N	2:B:1799:SER:O	2.44	0.50
2:B:3910:THR:HG23	2:B:3911:THR:HG23	1.93	0.50
2:B:4634:GLU:HG3	2:B:4636:THR:H	1.77	0.50
2:E:671:VAL:HG22	2:E:740:PRO:HG3	1.93	0.50
2:E:1071:ARG:HD3	2:E:1241:SER:HB3	1.92	0.50
2:E:2466:LEU:HA	2:E:2469:ILE:HD12	1.94	0.50
2:G:69:LEU:HD22	2:G:107:ILE:HD11	1.93	0.50
2:G:1721:GLU:O	2:G:1725:ARG:NH2	2.45	0.50
2:G:2013:LYS:HA	2:G:2028:ARG:HB2	1.93	0.50
2:G:2927:LEU:HD23	2:G:2930:LEU:HD12	1.94	0.50
2:G:4998:LYS:HB3	2:G:5003:HIS:HE1	1.76	0.50
2:I:639:ASN:H	2:I:678:GLN:HE22	1.59	0.50
2:I:2770:LYS:HB3	2:I:2775:TRP:HB2	1.94	0.50
2:I:3552:UNK:O	2:I:3556:UNK:N	2.44	0.50
2:I:4634:GLU:HG3	2:I:4636:THR:H	1.77	0.50
2:B:488:LEU:O	2:B:492:ASP:N	2.39	0.50
2:B:671:VAL:HG22	2:B:740:PRO:HG3	1.93	0.50
2:B:2013:LYS:HA	2:B:2028:ARG:HB2	1.93	0.50
2:B:4843:LEU:HD22	2:B:4928:LEU:HD11	1.93	0.50
2:E:932:LEU:HD23	2:E:935:LEU:HD12	1.94	0.50
2:E:1163:THR:HA	2:E:1168:VAL:HA	1.94	0.50
2:G:1865:MET:HB3	2:G:1926:LEU:HB2	1.94	0.50
2:G:4634:GLU:HG3	2:G:4636:THR:H	1.77	0.50
1:H:25:HIS:HB3	1:H:40:ARG:HD3	1.92	0.50
2:I:134:ASP:HA	2:I:192:ASP:HA	1.94	0.50
2:I:709:ASP:O	2:I:725:HIS:ND1	2.44	0.50
2:I:1721:GLU:O	2:I:1725:ARG:NH2	2.45	0.50
2:I:3910:THR:HG23	2:I:3911:THR:HG23	1.93	0.50
2:B:3889:GLN:OE1	2:B:3960:GLN:NE2	2.45	0.50
2:B:4184:MET:HE2	2:B:4188:ARG:HA	1.94	0.50
2:E:124:SER:HA	2:E:132:ALA:HB3	1.93	0.50
2:E:1721:GLU:O	2:E:1725:ARG:NH2	2.45	0.50
2:E:4634:GLU:HG3	2:E:4636:THR:H	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:670:GLU:H	2:G:740:PRO:HB3	1.77	0.50
2:G:1241:SER:HA	2:G:1603:VAL:HA	1.92	0.50
2:G:2420:HIS:ND1	2:G:2493:UNK:O	2.33	0.50
2:G:3889:GLN:OE1	2:G:3960:GLN:NE2	2.45	0.50
2:I:379:HIS:CD2	2:I:382:GLY:H	2.27	0.50
2:I:1778:SER:N	2:I:1799:SER:O	2.44	0.50
2:B:4571:PHE:O	2:B:4575:PHE:N	2.43	0.49
2:E:684:VAL:HG23	2:E:781:VAL:HB	1.94	0.49
2:E:709:ASP:O	2:E:725:HIS:ND1	2.44	0.49
2:E:3904:ARG:NH2	2:E:3973:CYS:SG	2.84	0.49
2:E:4571:PHE:O	2:E:4575:PHE:N	2.43	0.49
2:G:134:ASP:HA	2:G:192:ASP:HA	1.94	0.49
2:G:3761:GLN:HB3	2:G:4754:ASN:HA	1.93	0.49
2:G:3772:THR:OG1	2:G:3815:LYS:NZ	2.44	0.49
2:G:4560:TYR:O	2:G:4564:PHE:N	2.45	0.49
2:G:5012:LYS:O	2:G:5016:GLU:N	2.44	0.49
2:I:1865:MET:HB3	2:I:1926:LEU:HB2	1.94	0.49
2:I:2257:LEU:O	2:I:2261:SER:N	2.45	0.49
2:I:4924:VAL:O	2:I:4928:LEU:N	2.35	0.49
1:J:87:HIS:N	1:J:91:ILE:O	2.44	0.49
2:B:2132:GLY:O	2:B:2136:ARG:N	2.46	0.49
2:B:3756:LYS:O	2:B:3760:LYS:NZ	2.37	0.49
2:B:4582:VAL:HG11	2:I:4860:ARG:HD2	1.94	0.49
2:E:1931:LEU:HB3	2:E:1935:VAL:HB	1.94	0.49
2:I:637:LEU:HD23	2:I:1637:MET:HB3	1.92	0.49
2:I:1241:SER:HA	2:I:1603:VAL:HA	1.92	0.49
2:I:3904:ARG:NH2	2:I:3973:CYS:SG	2.84	0.49
1:A:25:HIS:HB3	1:A:40:ARG:HD3	1.92	0.49
2:B:124:SER:HA	2:B:132:ALA:HB3	1.94	0.49
2:B:670:GLU:H	2:B:740:PRO:HB3	1.77	0.49
2:E:670:GLU:H	2:E:740:PRO:HB3	1.77	0.49
2:E:2257:LEU:O	2:E:2261:SER:N	2.45	0.49
2:E:2758:PHE:O	2:E:2762:THR:N	2.44	0.49
2:E:3910:THR:HG23	2:E:3911:THR:HG23	1.93	0.49
2:E:4875:LYS:HB3	2:E:4882:CYS:HA	1.95	0.49
2:G:124:SER:HA	2:G:132:ALA:HB3	1.94	0.49
2:G:1111:PRO:HD3	2:G:1605:TRP:HE1	1.78	0.49
2:G:4875:LYS:HB3	2:G:4882:CYS:HA	1.95	0.49
2:I:670:GLU:H	2:I:740:PRO:HB3	1.77	0.49
2:I:2466:LEU:HA	2:I:2469:ILE:HD12	1.94	0.49
2:B:684:VAL:HG23	2:B:781:VAL:HB	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2190:VAL:HA	2:B:2193:GLN:HB2	1.93	0.49
2:B:3761:GLN:HB3	2:B:4754:ASN:HA	1.93	0.49
2:E:1109:LEU:HA	2:E:1120:LEU:HD21	1.93	0.49
2:E:4040:ILE:O	2:E:4044:MET:N	2.41	0.49
2:E:4546:VAL:O	2:E:4550:LYS:N	2.42	0.49
2:G:232:THR:HB	2:G:252:VAL:HG11	1.93	0.49
2:G:4570:ALA:O	2:G:4574:ASN:ND2	2.44	0.49
2:G:4859:PHE:C	2:G:4862:PHE:HD2	2.20	0.49
2:I:124:SER:HA	2:I:132:ALA:HB3	1.94	0.49
2:B:1931:LEU:HB3	2:B:1935:VAL:HB	1.94	0.49
2:B:2927:LEU:HD23	2:B:2930:LEU:HD12	1.94	0.49
2:B:5012:LYS:O	2:B:5016:GLU:N	2.44	0.49
2:E:4710:SER:OG	2:E:4772:ASP:OD2	2.28	0.49
2:G:1163:THR:HA	2:G:1168:VAL:HA	1.94	0.49
2:G:2132:GLY:O	2:G:2136:ARG:N	2.46	0.49
2:G:3910:THR:HG23	2:G:3911:THR:HG23	1.93	0.49
2:I:164:ARG:N	2:I:167:ASP:OD2	2.46	0.49
2:I:1071:ARG:HD3	2:I:1241:SER:HB3	1.93	0.49
2:I:1931:LEU:HB3	2:I:1935:VAL:HB	1.94	0.49
2:I:2132:GLY:O	2:I:2136:ARG:N	2.46	0.49
2:I:3889:GLN:OE1	2:I:3960:GLN:NE2	2.45	0.49
2:I:5012:LYS:O	2:I:5016:GLU:N	2.44	0.49
2:B:3772:THR:OG1	2:B:3815:LYS:NZ	2.44	0.49
1:F:29:MET:HB3	1:F:98:ILE:HB	1.93	0.49
2:G:43:GLY:N	2:G:447:ASP:OD2	2.43	0.49
2:G:4184:MET:HE2	2:G:4188:ARG:HA	1.94	0.49
2:I:252:VAL:HA	2:I:255:HIS:HB2	1.94	0.49
2:I:988:LEU:O	2:I:992:GLY:N	2.44	0.49
2:I:1936:LYS:HZ3	2:I:2105:TRP:CG	2.30	0.49
2:I:2927:LEU:HD23	2:I:2930:LEU:HD12	1.94	0.49
2:I:4875:LYS:HB3	2:I:4882:CYS:HA	1.95	0.49
2:B:988:LEU:O	2:B:992:GLY:N	2.45	0.49
2:E:3761:GLN:HB3	2:E:4754:ASN:HA	1.93	0.49
2:E:3765:TYR:O	2:E:3769:ARG:N	2.36	0.49
2:E:3772:THR:OG1	2:E:3815:LYS:NZ	2.44	0.49
2:E:4184:MET:HE2	2:E:4188:ARG:HA	1.94	0.49
2:G:78:LEU:O	2:G:82:LEU:N	2.44	0.49
2:G:864:PRO:HD2	2:G:867:LEU:HD12	1.94	0.49
2:I:1841:VAL:HA	2:I:1844:LEU:HB3	1.95	0.49
2:I:3761:GLN:HB3	2:I:4754:ASN:HA	1.93	0.49
2:B:1841:VAL:HA	2:B:1844:LEU:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:3840:SER:OG	2:B:3875:MET:O	2.25	0.49
2:E:495:ASN:HD21	2:E:550:LYS:HD2	1.77	0.49
2:E:1841:VAL:HA	2:E:1844:LEU:HB3	1.95	0.49
2:G:1730:MET:HE1	2:G:1773:PRO:HG3	1.95	0.49
2:I:69:LEU:HD22	2:I:107:ILE:HD11	1.93	0.49
2:I:864:PRO:HD2	2:I:867:LEU:HD12	1.94	0.49
2:I:1163:THR:HA	2:I:1168:VAL:HA	1.94	0.49
2:I:3905:THR:HA	2:I:3912:THR:HG23	1.95	0.49
2:I:4560:TYR:O	2:I:4564:PHE:N	2.45	0.49
2:B:396:GLU:O	2:B:400:ALA:N	2.40	0.49
2:B:867:LEU:HD22	2:B:929:LEU:HD22	1.95	0.49
2:B:2466:LEU:HA	2:B:2469:ILE:HD12	1.94	0.49
2:B:4875:LYS:HB3	2:B:4882:CYS:HA	1.95	0.49
2:E:1111:PRO:HD3	2:E:1605:TRP:HE1	1.78	0.49
2:E:1229:ASN:O	2:E:1827:ARG:N	2.42	0.49
2:E:1737:PRO:HG2	2:E:1739:THR:HG23	1.95	0.49
2:E:3756:LYS:O	2:E:3760:LYS:NZ	2.37	0.49
2:G:1841:VAL:HA	2:G:1844:LEU:HB3	1.95	0.49
2:I:2336:ARG:NH2	2:I:2428:ALA:O	2.46	0.49
2:B:379:HIS:CD2	2:B:382:GLY:H	2.27	0.49
2:B:2143:THR:O	2:B:3651:ASN:ND2	2.38	0.49
2:B:2257:LEU:O	2:B:2261:SER:N	2.45	0.49
2:E:864:PRO:HD2	2:E:867:LEU:HD12	1.94	0.49
1:H:7:ILE:HG22	1:H:9:PRO:HD2	1.94	0.49
2:I:1111:PRO:HD3	2:I:1605:TRP:HE1	1.78	0.49
2:I:1663:HIS:O	2:I:1667:LEU:N	2.46	0.49
2:I:1965:TYR:OH	2:I:2027:ILE:O	2.26	0.49
2:I:3840:SER:OG	2:I:3875:MET:O	2.25	0.49
2:B:232:THR:HB	2:B:252:VAL:HG11	1.93	0.48
2:B:252:VAL:HA	2:B:255:HIS:HB2	1.95	0.48
2:B:797:HIS:HB3	2:B:1625:GLY:H	1.78	0.48
2:B:1163:THR:HA	2:B:1168:VAL:HA	1.94	0.48
2:G:54:ASN:O	2:G:58:VAL:N	2.43	0.48
2:G:867:LEU:HD22	2:G:929:LEU:HD22	1.95	0.48
2:G:988:LEU:O	2:G:992:GLY:N	2.45	0.48
2:I:867:LEU:HD22	2:I:929:LEU:HD22	1.95	0.48
2:I:1952:GLN:HA	2:I:1955:VAL:HG12	1.95	0.48
2:I:2104:ARG:HA	2:I:2107:GLN:HB3	1.95	0.48
2:I:2868:SER:O	2:I:2872:GLN:N	2.46	0.48
1:A:7:ILE:HG22	1:A:9:PRO:HD2	1.94	0.48
2:B:164:ARG:N	2:B:167:ASP:OD2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:629:ARG:HB3	2:B:634:GLN:NE2	2.29	0.48
2:B:1111:PRO:HD3	2:B:1605:TRP:HE1	1.78	0.48
2:E:2868:SER:O	2:E:2872:GLN:N	2.46	0.48
2:G:1229:ASN:O	2:G:1827:ARG:N	2.42	0.48
2:I:2318:TYR:OH	2:I:2414:ASN:N	2.45	0.48
1:A:29:MET:HB3	1:A:98:ILE:HB	1.93	0.48
2:B:54:ASN:O	2:B:58:VAL:N	2.43	0.48
2:B:69:LEU:HD22	2:B:107:ILE:HD11	1.93	0.48
2:B:864:PRO:HD2	2:B:867:LEU:HD12	1.94	0.48
2:B:1952:GLN:HA	2:B:1955:VAL:HG12	1.95	0.48
2:E:1659:LEU:O	2:E:1663:HIS:N	2.40	0.48
2:G:2868:SER:O	2:G:2872:GLN:N	2.46	0.48
2:I:266:ARG:NH2	2:I:269:TRP:O	2.46	0.48
2:I:1294:UNK:HA	2:I:1455:UNK:HA	1.96	0.48
2:B:1730:MET:HE1	2:B:1773:PRO:HG3	1.95	0.48
2:E:913:LEU:HD13	2:E:918:ARG:HA	1.96	0.48
1:F:7:ILE:HG22	1:F:9:PRO:HD2	1.94	0.48
2:G:266:ARG:NH2	2:G:269:TRP:O	2.46	0.48
2:G:629:ARG:HB3	2:G:634:GLN:NE2	2.28	0.48
2:I:485:SER:O	2:I:489:ASN:N	2.46	0.48
2:I:495:ASN:HD21	2:I:550:LYS:HD2	1.77	0.48
2:I:1730:MET:HE1	2:I:1773:PRO:HG3	1.95	0.48
2:B:1227:ALA:HB1	2:B:1230:MET:HG3	1.95	0.48
2:E:988:LEU:O	2:E:992:GLY:N	2.45	0.48
2:E:2318:TYR:OH	2:E:2414:ASN:N	2.45	0.48
2:E:4705:VAL:HB	2:E:4778:TRP:CG	2.48	0.48
2:G:1718:ILE:HG13	2:G:1719:HIS:CD2	2.48	0.48
2:G:2104:ARG:HA	2:G:2107:GLN:HB3	1.95	0.48
2:G:4928:LEU:HA	2:G:4931:ILE:HD12	1.95	0.48
2:I:913:LEU:HD13	2:I:918:ARG:HA	1.96	0.48
2:I:4705:VAL:HB	2:I:4778:TRP:CG	2.49	0.48
2:B:2104:ARG:HA	2:B:2107:GLN:HB3	1.95	0.48
2:B:2318:TYR:OH	2:B:2414:ASN:N	2.45	0.48
2:B:2868:SER:O	2:B:2872:GLN:N	2.46	0.48
2:E:266:ARG:NH2	2:E:269:TRP:O	2.47	0.48
2:E:629:ARG:HB3	2:E:634:GLN:NE2	2.29	0.48
2:E:867:LEU:HD22	2:E:929:LEU:HD22	1.95	0.48
2:E:3993:LEU:HA	2:E:3996:PHE:HB2	1.96	0.48
2:G:707:VAL:HG23	2:G:713:SER:HB2	1.96	0.48
2:I:232:THR:HB	2:I:252:VAL:HG11	1.93	0.48
2:I:1668:ARG:HA	2:I:1671:ARG:HH11	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:3992:PHE:O	2:I:3996:PHE:N	2.38	0.48
2:I:4745:LEU:O	2:I:4749:GLU:N	2.43	0.48
2:B:266:ARG:NH2	2:B:269:TRP:O	2.46	0.48
2:B:4705:VAL:HB	2:B:4778:TRP:CG	2.49	0.48
2:E:164:ARG:N	2:E:167:ASP:OD2	2.46	0.48
2:E:1668:ARG:HA	2:E:1671:ARG:HH11	1.79	0.48
2:G:164:ARG:N	2:G:167:ASP:OD2	2.46	0.48
2:G:252:VAL:HA	2:G:255:HIS:HB2	1.95	0.48
2:G:396:GLU:O	2:G:400:ALA:N	2.41	0.48
2:G:495:ASN:HD21	2:G:550:LYS:HD2	1.77	0.48
2:G:684:VAL:HG23	2:G:781:VAL:HB	1.94	0.48
2:G:1203:ASN:ND2	2:G:1210:SER:O	2.47	0.48
2:G:1952:GLN:HA	2:G:1955:VAL:HG12	1.95	0.48
2:G:4705:VAL:HB	2:G:4778:TRP:CG	2.48	0.48
2:I:668:VAL:HG22	2:I:789:VAL:HG23	1.96	0.48
2:I:1227:ALA:HB1	2:I:1230:MET:HG3	1.95	0.48
2:I:1718:ILE:HG13	2:I:1719:HIS:CD2	2.49	0.48
1:J:7:ILE:HG22	1:J:9:PRO:HD2	1.94	0.48
2:B:4138:ASP:OD1	2:B:4138:ASP:N	2.46	0.48
2:B:4745:LEU:O	2:B:4749:GLU:N	2.43	0.48
2:E:220:LEU:HD11	2:E:390:LEU:HD22	1.95	0.48
2:E:2336:ARG:NH2	2:E:2428:ALA:O	2.46	0.48
2:G:220:LEU:HD11	2:G:390:LEU:HD22	1.95	0.48
2:G:485:SER:O	2:G:489:ASN:N	2.46	0.48
2:I:707:VAL:HG23	2:I:713:SER:HB2	1.96	0.48
2:B:469:ARG:HH21	2:B:3712:GLU:HB3	1.79	0.48
2:B:495:ASN:HD21	2:B:550:LYS:HD2	1.77	0.48
2:B:1203:ASN:ND2	2:B:1210:SER:O	2.47	0.48
2:B:1764:GLY:HA3	2:B:1859:VAL:HG11	1.96	0.48
2:E:707:VAL:HG23	2:E:713:SER:HB2	1.96	0.48
2:E:914:PRO:O	2:E:918:ARG:N	2.46	0.48
2:E:1730:MET:HE1	2:E:1773:PRO:HG3	1.94	0.48
2:E:1854:PHE:HD1	2:E:1858:ASP:HB3	1.79	0.48
2:E:3829:PHE:HA	2:E:3832:ILE:HD12	1.95	0.48
2:G:637:LEU:HG	2:G:1693:GLN:HB3	1.96	0.48
2:G:797:HIS:HB3	2:G:1625:GLY:H	1.78	0.48
2:G:1659:LEU:O	2:G:1663:HIS:N	2.41	0.48
2:G:1976:ARG:NH1	2:G:1997:GLU:OE2	2.35	0.48
2:I:78:LEU:O	2:I:82:LEU:N	2.44	0.48
2:I:684:VAL:HG23	2:I:781:VAL:HB	1.94	0.48
2:I:1764:GLY:HA3	2:I:1859:VAL:HG11	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:497:TYR:HB3	2:B:500:ALA:HB2	1.96	0.48
2:B:1668:ARG:HA	2:B:1671:ARG:HH11	1.79	0.48
2:E:252:VAL:HA	2:E:255:HIS:HB2	1.95	0.48
2:E:1764:GLY:HA3	2:E:1859:VAL:HG11	1.96	0.48
2:E:1952:GLN:HA	2:E:1955:VAL:HG12	1.95	0.48
2:E:3905:THR:HA	2:E:3912:THR:HG23	1.95	0.48
2:G:288:GLY:HA3	2:G:405:HIS:CE1	2.49	0.48
2:G:379:HIS:CD2	2:G:382:GLY:H	2.27	0.48
2:G:1668:ARG:HA	2:G:1671:ARG:HH11	1.79	0.48
2:I:54:ASN:O	2:I:58:VAL:N	2.43	0.48
2:I:637:LEU:HG	2:I:1693:GLN:HB3	1.96	0.48
2:I:709:ASP:HB3	2:I:725:HIS:CE1	2.49	0.48
2:I:797:HIS:HB3	2:I:1625:GLY:H	1.78	0.48
2:I:4942:GLU:O	2:I:4946:GLN:N	2.43	0.48
2:B:2336:ARG:NH2	2:B:2428:ALA:O	2.46	0.47
2:E:469:ARG:HH21	2:E:3712:GLU:HB3	1.79	0.47
2:E:497:TYR:HB3	2:E:500:ALA:HB2	1.96	0.47
2:E:637:LEU:HG	2:E:1693:GLN:HB3	1.96	0.47
2:E:668:VAL:HG22	2:E:789:VAL:HG23	1.96	0.47
2:E:1203:ASN:ND2	2:E:1210:SER:O	2.47	0.47
2:E:1848:LEU:HB3	2:E:1853:ILE:HB	1.95	0.47
2:I:497:TYR:HB3	2:I:500:ALA:HB2	1.96	0.47
2:I:1203:ASN:ND2	2:I:1210:SER:O	2.47	0.47
2:I:3829:PHE:HA	2:I:3832:ILE:HD12	1.95	0.47
2:I:4928:LEU:HA	2:I:4931:ILE:HD12	1.96	0.47
2:B:1718:ILE:HG13	2:B:1719:HIS:CD2	2.49	0.47
2:B:3963:ASN:O	2:B:3966:THR:OG1	2.29	0.47
2:B:4560:TYR:O	2:B:4564:PHE:N	2.45	0.47
2:G:1227:ALA:HB1	2:G:1230:MET:HG3	1.95	0.47
2:G:3905:THR:HA	2:G:3912:THR:HG23	1.95	0.47
2:G:4571:PHE:O	2:G:4575:PHE:N	2.43	0.47
2:I:683:ARG:HG2	2:I:717:ASP:HB3	1.96	0.47
2:I:1737:PRO:HG2	2:I:1739:THR:HG23	1.95	0.47
2:B:913:LEU:HD13	2:B:918:ARG:HA	1.95	0.47
2:B:1229:ASN:O	2:B:1827:ARG:N	2.42	0.47
2:B:1737:PRO:HG2	2:B:1739:THR:HG23	1.95	0.47
2:E:809:ALA:O	2:E:811:CYS:N	2.47	0.47
2:E:1227:ALA:HB1	2:E:1230:MET:HG3	1.95	0.47
2:G:139:GLU:O	2:G:141:ALA:N	2.47	0.47
2:G:4780:PHE:O	2:G:4784:PHE:N	2.42	0.47
2:I:629:ARG:HB3	2:I:634:GLN:NE2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:4584:ASP:HA	2:I:4627:MET:HA	1.97	0.47
2:B:288:GLY:HA3	2:B:405:HIS:CE1	2.49	0.47
2:B:668:VAL:HG22	2:B:789:VAL:HG23	1.96	0.47
2:B:683:ARG:HG2	2:B:717:ASP:HB3	1.96	0.47
2:B:1817:GLU:O	2:B:1821:ASP:N	2.45	0.47
2:B:4584:ASP:HA	2:B:4627:MET:HA	1.97	0.47
2:E:1663:HIS:O	2:E:1667:LEU:N	2.46	0.47
2:E:1718:ILE:HG13	2:E:1719:HIS:CD2	2.48	0.47
2:E:4056:GLU:HA	2:E:4059:LEU:HB2	1.97	0.47
2:G:173:SER:OG	2:G:174:VAL:N	2.48	0.47
2:G:410:LEU:HD21	2:G:441:VAL:HA	1.96	0.47
2:G:497:TYR:HB3	2:G:500:ALA:HB2	1.96	0.47
2:G:709:ASP:HB3	2:G:725:HIS:CE1	2.50	0.47
2:G:913:LEU:HD13	2:G:918:ARG:HA	1.96	0.47
2:G:1044:ARG:HA	2:G:1047:LEU:HD12	1.97	0.47
2:G:1764:GLY:HA3	2:G:1859:VAL:HG11	1.96	0.47
2:G:3829:PHE:HA	2:G:3832:ILE:HD12	1.95	0.47
2:I:652:ARG:HB3	2:I:773:LEU:HD13	1.97	0.47
2:B:173:SER:OG	2:B:174:VAL:N	2.47	0.47
2:B:4928:LEU:HA	2:B:4931:ILE:HD12	1.96	0.47
2:E:288:GLY:HA3	2:E:405:HIS:CE1	2.49	0.47
2:E:797:HIS:HB3	2:E:1625:GLY:H	1.78	0.47
2:E:952:LYS:HB3	2:E:968:ALA:HB1	1.96	0.47
2:E:3927:GLN:O	2:E:3931:SER:N	2.43	0.47
2:G:1737:PRO:HG2	2:G:1739:THR:HG23	1.95	0.47
2:G:2318:TYR:OH	2:G:2414:ASN:N	2.45	0.47
2:I:2095:GLN:NE2	2:I:2127:GLN:O	2.48	0.47
2:I:4896:GLY:HA2	2:I:4921:PHE:HB2	1.97	0.47
2:B:220:LEU:HD11	2:B:390:LEU:HD22	1.95	0.47
2:B:637:LEU:HG	2:B:1693:GLN:HB3	1.96	0.47
2:B:2154:SER:O	2:B:2184:ASN:ND2	2.47	0.47
2:B:3674:ILE:HG13	2:B:3732:SER:HB3	1.96	0.47
2:B:3993:LEU:HA	2:B:3996:PHE:HB2	1.96	0.47
2:B:4546:VAL:O	2:B:4550:LYS:N	2.42	0.47
2:E:4059:LEU:O	2:E:4063:ASP:N	2.47	0.47
2:E:4858:PHE:O	2:E:4862:PHE:HE2	1.98	0.47
2:G:1848:LEU:HB3	2:G:1853:ILE:HB	1.95	0.47
2:G:4172:GLU:HA	2:G:4175:ARG:HE	1.79	0.47
2:I:952:LYS:HB3	2:I:968:ALA:HB1	1.96	0.47
2:I:1044:ARG:HA	2:I:1047:LEU:HD12	1.97	0.47
2:B:118:LEU:HD12	2:B:137:LEU:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:410:LEU:HD21	2:B:441:VAL:HA	1.96	0.47
2:B:707:VAL:HG23	2:B:713:SER:HB2	1.96	0.47
2:B:709:ASP:HB3	2:B:725:HIS:CE1	2.49	0.47
2:B:1848:LEU:HD22	2:B:1853:ILE:HG13	1.97	0.47
2:B:1848:LEU:HB3	2:B:1853:ILE:HB	1.95	0.47
2:B:4021:LYS:HA	2:B:4024:VAL:HG12	1.97	0.47
2:B:4109:GLN:O	2:B:4113:SER:N	2.43	0.47
2:B:4241:THR:HG22	2:B:4245:MET:HE2	1.97	0.47
2:B:4688:ILE:HG21	2:B:4728:HIS:HB3	1.96	0.47
2:B:4896:GLY:HA2	2:B:4921:PHE:HB2	1.97	0.47
2:E:546:TRP:O	2:E:550:LYS:NZ	2.31	0.47
2:E:652:ARG:HB3	2:E:773:LEU:HD13	1.97	0.47
2:E:709:ASP:HB3	2:E:725:HIS:CE1	2.49	0.47
2:E:1046:LEU:HB3	2:E:1051:TYR:HB2	1.97	0.47
2:E:2095:GLN:NE2	2:E:2127:GLN:O	2.48	0.47
2:E:2104:ARG:HA	2:E:2107:GLN:HB3	1.95	0.47
2:E:2132:GLY:O	2:E:2136:ARG:N	2.45	0.47
2:E:2154:SER:O	2:E:2184:ASN:ND2	2.47	0.47
2:E:4021:LYS:HA	2:E:4024:VAL:HG12	1.97	0.47
2:G:118:LEU:HD12	2:G:137:LEU:HB3	1.97	0.47
2:G:652:ARG:HB3	2:G:773:LEU:HD13	1.97	0.47
2:G:683:ARG:HG2	2:G:717:ASP:HB3	1.96	0.47
2:G:1516:UNK:N	2:G:1529:UNK:O	2.47	0.47
2:G:4056:GLU:HA	2:G:4059:LEU:HB2	1.97	0.47
2:G:4138:ASP:OD1	2:G:4138:ASP:N	2.46	0.47
2:G:4688:ILE:HG21	2:G:4728:HIS:HB3	1.96	0.47
2:I:220:LEU:HD11	2:I:390:LEU:HD22	1.95	0.47
2:I:1848:LEU:HB3	2:I:1853:ILE:HB	1.95	0.47
2:I:4172:GLU:HA	2:I:4175:ARG:HE	1.79	0.47
2:I:4241:THR:HG22	2:I:4245:MET:HE2	1.97	0.47
2:B:139:GLU:O	2:B:141:ALA:N	2.47	0.47
2:B:914:PRO:O	2:B:918:ARG:N	2.46	0.47
2:B:3905:THR:HA	2:B:3912:THR:HG23	1.95	0.47
2:E:139:GLU:O	2:E:141:ALA:N	2.47	0.47
2:E:485:SER:O	2:E:489:ASN:N	2.46	0.47
2:E:2430:ILE:HG21	2:E:2502:UNK:HA	1.97	0.47
2:E:4928:LEU:HA	2:E:4931:ILE:HD12	1.96	0.47
2:G:668:VAL:HG22	2:G:789:VAL:HG23	1.96	0.47
2:G:809:ALA:O	2:G:811:CYS:N	2.47	0.47
2:G:1046:LEU:HB3	2:G:1051:TYR:HB2	1.97	0.47
2:G:1854:PHE:HD1	2:G:1858:ASP:HB3	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:4201:ASN:ND2	2:G:4993:MET:SD	2.88	0.47
2:I:118:LEU:HD12	2:I:137:LEU:HB3	1.97	0.47
2:I:218:HIS:HB3	2:I:392:ARG:HD3	1.97	0.47
2:I:1665:HIS:HA	2:I:1668:ARG:HG2	1.97	0.47
2:I:1848:LEU:HD22	2:I:1853:ILE:HG13	1.97	0.47
2:B:475:GLN:NE2	2:B:528:SER:O	2.48	0.47
2:B:1046:LEU:HB3	2:B:1051:TYR:HB2	1.97	0.47
2:B:1665:HIS:HA	2:B:1668:ARG:HG2	1.97	0.47
2:B:1854:PHE:HD1	2:B:1858:ASP:HB3	1.79	0.47
2:B:4666:VAL:HG23	2:B:4669:VAL:HB	1.97	0.47
2:E:4083:ASP:HA	2:E:4085:ARG:HH11	1.80	0.47
2:E:4201:ASN:ND2	2:E:4993:MET:SD	2.88	0.47
2:E:4860:ARG:HD2	2:G:4582:VAL:HG11	1.97	0.47
2:G:1100:MET:HE2	2:G:1198:GLN:HB3	1.97	0.47
2:G:4584:ASP:HA	2:G:4627:MET:HA	1.96	0.47
2:I:3765:TYR:O	2:I:3769:ARG:N	2.36	0.47
1:A:23:VAL:HB	1:A:105:ASN:HA	1.97	0.47
2:B:176:SER:HB2	2:B:178:ARG:HD3	1.97	0.47
2:B:652:ARG:HB3	2:B:773:LEU:HD13	1.97	0.47
2:B:1044:ARG:HA	2:B:1047:LEU:HD12	1.97	0.47
2:E:173:SER:OG	2:E:174:VAL:N	2.48	0.47
2:E:410:LEU:HD21	2:E:441:VAL:HA	1.96	0.47
2:E:702:TRP:O	2:E:705:ASN:ND2	2.46	0.47
2:E:4138:ASP:N	2:E:4138:ASP:OD1	2.46	0.47
2:G:176:SER:HB2	2:G:178:ARG:HD3	1.97	0.47
2:G:241:GLN:O	2:G:289:ARG:NH1	2.42	0.47
2:G:952:LYS:HB3	2:G:968:ALA:HB1	1.96	0.47
2:G:2154:SER:O	2:G:2184:ASN:ND2	2.47	0.47
2:G:4896:GLY:HA2	2:G:4921:PHE:HB2	1.97	0.47
2:I:469:ARG:HH21	2:I:3712:GLU:HB3	1.80	0.47
2:I:4138:ASP:OD1	2:I:4138:ASP:N	2.46	0.47
2:B:460:GLN:HG2	2:B:462:GLU:H	1.80	0.46
2:E:379:HIS:CD2	2:E:382:GLY:H	2.27	0.46
2:E:4584:ASP:HA	2:E:4627:MET:HA	1.96	0.46
2:E:4666:VAL:HG23	2:E:4669:VAL:HB	1.97	0.46
1:F:23:VAL:HB	1:F:105:ASN:HA	1.97	0.46
2:G:469:ARG:HH21	2:G:3712:GLU:HB3	1.80	0.46
2:G:2095:GLN:NE2	2:G:2127:GLN:O	2.48	0.46
2:G:3674:ILE:HG13	2:G:3732:SER:HB3	1.96	0.46
2:G:3927:GLN:O	2:G:3931:SER:N	2.43	0.46
2:G:4083:ASP:HA	2:G:4085:ARG:HH11	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:4858:PHE:O	2:G:4862:PHE:HE2	1.98	0.46
2:I:139:GLU:O	2:I:141:ALA:N	2.48	0.46
2:I:173:SER:OG	2:I:174:VAL:N	2.47	0.46
2:I:410:LEU:HD21	2:I:441:VAL:HA	1.96	0.46
2:I:1046:LEU:HB3	2:I:1051:TYR:HB2	1.97	0.46
2:I:1149:VAL:HG22	2:I:1164:LEU:HD13	1.97	0.46
2:I:1976:ARG:NH1	2:I:1997:GLU:OE2	2.35	0.46
2:I:3993:LEU:HA	2:I:3996:PHE:HB2	1.96	0.46
2:B:34:LYS:N	2:B:53:SER:OG	2.43	0.46
2:B:1149:VAL:HG22	2:B:1164:LEU:HD13	1.97	0.46
2:B:2880:GLU:O	2:B:2884:ASN:N	2.45	0.46
2:B:3829:PHE:HA	2:B:3832:ILE:HD12	1.95	0.46
2:B:4083:ASP:HA	2:B:4085:ARG:HH11	1.80	0.46
2:E:118:LEU:HD12	2:E:137:LEU:HB3	1.97	0.46
2:E:218:HIS:HB3	2:E:392:ARG:HD3	1.97	0.46
2:E:1098:GLY:HA2	2:E:1127:HIS:CD2	2.51	0.46
2:E:4241:THR:HG22	2:E:4245:MET:HE2	1.97	0.46
2:E:4688:ILE:HG21	2:E:4728:HIS:HB3	1.96	0.46
2:G:111:HIS:N	2:G:116:MET:O	2.36	0.46
2:G:385:ASP:OD1	2:G:385:ASP:N	2.48	0.46
2:G:1098:GLY:HA2	2:G:1127:HIS:CD2	2.51	0.46
2:G:4563:ARG:NH1	2:G:4815:ASP:OD2	2.36	0.46
2:I:460:GLN:HG2	2:I:462:GLU:H	1.80	0.46
2:B:4172:GLU:HA	2:B:4175:ARG:HE	1.79	0.46
2:E:396:GLU:O	2:E:400:ALA:N	2.40	0.46
2:E:683:ARG:HG2	2:E:717:ASP:HB3	1.96	0.46
2:E:3674:ILE:HG13	2:E:3732:SER:HB3	1.97	0.46
2:E:4172:GLU:HA	2:E:4175:ARG:HE	1.80	0.46
2:G:2336:ARG:NH2	2:G:2428:ALA:O	2.46	0.46
2:I:475:GLN:NE2	2:I:528:SER:O	2.48	0.46
2:I:3674:ILE:HG13	2:I:3732:SER:HB3	1.97	0.46
2:I:4056:GLU:HA	2:I:4059:LEU:HB2	1.97	0.46
2:B:4861:LYS:HA	2:B:4874:MET:HE1	1.97	0.46
2:E:176:SER:HB2	2:E:178:ARG:HD3	1.97	0.46
2:E:2212:VAL:O	2:E:2216:GLY:N	2.46	0.46
2:E:4896:GLY:HA2	2:E:4921:PHE:HB2	1.97	0.46
2:G:426:ARG:HG2	2:G:431:PRO:HA	1.98	0.46
2:G:1665:HIS:HA	2:G:1668:ARG:HG2	1.97	0.46
2:G:2758:PHE:O	2:G:2762:THR:N	2.44	0.46
2:I:1100:MET:HE2	2:I:1198:GLN:HB3	1.97	0.46
2:I:1854:PHE:HD1	2:I:1858:ASP:HB3	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:4688:ILE:HG21	2:I:4728:HIS:HB3	1.96	0.46
2:I:4861:LYS:HA	2:I:4874:MET:HE1	1.97	0.46
2:B:426:ARG:HG2	2:B:431:PRO:HA	1.98	0.46
2:B:702:TRP:O	2:B:705:ASN:ND2	2.46	0.46
2:B:2095:GLN:NE2	2:B:2127:GLN:O	2.48	0.46
2:B:2430:ILE:HG21	2:B:2502:UNK:HA	1.98	0.46
2:B:4824:ARG:O	2:B:4828:SER:N	2.38	0.46
2:G:742:ASP:OD1	2:G:760:ASN:ND2	2.49	0.46
2:G:1848:LEU:HD22	2:G:1853:ILE:HG13	1.97	0.46
2:G:4021:LYS:HA	2:G:4024:VAL:HG12	1.97	0.46
2:G:4241:THR:HG22	2:G:4245:MET:HE2	1.97	0.46
2:I:176:SER:HB2	2:I:178:ARG:HD3	1.97	0.46
2:I:288:GLY:HA3	2:I:405:HIS:CE1	2.49	0.46
2:I:4546:VAL:O	2:I:4550:LYS:N	2.42	0.46
2:B:485:SER:O	2:B:489:ASN:N	2.46	0.46
2:B:952:LYS:HB3	2:B:968:ALA:HB1	1.96	0.46
2:B:1663:HIS:O	2:B:1667:LEU:N	2.46	0.46
2:E:1848:LEU:HD22	2:E:1853:ILE:HG13	1.97	0.46
2:G:264:PRO:HA	2:G:280:LEU:HA	1.97	0.46
2:G:355:LEU:HB3	2:G:378:LEU:HB3	1.97	0.46
2:G:1149:VAL:HG22	2:G:1164:LEU:HD13	1.97	0.46
2:G:3993:LEU:HA	2:G:3996:PHE:HB2	1.96	0.46
2:G:4666:VAL:HG23	2:G:4669:VAL:HB	1.98	0.46
2:I:2154:SER:O	2:I:2184:ASN:ND2	2.47	0.46
2:I:4021:LYS:HA	2:I:4024:VAL:HG12	1.97	0.46
2:I:4710:SER:OG	2:I:4772:ASP:OD2	2.28	0.46
2:I:4853:VAL:HA	2:I:4856:PHE:HB3	1.98	0.46
2:B:583:ILE:HA	2:B:586:ILE:HD12	1.98	0.46
2:E:426:ARG:HG2	2:E:431:PRO:HA	1.98	0.46
2:E:475:GLN:NE2	2:E:528:SER:O	2.48	0.46
2:E:1149:VAL:HG22	2:E:1164:LEU:HD13	1.97	0.46
2:E:1665:HIS:HA	2:E:1668:ARG:HG2	1.98	0.46
2:G:218:HIS:HB3	2:G:392:ARG:HD3	1.97	0.46
1:H:14:THR:N	1:H:67:SER:OG	2.49	0.46
2:I:34:LYS:N	2:I:53:SER:OG	2.43	0.46
2:I:385:ASP:N	2:I:385:ASP:OD1	2.48	0.46
2:I:426:ARG:HG2	2:I:431:PRO:HA	1.98	0.46
2:I:2143:THR:O	2:I:3651:ASN:ND2	2.38	0.46
2:B:2231:SER:HA	2:B:2234:ARG:HG2	1.98	0.46
2:E:1044:ARG:HA	2:E:1047:LEU:HD12	1.97	0.46
2:E:2158:CYS:HB2	2:E:2184:ASN:HD22	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:4105:GLY:HA2	2:E:4108:ILE:HD12	1.98	0.46
2:G:1647:CYS:SG	2:G:1648:MET:N	2.89	0.46
2:G:4934:GLY:HA3	2:I:4937:ILE:HD12	1.97	0.46
2:I:1098:GLY:HA2	2:I:1127:HIS:CD2	2.51	0.46
2:I:4083:ASP:HA	2:I:4085:ARG:HH11	1.80	0.46
2:B:218:HIS:HB3	2:B:392:ARG:HD3	1.97	0.46
2:B:650:VAL:HB	2:B:777:PHE:HB2	1.98	0.46
2:B:2158:CYS:HB2	2:B:2184:ASN:HD22	1.81	0.46
2:B:4710:SER:OG	2:B:4772:ASP:OD2	2.28	0.46
2:E:583:ILE:HA	2:E:586:ILE:HD12	1.98	0.46
2:E:635:THR:O	1:F:34:LYS:NZ	2.49	0.46
2:E:2231:SER:HA	2:E:2234:ARG:HG2	1.98	0.46
2:G:34:LYS:N	2:G:53:SER:OG	2.43	0.46
2:G:4861:LYS:HA	2:G:4874:MET:HE1	1.97	0.46
2:I:742:ASP:OD1	2:I:760:ASN:ND2	2.49	0.46
2:I:1817:GLU:O	2:I:1821:ASP:N	2.45	0.46
2:I:2231:SER:HA	2:I:2234:ARG:HG2	1.98	0.46
2:I:3963:ASN:O	2:I:3966:THR:OG1	2.28	0.46
2:I:4201:ASN:ND2	2:I:4993:MET:SD	2.88	0.46
2:B:278:GLN:N	2:B:315:CYS:SG	2.89	0.46
2:B:1100:MET:HE2	2:B:1198:GLN:HB3	1.97	0.46
2:B:4056:GLU:HA	2:B:4059:LEU:HB2	1.97	0.46
2:B:4201:ASN:ND2	2:B:4993:MET:SD	2.88	0.46
2:B:4942:GLU:O	2:B:4946:GLN:N	2.43	0.46
2:E:4003:LEU:HB2	2:E:4013:LEU:HD13	1.98	0.46
2:G:475:GLN:NE2	2:G:528:SER:O	2.48	0.46
2:G:2004:GLU:HA	2:G:2007:ASN:HD22	1.81	0.46
2:G:4059:LEU:O	2:G:4063:ASP:N	2.49	0.46
2:I:264:PRO:HA	2:I:280:LEU:HA	1.97	0.46
2:I:355:LEU:HB3	2:I:378:LEU:HB3	1.97	0.46
2:I:1647:CYS:SG	2:I:1648:MET:N	2.89	0.46
2:I:2243:SER:HB3	2:I:2246:ASN:H	1.81	0.46
2:I:2430:ILE:HG21	2:I:2502:UNK:HA	1.98	0.46
2:I:4666:VAL:HG23	2:I:4669:VAL:HB	1.97	0.46
2:B:666:VAL:HG21	2:B:684:VAL:HG21	1.98	0.45
2:B:1647:CYS:SG	2:B:1648:MET:N	2.89	0.45
2:B:3805:LEU:H	2:B:3805:LEU:HG	1.61	0.45
2:E:1965:TYR:HE1	2:E:2027:ILE:HB	1.82	0.45
2:E:4577:LEU:HG	2:E:4580:TYR:HE2	1.81	0.45
2:E:4813:LEU:HA	2:E:4816:ILE:HG12	1.99	0.45
1:F:14:THR:N	1:F:67:SER:OG	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:583:ILE:HA	2:G:586:ILE:HD12	1.98	0.45
2:G:650:VAL:HB	2:G:777:PHE:HB2	1.98	0.45
2:G:1694:LEU:O	2:G:1712:TYR:OH	2.24	0.45
2:G:4853:VAL:HA	2:G:4856:PHE:HB3	1.98	0.45
2:I:110:ARG:HH21	2:I:115:ARG:HB3	1.81	0.45
2:I:668:VAL:O	2:I:741:GLU:N	2.49	0.45
2:I:2004:GLU:HA	2:I:2007:ASN:HD22	1.81	0.45
2:I:4577:LEU:HG	2:I:4580:TYR:HE2	1.81	0.45
2:B:742:ASP:OD1	2:B:760:ASN:ND2	2.49	0.45
2:B:2869:ARG:HH12	2:B:2945:UNK:C	2.29	0.45
2:B:4895:GLY:O	2:E:4892:ARG:NH2	2.48	0.45
2:E:355:LEU:HB3	2:E:378:LEU:HB3	1.97	0.45
2:E:1100:MET:HE2	2:E:1198:GLN:HB3	1.97	0.45
2:E:5012:LYS:O	2:E:5016:GLU:N	2.44	0.45
2:G:110:ARG:HH21	2:G:115:ARG:HB3	1.81	0.45
2:G:2243:SER:HB3	2:G:2246:ASN:H	1.81	0.45
2:G:4003:LEU:HB2	2:G:4013:LEU:HD13	1.98	0.45
2:G:4105:GLY:HA2	2:G:4108:ILE:HD12	1.98	0.45
2:G:4109:GLN:O	2:G:4113:SER:N	2.43	0.45
2:I:3927:GLN:O	2:I:3931:SER:N	2.43	0.45
2:I:4961:CYS:HB3	2:I:4983:HIS:CE1	2.51	0.45
1:J:14:THR:N	1:J:67:SER:OG	2.49	0.45
2:B:264:PRO:HA	2:B:280:LEU:HA	1.97	0.45
2:B:668:VAL:O	2:B:741:GLU:N	2.49	0.45
2:B:2243:SER:HB3	2:B:2246:ASN:H	1.81	0.45
2:B:4041:ALA:HA	2:B:4044:MET:HB2	1.99	0.45
2:B:4813:LEU:HA	2:B:4816:ILE:HG12	1.98	0.45
2:E:264:PRO:HA	2:E:280:LEU:HA	1.97	0.45
2:E:460:GLN:HG2	2:E:462:GLU:H	1.80	0.45
2:E:742:ASP:OD1	2:E:760:ASN:ND2	2.49	0.45
2:E:1516:UNK:N	2:E:1529:UNK:O	2.50	0.45
2:G:702:TRP:O	2:G:705:ASN:ND2	2.46	0.45
2:G:2143:THR:O	2:G:3651:ASN:ND2	2.38	0.45
2:G:4041:ALA:HA	2:G:4044:MET:HB2	1.99	0.45
2:G:4546:VAL:O	2:G:4550:LYS:N	2.42	0.45
2:I:278:GLN:N	2:I:315:CYS:SG	2.89	0.45
2:I:583:ILE:HA	2:I:586:ILE:HD12	1.98	0.45
2:I:2869:ARG:HH12	2:I:2945:UNK:C	2.29	0.45
2:I:4813:LEU:HA	2:I:4816:ILE:HG12	1.98	0.45
2:B:983:THR:O	2:B:987:ARG:N	2.48	0.45
2:B:1098:GLY:HA2	2:B:1127:HIS:CD2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:4003:LEU:HB2	2:B:4013:LEU:HD13	1.98	0.45
2:B:4780:PHE:HA	2:B:4783:ILE:HD12	1.99	0.45
2:E:983:THR:O	2:E:987:ARG:N	2.48	0.45
2:E:4041:ALA:HA	2:E:4044:MET:HB2	1.99	0.45
2:E:4780:PHE:HA	2:E:4783:ILE:HD12	1.99	0.45
2:G:870:ILE:HD11	2:G:1049:TYR:CG	2.52	0.45
2:G:2231:SER:HA	2:G:2234:ARG:HG2	1.98	0.45
2:G:4710:SER:OG	2:G:4772:ASP:OD2	2.28	0.45
2:G:4780:PHE:HA	2:G:4783:ILE:HD12	1.99	0.45
1:H:23:VAL:HB	1:H:105:ASN:HA	1.97	0.45
2:I:838:HIS:CE1	2:I:1201:HIS:HD2	2.35	0.45
2:I:2212:VAL:O	2:I:2216:GLY:N	2.46	0.45
2:I:2869:ARG:HA	2:I:2872:GLN:HB3	1.98	0.45
2:I:2880:GLU:O	2:I:2884:ASN:N	2.45	0.45
2:I:4044:MET:HA	2:I:4047:MET:HG2	1.98	0.45
2:B:838:HIS:CE1	2:B:1201:HIS:HD2	2.35	0.45
2:B:1245:PHE:HE1	2:B:1600:LEU:HD23	1.82	0.45
2:B:2908:TYR:OH	2:B:2920:ARG:NE	2.44	0.45
2:B:3805:LEU:HA	2:B:3809:ASN:HD22	1.82	0.45
2:B:4105:GLY:HA2	2:B:4108:ILE:HD12	1.98	0.45
2:E:2004:GLU:HA	2:E:2007:ASN:HD22	1.81	0.45
2:E:2143:THR:O	2:E:3651:ASN:ND2	2.38	0.45
2:E:2869:ARG:HH12	2:E:2945:UNK:C	2.29	0.45
2:E:4861:LYS:HA	2:E:4874:MET:HE1	1.97	0.45
2:G:278:GLN:N	2:G:315:CYS:SG	2.89	0.45
2:G:1663:HIS:O	2:G:1667:LEU:N	2.46	0.45
2:G:1817:GLU:O	2:G:1821:ASP:N	2.45	0.45
2:G:2158:CYS:HB2	2:G:2184:ASN:HD22	1.81	0.45
1:J:23:VAL:HB	1:J:105:ASN:HA	1.97	0.45
1:A:14:THR:N	1:A:67:SER:OG	2.49	0.45
2:B:78:LEU:O	2:B:82:LEU:N	2.44	0.45
2:B:684:VAL:HA	2:B:781:VAL:HA	1.99	0.45
2:B:2004:GLU:HA	2:B:2007:ASN:HD22	1.81	0.45
2:B:4044:MET:HA	2:B:4047:MET:HG2	1.98	0.45
2:E:838:HIS:CE1	2:E:1201:HIS:HD2	2.35	0.45
2:E:1647:CYS:SG	2:E:1648:MET:N	2.89	0.45
2:E:1694:LEU:O	2:E:1712:TYR:OH	2.24	0.45
2:G:684:VAL:HA	2:G:781:VAL:HA	1.99	0.45
2:G:4044:MET:HA	2:G:4047:MET:HG2	1.98	0.45
2:I:229:GLU:OE2	2:I:374:LYS:NZ	2.47	0.45
2:I:1245:PHE:HE1	2:I:1600:LEU:HD23	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:4780:PHE:HA	2:I:4783:ILE:HD12	1.99	0.45
2:B:1092:PHE:N	2:B:1149:VAL:O	2.37	0.45
2:E:110:ARG:HH21	2:E:115:ARG:HB3	1.82	0.45
2:E:278:GLN:N	2:E:315:CYS:SG	2.89	0.45
2:E:666:VAL:HG21	2:E:684:VAL:HG21	1.98	0.45
2:E:4853:VAL:HA	2:E:4856:PHE:HB3	1.98	0.45
2:G:3649:ALA:O	2:G:3653:PHE:N	2.47	0.45
2:G:3805:LEU:HA	2:G:3809:ASN:HD22	1.82	0.45
2:G:4031:LEU:HB3	2:G:4034:ASN:HB2	1.99	0.45
2:I:2158:CYS:HB2	2:I:2184:ASN:HD22	1.81	0.45
2:I:4003:LEU:HB2	2:I:4013:LEU:HD13	1.98	0.45
2:B:229:GLU:OE2	2:B:374:LYS:NZ	2.47	0.45
2:B:809:ALA:O	2:B:811:CYS:N	2.47	0.45
2:B:1679:ASN:O	2:B:1683:HIS:ND1	2.36	0.45
2:B:3927:GLN:O	2:B:3931:SER:N	2.43	0.45
2:B:4031:LEU:HB3	2:B:4034:ASN:HB2	1.99	0.45
2:E:684:VAL:HA	2:E:781:VAL:HA	1.99	0.45
2:E:840:VAL:HB	2:E:1199:VAL:HG12	1.99	0.45
2:E:2869:ARG:HA	2:E:2872:GLN:HB3	1.98	0.45
2:E:2950:UNK:O	2:E:2954:UNK:N	2.50	0.45
2:G:666:VAL:HG21	2:G:684:VAL:HG21	1.98	0.45
2:G:840:VAL:HB	2:G:1199:VAL:HG12	1.99	0.45
2:G:4942:GLU:O	2:G:4946:GLN:N	2.43	0.45
2:I:4105:GLY:HA2	2:I:4108:ILE:HD12	1.98	0.45
2:B:349:GLN:HA	2:B:356:TRP:HA	1.99	0.45
2:B:355:LEU:HB3	2:B:378:LEU:HB3	1.97	0.45
2:B:870:ILE:HD11	2:B:1049:TYR:CG	2.52	0.45
2:B:4853:VAL:HA	2:B:4856:PHE:HB3	1.98	0.45
2:B:4961:CYS:HB3	2:B:4983:HIS:CE1	2.51	0.45
2:E:1817:GLU:O	2:E:1821:ASP:N	2.45	0.45
2:E:4031:LEU:HB3	2:E:4034:ASN:HB2	1.99	0.45
2:E:4169:SER:HA	2:E:4172:GLU:HB3	1.99	0.45
2:G:4813:LEU:HA	2:G:4816:ILE:HG12	1.99	0.45
2:G:4961:CYS:HB3	2:G:4983:HIS:CE1	2.51	0.45
2:I:666:VAL:HG21	2:I:684:VAL:HG21	1.98	0.45
2:I:3805:LEU:HA	2:I:3809:ASN:HD22	1.82	0.45
2:I:4735:GLU:HA	2:I:4738:ALA:HB3	1.99	0.45
2:B:1735:ILE:HG23	2:B:1771:LEU:HD23	1.99	0.45
2:B:2950:UNK:O	2:B:2954:UNK:N	2.50	0.45
2:B:4577:LEU:HG	2:B:4580:TYR:HE2	1.81	0.45
2:G:349:GLN:HA	2:G:356:TRP:HA	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:1735:ILE:HG23	2:G:1771:LEU:HD23	1.99	0.45
2:G:2950:UNK:O	2:G:2954:UNK:N	2.50	0.45
2:G:4735:GLU:HA	2:G:4738:ALA:HB3	1.99	0.45
2:I:4031:LEU:HB3	2:I:4034:ASN:HB2	1.99	0.45
2:I:4968:PHE:HE1	2:I:5029:ARG:HD3	1.82	0.45
2:B:317:ARG:N	2:B:347:PHE:O	2.50	0.44
2:B:2869:ARG:HA	2:B:2872:GLN:HB3	1.98	0.44
2:E:1679:ASN:O	2:E:1683:HIS:ND1	2.36	0.44
2:E:2116:LEU:O	2:E:2120:MET:N	2.46	0.44
2:E:4109:GLN:O	2:E:4113:SER:N	2.43	0.44
2:E:4735:GLU:HA	2:E:4738:ALA:HB3	1.99	0.44
2:E:4961:CYS:HB3	2:E:4983:HIS:CE1	2.51	0.44
2:E:4968:PHE:HE1	2:E:5029:ARG:HD3	1.82	0.44
2:G:1965:TYR:HE1	2:G:2027:ILE:HB	1.82	0.44
2:I:870:ILE:HD11	2:I:1049:TYR:CG	2.52	0.44
2:B:385:ASP:OD1	2:B:385:ASP:N	2.48	0.44
2:B:546:TRP:O	2:B:550:LYS:NZ	2.31	0.44
2:E:317:ARG:N	2:E:347:PHE:O	2.50	0.44
2:E:650:VAL:HB	2:E:777:PHE:HB2	1.98	0.44
2:E:1245:PHE:HE1	2:E:1600:LEU:HD23	1.82	0.44
2:E:2243:SER:HB3	2:E:2246:ASN:H	1.81	0.44
2:E:2908:TYR:OH	2:E:2920:ARG:NE	2.44	0.44
2:E:3974:THR:HA	2:E:3977:GLN:HB2	1.99	0.44
2:G:281:ARG:HA	2:G:312:THR:HG21	2.00	0.44
2:G:460:GLN:HG2	2:G:462:GLU:H	1.80	0.44
2:G:983:THR:O	2:G:987:ARG:N	2.48	0.44
2:G:1245:PHE:HE1	2:G:1600:LEU:HD23	1.82	0.44
2:G:1497:UNK:HA	2:G:1535:UNK:HA	1.99	0.44
2:G:2116:LEU:O	2:G:2120:MET:N	2.46	0.44
2:G:4169:SER:HA	2:G:4172:GLU:HB3	1.99	0.44
2:G:4558:ASN:HB2	2:G:4561:THR:HB	2.00	0.44
2:I:392:ARG:HH12	2:I:398:SER:HB2	1.83	0.44
2:I:580:GLU:HG3	2:I:620:LEU:HD22	1.99	0.44
2:I:2950:UNK:O	2:I:2954:UNK:N	2.50	0.44
2:B:264:PRO:HG2	2:B:270:SER:HB2	2.00	0.44
2:B:4735:GLU:HA	2:B:4738:ALA:HB3	1.99	0.44
2:B:4989:MET:HE2	2:B:4989:MET:HB3	1.79	0.44
2:E:349:GLN:HA	2:E:356:TRP:HA	1.99	0.44
2:E:870:ILE:HD11	2:E:1049:TYR:CG	2.52	0.44
2:E:4560:TYR:O	2:E:4564:PHE:N	2.45	0.44
2:G:317:ARG:N	2:G:347:PHE:O	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:580:GLU:HG3	2:G:620:LEU:HD22	1.99	0.44
2:G:4577:LEU:HG	2:G:4580:TYR:HE2	1.81	0.44
2:I:349:GLN:HA	2:I:356:TRP:HA	1.99	0.44
2:I:4041:ALA:HA	2:I:4044:MET:HB2	1.99	0.44
2:B:1965:TYR:HE1	2:B:2027:ILE:HB	1.82	0.44
2:B:2452:ARG:HH12	2:I:177:GLU:HG3	1.83	0.44
2:E:1735:ILE:HG23	2:E:1771:LEU:HD23	2.00	0.44
2:G:392:ARG:HH12	2:G:398:SER:HB2	1.83	0.44
2:G:3676:ASP:OD1	2:G:3676:ASP:N	2.49	0.44
2:G:3963:ASN:O	2:G:3966:THR:OG1	2.29	0.44
2:G:4568:PHE:HA	2:G:4571:PHE:HD2	1.83	0.44
2:G:4968:PHE:HE1	2:G:5029:ARG:HD3	1.83	0.44
2:I:684:VAL:HA	2:I:781:VAL:HA	1.99	0.44
2:I:1735:ILE:HG23	2:I:1771:LEU:HD23	1.99	0.44
2:I:4568:PHE:HA	2:I:4571:PHE:HD2	1.82	0.44
2:B:110:ARG:HH21	2:B:115:ARG:HB3	1.81	0.44
2:B:392:ARG:HH12	2:B:398:SER:HB2	1.83	0.44
2:B:772:ASN:ND2	2:B:774:ASP:OD2	2.50	0.44
2:B:1931:LEU:HD22	2:B:1935:VAL:HG11	2.00	0.44
2:B:2212:VAL:O	2:B:2216:GLY:N	2.46	0.44
2:E:772:ASN:ND2	2:E:774:ASP:OD2	2.50	0.44
2:E:3361:UNK:O	2:E:3365:UNK:N	2.51	0.44
2:E:4139:ILE:HA	2:E:4142:ASN:HD22	1.82	0.44
2:G:360:ALA:N	2:G:375:LYS:O	2.50	0.44
2:I:650:VAL:HB	2:I:777:PHE:HB2	1.98	0.44
2:I:1931:LEU:HD22	2:I:1935:VAL:HG11	2.00	0.44
2:I:4558:ASN:HB2	2:I:4561:THR:HB	2.00	0.44
2:B:16:THR:OG1	2:B:97:GLY:O	2.35	0.44
2:B:3676:ASP:OD1	2:B:3676:ASP:N	2.49	0.44
2:B:4139:ILE:HA	2:B:4142:ASN:HD22	1.82	0.44
2:B:4990:PHE:O	2:B:4994:TYR:N	2.48	0.44
2:E:16:THR:OG1	2:E:97:GLY:O	2.35	0.44
2:E:392:ARG:HH12	2:E:398:SER:HB2	1.83	0.44
2:E:1976:ARG:NH1	2:E:1997:GLU:OE2	2.35	0.44
2:E:2142:TYR:CG	2:E:2197:LEU:HD13	2.53	0.44
2:G:978:THR:HB	2:G:980:ALA:H	1.83	0.44
2:G:3974:THR:HA	2:G:3977:GLN:HB2	1.99	0.44
2:I:264:PRO:HG2	2:I:270:SER:HB2	2.00	0.44
2:I:283:ARG:HH21	2:I:402:ARG:HH12	1.65	0.44
2:I:2420:HIS:ND1	2:I:2493:UNK:O	2.35	0.44
2:B:4059:LEU:O	2:B:4063:ASP:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:876:GLU:O	2:E:880:GLU:N	2.48	0.44
2:E:3805:LEU:HA	2:E:3809:ASN:HD22	1.82	0.44
2:G:668:VAL:O	2:G:741:GLU:N	2.49	0.44
2:G:3817:LEU:HD13	2:G:3899:PHE:HD1	1.83	0.44
2:G:4745:LEU:O	2:G:4749:GLU:N	2.43	0.44
2:I:840:VAL:HB	2:I:1199:VAL:HG12	1.99	0.44
2:I:1965:TYR:HE1	2:I:2027:ILE:HB	1.82	0.44
2:I:3676:ASP:N	2:I:3676:ASP:OD1	2.49	0.44
2:B:580:GLU:HG3	2:B:620:LEU:HD22	1.99	0.44
2:B:1497:UNK:HA	2:B:1535:UNK:HA	2.00	0.44
2:B:3361:UNK:O	2:B:3365:UNK:N	2.50	0.44
2:E:38:ALA:HB1	2:E:64:ILE:HG13	1.99	0.44
2:E:668:VAL:O	2:E:741:GLU:N	2.49	0.44
2:E:4044:MET:HA	2:E:4047:MET:HG2	1.98	0.44
2:G:533:ASN:HB3	2:G:536:ASN:HB2	2.00	0.44
2:G:838:HIS:CE1	2:G:1201:HIS:HD2	2.35	0.44
2:G:3361:UNK:O	2:G:3365:UNK:N	2.51	0.44
2:I:983:THR:O	2:I:987:ARG:N	2.48	0.44
2:I:1232:ARG:HD3	2:I:1702:HIS:HB3	2.00	0.44
2:B:283:ARG:HH21	2:B:402:ARG:HH12	1.65	0.44
2:B:840:VAL:HB	2:B:1199:VAL:HG12	1.99	0.44
2:B:3713:LYS:HG2	2:B:3715:LYS:H	1.83	0.44
2:B:4169:SER:HA	2:B:4172:GLU:HB3	1.99	0.44
2:B:4968:PHE:HE1	2:B:5029:ARG:HD3	1.83	0.44
2:E:385:ASP:OD1	2:E:385:ASP:N	2.48	0.44
2:E:1676:LEU:HD22	2:E:2167:ILE:HG13	2.00	0.44
2:E:1779:PRO:HG2	1:F:44:LYS:HE3	2.00	0.44
2:G:2869:ARG:HA	2:G:2872:GLN:HB3	1.98	0.44
2:I:281:ARG:HA	2:I:312:THR:HG21	2.00	0.44
2:I:463:GLU:OE2	2:I:467:LYS:NZ	2.51	0.44
2:I:596:ASN:HB3	2:I:599:VAL:HG22	2.00	0.44
2:I:1676:LEU:HD22	2:I:2167:ILE:HG13	2.00	0.44
2:I:2142:TYR:CG	2:I:2197:LEU:HD13	2.53	0.44
2:I:2186:MET:HE3	2:I:2186:MET:HB3	1.91	0.44
2:B:635:THR:HB	2:B:1639:LEU:HD23	2.00	0.43
2:B:2142:TYR:CG	2:B:2197:LEU:HD13	2.53	0.43
2:E:177:GLU:HG3	2:G:2452:ARG:HH12	1.83	0.43
2:E:1577:ALA:HB1	2:E:1584:ARG:HA	2.00	0.43
2:E:4215:ARG:HA	2:E:4218:ILE:HD12	2.00	0.43
2:E:4942:GLU:O	2:E:4946:GLN:N	2.43	0.43
2:G:1232:ARG:HD3	2:G:1702:HIS:HB3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:1286:UNK:HA	2:G:1461:UNK:HA	1.99	0.43
2:I:702:TRP:O	2:I:705:ASN:ND2	2.46	0.43
2:I:4139:ILE:HA	2:I:4142:ASN:HD22	1.82	0.43
2:B:213:TYR:CG	2:B:337:PRO:HB2	2.53	0.43
2:B:1294:UNK:HA	2:B:1455:UNK:HA	1.98	0.43
2:E:4568:PHE:HA	2:E:4571:PHE:HD2	1.83	0.43
2:G:113:HIS:CE1	2:G:399:GLN:HA	2.53	0.43
2:G:1577:ALA:HB1	2:G:1584:ARG:HA	2.01	0.43
2:G:2124:LEU:HD23	2:G:3673:MET:HE3	2.00	0.43
2:I:655:GLY:HA2	2:I:1002:ALA:HB2	2.01	0.43
2:B:1738:LEU:H	2:B:2146:PRO:HD3	1.83	0.43
2:B:4918:ILE:HD13	2:E:4892:ARG:HD3	2.01	0.43
2:E:463:GLU:OE2	2:E:467:LYS:NZ	2.51	0.43
2:E:866:HIS:O	2:E:1051:TYR:OH	2.36	0.43
2:G:38:ALA:HB1	2:G:64:ILE:HG13	1.99	0.43
2:G:530:ILE:HA	2:G:536:ASN:HB3	2.00	0.43
2:G:914:PRO:O	2:G:918:ARG:N	2.46	0.43
2:G:3731:LYS:O	2:G:3735:LEU:N	2.50	0.43
2:I:113:HIS:CE1	2:I:399:GLN:HA	2.53	0.43
2:I:261:ARG:N	2:I:283:ARG:O	2.44	0.43
2:I:360:ALA:N	2:I:375:LYS:O	2.50	0.43
2:I:4059:LEU:O	2:I:4063:ASP:N	2.51	0.43
1:J:2:VAL:HG21	1:J:61:GLU:HB2	2.00	0.43
2:B:655:GLY:HA2	2:B:1002:ALA:HB2	2.01	0.43
2:B:831:ARG:HH21	2:B:840:VAL:HG11	1.84	0.43
2:B:3953:LYS:O	2:B:3956:SER:OG	2.29	0.43
2:B:4558:ASN:HB2	2:B:4561:THR:HB	1.99	0.43
2:B:4568:PHE:HA	2:B:4571:PHE:HD2	1.83	0.43
2:E:113:HIS:CE1	2:E:399:GLN:HA	2.53	0.43
2:E:3731:LYS:O	2:E:3735:LEU:N	2.50	0.43
2:E:4651:THR:HA	2:E:4799:SER:HB3	2.00	0.43
2:G:215:THR:HG22	2:G:273:HIS:HA	2.00	0.43
2:G:2142:TYR:CG	2:G:2197:LEU:HD13	2.53	0.43
2:G:4139:ILE:HA	2:G:4142:ASN:HD22	1.82	0.43
2:I:213:TYR:CG	2:I:337:PRO:HB2	2.53	0.43
2:I:658:GLN:O	2:I:662:TRP:NE1	2.51	0.43
2:I:1738:LEU:H	2:I:2146:PRO:HD3	1.83	0.43
2:B:596:ASN:HB3	2:B:599:VAL:HG22	2.00	0.43
2:B:733:PRO:HD2	2:B:763:PRO:HD2	2.00	0.43
2:B:1516:UNK:N	2:B:1529:UNK:O	2.51	0.43
2:B:3674:ILE:HD11	2:B:3728:ILE:HG22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:281:ARG:HA	2:E:312:THR:HG21	2.00	0.43
2:E:978:THR:HB	2:E:980:ALA:H	1.83	0.43
2:E:1232:ARG:HD3	2:E:1702:HIS:HB3	1.99	0.43
2:E:3817:LEU:HD13	2:E:3899:PHE:HD1	1.83	0.43
2:G:264:PRO:HG2	2:G:270:SER:HB2	1.99	0.43
2:G:1738:LEU:H	2:G:2146:PRO:HD3	1.83	0.43
2:G:2869:ARG:HH12	2:G:2945:UNK:C	2.32	0.43
2:G:2880:GLU:O	2:G:2884:ASN:N	2.45	0.43
2:I:215:THR:HG22	2:I:273:HIS:HA	2.01	0.43
2:I:317:ARG:N	2:I:347:PHE:O	2.50	0.43
2:B:1232:ARG:HD3	2:B:1702:HIS:HB3	1.99	0.43
2:B:1577:ALA:HB1	2:B:1584:ARG:HA	2.01	0.43
2:B:4147:LEU:O	2:B:4151:SER:OG	2.35	0.43
2:B:4215:ARG:HA	2:B:4218:ILE:HD12	2.00	0.43
2:E:264:PRO:HG2	2:E:270:SER:HB2	2.00	0.43
2:E:2286:LEU:HA	2:E:2289:ALA:HB3	2.01	0.43
2:E:4918:ILE:HD11	2:G:4888:TYR:HA	2.01	0.43
2:G:379:HIS:CD2	2:G:381:GLU:H	2.37	0.43
2:G:596:ASN:HB3	2:G:599:VAL:HG22	2.00	0.43
2:G:2155:LEU:HD23	2:G:2185:ILE:HG22	2.01	0.43
2:G:2286:LEU:HA	2:G:2289:ALA:HB3	2.01	0.43
2:G:3674:ILE:HD11	2:G:3728:ILE:HG22	2.01	0.43
2:I:545:ASP:HA	2:I:582:HIS:CE1	2.54	0.43
2:I:2102:VAL:HB	2:I:2124:LEU:HD12	2.01	0.43
2:I:2124:LEU:HD23	2:I:3673:MET:HE3	2.00	0.43
2:I:3713:LYS:HG2	2:I:3715:LYS:H	1.83	0.43
2:I:3817:LEU:HD13	2:I:3899:PHE:HD1	1.83	0.43
2:I:4169:SER:HA	2:I:4172:GLU:HB3	1.99	0.43
1:J:7:ILE:N	1:J:71:ARG:O	2.47	0.43
2:B:342:GLY:HA2	2:B:389:PHE:HD2	1.83	0.43
2:B:463:GLU:OE2	2:B:467:LYS:NZ	2.51	0.43
2:B:614:VAL:HG22	2:B:616:SER:H	1.84	0.43
2:B:1229:ASN:HB3	2:B:1826:ALA:HA	2.01	0.43
2:E:215:THR:HG22	2:E:273:HIS:HA	2.01	0.43
2:E:360:ALA:N	2:E:375:LYS:O	2.50	0.43
2:E:1661:ARG:O	2:E:1664:SER:OG	2.32	0.43
2:E:2124:LEU:HD23	2:E:3673:MET:HE3	2.00	0.43
2:E:2155:LEU:HD23	2:E:2185:ILE:HG22	2.01	0.43
2:E:3676:ASP:OD1	2:E:3676:ASP:N	2.49	0.43
2:G:213:TYR:CG	2:G:337:PRO:HB2	2.53	0.43
2:G:313:SER:HB3	2:G:352:ALA:H	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:2185:ILE:HA	2:G:2188:ASN:HD21	1.84	0.43
2:G:4791:TYR:HD2	2:G:4792:LEU:HD22	1.84	0.43
2:G:4822:THR:O	2:G:4825:THR:OG1	2.30	0.43
2:G:4895:GLY:O	2:I:4892:ARG:NH2	2.50	0.43
2:I:38:ALA:HB1	2:I:64:ILE:HG13	1.99	0.43
2:I:831:ARG:HH21	2:I:840:VAL:HG11	1.84	0.43
2:I:3674:ILE:HD11	2:I:3728:ILE:HG22	2.01	0.43
2:B:2286:LEU:HA	2:B:2289:ALA:HB3	2.01	0.43
2:E:283:ARG:HH21	2:E:402:ARG:HH12	1.66	0.43
2:E:655:GLY:HA2	2:E:1002:ALA:HB2	2.01	0.43
2:G:772:ASN:ND2	2:G:774:ASP:OD2	2.50	0.43
2:G:2102:VAL:HB	2:G:2124:LEU:HD12	2.00	0.43
2:G:5026:ASP:OD1	2:G:5027:CYS:N	2.52	0.43
2:I:530:ILE:HA	2:I:536:ASN:HB3	2.00	0.43
2:I:809:ALA:O	2:I:811:CYS:N	2.47	0.43
2:I:1229:ASN:HB3	2:I:1826:ALA:HA	2.01	0.43
2:I:1649:ASP:OD1	2:I:1650:ILE:N	2.52	0.43
2:I:3974:THR:HA	2:I:3977:GLN:HB2	1.99	0.43
2:B:38:ALA:HB1	2:B:64:ILE:HG13	1.99	0.43
2:B:313:SER:HB3	2:B:352:ALA:H	1.84	0.43
2:B:530:ILE:HA	2:B:536:ASN:HB3	2.00	0.43
2:B:5026:ASP:OD1	2:B:5027:CYS:N	2.52	0.43
2:E:213:TYR:CG	2:E:337:PRO:HB2	2.53	0.43
2:E:313:SER:HB3	2:E:352:ALA:H	1.84	0.43
2:E:342:GLY:HA2	2:E:389:PHE:HD2	1.83	0.43
2:E:703:GLY:H	2:E:1647:CYS:HB3	1.84	0.43
2:E:3674:ILE:HD11	2:E:3728:ILE:HG22	2.01	0.43
2:E:4558:ASN:HB2	2:E:4561:THR:HB	2.00	0.43
2:G:342:GLY:HA2	2:G:389:PHE:HD2	1.83	0.43
2:G:635:THR:HB	2:G:1639:LEU:HD23	2.00	0.43
2:G:831:ARG:HH21	2:G:840:VAL:HG11	1.84	0.43
2:G:3713:LYS:HG2	2:G:3715:LYS:H	1.83	0.43
1:H:16:PRO:HD2	1:H:64:ALA:HA	2.01	0.43
2:I:1152:MET:HB2	2:I:1161:ILE:HB	2.01	0.43
2:I:1229:ASN:O	2:I:1827:ARG:N	2.42	0.43
2:I:1577:ALA:HB1	2:I:1584:ARG:HA	2.01	0.43
2:I:2286:LEU:HA	2:I:2289:ALA:HB3	2.01	0.43
1:J:16:PRO:HD2	1:J:64:ALA:HA	2.00	0.43
2:B:113:HIS:CE1	2:B:399:GLN:HA	2.53	0.43
2:B:281:ARG:HA	2:B:312:THR:HG21	2.00	0.43
2:B:978:THR:HB	2:B:980:ALA:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2185:ILE:HA	2:B:2188:ASN:HD21	1.84	0.43
2:B:3974:THR:HA	2:B:3977:GLN:HB2	1.99	0.43
2:E:530:ILE:HA	2:E:536:ASN:HB3	1.99	0.43
2:E:580:GLU:HG3	2:E:620:LEU:HD22	1.99	0.43
2:E:635:THR:HB	2:E:1639:LEU:HD23	2.01	0.43
2:E:1738:LEU:H	2:E:2146:PRO:HD3	1.83	0.43
2:E:1931:LEU:HD22	2:E:1935:VAL:HG11	2.00	0.43
2:E:2880:GLU:O	2:E:2884:ASN:N	2.45	0.43
2:E:3805:LEU:H	2:E:3805:LEU:HG	1.61	0.43
2:E:4990:PHE:O	2:E:4994:TYR:N	2.48	0.43
2:E:4995:LEU:HA	2:E:4995:LEU:HD22	1.81	0.43
2:G:866:HIS:O	2:G:1051:TYR:OH	2.36	0.43
2:G:1676:LEU:HD22	2:G:2167:ILE:HG13	2.00	0.43
2:G:2006:ILE:O	2:G:2010:LEU:N	2.45	0.43
2:G:2208:MET:HE1	2:G:2253:HIS:HB3	2.01	0.43
2:G:4651:THR:HA	2:G:4799:SER:HB3	2.00	0.43
2:G:4670:ILE:O	2:G:4674:GLU:N	2.44	0.43
1:H:2:VAL:HG21	1:H:61:GLU:HB2	2.00	0.43
2:I:313:SER:HB3	2:I:352:ALA:H	1.84	0.43
2:I:1516:UNK:N	2:I:1529:UNK:O	2.52	0.43
2:I:3731:LYS:O	2:I:3735:LEU:N	2.50	0.43
2:I:3825:GLU:OE1	2:I:3825:GLU:N	2.52	0.43
2:I:4990:PHE:O	2:I:4994:TYR:N	2.48	0.43
1:J:26:TYR:OH	1:J:42:ARG:NH2	2.39	0.43
2:B:404:ILE:HG21	2:B:481:GLU:HG3	2.01	0.42
2:E:545:ASP:HA	2:E:582:HIS:CE1	2.54	0.42
2:E:614:VAL:HG22	2:E:616:SER:H	1.84	0.42
2:E:831:ARG:HH21	2:E:840:VAL:HG11	1.84	0.42
2:E:1649:ASP:OD1	2:E:1650:ILE:N	2.52	0.42
2:E:2102:VAL:HB	2:E:2124:LEU:HD12	2.01	0.42
2:E:3649:ALA:O	2:E:3653:PHE:N	2.48	0.42
1:F:83:GLY:O	1:F:94:ASN:N	2.52	0.42
2:G:283:ARG:HH21	2:G:402:ARG:HH12	1.65	0.42
2:G:545:ASP:HA	2:G:582:HIS:CE1	2.54	0.42
2:G:4215:ARG:HA	2:G:4218:ILE:HD12	2.00	0.42
2:I:342:GLY:HA2	2:I:389:PHE:HD2	1.83	0.42
2:I:703:GLY:H	2:I:1647:CYS:HB3	1.84	0.42
2:B:2102:VAL:HB	2:B:2124:LEU:HD12	2.01	0.42
2:E:345:LEU:HD23	2:E:389:PHE:HB3	2.01	0.42
2:G:463:GLU:OE2	2:G:467:LYS:NZ	2.51	0.42
2:G:655:GLY:HA2	2:G:1002:ALA:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:733:PRO:HD2	2:G:763:PRO:HD2	2.00	0.42
2:I:379:HIS:CD2	2:I:381:GLU:H	2.37	0.42
2:I:404:ILE:HG21	2:I:481:GLU:HG3	2.01	0.42
2:I:947:GLU:HG3	2:I:1049:TYR:HD1	1.84	0.42
2:I:3361:UNK:O	2:I:3365:UNK:N	2.52	0.42
2:I:5026:ASP:OD1	2:I:5027:CYS:N	2.52	0.42
2:B:215:THR:HG22	2:B:273:HIS:HA	2.01	0.42
2:B:545:ASP:HA	2:B:582:HIS:CE1	2.54	0.42
2:B:2124:LEU:HD23	2:B:3673:MET:HE3	2.00	0.42
2:E:596:ASN:HB3	2:E:599:VAL:HG22	2.00	0.42
2:E:4147:LEU:O	2:E:4151:SER:OG	2.35	0.42
2:G:404:ILE:HG21	2:G:481:GLU:HG3	2.01	0.42
2:G:1931:LEU:HD22	2:G:1935:VAL:HG11	1.99	0.42
2:G:3880:PHE:O	2:G:3884:LEU:N	2.52	0.42
2:I:614:VAL:HG22	2:I:616:SER:H	1.84	0.42
2:I:772:ASN:ND2	2:I:774:ASP:OD2	2.50	0.42
2:I:2101:MET:HE2	2:I:2101:MET:HB3	1.96	0.42
2:I:2185:ILE:HA	2:I:2188:ASN:HD21	1.84	0.42
2:I:2208:MET:HE1	2:I:2253:HIS:HB3	2.01	0.42
2:I:3229:UNK:HA	2:I:3302:UNK:HA	2.02	0.42
2:B:260:TRP:CE2	2:B:284:HIS:HD2	2.38	0.42
2:B:533:ASN:HB3	2:B:536:ASN:HB2	2.00	0.42
2:B:703:GLY:H	2:B:1647:CYS:HB3	1.84	0.42
2:B:947:GLU:HG3	2:B:1049:TYR:HD1	1.85	0.42
2:B:1152:MET:HB2	2:B:1161:ILE:HB	2.01	0.42
2:B:3817:LEU:HD13	2:B:3899:PHE:HD1	1.83	0.42
2:B:3825:GLU:OE1	2:B:3825:GLU:N	2.52	0.42
2:E:404:ILE:HG21	2:E:481:GLU:HG3	2.01	0.42
2:E:733:PRO:HD2	2:E:763:PRO:HD2	2.00	0.42
2:E:3880:PHE:O	2:E:3884:LEU:N	2.52	0.42
2:E:4670:ILE:O	2:E:4674:GLU:N	2.44	0.42
2:E:4791:TYR:HD2	2:E:4792:LEU:HD22	1.84	0.42
2:G:229:GLU:OE2	2:G:374:LYS:NZ	2.47	0.42
2:G:703:GLY:H	2:G:1647:CYS:HB3	1.84	0.42
2:G:1649:ASP:OD1	2:G:1650:ILE:N	2.52	0.42
2:G:2212:VAL:O	2:G:2216:GLY:N	2.46	0.42
2:I:16:THR:OG1	2:I:97:GLY:O	2.35	0.42
2:I:533:ASN:HB3	2:I:536:ASN:HB2	2.00	0.42
2:I:733:PRO:HD2	2:I:763:PRO:HD2	2.00	0.42
2:I:870:ILE:HD12	2:I:870:ILE:HA	1.87	0.42
2:I:4651:THR:HA	2:I:4799:SER:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:4791:TYR:HD2	2:I:4792:LEU:HD22	1.84	0.42
1:A:2:VAL:HG21	1:A:61:GLU:HB2	2.00	0.42
2:B:1649:ASP:OD1	2:B:1650:ILE:N	2.52	0.42
2:B:2144:ILE:H	2:B:2144:ILE:HG13	1.72	0.42
2:B:2155:LEU:HD23	2:B:2185:ILE:HG22	2.01	0.42
2:B:2186:MET:HE3	2:B:2186:MET:HB3	1.91	0.42
2:B:3880:PHE:O	2:B:3884:LEU:N	2.52	0.42
2:E:119:SER:HA	2:E:146:CYS:HA	2.01	0.42
2:E:379:HIS:CD2	2:E:381:GLU:H	2.37	0.42
2:E:3825:GLU:OE1	2:E:3825:GLU:N	2.52	0.42
1:F:2:VAL:HG21	1:F:61:GLU:HB2	2.00	0.42
1:F:55:VAL:HG23	1:F:60:GLU:HB2	2.02	0.42
2:G:614:VAL:HG22	2:G:616:SER:H	1.84	0.42
2:G:1771:LEU:HD11	2:G:2149:VAL:HB	2.01	0.42
2:I:260:TRP:CE2	2:I:284:HIS:HD2	2.38	0.42
2:I:873:LYS:HB3	2:I:1049:TYR:CZ	2.55	0.42
2:I:886:ARG:HB3	2:I:891:TRP:HB2	2.02	0.42
2:I:2155:LEU:HD23	2:I:2185:ILE:HG22	2.01	0.42
1:A:16:PRO:HD2	1:A:64:ALA:HA	2.00	0.42
2:B:1676:LEU:HD22	2:B:2167:ILE:HG13	2.00	0.42
2:B:4651:THR:HA	2:B:4799:SER:HB3	2.00	0.42
2:E:273:HIS:CE1	2:E:337:PRO:HB3	2.55	0.42
1:F:16:PRO:HD2	1:F:64:ALA:HA	2.00	0.42
2:G:3663:LEU:H	2:G:3663:LEU:HG	1.64	0.42
2:I:345:LEU:HD23	2:I:389:PHE:HB3	2.01	0.42
2:I:1771:LEU:HD11	2:I:2149:VAL:HB	2.01	0.42
2:I:4960:ILE:HD12	2:I:4983:HIS:HB3	2.02	0.42
2:B:119:SER:HA	2:B:146:CYS:HA	2.01	0.42
2:B:345:LEU:HD23	2:B:389:PHE:HB3	2.01	0.42
2:B:3770:LEU:HD22	2:B:3804:ILE:HD11	2.01	0.42
2:B:4960:ILE:HD12	2:B:4983:HIS:HB3	2.02	0.42
2:E:790:ARG:HG2	2:E:1627:ALA:HA	2.02	0.42
2:E:1229:ASN:HB3	2:E:1826:ALA:HA	2.01	0.42
2:E:2185:ILE:HA	2:E:2188:ASN:HD21	1.84	0.42
2:E:3713:LYS:HG2	2:E:3715:LYS:H	1.83	0.42
2:G:345:LEU:HD23	2:G:389:PHE:HB3	2.01	0.42
2:G:1152:MET:HB2	2:G:1161:ILE:HB	2.01	0.42
1:H:7:ILE:N	1:H:71:ARG:O	2.47	0.42
1:H:83:GLY:O	1:H:94:ASN:N	2.52	0.42
2:I:4215:ARG:HA	2:I:4218:ILE:HD12	2.00	0.42
1:A:55:VAL:HG23	1:A:60:GLU:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:273:HIS:CE1	2:B:337:PRO:HB3	2.55	0.42
2:B:2318:TYR:HA	2:B:2319:PRO:HD3	1.87	0.42
2:B:2862:LEU:HB3	2:B:2928:LYS:HB3	2.02	0.42
2:E:260:TRP:CE2	2:E:284:HIS:HD2	2.38	0.42
2:E:1152:MET:HE1	2:E:1217:CYS:HB3	2.02	0.42
2:E:2862:LEU:HB3	2:E:2928:LYS:HB3	2.02	0.42
2:G:886:ARG:HB3	2:G:891:TRP:HB2	2.02	0.42
2:G:1229:ASN:HB3	2:G:1826:ALA:HA	2.01	0.42
2:G:3770:LEU:HD22	2:G:3804:ILE:HD11	2.01	0.42
2:G:3825:GLU:OE1	2:G:3825:GLU:N	2.52	0.42
2:G:4692:PRO:HG2	2:G:4703:ARG:HH21	1.84	0.42
2:G:4852:THR:HG21	2:G:4883:TYR:HB2	2.02	0.42
2:I:102:LEU:HB3	2:I:160:GLY:HA2	2.02	0.42
2:I:241:GLN:O	2:I:289:ARG:NH1	2.42	0.42
2:B:379:HIS:CD2	2:B:381:GLU:H	2.37	0.42
2:B:1771:LEU:HD11	2:B:2149:VAL:HB	2.02	0.42
2:B:1976:ARG:NH1	2:B:1997:GLU:OE2	2.35	0.42
2:E:533:ASN:HB3	2:E:536:ASN:HB2	2.00	0.42
2:E:1152:MET:HB2	2:E:1161:ILE:HB	2.01	0.42
2:E:1936:LYS:O	2:E:1940:CYS:N	2.48	0.42
2:E:2208:MET:HE1	2:E:2253:HIS:HB3	2.01	0.42
2:E:4736:ARG:O	2:E:4740:LEU:N	2.53	0.42
2:E:4960:ILE:HD12	2:E:4983:HIS:HB3	2.02	0.42
2:E:5026:ASP:OD1	2:E:5027:CYS:N	2.52	0.42
2:G:349:GLN:HE21	2:G:354:GLY:HA2	1.85	0.42
2:G:873:LYS:HB3	2:G:1049:TYR:CZ	2.55	0.42
2:G:1936:LYS:O	2:G:1940:CYS:N	2.48	0.42
2:G:4736:ARG:O	2:G:4740:LEU:N	2.53	0.42
2:B:3716:LEU:HD22	2:B:3785:ALA:HB1	2.02	0.42
2:B:3927:GLN:NE2	2:B:3988:ALA:O	2.46	0.42
2:B:4791:TYR:HD2	2:B:4792:LEU:HD22	1.84	0.42
2:E:488:LEU:HA	2:E:491:ILE:HB	2.02	0.42
2:E:947:GLU:HG3	2:E:1049:TYR:HD1	1.84	0.42
2:G:35:LEU:HD13	2:G:49:LEU:HD13	2.02	0.42
2:G:131:LEU:HD22	2:G:178:ARG:NH1	2.35	0.42
2:G:1152:MET:HE1	2:G:1217:CYS:HB3	2.02	0.42
2:G:4859:PHE:HA	2:G:4862:PHE:CE2	2.47	0.42
2:G:4956:THR:O	2:G:4965:SER:N	2.52	0.42
2:I:273:HIS:CE1	2:I:337:PRO:HB3	2.55	0.42
2:I:349:GLN:HE21	2:I:354:GLY:HA2	1.84	0.42
1:A:83:GLY:O	1:A:94:ASN:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:35:LEU:HD13	2:B:49:LEU:HD13	2.02	0.41
2:B:102:LEU:HB3	2:B:160:GLY:HA2	2.02	0.41
2:B:110:ARG:NH2	2:B:115:ARG:HB3	2.35	0.41
2:B:150:MET:HE2	2:B:150:MET:HB3	1.97	0.41
2:B:873:LYS:HB3	2:B:1049:TYR:CZ	2.55	0.41
2:B:946:ALA:HA	2:B:949:ASN:HB2	2.02	0.41
2:B:1256:GLU:HG2	2:B:1273:ALA:HB3	2.02	0.41
2:B:3766:GLN:O	2:B:3770:LEU:N	2.50	0.41
2:B:3773:ARG:HG2	2:B:3815:LYS:HD3	2.03	0.41
2:B:4167:ALA:HA	2:B:4170:ILE:HD12	2.02	0.41
2:E:261:ARG:N	2:E:283:ARG:O	2.44	0.41
2:E:658:GLN:O	2:E:662:TRP:NE1	2.51	0.41
2:E:3716:LEU:HD22	2:E:3785:ALA:HB1	2.02	0.41
2:E:3770:LEU:HD22	2:E:3804:ILE:HD11	2.01	0.41
2:E:4167:ALA:HA	2:E:4170:ILE:HD12	2.02	0.41
2:E:4208:PRO:HA	2:E:4211:LYS:HB3	2.02	0.41
2:G:260:TRP:CE2	2:G:284:HIS:HD2	2.38	0.41
2:G:273:HIS:CE1	2:G:337:PRO:HB3	2.55	0.41
2:G:488:LEU:HA	2:G:491:ILE:HB	2.02	0.41
2:G:947:GLU:HG3	2:G:1049:TYR:HD1	1.84	0.41
2:G:2430:ILE:HG21	2:G:2502:UNK:HA	2.02	0.41
2:G:4960:ILE:HD12	2:G:4983:HIS:HB3	2.02	0.41
2:I:110:ARG:NH2	2:I:115:ARG:HB3	2.35	0.41
2:I:978:THR:HB	2:I:980:ALA:H	1.83	0.41
2:I:3880:PHE:O	2:I:3884:LEU:N	2.52	0.41
1:J:83:GLY:O	1:J:94:ASN:N	2.52	0.41
1:A:34:LYS:NZ	2:B:634:GLN:HB3	2.35	0.41
2:B:299:LEU:HD12	2:B:299:LEU:HA	1.89	0.41
2:B:1268:PRO:HB2	2:B:1591:CYS:HB2	2.03	0.41
2:E:639:ASN:HD22	2:E:1635:THR:HA	1.85	0.41
2:E:873:LYS:HB3	2:E:1049:TYR:CZ	2.55	0.41
2:E:1771:LEU:HD11	2:E:2149:VAL:HB	2.02	0.41
2:E:3901:ASN:OD1	2:E:3904:ARG:NH1	2.49	0.41
2:G:546:TRP:O	2:G:550:LYS:NZ	2.31	0.41
2:G:1096:THR:OG1	2:G:1199:VAL:O	2.37	0.41
2:I:488:LEU:HA	2:I:491:ILE:HB	2.02	0.41
2:I:639:ASN:HD22	2:I:1635:THR:HA	1.85	0.41
2:I:1679:ASN:O	2:I:1683:HIS:ND1	2.36	0.41
2:I:3770:LEU:HD22	2:I:3804:ILE:HD11	2.01	0.41
2:I:4692:PRO:HG2	2:I:4703:ARG:HH21	1.84	0.41
2:I:4852:THR:HG21	2:I:4883:TYR:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1041:GLN:O	2:B:1045:THR:OG1	2.30	0.41
2:E:131:LEU:HB3	2:G:2459:SER:HB2	2.01	0.41
2:E:3963:ASN:O	2:E:3966:THR:OG1	2.29	0.41
2:G:639:ASN:HD22	2:G:1635:THR:HA	1.85	0.41
2:G:658:GLN:O	2:G:662:TRP:NE1	2.51	0.41
2:G:3646:THR:O	2:G:3650:CYS:N	2.51	0.41
2:G:3716:LEU:HD22	2:G:3785:ALA:HB1	2.02	0.41
2:G:3756:LYS:O	2:G:3760:LYS:NZ	2.37	0.41
2:G:4208:PRO:HA	2:G:4211:LYS:HB3	2.02	0.41
2:I:635:THR:HB	2:I:1639:LEU:HD23	2.00	0.41
2:I:1076:ARG:HD3	2:I:1237:TRP:HB2	2.02	0.41
2:I:1152:MET:HE1	2:I:1217:CYS:HB3	2.02	0.41
2:I:1268:PRO:HB2	2:I:1591:CYS:HB2	2.03	0.41
2:I:2862:LEU:HB3	2:I:2928:LYS:HB3	2.02	0.41
1:J:55:VAL:HG23	1:J:60:GLU:HB2	2.02	0.41
1:A:26:TYR:OH	1:A:42:ARG:NH2	2.39	0.41
2:B:728:ARG:NH2	2:B:1527:UNK:O	2.53	0.41
2:B:3915:ILE:H	2:B:3915:ILE:HG13	1.63	0.41
2:B:4692:PRO:HG2	2:B:4703:ARG:HH21	1.84	0.41
2:B:4736:ARG:O	2:B:4740:LEU:N	2.53	0.41
2:B:4801:LEU:HB3	2:B:4808:PHE:CG	2.56	0.41
2:E:78:LEU:O	2:E:82:LEU:N	2.44	0.41
2:E:229:GLU:OE2	2:E:374:LYS:NZ	2.47	0.41
2:E:241:GLN:O	2:E:289:ARG:NH1	2.42	0.41
2:E:1096:THR:OG1	2:E:1199:VAL:O	2.37	0.41
2:G:790:ARG:HG2	2:G:1627:ALA:HA	2.02	0.41
2:G:2265:LEU:HD21	2:G:2273:LEU:HD13	2.02	0.41
2:G:3927:GLN:NE2	2:G:3988:ALA:O	2.46	0.41
2:G:4989:MET:HE2	2:G:4989:MET:HB3	1.79	0.41
2:I:1256:GLU:HG2	2:I:1273:ALA:HB3	2.02	0.41
2:B:131:LEU:HD22	2:B:178:ARG:NH1	2.35	0.41
2:B:639:ASN:HD22	2:B:1635:THR:HA	1.85	0.41
2:B:790:ARG:HG2	2:B:1627:ALA:HA	2.02	0.41
2:B:4195:PHE:HZ	2:B:4987:ASN:HB3	1.86	0.41
2:E:35:LEU:HD13	2:E:49:LEU:HD13	2.02	0.41
2:E:1076:ARG:HD3	2:E:1237:TRP:HB2	2.02	0.41
2:E:3645:PRO:O	2:E:3649:ALA:N	2.53	0.41
2:E:4692:PRO:HG2	2:E:4703:ARG:HH21	1.84	0.41
2:E:4801:LEU:HB3	2:E:4808:PHE:CG	2.56	0.41
2:G:119:SER:HA	2:G:146:CYS:HA	2.01	0.41
2:G:3229:UNK:HA	2:G:3302:UNK:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:55:VAL:HG23	1:H:60:GLU:HB2	2.02	0.41
2:I:914:PRO:O	2:I:918:ARG:N	2.46	0.41
2:I:3773:ARG:HG2	2:I:3815:LYS:HD3	2.02	0.41
2:B:349:GLN:HE21	2:B:354:GLY:HA2	1.85	0.41
2:B:4707:ASN:OD1	2:B:4742:GLY:N	2.49	0.41
2:B:4822:THR:O	2:B:4825:THR:OG1	2.30	0.41
2:B:4957:LYS:HE3	2:B:4957:LYS:HB3	1.83	0.41
2:E:131:LEU:HD22	2:E:178:ARG:NH1	2.35	0.41
2:E:1497:UNK:HA	2:E:1535:UNK:HA	2.02	0.41
2:G:110:ARG:NH2	2:G:115:ARG:HB3	2.35	0.41
2:G:1256:GLU:HG2	2:G:1273:ALA:HB3	2.02	0.41
2:G:1661:ARG:O	2:G:1664:SER:OG	2.32	0.41
2:G:2862:LEU:HB3	2:G:2928:LYS:HB3	2.02	0.41
2:G:2908:TYR:OH	2:G:2920:ARG:NE	2.44	0.41
2:I:876:GLU:O	2:I:880:GLU:N	2.48	0.41
2:B:1088:TRP:HB2	2:B:1153:ILE:HG22	2.03	0.41
2:B:1152:MET:HE1	2:B:1217:CYS:HB3	2.02	0.41
2:B:3649:ALA:O	2:B:3653:PHE:N	2.48	0.41
2:E:110:ARG:NH2	2:E:115:ARG:HB3	2.35	0.41
2:E:1116:GLY:HA3	2:E:1123:VAL:HG12	2.02	0.41
2:E:1270:LEU:HD11	2:E:1595:LEU:HB3	2.03	0.41
2:E:4989:MET:HE2	2:E:4989:MET:HB3	1.79	0.41
2:G:16:THR:OG1	2:G:97:GLY:O	2.35	0.41
2:G:946:ALA:HA	2:G:949:ASN:HB2	2.02	0.41
2:G:4990:PHE:O	2:G:4994:TYR:N	2.48	0.41
2:B:805:PRO:HA	2:B:806:PRO:HD3	1.95	0.41
2:B:1808:ARG:HD3	2:B:1853:ILE:HG22	2.03	0.41
2:E:34:LYS:N	2:E:53:SER:OG	2.43	0.41
2:E:308:HIS:CE1	2:E:310:LYS:HB2	2.56	0.41
2:E:349:GLN:HE21	2:E:354:GLY:HA2	1.85	0.41
2:E:2144:ILE:H	2:E:2144:ILE:HG13	1.72	0.41
2:E:3773:ARG:HG2	2:E:3815:LYS:HD3	2.03	0.41
2:E:4195:PHE:HZ	2:E:4987:ASN:HB3	1.86	0.41
2:E:4639:MET:HE2	2:E:4639:MET:HB3	1.93	0.41
2:E:4847:VAL:HG11	2:E:4924:VAL:HG11	2.03	0.41
2:G:102:LEU:HB3	2:G:160:GLY:HA2	2.02	0.41
2:G:805:PRO:HA	2:G:806:PRO:HD3	1.94	0.41
2:G:1088:TRP:HB2	2:G:1153:ILE:HG22	2.03	0.41
2:G:1808:ARG:HD3	2:G:1853:ILE:HG22	2.03	0.41
2:G:3921:ASP:HA	2:G:3924:LEU:HB3	2.03	0.41
2:G:4847:VAL:HG11	2:G:4924:VAL:HG11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:119:SER:HA	2:I:146:CYS:HA	2.01	0.41
2:I:3915:ILE:H	2:I:3915:ILE:HG13	1.63	0.41
2:I:4049:VAL:HG21	2:I:4159:ARG:HD2	2.03	0.41
2:B:17:ASP:HB2	2:B:98:HIS:CE1	2.55	0.41
2:B:866:HIS:O	2:B:1051:TYR:OH	2.36	0.41
2:B:886:ARG:HB3	2:B:891:TRP:HB2	2.02	0.41
2:B:1116:GLY:HA3	2:B:1123:VAL:HG12	2.02	0.41
2:B:2121:PHE:O	2:B:3725:TYR:OH	2.39	0.41
2:B:2208:MET:HE1	2:B:2253:HIS:HB3	2.01	0.41
2:B:2265:LEU:HD21	2:B:2273:LEU:HD13	2.02	0.41
2:B:2342:ASN:OD1	2:B:2342:ASN:N	2.54	0.41
2:B:3153:UNK:O	2:B:3157:UNK:N	2.54	0.41
2:B:3921:ASP:HA	2:B:3924:LEU:HB3	2.03	0.41
2:B:4826:ILE:O	2:B:4829:SER:OG	2.30	0.41
2:B:4852:THR:HG21	2:B:4883:TYR:HB2	2.02	0.41
2:E:259:LEU:HA	2:E:259:LEU:HD23	1.87	0.41
2:E:913:LEU:O	2:E:918:ARG:NH2	2.54	0.41
2:E:1088:TRP:HB2	2:E:1153:ILE:HG22	2.03	0.41
2:E:2265:LEU:HD22	2:E:2330:ARG:HB3	2.03	0.41
2:E:3229:UNK:HA	2:E:3302:UNK:HA	2.02	0.41
2:E:3663:LEU:H	2:E:3663:LEU:HG	1.64	0.41
2:E:4958:CYS:SG	2:E:4959:PHE:N	2.94	0.41
2:G:259:LEU:HD23	2:G:259:LEU:HA	1.87	0.41
2:G:1076:ARG:HD3	2:G:1237:TRP:HB2	2.02	0.41
2:G:1116:GLY:HA3	2:G:1123:VAL:HG12	2.02	0.41
2:G:2002:PRO:HA	2:G:2005:GLN:HB3	2.02	0.41
2:G:3773:ARG:HG2	2:G:3815:LYS:HD3	2.03	0.41
2:G:4049:VAL:HG21	2:G:4159:ARG:HD2	2.03	0.41
2:G:4957:LYS:HE3	2:G:4957:LYS:HB3	1.83	0.41
2:I:591:ASP:O	2:I:1594:ARG:NH2	2.54	0.41
2:I:728:ARG:NH2	2:I:1527:UNK:O	2.54	0.41
2:I:946:ALA:HA	2:I:949:ASN:HB2	2.02	0.41
2:I:1025:ARG:O	2:I:1032:LYS:NZ	2.53	0.41
2:I:1088:TRP:HB2	2:I:1153:ILE:HG22	2.03	0.41
2:I:1116:GLY:HA3	2:I:1123:VAL:HG12	2.02	0.41
2:I:1497:UNK:HA	2:I:1535:UNK:HA	2.02	0.41
2:I:2116:LEU:O	2:I:2120:MET:N	2.46	0.41
2:I:2121:PHE:O	2:I:3725:TYR:OH	2.39	0.41
2:I:2265:LEU:HD21	2:I:2273:LEU:HD13	2.02	0.41
2:I:2384:ILE:O	2:I:2388:GLU:N	2.54	0.41
2:I:3663:LEU:H	2:I:3663:LEU:HG	1.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:3716:LEU:HD22	2:I:3785:ALA:HB1	2.02	0.41
2:I:4167:ALA:HA	2:I:4170:ILE:HD12	2.02	0.41
2:I:4195:PHE:HZ	2:I:4987:ASN:HB3	1.86	0.41
2:I:4707:ASN:OD1	2:I:4742:GLY:N	2.49	0.41
2:I:4736:ARG:O	2:I:4740:LEU:N	2.53	0.41
2:I:4847:VAL:HG11	2:I:4924:VAL:HG11	2.03	0.41
2:I:4957:LYS:HB3	2:I:4957:LYS:HE3	1.83	0.41
2:I:5013:MET:HA	2:I:5016:GLU:HB3	2.03	0.41
2:B:308:HIS:CE1	2:B:310:LYS:HB2	2.56	0.41
2:B:1092:PHE:HE2	2:B:1094:ALA:HB2	1.85	0.41
2:B:1936:LYS:O	2:B:1940:CYS:N	2.48	0.41
2:B:2116:LEU:O	2:B:2120:MET:N	2.46	0.41
2:B:2517:UNK:O	2:B:2521:UNK:N	2.54	0.41
2:B:4191:GLU:OE1	2:B:5006:GLN:NE2	2.54	0.41
2:B:4208:PRO:HA	2:B:4211:LYS:HB3	2.03	0.41
2:B:5013:MET:HA	2:B:5016:GLU:HB3	2.03	0.41
2:E:886:ARG:HB3	2:E:891:TRP:HB2	2.02	0.41
2:E:1256:GLU:HG2	2:E:1273:ALA:HB3	2.02	0.41
2:E:1808:ARG:HD3	2:E:1853:ILE:HG22	2.03	0.41
2:E:4191:GLU:OE1	2:E:5006:GLN:NE2	2.54	0.41
1:F:7:ILE:N	1:F:71:ARG:O	2.47	0.41
2:G:1270:LEU:HD11	2:G:1595:LEU:HB3	2.03	0.41
2:G:2342:ASN:OD1	2:G:2342:ASN:N	2.54	0.41
2:G:4191:GLU:OE1	2:G:5006:GLN:NE2	2.54	0.41
2:I:42:PHE:HD1	2:I:447:ASP:HB3	1.86	0.41
2:I:131:LEU:HD22	2:I:178:ARG:NH1	2.35	0.41
2:I:308:HIS:CE1	2:I:310:LYS:HB2	2.56	0.41
2:I:1808:ARG:HD3	2:I:1853:ILE:HG22	2.03	0.41
2:I:3362:UNK:O	2:I:3366:UNK:N	2.54	0.41
2:I:4191:GLU:OE1	2:I:5006:GLN:NE2	2.54	0.41
2:I:4204:GLN:NE2	2:I:4245:MET:SD	2.94	0.41
2:I:4569:LEU:HD11	2:I:4646:LEU:HD22	2.03	0.41
2:I:4801:LEU:HB3	2:I:4808:PHE:CG	2.56	0.41
2:B:488:LEU:HA	2:B:491:ILE:HB	2.02	0.40
2:B:4091:LYS:HD3	2:B:4091:LYS:HA	1.90	0.40
2:B:4581:LYS:HD2	2:B:4632:LEU:HD13	2.04	0.40
2:E:17:ASP:HB2	2:E:98:HIS:CE1	2.55	0.40
2:E:591:ASP:O	2:E:1594:ARG:NH2	2.54	0.40
2:E:3645:PRO:HB2	2:E:3648:ARG:HB3	2.03	0.40
2:E:3658:LYS:HA	2:E:3661:TRP:CD2	2.56	0.40
2:E:3921:ASP:HA	2:E:3924:LEU:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:3953:LYS:O	2:E:3956:SER:OG	2.29	0.40
2:E:4138:ASP:O	2:E:4142:ASN:ND2	2.54	0.40
2:E:4852:THR:HG21	2:E:4883:TYR:HB2	2.02	0.40
2:G:414:PHE:HE1	2:G:436:LEU:HB3	1.86	0.40
2:G:4569:LEU:HD11	2:G:4646:LEU:HD22	2.03	0.40
2:I:35:LEU:HD13	2:I:49:LEU:HD13	2.02	0.40
2:I:4930:ALA:HA	2:I:4933:GLN:HB3	2.03	0.40
2:B:42:PHE:HD1	2:B:447:ASP:HB3	1.86	0.40
2:B:2006:ILE:O	2:B:2010:LEU:N	2.45	0.40
2:B:2196:ASN:OD1	2:B:2199:ARG:NH1	2.54	0.40
2:B:2674:UNK:O	2:B:2676:UNK:N	2.54	0.40
2:B:3645:PRO:HB2	2:B:3648:ARG:HB3	2.03	0.40
2:E:320:LYS:HG2	2:E:356:TRP:CD1	2.57	0.40
2:E:627:PRO:HB2	1:F:92:PRO:HD3	2.04	0.40
2:E:836:GLY:HA3	2:E:1201:HIS:ND1	2.37	0.40
2:E:1693:GLN:HA	2:E:1696:HIS:HB3	2.04	0.40
2:E:2255:SER:HA	2:E:2258:LEU:HB3	2.04	0.40
2:E:4837:LEU:HD11	2:E:4936:ILE:HD11	2.03	0.40
2:G:1092:PHE:HE2	2:G:1094:ALA:HB2	1.85	0.40
2:G:2121:PHE:O	2:G:3725:TYR:OH	2.39	0.40
2:G:3771:HIS:O	2:G:3774:GLY:N	2.52	0.40
2:I:790:ARG:HG2	2:I:1627:ALA:HA	2.02	0.40
2:I:2810:LYS:O	2:I:2814:LYS:N	2.52	0.40
2:I:4989:MET:HB3	2:I:4989:MET:HE2	1.79	0.40
2:B:414:PHE:HE1	2:B:436:LEU:HB3	1.86	0.40
2:B:591:ASP:O	2:B:1594:ARG:NH2	2.54	0.40
2:B:688:LEU:HB3	2:B:777:PHE:CE1	2.57	0.40
2:B:1270:LEU:HD11	2:B:1595:LEU:HB3	2.03	0.40
2:B:2265:LEU:HD22	2:B:2330:ARG:HB3	2.03	0.40
2:B:4847:VAL:HG11	2:B:4924:VAL:HG11	2.03	0.40
2:B:4875:LYS:HA	2:B:4881:THR:HG22	2.03	0.40
2:E:946:ALA:HA	2:E:949:ASN:HB2	2.02	0.40
2:E:1092:PHE:HE2	2:E:1094:ALA:HB2	1.85	0.40
2:E:2121:PHE:O	2:E:3725:TYR:OH	2.39	0.40
2:E:2318:TYR:HA	2:E:2319:PRO:HD3	1.88	0.40
2:E:3921:ASP:O	2:E:3925:ARG:N	2.51	0.40
2:E:4114:CYS:HB3	2:E:4131:ARG:HH22	1.86	0.40
2:G:149:THR:N	2:G:172:VAL:O	2.55	0.40
2:G:591:ASP:O	2:G:1594:ARG:NH2	2.54	0.40
2:G:913:LEU:O	2:G:918:ARG:NH2	2.54	0.40
2:G:2023:LEU:O	2:G:2025:GLU:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:2384:ILE:O	2:G:2388:GLU:N	2.54	0.40
2:G:2674:UNK:O	2:G:2676:UNK:N	2.55	0.40
2:G:4138:ASP:O	2:G:4142:ASN:ND2	2.55	0.40
2:G:4801:LEU:HB3	2:G:4808:PHE:CG	2.56	0.40
2:G:5013:MET:HA	2:G:5016:GLU:HB3	2.03	0.40
2:I:414:PHE:HE1	2:I:436:LEU:HB3	1.86	0.40
2:I:716:PHE:HE2	2:I:759:ILE:HD11	1.86	0.40
2:I:1092:PHE:HE2	2:I:1094:ALA:HB2	1.85	0.40
2:I:1270:LEU:HD11	2:I:1595:LEU:HB3	2.03	0.40
2:I:2265:LEU:HD22	2:I:2330:ARG:HB3	2.04	0.40
2:I:3766:GLN:O	2:I:3770:LEU:N	2.50	0.40
2:I:3832:ILE:O	2:I:3836:MET:N	2.45	0.40
2:I:3921:ASP:HA	2:I:3924:LEU:HB3	2.03	0.40
2:I:4040:ILE:HG22	2:I:4044:MET:HE3	2.04	0.40
2:B:221:ARG:NH2	2:B:255:HIS:O	2.55	0.40
2:B:360:ALA:N	2:B:375:LYS:O	2.50	0.40
2:B:2002:PRO:HA	2:B:2005:GLN:HB3	2.02	0.40
2:B:4850:LEU:HD22	2:E:4814:LEU:HD21	2.03	0.40
2:E:102:LEU:HB3	2:E:160:GLY:HA2	2.02	0.40
2:E:688:LEU:HB3	2:E:777:PHE:CE1	2.57	0.40
2:E:776:LEU:HG	2:E:848:HIS:HA	2.04	0.40
2:E:2342:ASN:OD1	2:E:2342:ASN:N	2.54	0.40
2:E:3363:UNK:O	2:E:3367:UNK:N	2.55	0.40
2:E:3915:ILE:H	2:E:3915:ILE:HG13	1.63	0.40
2:E:4956:THR:O	2:E:4965:SER:N	2.52	0.40
2:G:308:HIS:CE1	2:G:310:LYS:HB2	2.56	0.40
2:G:716:PHE:HE2	2:G:759:ILE:HD11	1.86	0.40
2:G:836:GLY:HA3	2:G:1201:HIS:ND1	2.37	0.40
2:G:1268:PRO:HB2	2:G:1591:CYS:HB2	2.03	0.40
2:G:1294:UNK:HA	2:G:1455:UNK:HA	2.03	0.40
2:G:4195:PHE:HZ	2:G:4987:ASN:HB3	1.86	0.40
2:G:4204:GLN:NE2	2:G:4245:MET:SD	2.94	0.40
2:I:913:LEU:O	2:I:918:ARG:NH2	2.54	0.40
2:I:2674:UNK:O	2:I:2676:UNK:N	2.55	0.40
2:I:4138:ASP:O	2:I:4142:ASN:ND2	2.55	0.40
2:I:4147:LEU:O	2:I:4151:SER:OG	2.35	0.40
2:I:4208:PRO:HA	2:I:4211:LYS:HB3	2.02	0.40
2:B:716:PHE:HE2	2:B:759:ILE:HD11	1.86	0.40
2:E:1268:PRO:HB2	2:E:1591:CYS:HB2	2.03	0.40
2:E:2236:LEU:HD23	2:E:2275:VAL:HG21	2.03	0.40
2:E:2265:LEU:HD21	2:E:2273:LEU:HD13	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:151:HIS:HB2	2:G:170:ILE:HB	2.04	0.40
2:G:663:TYR:HB2	2:G:808:TYR:HB3	2.04	0.40
2:G:2196:ASN:OD1	2:G:2199:ARG:NH1	2.54	0.40
2:G:2255:SER:HA	2:G:2258:LEU:HB3	2.04	0.40
2:G:4040:ILE:HG22	2:G:4044:MET:HE3	2.04	0.40
2:G:4167:ALA:HA	2:G:4170:ILE:HD12	2.02	0.40
2:I:4236:SER:O	2:I:4240:ASP:N	2.45	0.40
2:I:4978:HIS:O	2:I:4983:HIS:N	2.47	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	105/107 (98%)	95 (90%)	10 (10%)	0	100	100
1	F	105/107 (98%)	95 (90%)	10 (10%)	0	100	100
1	H	105/107 (98%)	95 (90%)	10 (10%)	0	100	100
1	J	105/107 (98%)	95 (90%)	10 (10%)	0	100	100
2	B	3235/4687 (69%)	2848 (88%)	382 (12%)	5 (0%)	43	77
2	E	3235/4687 (69%)	2849 (88%)	381 (12%)	5 (0%)	43	77
2	G	3235/4687 (69%)	2848 (88%)	382 (12%)	5 (0%)	43	77
2	I	3235/4687 (69%)	2850 (88%)	380 (12%)	5 (0%)	43	77
All	All	13360/19176 (70%)	11775 (88%)	1565 (12%)	20 (0%)	49	83

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	1708	ARG
2	E	1708	ARG

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Mol	Chain	Res	Type
2	G	1708	ARG
2	I	1708	ARG
2	B	1932	PRO
2	E	1932	PRO
2	G	1932	PRO
2	I	1932	PRO
2	B	4667	PRO
2	E	4667	PRO
2	G	4667	PRO
2	I	4667	PRO
2	B	1840	PRO
2	E	1840	PRO
2	G	1840	PRO
2	I	1840	PRO
2	B	4641	PRO
2	E	4641	PRO
2	G	4641	PRO
2	I	4641	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	88/88 (100%)	88 (100%)	0	100	100
1	F	88/88 (100%)	88 (100%)	0	100	100
1	H	88/88 (100%)	88 (100%)	0	100	100
1	J	88/88 (100%)	88 (100%)	0	100	100
2	B	2493/3209 (78%)	2481 (100%)	12 (0%)	81	81
2	E	2493/3209 (78%)	2481 (100%)	12 (0%)	81	81
2	G	2493/3209 (78%)	2481 (100%)	12 (0%)	81	81
2	I	2493/3209 (78%)	2481 (100%)	12 (0%)	81	81
All	All	10324/13188 (78%)	10276 (100%)	48 (0%)	78	81

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	131	LEU
2	B	688	LEU
2	B	781	VAL
2	B	978	THR
2	B	2144	ILE
2	B	2339	VAL
2	B	3663	LEU
2	B	3805	LEU
2	B	4154	VAL
2	B	4871	GLU
2	B	4913	ARG
2	B	4995	LEU
2	E	131	LEU
2	E	688	LEU
2	E	781	VAL
2	E	978	THR
2	E	2144	ILE
2	E	2339	VAL
2	E	3663	LEU
2	E	3805	LEU
2	E	4154	VAL
2	E	4871	GLU
2	E	4913	ARG
2	E	4995	LEU
2	G	131	LEU
2	G	688	LEU
2	G	781	VAL
2	G	978	THR
2	G	2144	ILE
2	G	2339	VAL
2	G	3663	LEU
2	G	3805	LEU
2	G	4154	VAL
2	G	4871	GLU
2	G	4913	ARG
2	G	4995	LEU
2	I	131	LEU
2	I	688	LEU
2	I	781	VAL
2	I	978	THR
2	I	2144	ILE
2	I	2339	VAL
2	I	3663	LEU

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Mol	Chain	Res	Type
2	I	3805	LEU
2	I	4154	VAL
2	I	4871	GLU
2	I	4913	ARG
2	I	4995	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (219) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	HIS
2	B	44	ASN
2	B	113	HIS
2	B	151	HIS
2	B	224	HIS
2	B	308	HIS
2	B	379	HIS
2	B	395	GLN
2	B	405	HIS
2	B	479	GLN
2	B	495	ASN
2	B	678	GLN
2	B	797	HIS
2	B	838	HIS
2	B	877	ASN
2	B	1035	ASN
2	B	1158	ASN
2	B	1598	GLN
2	B	1679	ASN
2	B	1691	GLN
2	B	1696	HIS
2	B	1719	HIS
2	B	1760	HIS
2	B	1775	HIS
2	B	1861	GLN
2	B	1949	GLN
2	B	1972	ASN
2	B	2005	GLN
2	B	2036	GLN
2	B	2041	HIS
2	B	2127	GLN
2	B	2260	ASN
2	B	2773	ASN

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Mol	Chain	Res	Type
2	B	3809	ASN
2	B	3814	GLN
2	B	3882	GLN
2	B	3889	GLN
2	B	3896	ASN
2	B	3946	GLN
2	B	3950	ASN
2	B	3960	GLN
2	B	3963	ASN
2	B	3970	GLN
2	B	4094	GLN
2	B	4109	GLN
2	B	4120	ASN
2	B	4142	ASN
2	B	4201	ASN
2	B	4209	GLN
2	B	4246	GLN
2	B	4553	ASN
2	B	4728	HIS
2	B	4886	HIS
2	B	4949	GLN
2	B	5003	HIS
2	E	44	ASN
2	E	113	HIS
2	E	151	HIS
2	E	224	HIS
2	E	273	HIS
2	E	308	HIS
2	E	379	HIS
2	E	395	GLN
2	E	405	HIS
2	E	479	GLN
2	E	495	ASN
2	E	678	GLN
2	E	838	HIS
2	E	877	ASN
2	E	1035	ASN
2	E	1158	ASN
2	E	1220	GLN
2	E	1598	GLN
2	E	1679	ASN
2	E	1691	GLN

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Mol	Chain	Res	Type
2	E	1696	HIS
2	E	1719	HIS
2	E	1760	HIS
2	E	1775	HIS
2	E	1861	GLN
2	E	1941	ASN
2	E	1949	GLN
2	E	2005	GLN
2	E	2036	GLN
2	E	2041	HIS
2	E	2127	GLN
2	E	2260	ASN
2	E	2773	ASN
2	E	3809	ASN
2	E	3814	GLN
2	E	3882	GLN
2	E	3889	GLN
2	E	3896	ASN
2	E	3946	GLN
2	E	3950	ASN
2	E	3960	GLN
2	E	3963	ASN
2	E	4094	GLN
2	E	4109	GLN
2	E	4120	ASN
2	E	4130	ASN
2	E	4142	ASN
2	E	4201	ASN
2	E	4246	GLN
2	E	4553	ASN
2	E	4728	HIS
2	E	4806	ASN
2	E	4832	HIS
2	E	4833	ASN
2	E	4886	HIS
2	E	4949	GLN
2	E	5003	HIS
2	E	5031	GLN
2	G	113	HIS
2	G	151	HIS
2	G	224	HIS
2	G	308	HIS

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Mol	Chain	Res	Type
2	G	379	HIS
2	G	395	GLN
2	G	405	HIS
2	G	495	ASN
2	G	678	GLN
2	G	765	GLN
2	G	797	HIS
2	G	838	HIS
2	G	877	ASN
2	G	1035	ASN
2	G	1158	ASN
2	G	1598	GLN
2	G	1679	ASN
2	G	1691	GLN
2	G	1696	HIS
2	G	1719	HIS
2	G	1760	HIS
2	G	1775	HIS
2	G	1861	GLN
2	G	1941	ASN
2	G	1949	GLN
2	G	2005	GLN
2	G	2041	HIS
2	G	2127	GLN
2	G	2260	ASN
2	G	2773	ASN
2	G	3809	ASN
2	G	3814	GLN
2	G	3882	GLN
2	G	3889	GLN
2	G	3896	ASN
2	G	3960	GLN
2	G	3963	ASN
2	G	3970	GLN
2	G	4094	GLN
2	G	4109	GLN
2	G	4120	ASN
2	G	4130	ASN
2	G	4142	ASN
2	G	4201	ASN
2	G	4246	GLN
2	G	4553	ASN

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Mol	Chain	Res	Type
2	G	4728	HIS
2	G	4832	HIS
2	G	4833	ASN
2	G	4864	ASN
2	G	4886	HIS
2	G	4949	GLN
2	G	5003	HIS
2	G	5031	GLN
2	I	113	HIS
2	I	151	HIS
2	I	224	HIS
2	I	308	HIS
2	I	379	HIS
2	I	395	GLN
2	I	405	HIS
2	I	479	GLN
2	I	495	ASN
2	I	678	GLN
2	I	838	HIS
2	I	877	ASN
2	I	1035	ASN
2	I	1158	ASN
2	I	1220	GLN
2	I	1598	GLN
2	I	1679	ASN
2	I	1691	GLN
2	I	1719	HIS
2	I	1760	HIS
2	I	1775	HIS
2	I	1861	GLN
2	I	1941	ASN
2	I	1949	GLN
2	I	1972	ASN
2	I	2005	GLN
2	I	2041	HIS
2	I	2127	GLN
2	I	2260	ASN
2	I	2773	ASN
2	I	3809	ASN
2	I	3814	GLN
2	I	3882	GLN
2	I	3889	GLN

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Mol	Chain	Res	Type
2	I	3896	ASN
2	I	3946	GLN
2	I	3950	ASN
2	I	3960	GLN
2	I	3963	ASN
2	I	4094	GLN
2	I	4109	GLN
2	I	4120	ASN
2	I	4130	ASN
2	I	4142	ASN
2	I	4201	ASN
2	I	4246	GLN
2	I	4553	ASN
2	I	4728	HIS
2	I	4886	HIS
2	I	4949	GLN
2	I	5003	HIS
2	I	5031	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	12
2	I	12
2	E	12
2	G	12

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	3613:UNK	C	3639:THR	N	44.41
1	I	3613:UNK	C	3639:THR	N	44.36
1	E	3613:UNK	C	3639:THR	N	44.35
1	G	3613:UNK	C	3639:THR	N	44.35
1	B	3163:UNK	C	3170:UNK	N	16.42
1	E	3163:UNK	C	3170:UNK	N	16.36
1	G	3163:UNK	C	3170:UNK	N	16.35
1	I	3163:UNK	C	3170:UNK	N	16.29
1	G	3468:UNK	C	3511:UNK	N	14.86
1	E	3468:UNK	C	3511:UNK	N	14.84
1	I	3468:UNK	C	3511:UNK	N	14.84
1	B	3468:UNK	C	3511:UNK	N	14.79
1	I	3063:UNK	C	3134:UNK	N	14.53
1	G	3063:UNK	C	3134:UNK	N	14.50
1	G	2703:UNK	C	2734:ASN	N	14.49
1	E	3063:UNK	C	3134:UNK	N	14.48
1	I	2703:UNK	C	2734:ASN	N	14.48
1	B	3063:UNK	C	3134:UNK	N	14.46
1	B	2703:UNK	C	2734:ASN	N	14.44
1	E	2703:UNK	C	2734:ASN	N	14.34
1	B	3236:UNK	C	3241:UNK	N	13.22
1	G	3236:UNK	C	3241:UNK	N	13.20
1	E	3236:UNK	C	3241:UNK	N	13.17

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	3236:UNK	C	3241:UNK	N	13.16
1	I	1564:UNK	C	1573:MET	N	12.84
1	B	1564:UNK	C	1573:MET	N	12.82
1	E	1564:UNK	C	1573:MET	N	12.72
1	G	1564:UNK	C	1573:MET	N	12.61
1	B	2976:UNK	C	2995:UNK	N	12.18
1	E	2976:UNK	C	2995:UNK	N	12.15
1	I	2976:UNK	C	2995:UNK	N	12.07
1	G	2976:UNK	C	2995:UNK	N	12.06
1	G	3254:UNK	C	3261:UNK	N	8.57
1	I	3254:UNK	C	3261:UNK	N	8.57
1	B	3254:UNK	C	3261:UNK	N	8.56
1	E	3254:UNK	C	3261:UNK	N	8.53
1	E	1297:UNK	C	1430:UNK	N	5.79
1	I	1297:UNK	C	1430:UNK	N	5.74
1	G	1297:UNK	C	1430:UNK	N	5.65
1	B	1297:UNK	C	1430:UNK	N	5.48
1	B	2479:LEU	C	2487:UNK	N	3.92
1	E	2479:LEU	C	2487:UNK	N	3.92
1	I	2479:LEU	C	2487:UNK	N	3.89
1	G	2479:LEU	C	2487:UNK	N	3.81
1	G	2939:ARG	C	2942:UNK	N	3.63
1	I	2939:ARG	C	2942:UNK	N	3.56
1	B	2939:ARG	C	2942:UNK	N	3.53
1	E	2939:ARG	C	2942:UNK	N	3.53

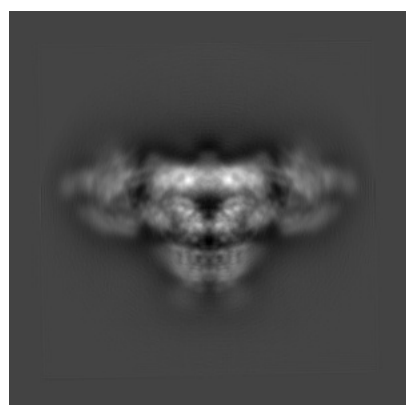
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22394. These allow visual inspection of the internal detail of the map and identification of artifacts.

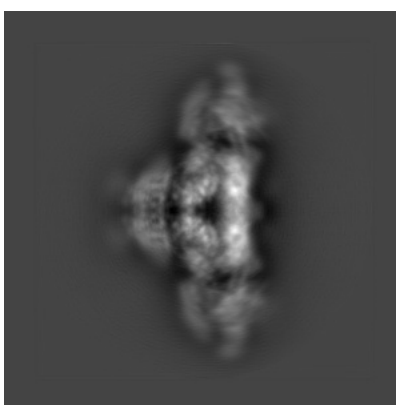
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

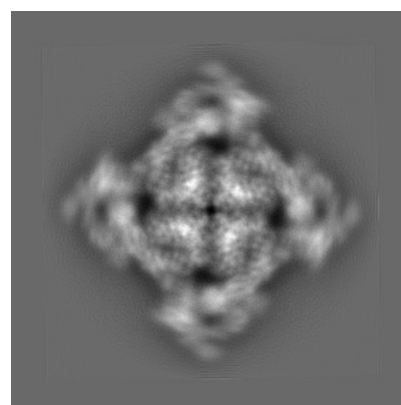
6.1.1 Primary map



X



Y

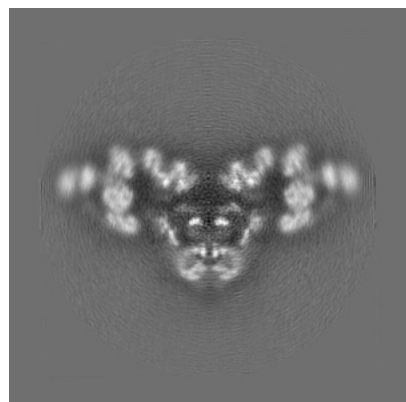


Z

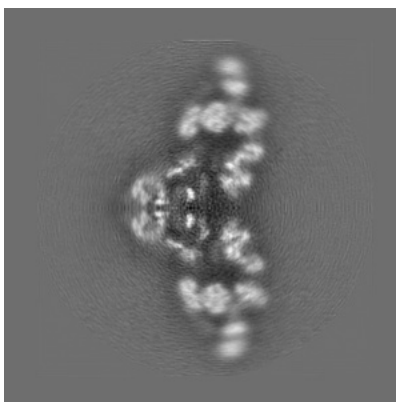
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

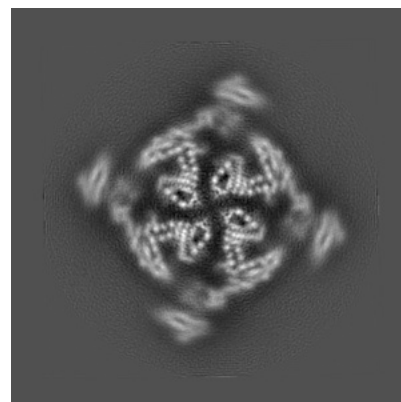
6.2.1 Primary map



X Index: 200



Y Index: 200

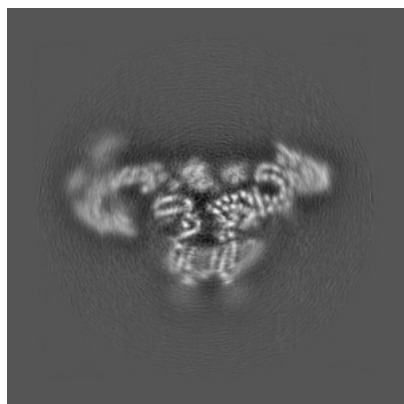


Z Index: 200

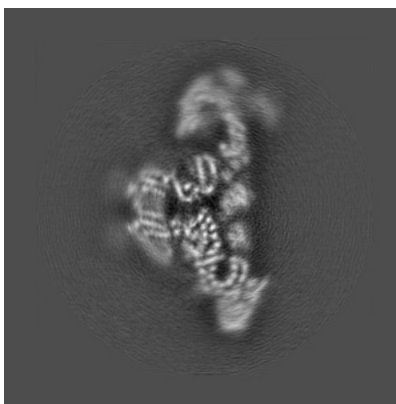
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

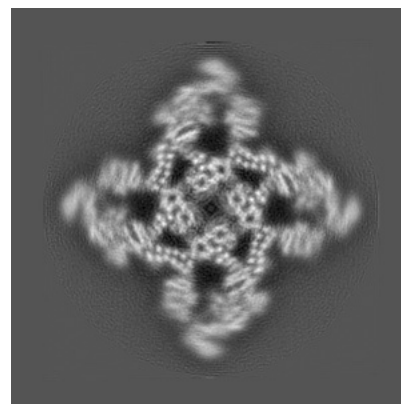
6.3.1 Primary map



X Index: 177



Y Index: 177



Z Index: 227

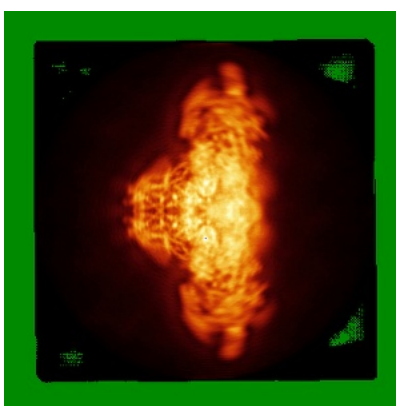
The images above show the largest variance slices of the map in three orthogonal directions.

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

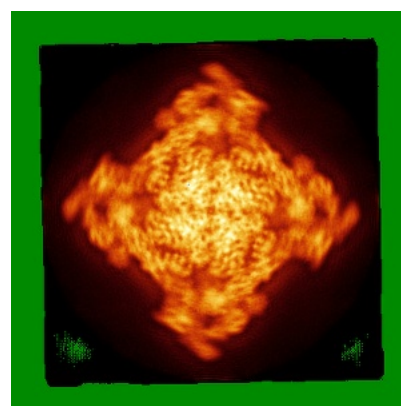
6.4.1 Primary map



X



Y

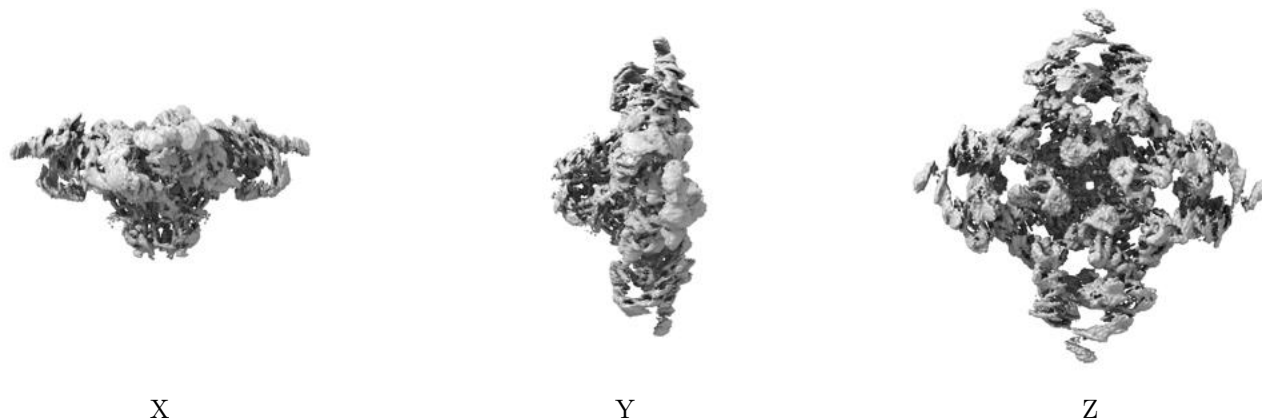


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.16. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

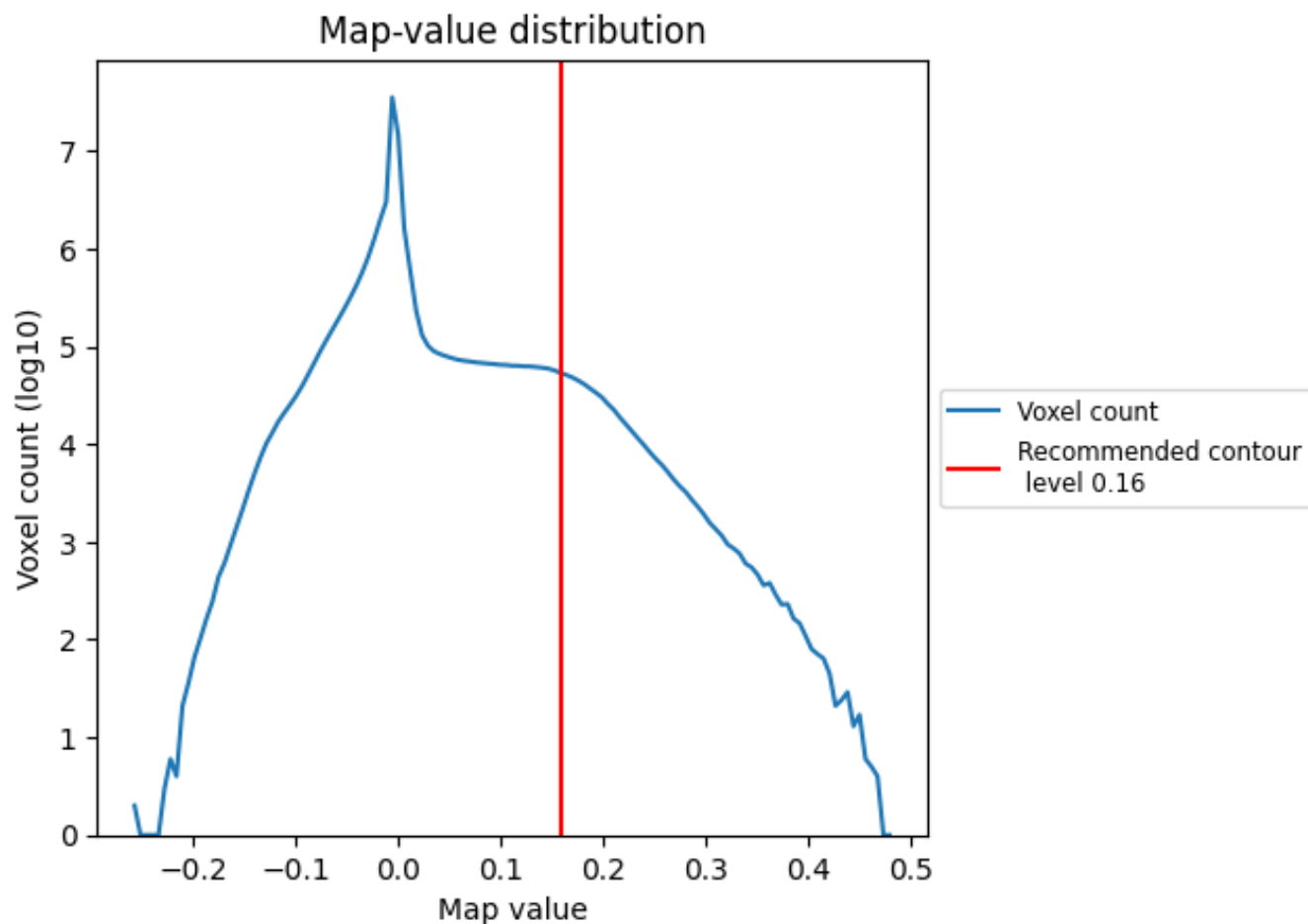
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

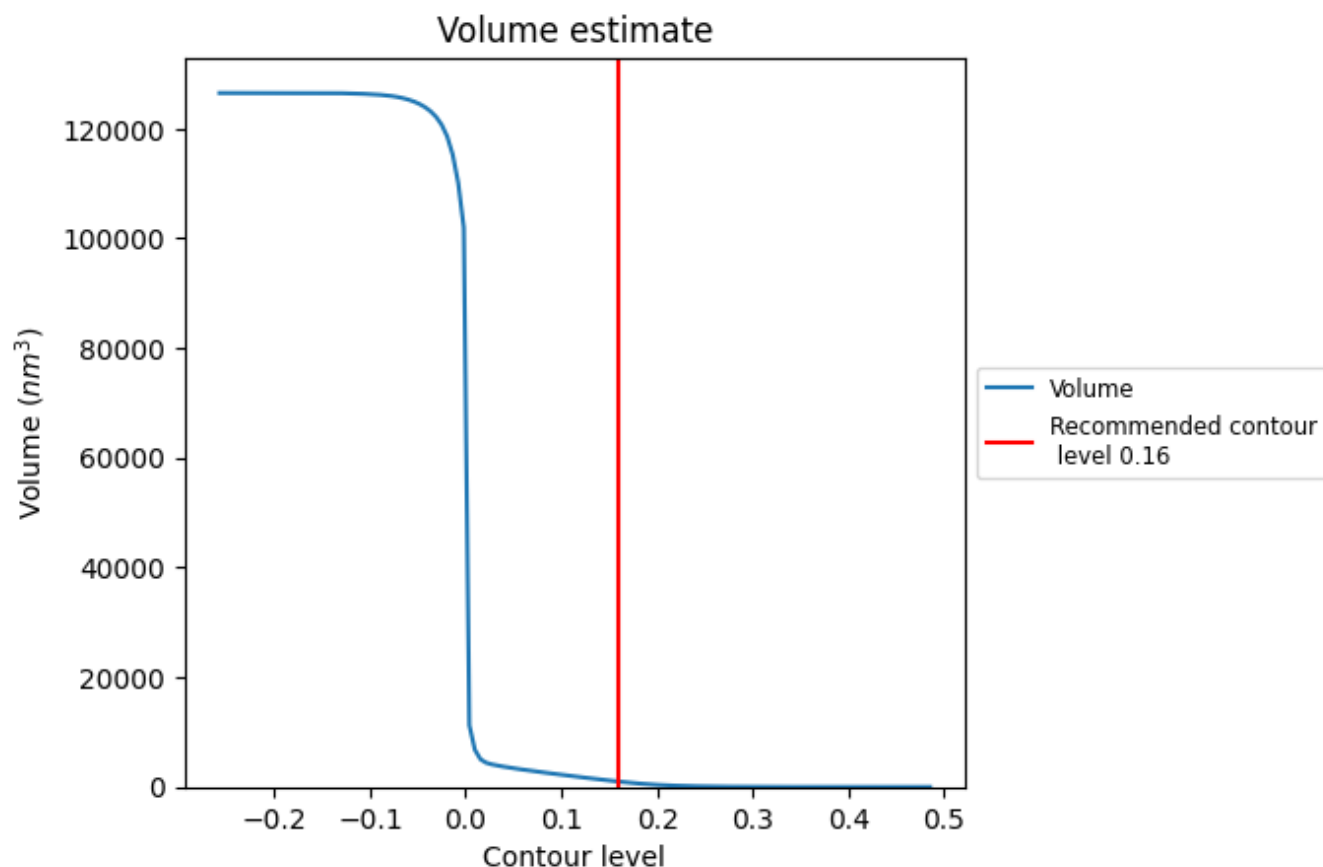
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

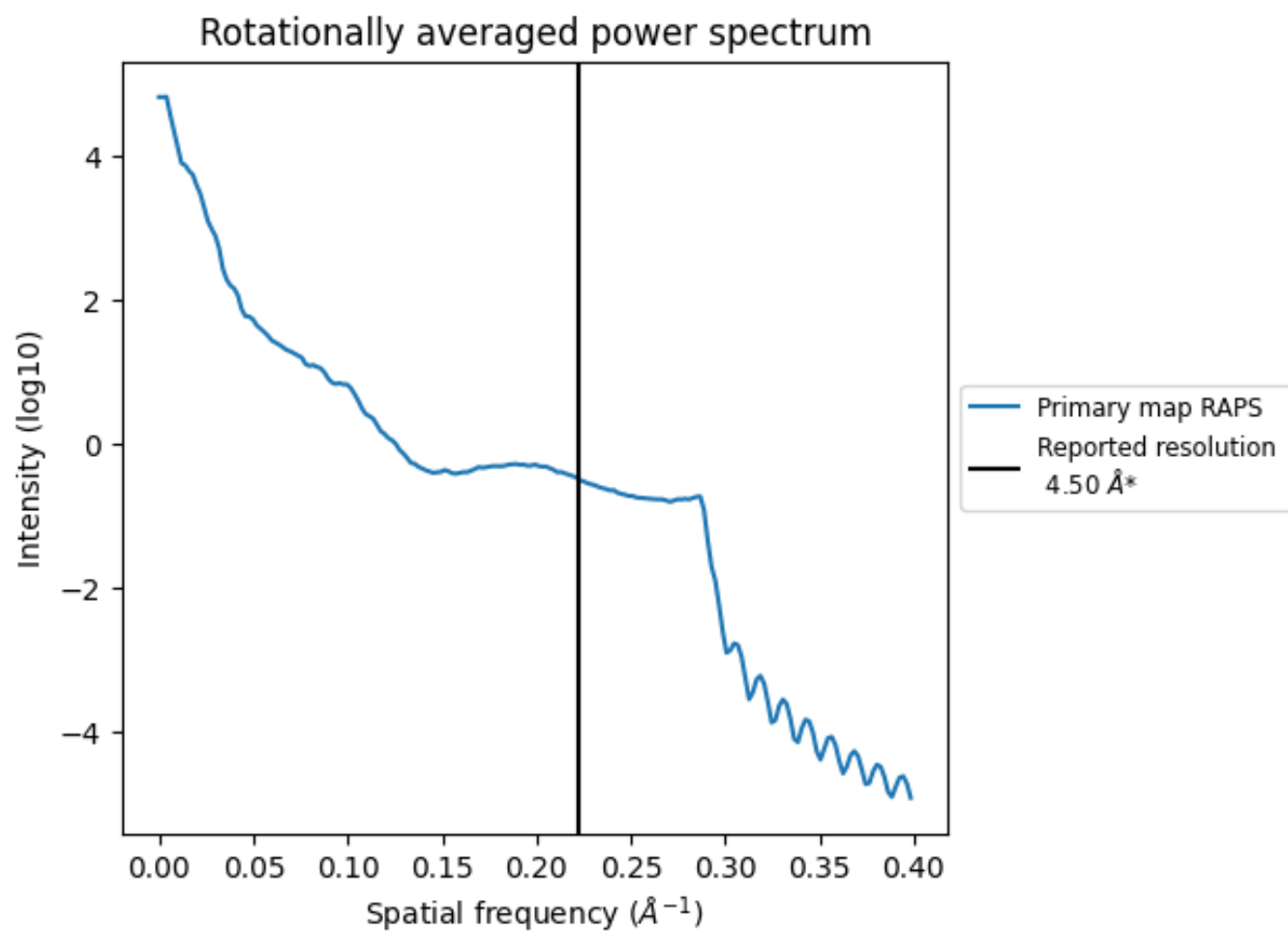
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 979 nm^3 ; this corresponds to an approximate mass of 884 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 0.222 Å⁻¹

8 Fourier-Shell correlation

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

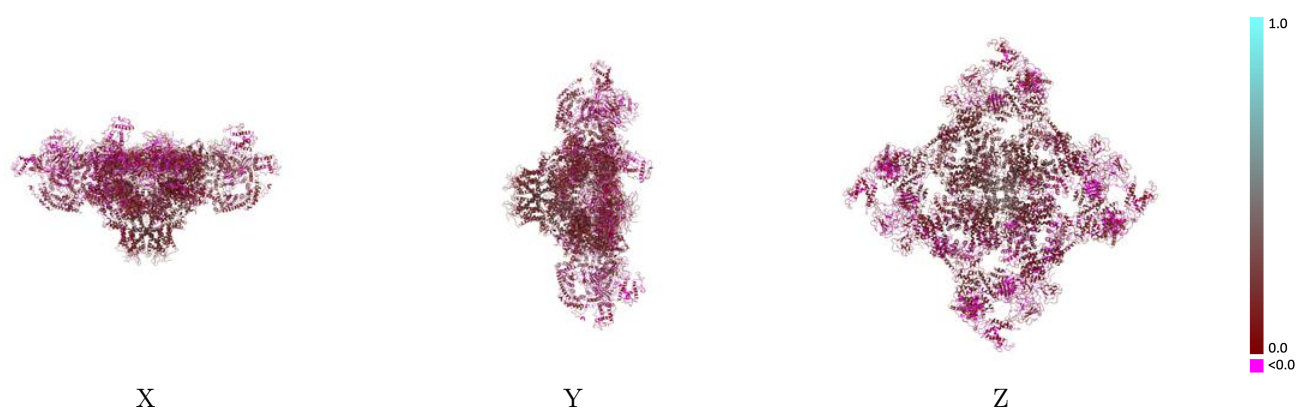
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22394 and PDB model 7JMH. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)

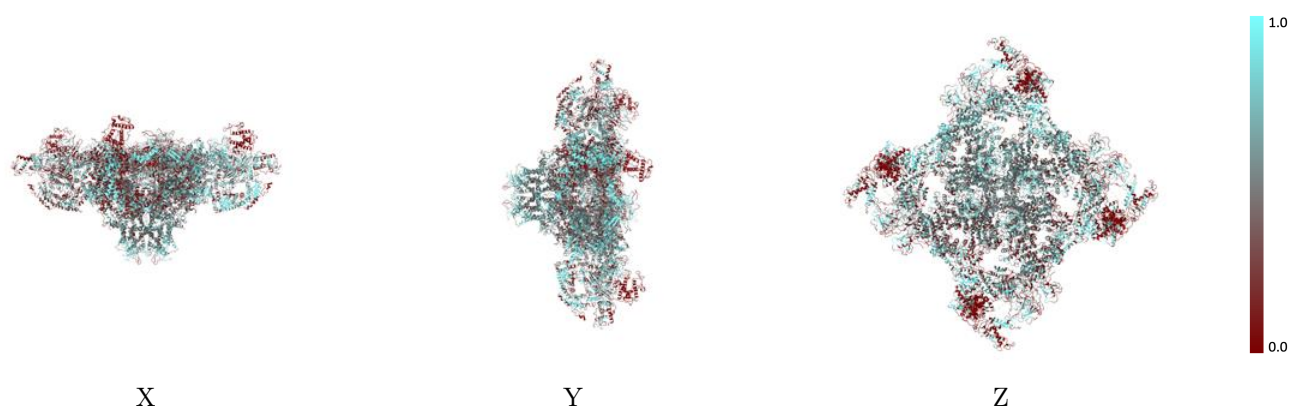
This section was not generated.

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



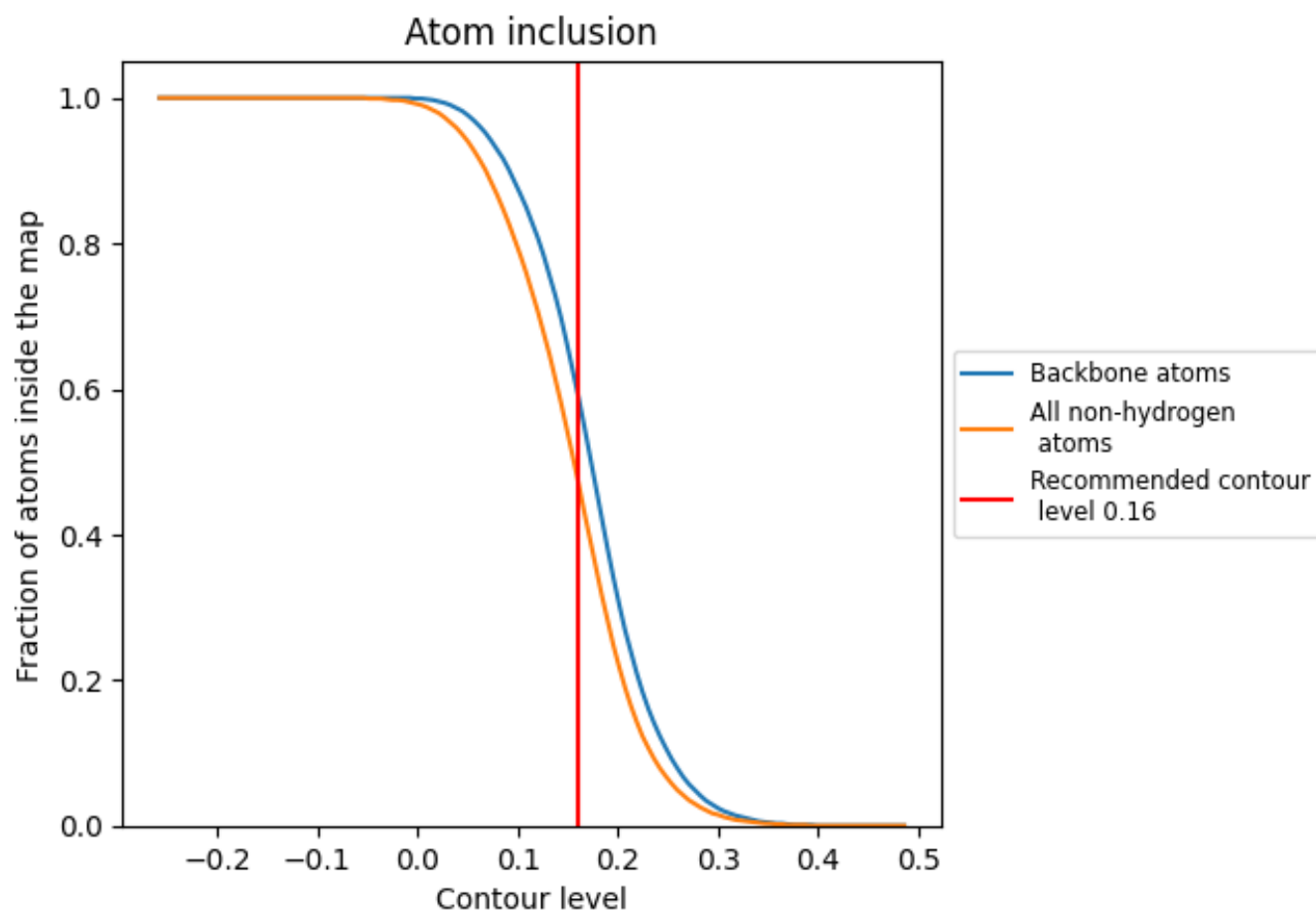
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.16).

9.4 Atom inclusion [i](#)



At the recommended contour level, 59% of all backbone atoms, 48% 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 (0.16) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4750	0.1320
A	0.5620	0.1390
B	0.5150	0.1680
E	0.4810	0.1330
F	0.4890	0.1070
G	0.4450	0.1070
H	0.4530	0.1190
I	0.4560	0.1230
J	0.4690	0.1180

