



Full wwPDB EM Validation Report ⓘ

Nov 8, 2022 – 09:33 AM EST

PDB ID : 6PV6
EMDB ID : EMD-20486
Title : Functional Pathways of Biomolecules Retrieved from Single-particle Snapshots
Authors : Dashti, A.; des Georges, A.; Frank, J.; Ourmazd, A.
Deposited on : 2019-07-19
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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

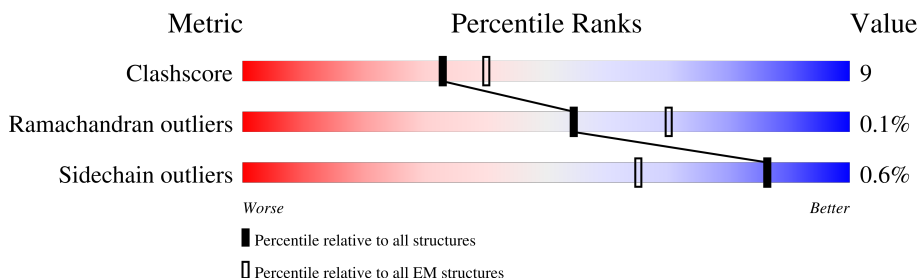
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.50 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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

Mol	Chain	Length	Quality of chain
1	B	4687	<div> <div>33%</div> <div>70%</div> <div>18%</div> <div>11%</div> </div>
1	E	4687	<div> <div>37%</div> <div>70%</div> <div>18%</div> <div>11%</div> </div>
1	G	4687	<div> <div>40%</div> <div>70%</div> <div>19%</div> <div>11%</div> </div>
1	I	4687	<div> <div>36%</div> <div>70%</div> <div>18%</div> <div>11%</div> </div>
2	A	108	<div> <div>37%</div> <div>69%</div> <div>31%</div> <div>.</div> </div>
2	F	108	<div> <div>47%</div> <div>70%</div> <div>29%</div> <div>.</div> </div>
2	H	108	<div> <div>54%</div> <div>69%</div> <div>31%</div> <div>.</div> </div>
2	J	108	<div> <div>43%</div> <div>67%</div> <div>32%</div> <div>.</div> </div>

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 Ryanodine receptor 1.

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

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

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

- Molecule 3 is ZINC ION (three-letter code: 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	I	1	Total	Zn	0
			1	1	
3	G	1	Total	Zn	0
			1	1	

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of

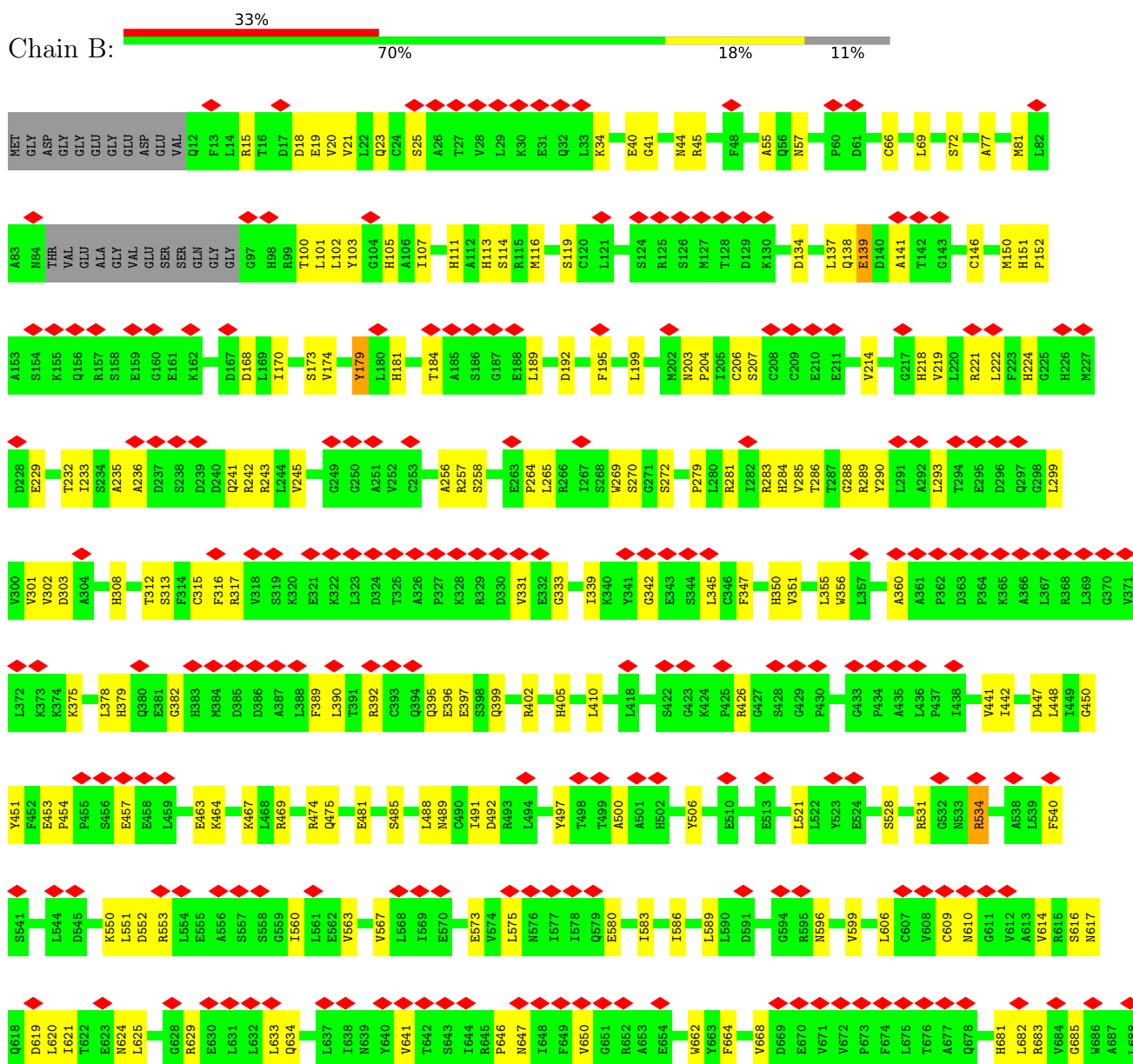
Interest" by depositor).

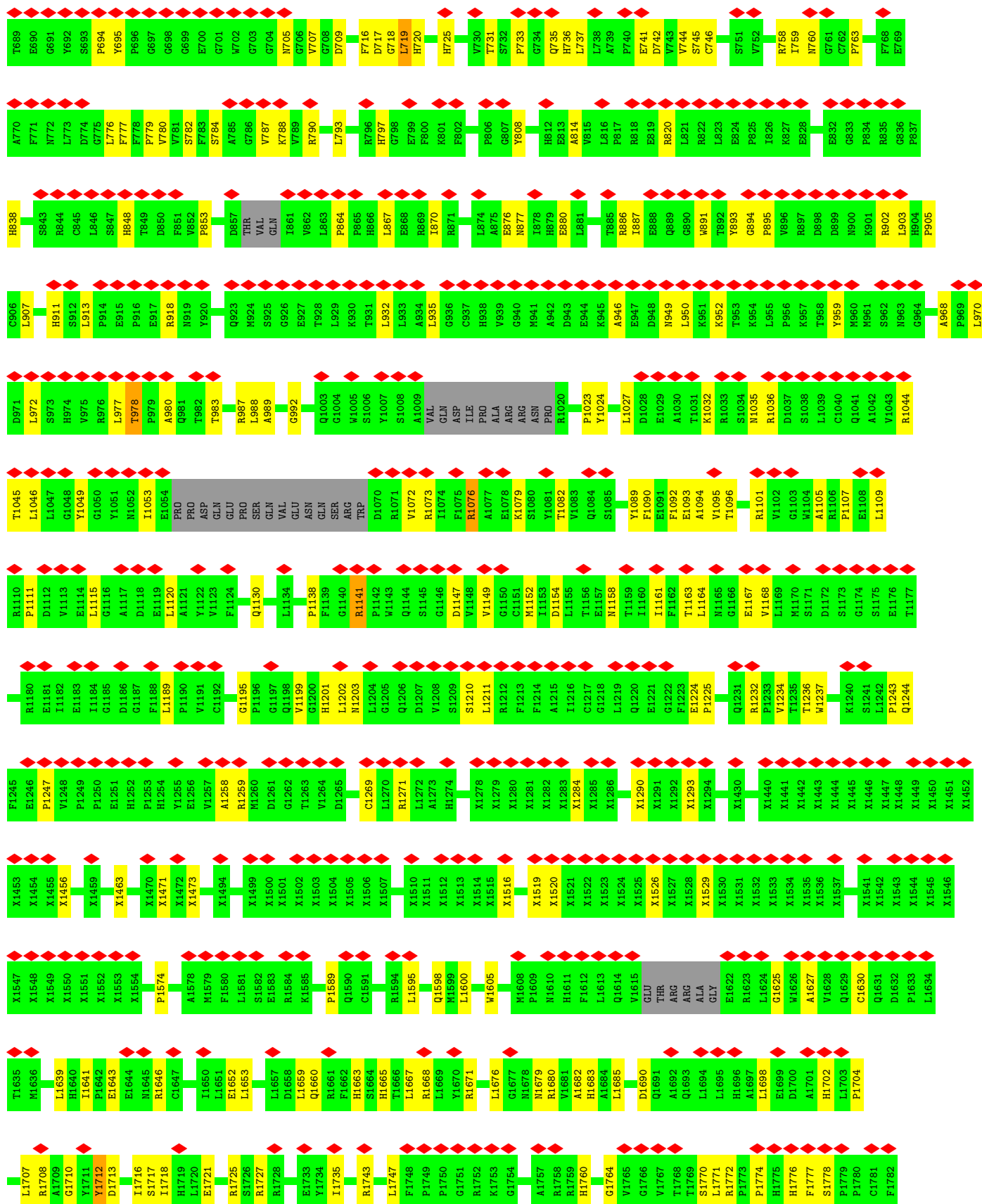
Mol	Chain	Residues	Atoms		AltConf
4	B	1	Total 1	Ca 1	0
4	E	1	Total 1	Ca 1	0
4	I	1	Total 1	Ca 1	0
4	G	1	Total 1	Ca 1	0

3 Residue-property plots

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

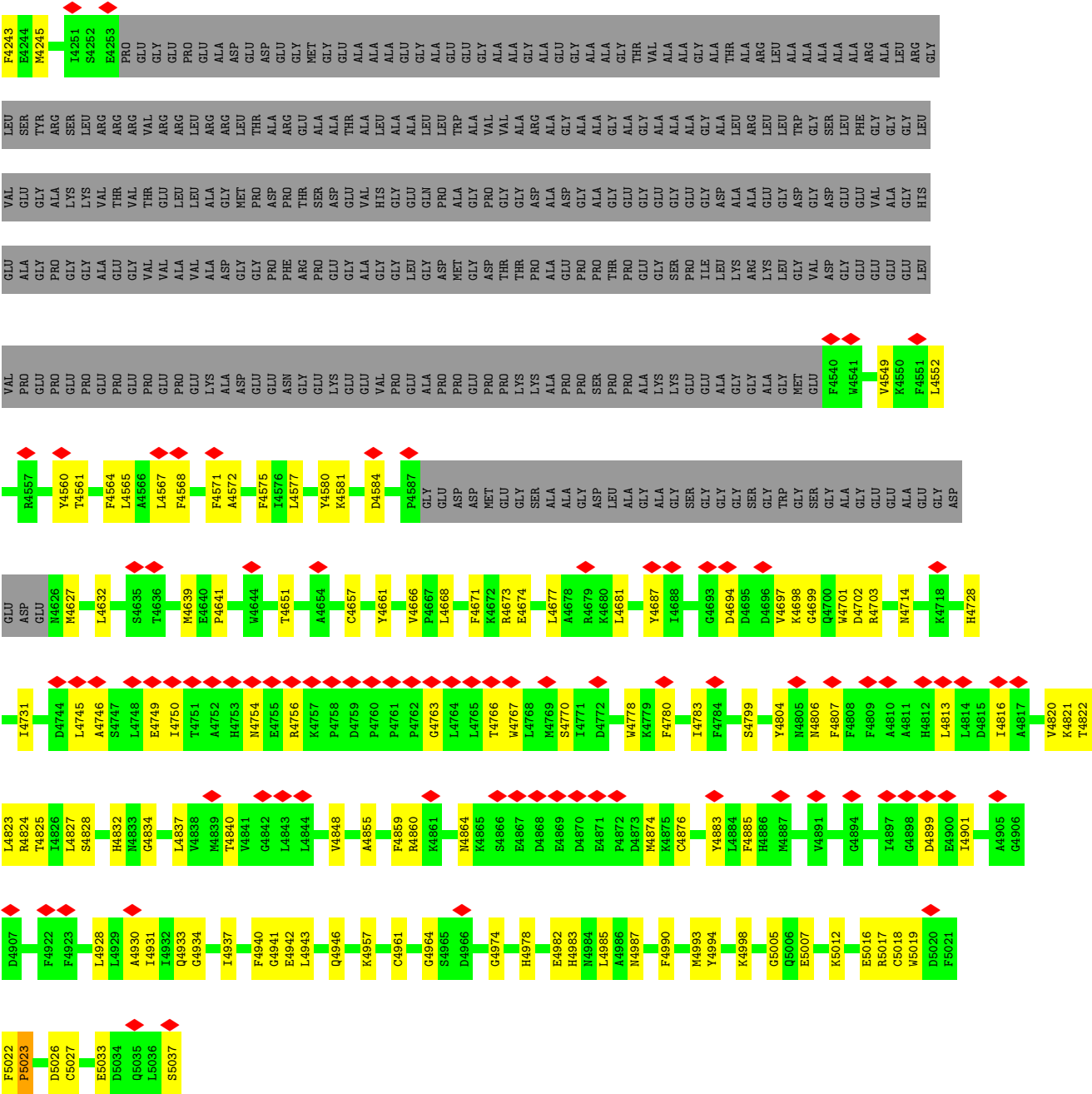
• Molecule 1: Ryanodine receptor 1



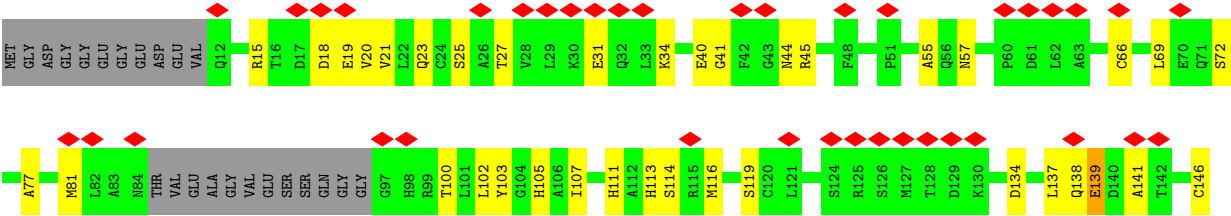


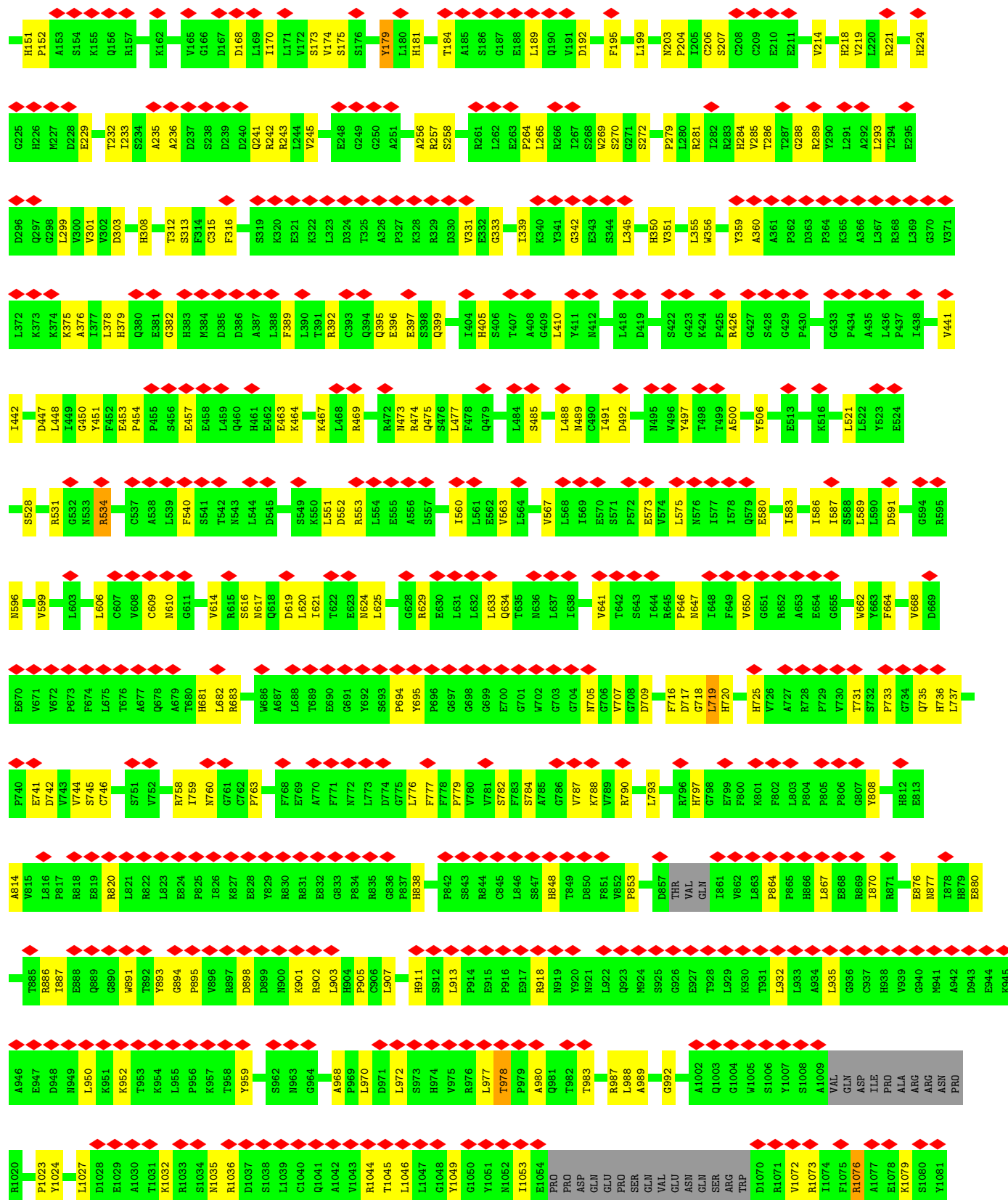


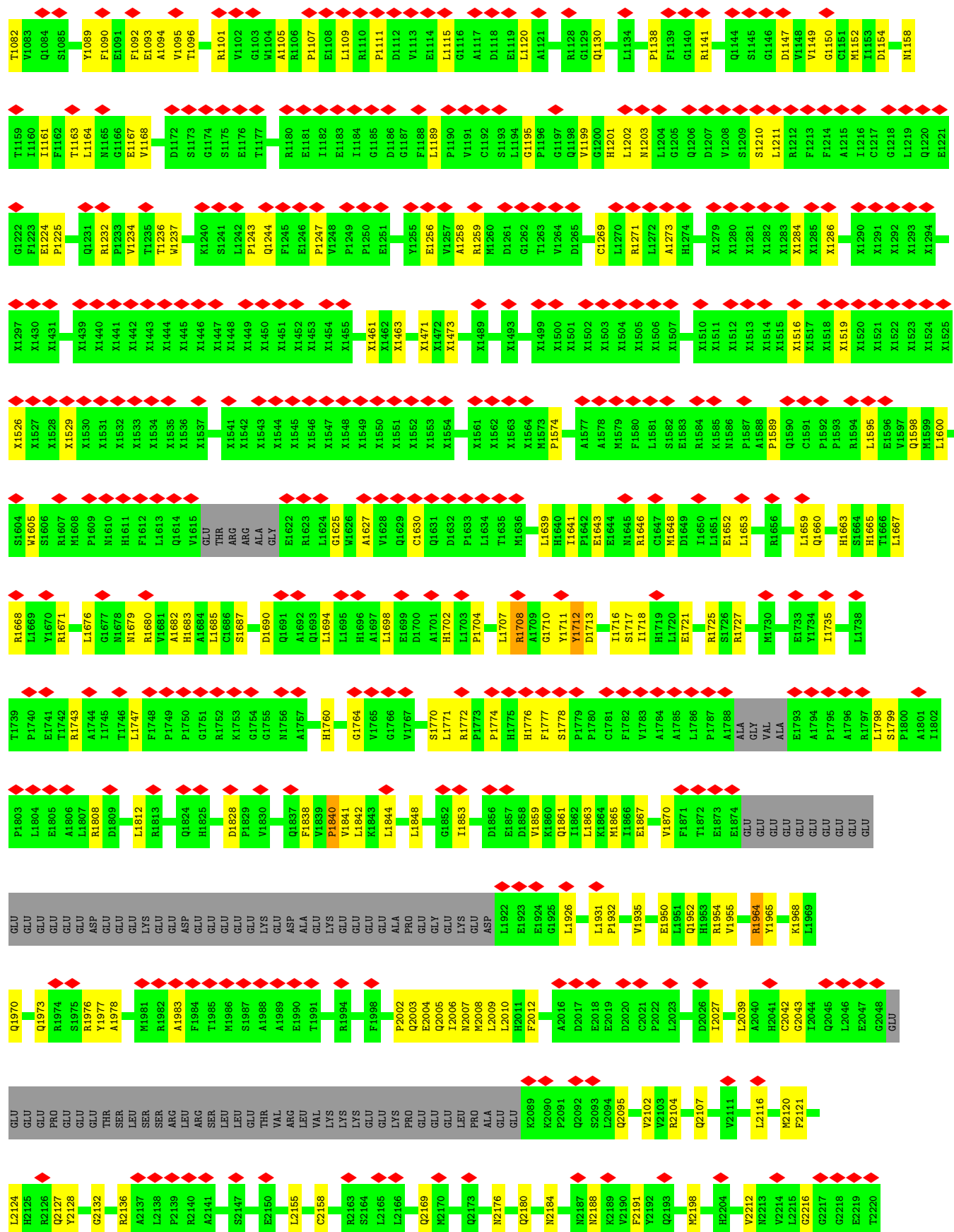
R4137 D4138 R4142 V4145 L4146 L4147 L4150 S4151 E4152 P4155 H4156 R4159 L4164 S4169 E4172 Y4173 F4174 R4175 R4180 L4181 E4182 R4188 R4192 L4193 Y4194 T4200 M4201 Q4204 R4215 L4218 E4224 Q4225 Q4226 E4227 A4228 E4229 E4232 S4236 D4240	V4072 G4073 S4074 E4075 M4076 F4077 Q4078 D4079 Y4080 V4081 T4082 D4083 P4084 R4085 I4088 S4089 K4090 K4091 Q4094 K4095 A4096 M4097 D4098 S4099 Q4100 K4101 Q4102 F4103 T4104 G4105 L4106 E4107 I4108 Q4109 F4110 L4111 L4112 S4113 C4114 S4115 E4116 A4117 D4118 E4119 M4120 E4121 M4122 I4123 M4124 F4125 E4126 E4127 F4128 A4129 M4130 R4131 F4132 Q4133	N3963 G3971 C3973 R3976 H3982 K3986 Y3990 L3993 H3994 V3995 F3996 S3997 H3998 K4002 Q4005 D4006 S4007 S4008 Q4009 L4019 D4022 M4023 V4024 M4025 M4026 L4027 L4028 M4034 A4041 R4042 Q4043 M4044 E4050 S4051 K4060 F4061 F4062 D4063 M4064 F4065 L4066 K4069 D4070 I4071	L3780 Q3781 S3784 C3785 C3786 K3787 R3788 E3789 T3790 L3805 N3806 G3807 L3888 Q3889 L3890 V3812 M3816 L3817 D3818 Y3819 D3822 F3829 Q3830 S3831 T3832 Q3833 M3836 S3840 V3841 L3842 D3843 Q3850 N3851 K3852 E3854 G3855 L3856 G3857 M3858 V3859 N3860 E3861 D3862 Q3863 T3864 V3865 I3866 N3867 R3868 Q3869 N3870	G3871 E3872 K3873 M3874 K3875 A3876 D3877 D3878 E3879 F3885 R3886 F3887 L3888 Q3889 L3890 L3891 C3892 E3893 N3896 N3897 D3898 F3899 Q3900 N3901 Y3902 Q3906 T3912 Y3922 L3926 Q3927 E3928 S3929 I3930 S3931 D3932 W3935 Y3936 Y3937 S3938 G3939 K3940 D3941 E3945 Q3946 R3949 N3950 F3951 T3952 V3953 I3954 E3955 E3956 E3957 M3958 E3959 K3960 Q3961 T3962 L3970 H3971 T3972 R3973 A3976	V3702 L3703 H3704 F3705 S3706 R3707 L3710 T3711 E3712 K3713 S3714 K3715 L3716 D3717 E3718 D3719 Y3720 Y3725 A3730 H3734 L3735 E3736 E3737 Q3738 Q3739 E3740 GLY GLU ALA GLU E3747 E3748 V3749 E3750 V3751 S3752 F3753 E3754 E3755 K3756 E3757 M3758 E3759 K3760 Q3761 R3762 L3770 H3771 T3772 R3773 A3776	X3583 X3584 X3585 X3586 X3587 X3588 X3591 X3606 X3607 X3608 X3609 X3610 X3611 X3612 X3613 L3641 Y3642 P3645 T3646 A3649 C3650 F3653 K3658 A3659 A3660 V3661 I3662 L3663 T3664 E3665 D3666 H3667 S3668 F3669 D3676 K3679 A3680 G3681 E3682 Q3683 E3684 E3685 E3686 E3687 E3688 E3689 V3690 E3691 E3692 K3693	X3436 X3462 X3461 X3465 X3466 X3467 X3468 X3511 X3512 X3513 X3516 X3520 X3521 X3524 X3528 X3529 X3533 X3534 X3535 X3539 X3540 X3543 X3549 X3552 X3556 X3560 X3561 X3562 X3563 X3564 X3565 X3566 X3567 X3568 X3569 X3570 X3571 X3572 X3576 X3577 X3578 X3579 X3580 X3581 X3582	X3351 X3352 X3353 X3354 X3355 X3356 X3357 X3358 X3359 X3360 X3361 X3362 X3363 X3364 X3365 X3369 X3372 X3373 X3376 X3381 X3387 X3388 X3389 X3390 X3391 X3392 X3393 X3394 X3395 X3396 X3397 X3398 X3411 X3412 X3413 X3414 X3415 X3416 X3419 X3423 X3424 X3425 X3426 X3427 X3428 X3429 X3430 X3431 X3432 X3433 X3434 X3435	X3285 X3286 X3287 X3288 X3289 X3290 X3291 X3292 Q2924 E2925 L2926 L2927 K2928 F2929 L2930 Q2931 L2932 H2933 Q2934 Y2935 K2936 V2937 T2938 D2939 K2942 X2943 X2944 X2945 X2946 X2947 X2948 X2949 X2950 X2951 X2952 X2953 X2954 X2955 X2956 X2959 X2965 X2968	X3163 X3170 X3171 X3172 X3173 X3174 X3175 X3176 X3179 X3186 X3189 X3190 X3191 X3192 X3193 X3194 X3195 X3196 X3197 X3209 X3213 X3214 X3215 X3216 X3217 X3218 X3219 X3220 X3221 X3222 X3223 X3226 X3234 X3235 X3236 X3241 X3242 X3243 X3244 X3245 X3246 X3247 X3248 X3249 X3250 X3251 X3252 X3253 X3254 X3256 X3262 X3263 X3264	X3053 X3057 X3060 X3061 X3063 X3064 X3134 X3135 X3136 X3137 X3138 X3139 X3140 X3141 X3142 X3143 X3146 X3162	X2973 X2974 X2975 X2976 X2977 X2978 X2979 X2980 X2981 X2982 X2983 X2984 X2985 X2986 X2987 X2988 X3003 X3006 X3010 X3013 X3014 X3015 X3016 X3017 X3018 X3019 X3020 X3021 X3022 X3023 X3027 X3044 X3045 X3046 X3047 X3048 X3049 X3050
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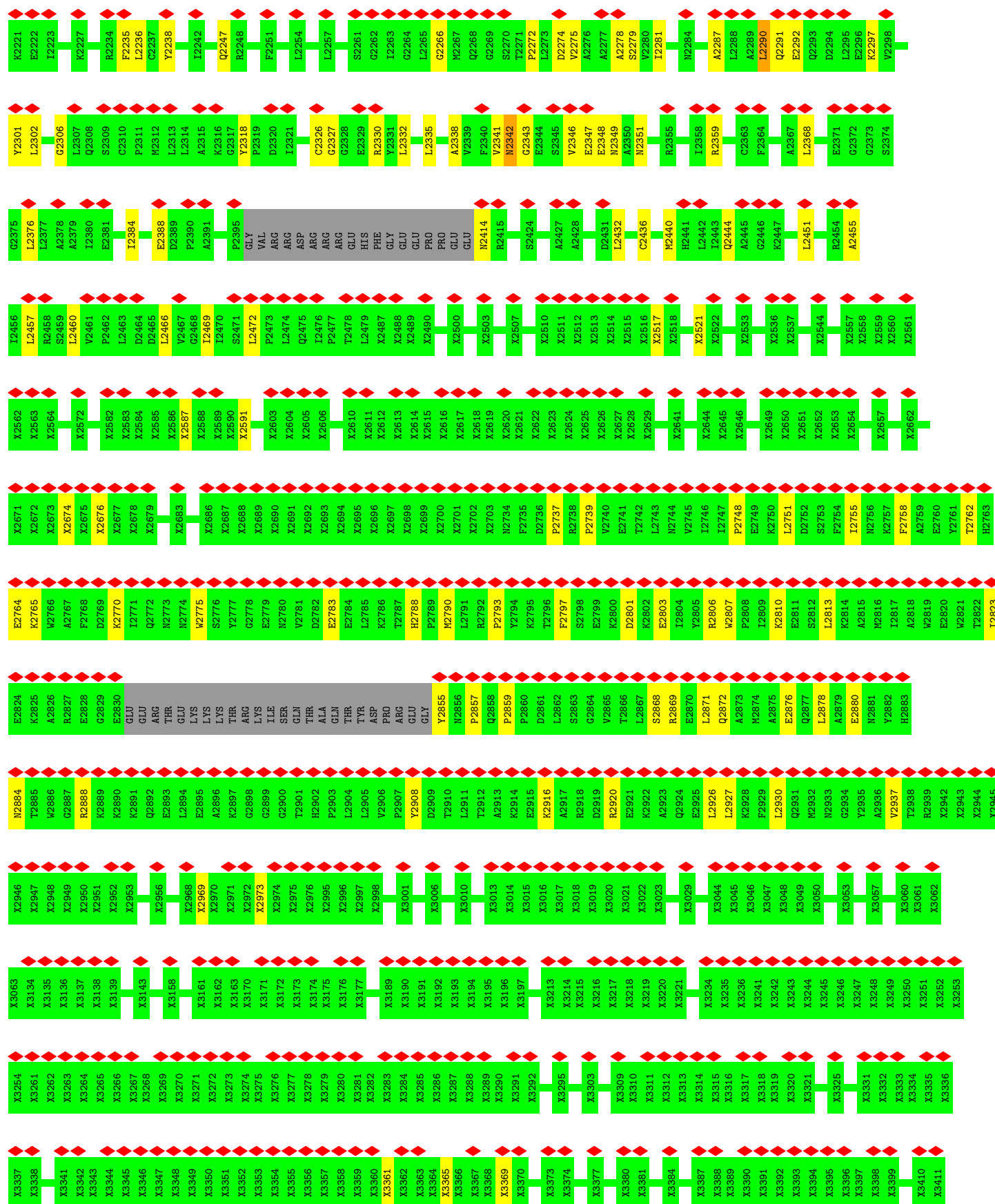


● Molecule 1: Ryanodine receptor 1

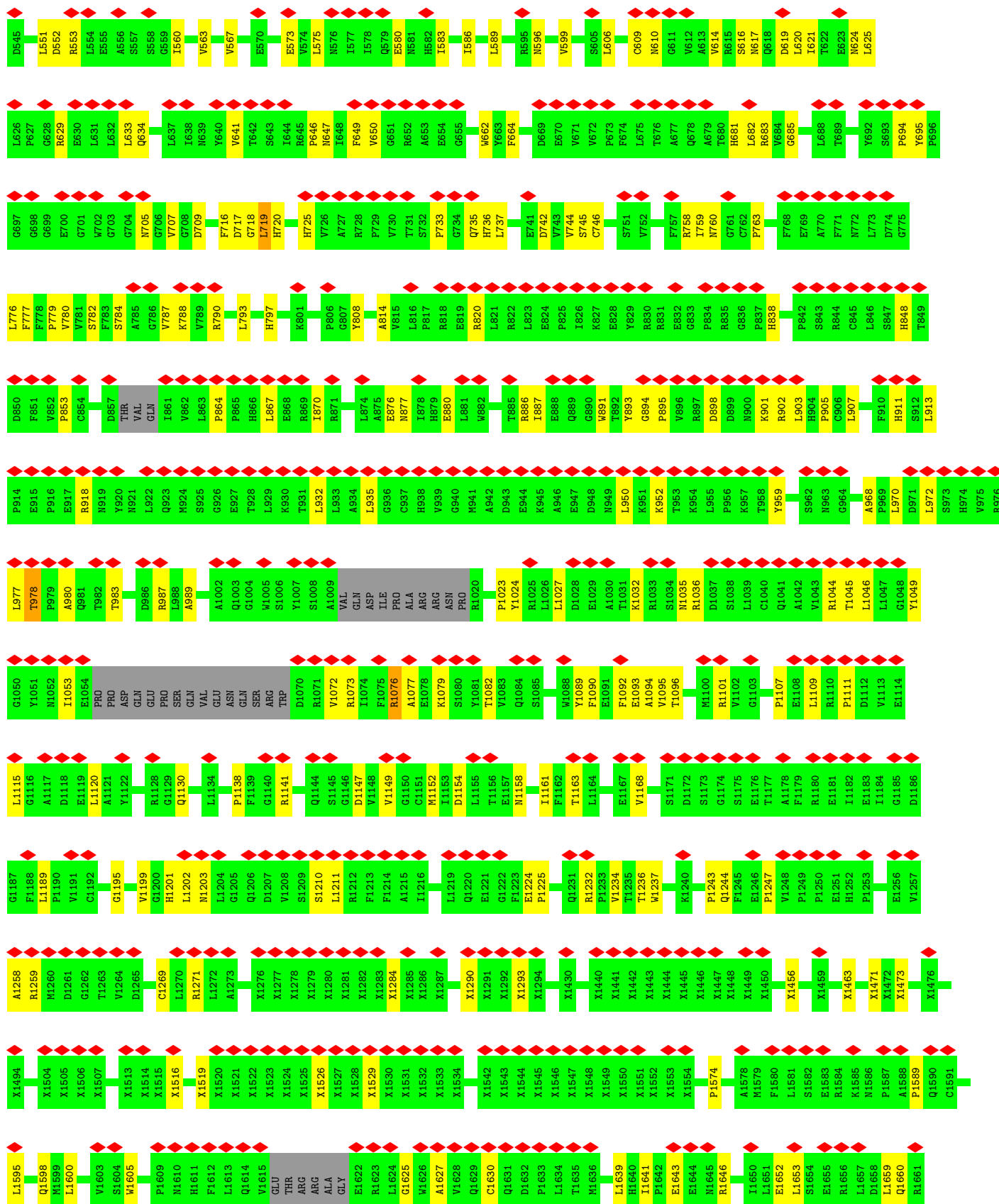






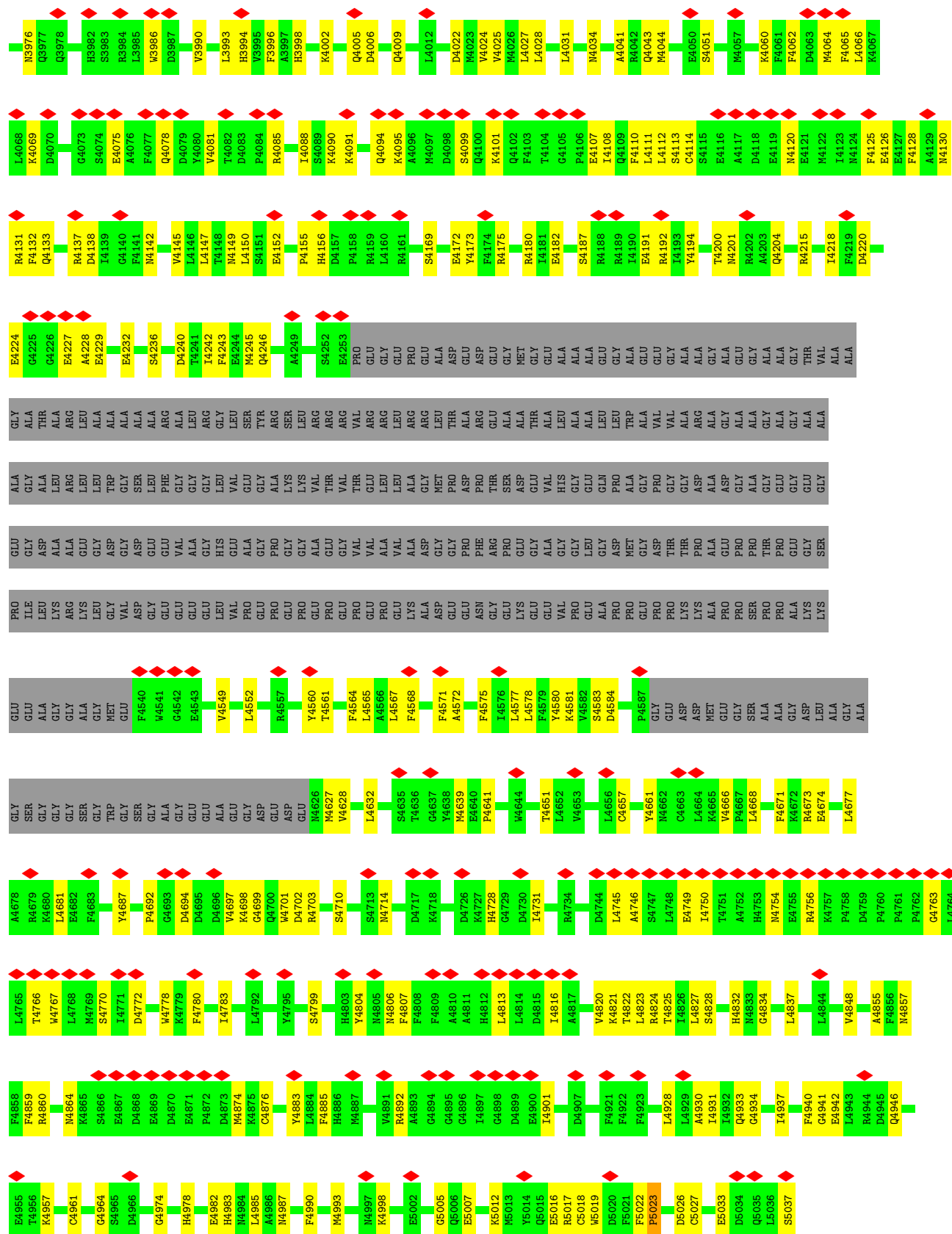










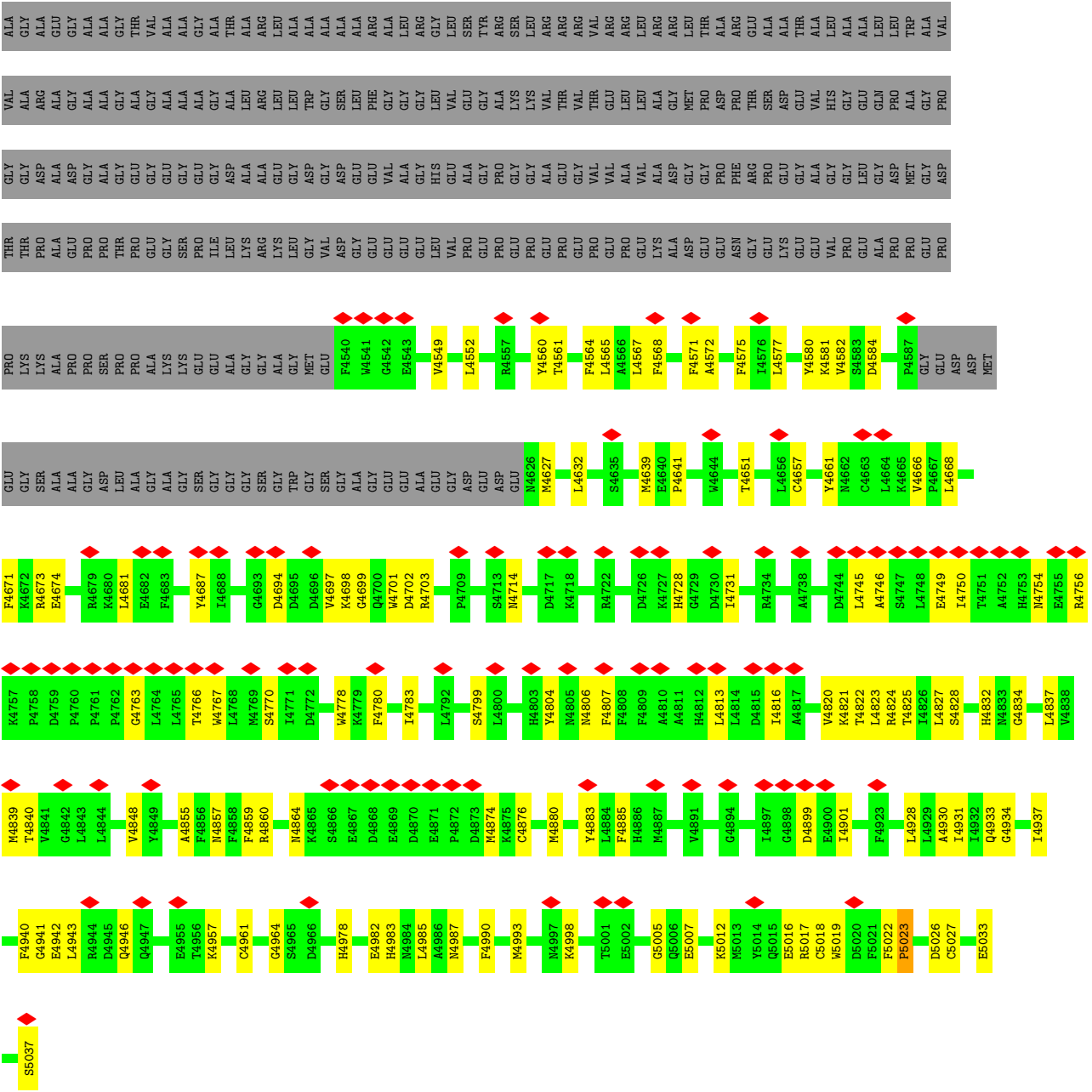




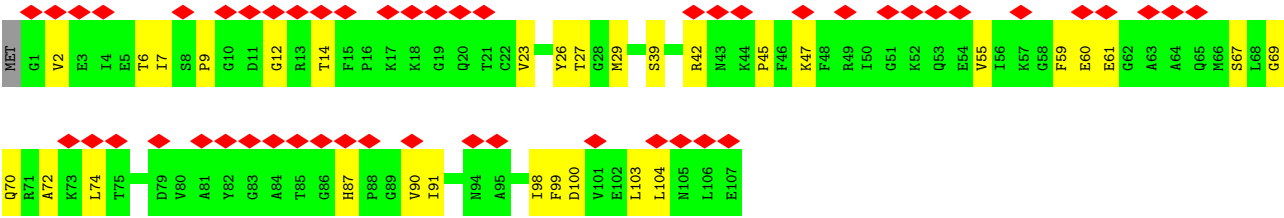


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LEU	GLU	THR	VAL	ARG	LEU	VAL	LYS	LYS	LYS	PRO	GLU	GLU	LEU	PRO	ALA	GLU	K2089	K2090	P2091	Q2092	S2093	L2094	Q2095	V2102	V2103	R2104	V2105	A2106	Q2107	V2111	E2115	L2116	V2117	R2118	A2119	M2120	F2121	L2124	H2125	R2126	Q2127	Y2128	G2132	L2135	R2136	A2137	L2138	P2139											
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E2222	I2223	R2234	F2235	L2236	C2237	Y2238	R2241	I2242	S2243	R2244	Q2245	N2246	Q2247	R2248	S2249	M2250	F2251	L2254	L2258	S2261	Q2262	L2263	G2264	L2265	G2266	M2267	Q2268	G2269	S2270	T2271	P2272	L2273	D2274	V2275	A2276	A2277	A2278	S2279	I2281	D2282	N2283	N2284	A2287	L2288	A2289	L2290	Q2291	E2292	L2295	E2296	K2297								
V2298	V2299	S2300	Y2301	L2302	A2303	Q2306	L2307	Q2308	S2309	C2310	L2313	L2314	A2315	Y2318	P2319	D2320	I2321	C2326	G2327	R2330	Y2331	L2332	L2335	R2336	F2337	A2338	V2339	F2340	V2341	N2342	G2343	E2344	S2345	V2346	E2347	E2348	N2349	A2350	N2351	V2354	R2355	L2356	L2357	L2358	R2359	K2360	P2361	E2362	C2363	F2364	L2368								
R2369	Q2370	E2371	G2372	G2373	S2374	G2375	L2376	L2377	A2378	E2381	E2382	L2383	T2384	R2385	E2388	D2389	P2390	A2391	P2395	GLY	VAL	ARG	ASP	ARG	ARG	ARG	GLU	PHE	HIS	GLY	GLU	PRO	PRO	GLU	N2414	H2420	A2427	L2430	D2431	L2432	C2436	P2438	E2439	M2440	H2441	Q2444	A2445												
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X2623	X2624	X2625	X2626	X2627	X2628	X2629	X2644	X2645	X2646	X2647	X2648	X2649	X2650	X2651	X2652	X2653	X2654	X2655	X2658	X2672	X2673	X2674	X2675	X2676	X2677	X2678	X2683	X2686	X2687	X2688	X2689	X2690	X2691	X2692	X2693	X2694	X2695	X2696	X2697	X2700	X2701	X2702	X2703	N2734	F2735	D2736	T2737	R2738	Y2739	V2740	E2741	T2742							
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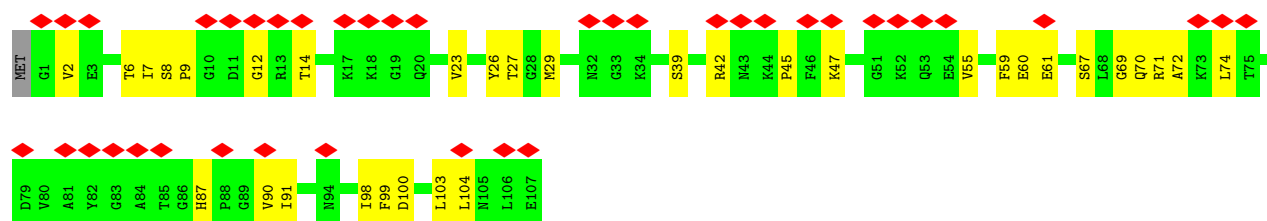




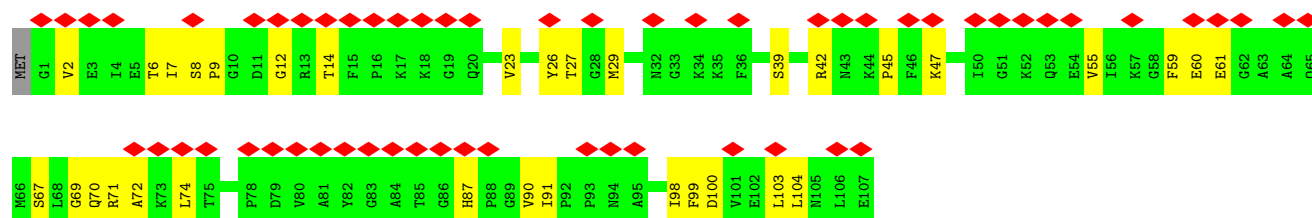
● Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B



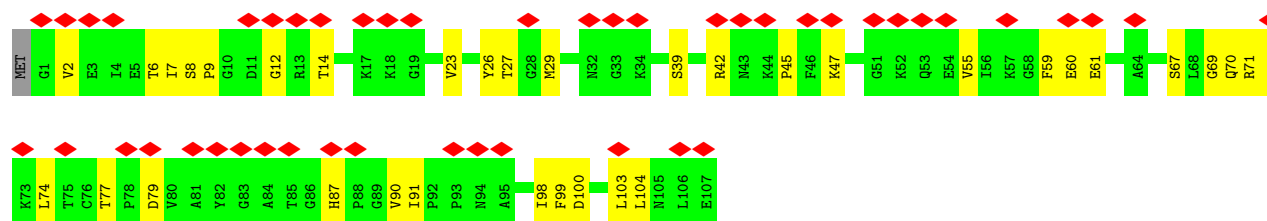
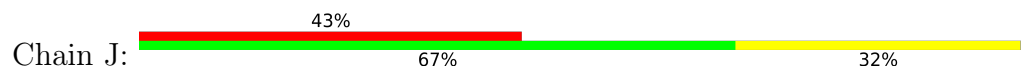
● Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B



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



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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, 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	0.535	Depositor
Minimum map value	-0.203	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.166	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: ZN, CA

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	B	0.35	0/25428	0.59	6/34534 (0.0%)
1	E	0.35	0/25428	0.59	6/34534 (0.0%)
1	G	0.35	0/25428	0.59	6/34534 (0.0%)
1	I	0.35	0/25428	0.59	6/34534 (0.0%)
2	A	0.35	0/834	0.61	0/1123
2	F	0.35	0/834	0.61	0/1123
2	H	0.35	0/834	0.61	0/1123
2	J	0.35	0/834	0.61	0/1123
All	All	0.35	0/105048	0.59	24/142628 (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
1	B	0	22
1	E	0	22
1	G	0	22
1	I	0	22
All	All	0	88

There are no bond length outliers.

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	1667	LEU	CA-CB-CG	6.67	130.64	115.30
1	B	1667	LEU	CA-CB-CG	6.66	130.62	115.30
1	G	1667	LEU	CA-CB-CG	6.64	130.56	115.30
1	I	1667	LEU	CA-CB-CG	6.62	130.53	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	977	LEU	CA-CB-CG	5.60	128.18	115.30
1	I	977	LEU	CA-CB-CG	5.57	128.12	115.30
1	G	977	LEU	CA-CB-CG	5.57	128.11	115.30
1	E	977	LEU	CA-CB-CG	5.54	128.05	115.30
1	E	2291	GLN	C-N-CA	5.48	135.40	121.70
1	I	2291	GLN	C-N-CA	5.48	135.41	121.70
1	B	2291	GLN	C-N-CA	5.47	135.37	121.70
1	G	2291	GLN	C-N-CA	5.46	135.35	121.70
1	G	719	LEU	CA-CB-CG	5.28	127.45	115.30
1	I	719	LEU	CA-CB-CG	5.28	127.45	115.30
1	E	719	LEU	CA-CB-CG	5.27	127.41	115.30
1	B	719	LEU	CA-CB-CG	5.26	127.41	115.30
1	B	2290	LEU	CA-CB-CG	5.15	127.15	115.30
1	I	2290	LEU	CA-CB-CG	5.15	127.14	115.30
1	G	2290	LEU	CA-CB-CG	5.15	127.14	115.30
1	E	2290	LEU	CA-CB-CG	5.14	127.12	115.30
1	E	4639	MET	C-N-CA	5.12	134.50	121.70
1	G	4639	MET	C-N-CA	5.11	134.47	121.70
1	B	4639	MET	C-N-CA	5.10	134.45	121.70
1	I	4639	MET	C-N-CA	5.08	134.41	121.70

There are no chirality outliers.

All (88) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	139	GLU	Peptide
1	B	1676	LEU	Peptide
1	B	1690	ASP	Peptide
1	B	1712	TYR	Peptide
1	B	179	TYR	Peptide
1	B	1828	ASP	Peptide
1	B	1840	PRO	Peptide
1	B	2169	GLN	Peptide
1	B	2292	GLU	Peptide
1	B	2342	ASN	Peptide
1	B	2343	GLY	Peptide
1	B	2472	LEU	Peptide
1	B	2807	TRP	Peptide
1	B	3760	LYS	Peptide
1	B	3771	HIS	Peptide
1	B	3786	CYS	Peptide
1	B	3971	GLY	Peptide

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Mol	Chain	Res	Type	Group
1	B	4666	VAL	Peptide
1	B	4694	ASP	Peptide
1	B	552	ASP	Peptide
1	B	694	PRO	Peptide
1	B	808	TYR	Peptide
1	E	139	GLU	Peptide
1	E	1676	LEU	Peptide
1	E	1690	ASP	Peptide
1	E	1712	TYR	Peptide
1	E	179	TYR	Peptide
1	E	1828	ASP	Peptide
1	E	1840	PRO	Peptide
1	E	2169	GLN	Peptide
1	E	2292	GLU	Peptide
1	E	2342	ASN	Peptide
1	E	2343	GLY	Peptide
1	E	2472	LEU	Peptide
1	E	2807	TRP	Peptide
1	E	3760	LYS	Peptide
1	E	3771	HIS	Peptide
1	E	3786	CYS	Peptide
1	E	3971	GLY	Peptide
1	E	4666	VAL	Peptide
1	E	4694	ASP	Peptide
1	E	552	ASP	Peptide
1	E	694	PRO	Peptide
1	E	808	TYR	Peptide
1	G	139	GLU	Peptide
1	G	1676	LEU	Peptide
1	G	1690	ASP	Peptide
1	G	1712	TYR	Peptide
1	G	179	TYR	Peptide
1	G	1828	ASP	Peptide
1	G	1840	PRO	Peptide
1	G	2169	GLN	Peptide
1	G	2292	GLU	Peptide
1	G	2342	ASN	Peptide
1	G	2343	GLY	Peptide
1	G	2472	LEU	Peptide
1	G	2807	TRP	Peptide
1	G	3760	LYS	Peptide
1	G	3771	HIS	Peptide

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Mol	Chain	Res	Type	Group
1	G	3786	CYS	Peptide
1	G	3971	GLY	Peptide
1	G	4666	VAL	Peptide
1	G	4694	ASP	Peptide
1	G	552	ASP	Peptide
1	G	694	PRO	Peptide
1	G	808	TYR	Peptide
1	I	139	GLU	Peptide
1	I	1676	LEU	Peptide
1	I	1690	ASP	Peptide
1	I	1712	TYR	Peptide
1	I	179	TYR	Peptide
1	I	1828	ASP	Peptide
1	I	1840	PRO	Peptide
1	I	2169	GLN	Peptide
1	I	2292	GLU	Peptide
1	I	2342	ASN	Peptide
1	I	2343	GLY	Peptide
1	I	2472	LEU	Peptide
1	I	2807	TRP	Peptide
1	I	3760	LYS	Peptide
1	I	3771	HIS	Peptide
1	I	3786	CYS	Peptide
1	I	3971	GLY	Peptide
1	I	4666	VAL	Peptide
1	I	4694	ASP	Peptide
1	I	552	ASP	Peptide
1	I	694	PRO	Peptide
1	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	B	29369	0	24717	498	0
1	E	29369	0	24716	494	0
1	G	29369	0	24717	506	0
1	I	29369	0	24717	497	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	818	0	824	19	0
2	F	818	0	824	19	0
2	H	818	0	824	19	0
2	J	818	0	824	20	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	102163	2047	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 (2047) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:2318:TYR:HH	1:G:2414:ASN:N	1.80	0.79
1:I:2318:TYR:HH	1:I:2414:ASN:N	1.80	0.79
1:E:2318:TYR:HH	1:E:2414:ASN:N	1.81	0.79
1:B:2318:TYR:HH	1:B:2414:ASN:N	1.81	0.79
1:E:179:TYR:OH	1:G:2359:ARG:NH1	2.18	0.76
1:E:4674:GLU:HG3	1:E:4714:ASN:HB3	1.73	0.71
1:E:4731:ILE:HA	1:G:4101:LYS:HG3	1.71	0.71
1:B:4674:GLU:HG3	1:B:4714:ASN:HB3	1.73	0.70
1:G:4674:GLU:HG3	1:G:4714:ASN:HB3	1.73	0.70
1:G:1671:ARG:NH2	1:G:1710:GLY:O	2.25	0.70
1:I:4674:GLU:HG3	1:I:4714:ASN:HB3	1.73	0.69
1:E:1671:ARG:NH2	1:E:1710:GLY:O	2.25	0.69
1:I:1671:ARG:NH2	1:I:1710:GLY:O	2.25	0.69
1:B:1671:ARG:NH2	1:B:1710:GLY:O	2.25	0.69
1:G:4855:ALA:HA	1:G:4859:PHE:HB2	1.75	0.69
1:I:4855:ALA:HA	1:I:4859:PHE:HB2	1.75	0.69
1:B:2266:GLY:O	1:B:2330:ARG:NH2	2.27	0.68
1:B:4855:ALA:HA	1:B:4859:PHE:HB2	1.75	0.68
1:E:4855:ALA:HA	1:E:4859:PHE:HB2	1.75	0.68
1:I:219:VAL:HG13	1:I:285:VAL:HG21	1.75	0.68
1:G:646:PRO:HD2	1:G:779:PRO:HB2	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:2266:GLY:O	1:I:2330:ARG:NH2	2.27	0.68
1:G:2266:GLY:O	1:G:2330:ARG:NH2	2.26	0.68
1:E:646:PRO:HD2	1:E:779:PRO:HB2	1.76	0.67
1:B:219:VAL:HG13	1:B:285:VAL:HG21	1.75	0.67
1:E:219:VAL:HG13	1:E:285:VAL:HG21	1.75	0.67
1:B:788:LYS:HG2	1:B:1630:CYS:H	1.59	0.67
1:E:2266:GLY:O	1:E:2330:ARG:NH2	2.27	0.67
1:I:646:PRO:HD2	1:I:779:PRO:HB2	1.76	0.67
1:E:788:LYS:HG2	1:E:1630:CYS:H	1.59	0.67
1:G:331:VAL:HG12	1:G:333:GLY:H	1.60	0.67
1:B:646:PRO:HD2	1:B:779:PRO:HB2	1.76	0.67
1:G:219:VAL:HG13	1:G:285:VAL:HG21	1.75	0.67
1:I:331:VAL:HG12	1:I:333:GLY:H	1.60	0.66
1:E:331:VAL:HG12	1:E:333:GLY:H	1.60	0.66
1:G:788:LYS:HG2	1:G:1630:CYS:H	1.59	0.66
1:B:151:HIS:HB2	1:B:170:ILE:HB	1.78	0.66
1:I:788:LYS:HG2	1:I:1630:CYS:H	1.59	0.65
1:B:103:TYR:HB3	1:B:152:PRO:HD3	1.79	0.65
1:B:2755:ILE:HD13	1:B:2810:LYS:HG2	1.77	0.65
1:G:2755:ILE:HD13	1:G:2810:LYS:HG2	1.78	0.65
1:I:1092:PHE:HB3	1:I:1149:VAL:HB	1.77	0.65
1:E:2755:ILE:HD13	1:E:2810:LYS:HG2	1.77	0.65
1:E:1777:PHE:HA	1:E:1799:SER:HB2	1.78	0.65
1:I:103:TYR:HB3	1:I:152:PRO:HD3	1.79	0.65
1:I:151:HIS:HB2	1:I:170:ILE:HB	1.78	0.65
1:I:2755:ILE:HD13	1:I:2810:LYS:HG2	1.78	0.65
1:G:103:TYR:HB3	1:G:152:PRO:HD3	1.79	0.65
1:G:742:ASP:HA	1:G:760:ASN:HD21	1.62	0.65
1:E:103:TYR:HB3	1:E:152:PRO:HD3	1.79	0.65
1:G:1092:PHE:HB3	1:G:1149:VAL:HB	1.77	0.65
1:B:331:VAL:HG12	1:B:333:GLY:H	1.60	0.65
1:B:1092:PHE:HB3	1:B:1149:VAL:HB	1.77	0.65
1:E:4961:CYS:SG	1:E:4978:HIS:NE2	2.70	0.65
1:E:2287:ALA:HA	1:E:2290:LEU:HD13	1.79	0.64
1:I:1519:UNK:HA	1:I:1526:UNK:HA	1.79	0.64
1:E:745:SER:HB2	1:E:758:ARG:HB3	1.79	0.64
1:G:4961:CYS:SG	1:G:4978:HIS:NE2	2.70	0.64
1:B:1777:PHE:HA	1:B:1799:SER:HB2	1.78	0.64
1:E:151:HIS:HB2	1:E:170:ILE:HB	1.79	0.64
1:I:742:ASP:HA	1:I:760:ASN:HD21	1.62	0.64
1:B:4813:LEU:HD12	1:B:4816:ILE:HD11	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:1777:PHE:HA	1:I:1799:SER:HB2	1.78	0.64
1:G:151:HIS:HB2	1:G:170:ILE:HB	1.79	0.64
1:G:4813:LEU:HD12	1:G:4816:ILE:HD11	1.79	0.64
1:B:742:ASP:HA	1:B:760:ASN:HD21	1.62	0.64
1:E:742:ASP:HA	1:E:760:ASN:HD21	1.62	0.64
1:E:1092:PHE:HB3	1:E:1149:VAL:HB	1.77	0.64
1:I:2287:ALA:HA	1:I:2290:LEU:HD13	1.79	0.64
1:G:745:SER:HB2	1:G:758:ARG:HB3	1.79	0.64
1:G:1777:PHE:HA	1:G:1799:SER:HB2	1.78	0.64
1:G:2095:GLN:O	1:G:2127:GLN:NE2	2.31	0.64
1:G:2876:GLU:OE1	1:G:2920:ARG:NH2	2.31	0.64
1:B:745:SER:HB2	1:B:758:ARG:HB3	1.79	0.64
1:G:1519:UNK:HA	1:G:1526:UNK:HA	1.80	0.64
1:B:4961:CYS:SG	1:B:4978:HIS:NE2	2.71	0.63
1:E:1079:LYS:NZ	1:E:1107:PRO:O	2.31	0.63
1:I:745:SER:HB2	1:I:758:ARG:HB3	1.79	0.63
1:I:4961:CYS:SG	1:I:4978:HIS:NE2	2.71	0.63
1:B:1079:LYS:NZ	1:B:1107:PRO:O	2.31	0.63
1:E:4813:LEU:HD12	1:E:4816:ILE:HD11	1.79	0.63
1:I:2095:GLN:O	1:I:2127:GLN:NE2	2.31	0.63
1:I:1079:LYS:NZ	1:I:1107:PRO:O	2.31	0.63
2:F:26:TYR:OH	2:F:42:ARG:NH2	2.32	0.63
1:G:454:PRO:HG2	1:G:531:ARG:HH12	1.64	0.63
2:H:74:LEU:HB2	2:H:99:PHE:HB2	1.80	0.63
1:I:2876:GLU:OE1	1:I:2920:ARG:NH2	2.31	0.63
2:A:26:TYR:OH	2:A:42:ARG:NH2	2.32	0.63
1:B:853:PRO:HB3	1:B:1024:TYR:H	1.64	0.63
1:I:4807:PHE:HZ	1:G:4857:ASN:HB2	1.64	0.63
1:G:853:PRO:HB3	1:G:1024:TYR:H	1.64	0.63
1:B:2876:GLU:OE1	1:B:2920:ARG:NH2	2.31	0.63
1:E:454:PRO:HG2	1:E:531:ARG:HH12	1.64	0.63
1:I:454:PRO:HG2	1:I:531:ARG:HH12	1.64	0.63
1:G:2287:ALA:HA	1:G:2290:LEU:HD13	1.79	0.63
1:B:454:PRO:HG2	1:B:531:ARG:HH12	1.64	0.62
1:E:2876:GLU:OE1	1:E:2920:ARG:NH2	2.31	0.62
2:F:74:LEU:HB2	2:F:99:PHE:HB2	1.80	0.62
2:A:6:THR:HA	2:A:72:ALA:HA	1.82	0.62
1:B:609:CYS:SG	1:B:610:ASN:N	2.72	0.62
1:B:3993:LEU:HA	1:B:3996:PHE:HB2	1.82	0.62
1:E:2095:GLN:O	1:E:2127:GLN:NE2	2.31	0.62
1:G:609:CYS:SG	1:G:610:ASN:N	2.72	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:26:TYR:OH	2:H:42:ARG:NH2	2.32	0.62
1:B:2287:ALA:HA	1:B:2290:LEU:HD13	1.79	0.62
1:I:609:CYS:SG	1:I:610:ASN:N	2.72	0.62
1:I:4892:ARG:NH2	1:G:4899:ASP:OD1	2.28	0.62
1:E:606:LEU:O	1:E:617:ASN:ND2	2.33	0.62
1:I:606:LEU:O	1:I:617:ASN:ND2	2.33	0.62
2:J:74:LEU:HB2	2:J:99:PHE:HB2	1.80	0.62
1:B:2095:GLN:O	1:B:2127:GLN:NE2	2.31	0.62
1:I:4813:LEU:HD12	1:I:4816:ILE:HD11	1.79	0.62
1:E:853:PRO:HB3	1:E:1024:TYR:H	1.64	0.62
1:E:3993:LEU:HA	1:E:3996:PHE:HB2	1.82	0.62
1:G:3993:LEU:HA	1:G:3996:PHE:HB2	1.82	0.62
1:B:606:LEU:O	1:B:617:ASN:ND2	2.33	0.62
1:E:3937:TYR:O	1:E:4002:LYS:NZ	2.33	0.62
1:I:3973:CYS:SG	1:I:3976:ASN:ND2	2.73	0.62
1:G:606:LEU:O	1:G:617:ASN:ND2	2.33	0.62
1:I:853:PRO:HB3	1:I:1024:TYR:H	1.64	0.61
2:J:6:THR:HA	2:J:72:ALA:HA	1.82	0.61
2:J:26:TYR:OH	2:J:42:ARG:NH2	2.32	0.61
1:I:1244:GLN:HB3	1:I:1646:ARG:HH12	1.65	0.61
1:G:3937:TYR:O	1:G:4002:LYS:NZ	2.33	0.61
1:G:3973:CYS:SG	1:G:3976:ASN:ND2	2.73	0.61
1:B:1244:GLN:HB3	1:B:1646:ARG:HH12	1.65	0.61
1:G:1079:LYS:NZ	1:G:1107:PRO:O	2.31	0.61
2:H:6:THR:HA	2:H:72:ALA:HA	1.82	0.61
1:B:3973:CYS:SG	1:B:3976:ASN:ND2	2.73	0.61
1:E:609:CYS:SG	1:E:610:ASN:N	2.72	0.61
1:E:1247:PRO:HA	1:E:1598:GLN:HA	1.83	0.61
1:B:3937:TYR:O	1:B:4002:LYS:NZ	2.33	0.61
2:A:74:LEU:HB2	2:A:99:PHE:HB2	1.80	0.61
2:H:23:VAL:HG22	2:H:47:LYS:HG2	1.83	0.61
1:B:575:LEU:HD22	1:B:609:CYS:HB3	1.83	0.61
1:G:4673:ARG:HH22	1:G:4698:LYS:HB2	1.66	0.61
2:J:87:HIS:N	2:J:91:ILE:O	2.34	0.61
1:B:1808:ARG:NH1	1:B:1853:ILE:O	2.34	0.60
1:I:575:LEU:HD22	1:I:609:CYS:HB3	1.83	0.60
2:F:23:VAL:HG22	2:F:47:LYS:HG2	1.83	0.60
2:F:87:HIS:N	2:F:91:ILE:O	2.34	0.60
2:F:6:THR:HA	2:F:72:ALA:HA	1.82	0.60
2:A:87:HIS:N	2:A:91:ILE:O	2.34	0.60
1:B:1247:PRO:HA	1:B:1598:GLN:HA	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:4673:ARG:HH22	1:E:4698:LYS:HB2	1.66	0.60
1:I:1203:ASN:ND2	1:I:1210:SER:O	2.35	0.60
1:B:1203:ASN:ND2	1:B:1210:SER:O	2.34	0.60
1:E:3973:CYS:SG	1:E:3976:ASN:ND2	2.73	0.60
1:I:3937:TYR:O	1:I:4002:LYS:NZ	2.33	0.60
1:I:4673:ARG:HH22	1:I:4698:LYS:HB2	1.66	0.60
1:G:41:GLY:O	1:G:45:ARG:NH1	2.35	0.60
1:G:1244:GLN:HB3	1:G:1646:ARG:HH12	1.65	0.60
1:I:1247:PRO:HA	1:I:1598:GLN:HA	1.83	0.60
1:B:1519:UNK:HA	1:B:1526:UNK:HA	1.84	0.60
1:E:1203:ASN:ND2	1:E:1210:SER:O	2.35	0.60
1:E:1244:GLN:HB3	1:E:1646:ARG:HH12	1.65	0.60
1:I:3993:LEU:HA	1:I:3996:PHE:HB2	1.82	0.60
1:G:1101:ARG:HE	1:G:1115:LEU:HB3	1.66	0.60
1:E:575:LEU:HD22	1:E:609:CYS:HB3	1.82	0.60
1:B:4673:ARG:HH22	1:B:4698:LYS:HB2	1.66	0.60
1:E:1808:ARG:NH1	1:E:1853:ILE:O	2.34	0.60
1:I:4821:LYS:HA	1:I:4824:ARG:HE	1.67	0.60
2:A:23:VAL:HG22	2:A:47:LYS:HG2	1.83	0.60
2:H:87:HIS:N	2:H:91:ILE:O	2.34	0.60
1:B:2338:ALA:HB1	1:B:2349:ASN:HB3	1.84	0.60
1:I:1808:ARG:NH1	1:I:1853:ILE:O	2.34	0.60
1:G:1808:ARG:NH1	1:G:1853:ILE:O	2.34	0.60
1:G:2748:PRO:HD2	1:G:2751:LEU:HD12	1.84	0.60
1:G:3762:ARG:H	1:G:4754:ASN:HA	1.67	0.60
1:G:4821:LYS:HA	1:G:4824:ARG:HE	1.67	0.60
1:B:256:ALA:HB1	1:B:286:THR:HG21	1.84	0.60
1:E:1101:ARG:HE	1:E:1115:LEU:HB3	1.66	0.60
1:I:1101:ARG:HE	1:I:1115:LEU:HB3	1.66	0.60
2:J:23:VAL:HG22	2:J:47:LYS:HG2	1.82	0.60
1:E:2338:ALA:HB1	1:E:2349:ASN:HB3	1.84	0.59
1:E:4821:LYS:HA	1:E:4824:ARG:HE	1.67	0.59
1:G:256:ALA:HB1	1:G:286:THR:HG21	1.83	0.59
1:G:1203:ASN:ND2	1:G:1210:SER:O	2.35	0.59
1:E:3762:ARG:H	1:E:4754:ASN:HA	1.67	0.59
1:I:2338:ALA:HB1	1:I:2349:ASN:HB3	1.84	0.59
1:I:4848:VAL:HG23	1:I:4883:TYR:HE1	1.66	0.59
1:G:575:LEU:HD22	1:G:609:CYS:HB3	1.83	0.59
1:B:4848:VAL:HG23	1:B:4883:TYR:HE1	1.66	0.59
1:E:1641:ILE:HG13	1:E:1643:GLU:H	1.68	0.59
1:I:41:GLY:O	1:I:45:ARG:NH1	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:90:VAL:HG12	2:F:91:ILE:HG12	1.84	0.59
1:E:41:GLY:O	1:E:45:ARG:NH1	2.35	0.59
1:E:175:SER:O	1:G:2452:ARG:NH1	2.32	0.59
1:E:718:GLY:HA3	1:E:737:LEU:HA	1.85	0.59
1:I:2359:ARG:NH1	1:G:179:TYR:OH	2.35	0.59
1:G:718:GLY:HA3	1:G:737:LEU:HA	1.84	0.59
1:G:1247:PRO:HA	1:G:1598:GLN:HA	1.83	0.59
1:G:315:CYS:SG	1:G:316:PHE:N	2.76	0.59
2:A:90:VAL:HG12	2:A:91:ILE:HG12	1.84	0.59
1:B:718:GLY:HA3	1:B:737:LEU:HA	1.84	0.59
1:E:4848:VAL:HG23	1:E:4883:TYR:HE1	1.66	0.59
1:I:19:GLU:HB2	1:I:206:CYS:HB3	1.84	0.59
1:I:315:CYS:SG	1:I:316:PHE:N	2.76	0.59
1:G:4848:VAL:HG23	1:G:4883:TYR:HE1	1.66	0.59
1:B:41:GLY:O	1:B:45:ARG:NH1	2.35	0.59
1:B:1101:ARG:HE	1:B:1115:LEU:HB3	1.66	0.59
1:B:4075:GLU:HA	1:B:4078:GLN:HB2	1.85	0.59
1:E:256:ALA:HB1	1:E:286:THR:HG21	1.83	0.59
1:I:3762:ARG:H	1:I:4754:ASN:HA	1.67	0.59
1:G:1641:ILE:HG13	1:G:1643:GLU:H	1.68	0.59
1:B:19:GLU:HB2	1:B:206:CYS:HB3	1.84	0.59
1:E:1519:UNK:HA	1:E:1526:UNK:HA	1.84	0.59
1:E:2748:PRO:HD2	1:E:2751:LEU:HD12	1.84	0.59
1:E:4075:GLU:HA	1:E:4078:GLN:HB2	1.85	0.59
1:G:2420:HIS:ND1	1:G:2493:UNK:O	2.25	0.59
1:I:2748:PRO:HD2	1:I:2751:LEU:HD12	1.84	0.58
1:E:315:CYS:SG	1:E:316:PHE:N	2.76	0.58
1:I:256:ALA:HB1	1:I:286:THR:HG21	1.83	0.58
1:I:716:PHE:HE2	1:I:759:ILE:HD11	1.68	0.58
1:G:19:GLU:HB2	1:G:206:CYS:HB3	1.84	0.58
1:G:716:PHE:HE2	1:G:759:ILE:HD11	1.68	0.58
1:B:315:CYS:SG	1:B:316:PHE:N	2.76	0.58
1:E:2871:LEU:HD22	1:E:2927:LEU:HD22	1.85	0.58
1:B:4821:LYS:HA	1:B:4824:ARG:HE	1.67	0.58
1:E:281:ARG:HG2	1:E:312:THR:HG21	1.85	0.58
1:I:718:GLY:HA3	1:I:737:LEU:HA	1.84	0.58
1:I:1641:ILE:HG13	1:I:1643:GLU:H	1.67	0.58
1:I:3805:LEU:HA	1:I:3809:ASN:HD22	1.68	0.58
1:G:2347:GLU:O	1:G:2351:ASN:N	2.37	0.58
1:G:2871:LEU:HD22	1:G:2927:LEU:HD22	1.85	0.58
1:E:265:LEU:HD12	1:E:279:PRO:HB2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:488:LEU:O	1:E:492:ASP:N	2.36	0.58
1:G:281:ARG:HG2	1:G:312:THR:HG21	1.85	0.58
1:G:2338:ALA:HB1	1:G:2349:ASN:HB3	1.84	0.58
1:B:2347:GLU:O	1:B:2351:ASN:N	2.37	0.58
1:B:2748:PRO:HD2	1:B:2751:LEU:HD12	1.84	0.58
1:B:3762:ARG:H	1:B:4754:ASN:HA	1.67	0.58
1:I:21:VAL:HG12	1:I:66:CYS:HA	1.86	0.58
1:G:21:VAL:HG12	1:G:66:CYS:HA	1.86	0.58
1:I:683:ARG:HB2	1:I:782:SER:HB3	1.86	0.58
1:E:19:GLU:HB2	1:E:206:CYS:HB3	1.84	0.58
1:I:650:VAL:HB	1:I:777:PHE:HB2	1.85	0.58
1:B:265:LEU:HD12	1:B:279:PRO:HB2	1.85	0.58
1:B:716:PHE:HE2	1:B:759:ILE:HD11	1.68	0.58
1:B:1641:ILE:HG13	1:B:1643:GLU:H	1.68	0.58
1:I:1109:LEU:HA	1:I:1120:LEU:HD21	1.86	0.58
1:I:4228:ALA:O	1:I:4232:GLU:N	2.37	0.58
1:I:4232:GLU:OE1	1:I:5019:TRP:NE1	2.37	0.58
1:I:4933:GLN:NE2	1:G:4933:GLN:OE1	2.36	0.58
1:G:4065:PHE:O	1:G:4133:GLN:NE2	2.37	0.58
1:B:4228:ALA:O	1:B:4232:GLU:N	2.36	0.58
1:I:4065:PHE:O	1:I:4133:GLN:NE2	2.37	0.58
1:G:1743:ARG:O	1:G:1964:ARG:NH2	2.37	0.58
1:B:4065:PHE:O	1:B:4133:GLN:NE2	2.37	0.57
1:E:3932:ASP:HA	1:E:3935:TRP:HD1	1.69	0.57
1:I:4075:GLU:HA	1:I:4078:GLN:HB2	1.85	0.57
1:G:3932:ASP:HA	1:G:3935:TRP:HD1	1.69	0.57
2:H:90:VAL:HG12	2:H:91:ILE:HG12	1.84	0.57
1:B:3805:LEU:HA	1:B:3809:ASN:HD22	1.68	0.57
1:E:21:VAL:HG12	1:E:66:CYS:HA	1.86	0.57
1:I:265:LEU:HD12	1:I:279:PRO:HB2	1.85	0.57
1:I:1271:ARG:HA	1:I:1471:UNK:HA	1.86	0.57
1:I:2871:LEU:HD22	1:I:2927:LEU:HD22	1.85	0.57
1:G:1109:LEU:HA	1:G:1120:LEU:HD21	1.86	0.57
1:G:4075:GLU:HA	1:G:4078:GLN:HB2	1.85	0.57
1:B:206:CYS:SG	1:B:207:SER:N	2.78	0.57
1:B:3990:VAL:HG13	1:B:4051:SER:HB2	1.87	0.57
1:E:650:VAL:HB	1:E:777:PHE:HB2	1.85	0.57
1:E:3890:LEU:HA	1:E:3893:GLU:HB2	1.86	0.57
1:G:206:CYS:SG	1:G:207:SER:N	2.78	0.57
1:G:265:LEU:HD12	1:G:279:PRO:HB2	1.85	0.57
1:G:650:VAL:HB	1:G:777:PHE:HB2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:683:ARG:HB2	1:G:782:SER:HB3	1.86	0.57
1:B:281:ARG:HG2	1:B:312:THR:HG21	1.85	0.57
1:B:3890:LEU:HA	1:B:3893:GLU:HB2	1.86	0.57
1:E:716:PHE:HE2	1:E:759:ILE:HD11	1.68	0.57
1:I:281:ARG:HG2	1:I:312:THR:HG21	1.85	0.57
1:I:2347:GLU:O	1:I:2351:ASN:N	2.37	0.57
1:I:3932:ASP:HA	1:I:3935:TRP:HD1	1.69	0.57
1:B:683:ARG:HB2	1:B:782:SER:HB3	1.86	0.57
1:B:4182:GLU:OE2	1:B:4983:HIS:NE2	2.38	0.57
1:E:4182:GLU:OE2	1:E:4983:HIS:NE2	2.38	0.57
1:I:206:CYS:SG	1:I:207:SER:N	2.78	0.57
1:I:4182:GLU:OE2	1:I:4983:HIS:NE2	2.38	0.57
1:B:2871:LEU:HD22	1:B:2927:LEU:HD22	1.85	0.57
1:I:235:ALA:HA	1:I:257:ARG:HD3	1.86	0.57
1:I:3990:VAL:HG13	1:I:4051:SER:HB2	1.86	0.57
1:G:3805:LEU:HA	1:G:3809:ASN:HD22	1.68	0.57
1:G:3890:LEU:HA	1:G:3893:GLU:HB2	1.86	0.57
2:J:90:VAL:HG12	2:J:91:ILE:HG12	1.84	0.57
1:B:650:VAL:HB	1:B:777:PHE:HB2	1.85	0.57
1:B:1109:LEU:HA	1:B:1120:LEU:HD21	1.86	0.57
1:B:4232:GLU:OE1	1:B:5019:TRP:NE1	2.37	0.57
1:G:4232:GLU:OE1	1:G:5019:TRP:NE1	2.37	0.57
1:E:641:VAL:HG21	1:E:705:ASN:HA	1.86	0.57
1:I:4126:GLU:O	1:I:4130:ASN:ND2	2.38	0.57
1:G:4182:GLU:OE2	1:G:4983:HIS:NE2	2.38	0.57
1:B:1973:GLN:O	1:B:1977:TYR:N	2.38	0.57
1:E:4228:ALA:O	1:E:4232:GLU:N	2.36	0.57
1:E:4232:GLU:OE1	1:E:5019:TRP:NE1	2.37	0.57
1:G:475:GLN:NE2	1:G:528:SER:O	2.38	0.57
1:B:21:VAL:HG12	1:B:66:CYS:HA	1.86	0.57
1:E:4065:PHE:O	1:E:4133:GLN:NE2	2.37	0.57
1:B:488:LEU:O	1:B:492:ASP:N	2.37	0.56
1:B:1237:TRP:HH2	1:B:1652:GLU:HA	1.70	0.56
1:B:3932:ASP:HA	1:B:3935:TRP:HD1	1.69	0.56
1:B:4933:GLN:OE1	1:E:4933:GLN:NE2	2.38	0.56
1:E:475:GLN:NE2	1:E:528:SER:O	2.38	0.56
1:I:1237:TRP:HH2	1:I:1652:GLU:HA	1.70	0.56
1:B:4152:GLU:OE1	1:B:4192:ARG:NH2	2.38	0.56
1:E:683:ARG:HB2	1:E:782:SER:HB3	1.86	0.56
1:E:3805:LEU:HA	1:E:3809:ASN:HD22	1.68	0.56
1:E:4126:GLU:O	1:E:4130:ASN:ND2	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:641:VAL:HG21	1:I:705:ASN:HA	1.86	0.56
1:G:4126:GLU:O	1:G:4130:ASN:ND2	2.38	0.56
1:G:4228:ALA:O	1:G:4232:GLU:N	2.36	0.56
1:B:683:ARG:NH1	1:B:707:VAL:O	2.39	0.56
1:B:2359:ARG:NH1	1:I:179:TYR:OH	2.38	0.56
1:B:3830:GLN:HA	1:B:3833:GLN:HG2	1.88	0.56
1:B:4126:GLU:O	1:B:4130:ASN:ND2	2.38	0.56
1:E:1109:LEU:HA	1:E:1120:LEU:HD21	1.86	0.56
1:E:4152:GLU:OE1	1:E:4192:ARG:NH2	2.38	0.56
1:I:475:GLN:NE2	1:I:528:SER:O	2.38	0.56
1:I:3830:GLN:HA	1:I:3833:GLN:HG2	1.88	0.56
1:I:4152:GLU:OE1	1:I:4192:ARG:NH2	2.38	0.56
1:G:20:VAL:HG12	1:G:204:PRO:HA	1.87	0.56
1:G:235:ALA:HA	1:G:257:ARG:HD3	1.86	0.56
1:B:257:ARG:O	1:B:284:HIS:NE2	2.37	0.56
1:E:1743:ARG:O	1:E:1964:ARG:NH2	2.37	0.56
1:E:3971:GLY:H	1:E:5005:GLY:HA3	1.71	0.56
1:E:3990:VAL:HG13	1:E:4051:SER:HB2	1.87	0.56
1:G:744:VAL:HG22	1:G:759:ILE:HG12	1.88	0.56
1:G:2003:GLN:O	1:G:2007:ASN:ND2	2.38	0.56
2:A:27:THR:HB	2:A:100:ASP:HB3	1.87	0.56
1:B:972:LEU:O	1:B:1044:ARG:NH2	2.39	0.56
1:E:2003:GLN:O	1:E:2007:ASN:ND2	2.39	0.56
1:I:683:ARG:NH1	1:I:707:VAL:O	2.38	0.56
1:I:1743:ARG:O	1:I:1964:ARG:NH2	2.37	0.56
1:I:4581:LYS:HB2	1:I:4632:LEU:HB2	1.88	0.56
1:G:4152:GLU:OE1	1:G:4192:ARG:NH2	2.38	0.56
1:B:641:VAL:HG21	1:B:705:ASN:HA	1.86	0.56
1:I:2003:GLN:O	1:I:2007:ASN:ND2	2.38	0.56
1:I:2368:LEU:HB2	1:I:2376:LEU:HD23	1.87	0.56
1:G:972:LEU:O	1:G:1044:ARG:NH2	2.39	0.56
1:G:1237:TRP:HH2	1:G:1652:GLU:HA	1.70	0.56
1:G:1973:GLN:O	1:G:1977:TYR:N	2.38	0.56
1:B:744:VAL:HG22	1:B:759:ILE:HG12	1.88	0.56
1:B:2003:GLN:O	1:B:2007:ASN:ND2	2.38	0.56
1:E:20:VAL:HG12	1:E:204:PRO:HA	1.87	0.56
1:E:683:ARG:HG2	1:E:717:ASP:HB3	1.88	0.56
1:E:1973:GLN:O	1:E:1977:TYR:N	2.38	0.56
1:G:1965:TYR:HA	1:G:1968:LYS:HE3	1.88	0.56
1:G:3830:GLN:HA	1:G:3833:GLN:HG2	1.88	0.56
2:J:27:THR:HB	2:J:100:ASP:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2104:ARG:HA	1:B:2107:GLN:HB3	1.88	0.56
1:B:4581:LYS:HB2	1:B:4632:LEU:HB2	1.88	0.56
1:E:1237:TRP:HH2	1:E:1652:GLU:HA	1.70	0.56
1:E:3830:GLN:HA	1:E:3833:GLN:HG2	1.88	0.56
1:G:683:ARG:HG2	1:G:717:ASP:HB3	1.88	0.56
1:B:235:ALA:HA	1:B:257:ARG:HD3	1.86	0.56
1:B:3971:GLY:H	1:B:5005:GLY:HA3	1.71	0.56
1:G:2235:PHE:HA	1:G:2238:TYR:HD2	1.71	0.56
2:H:27:THR:HB	2:H:100:ASP:HB3	1.87	0.56
1:B:683:ARG:HG2	1:B:717:ASP:HB3	1.88	0.55
1:B:1965:TYR:HA	1:B:1968:LYS:HE3	1.88	0.55
1:E:2104:ARG:HA	1:E:2107:GLN:HB3	1.88	0.55
1:E:2235:PHE:HA	1:E:2238:TYR:HD2	1.71	0.55
1:I:3890:LEU:HA	1:I:3893:GLU:HB2	1.86	0.55
1:E:2368:LEU:HB2	1:E:2376:LEU:HD23	1.88	0.55
1:I:1973:GLN:O	1:I:1977:TYR:N	2.38	0.55
1:G:3990:VAL:HG13	1:G:4051:SER:HB2	1.87	0.55
1:E:4998:LYS:NZ	1:E:5007:GLU:OE1	2.39	0.55
1:I:683:ARG:HG2	1:I:717:ASP:HB3	1.88	0.55
1:G:2104:ARG:HA	1:G:2107:GLN:HB3	1.88	0.55
1:B:1271:ARG:HA	1:B:1471:UNK:HA	1.88	0.55
1:B:1743:ARG:O	1:B:1964:ARG:NH2	2.37	0.55
1:E:206:CYS:SG	1:E:207:SER:N	2.78	0.55
1:E:235:ALA:HA	1:E:257:ARG:HD3	1.86	0.55
1:I:972:LEU:O	1:I:1044:ARG:NH2	2.39	0.55
1:G:257:ARG:O	1:G:284:HIS:NE2	2.37	0.55
1:G:695:TYR:OH	1:G:1073:ARG:NH1	2.39	0.55
1:E:257:ARG:O	1:E:284:HIS:NE2	2.37	0.55
1:E:683:ARG:NH1	1:E:707:VAL:O	2.38	0.55
1:I:887:ILE:HG21	1:I:959:TYR:HA	1.88	0.55
1:E:709:ASP:O	1:E:725:HIS:ND1	2.40	0.55
1:E:972:LEU:O	1:E:1044:ARG:NH2	2.39	0.55
1:I:20:VAL:HG12	1:I:204:PRO:HA	1.87	0.55
1:I:1232:ARG:HD2	1:I:1702:HIS:HB3	1.89	0.55
1:G:641:VAL:HG21	1:G:705:ASN:HA	1.86	0.55
1:B:709:ASP:O	1:B:725:HIS:ND1	2.40	0.55
1:B:2235:PHE:HA	1:B:2238:TYR:HD2	1.71	0.55
1:B:2368:LEU:HB2	1:B:2376:LEU:HD23	1.88	0.55
1:E:744:VAL:HG22	1:E:759:ILE:HG12	1.88	0.55
1:I:709:ASP:O	1:I:725:HIS:ND1	2.40	0.55
1:G:4581:LYS:HB2	1:G:4632:LEU:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:695:TYR:OH	1:E:1073:ARG:NH1	2.39	0.55
1:E:2803:GLU:OE2	1:E:2806:ARG:NH1	2.40	0.55
1:I:695:TYR:OH	1:I:1073:ARG:NH1	2.39	0.55
1:G:3971:GLY:H	1:G:5005:GLY:HA3	1.71	0.55
1:E:580:GLU:HG3	1:E:620:LEU:HD22	1.88	0.55
1:I:1965:TYR:HA	1:I:1968:LYS:HE3	1.88	0.55
1:I:2235:PHE:HA	1:I:2238:TYR:HD2	1.71	0.55
1:G:4998:LYS:NZ	1:G:5007:GLU:OE1	2.39	0.55
2:F:27:THR:HB	2:F:100:ASP:HB3	1.87	0.55
1:B:20:VAL:HG12	1:B:204:PRO:HA	1.87	0.55
1:B:887:ILE:HG21	1:B:959:TYR:HA	1.88	0.55
1:B:1659:LEU:O	1:B:1663:HIS:N	2.37	0.55
1:B:2042:CYS:SG	1:B:2043:GLY:N	2.80	0.55
1:B:4125:PHE:HA	1:B:4128:PHE:HB3	1.89	0.55
1:E:1965:TYR:HA	1:E:1968:LYS:HE3	1.88	0.55
1:E:2347:GLU:O	1:E:2351:ASN:N	2.37	0.55
1:I:1659:LEU:O	1:I:1663:HIS:N	2.37	0.55
1:I:2104:ARG:HA	1:I:2107:GLN:HB3	1.88	0.55
1:G:4229:GLU:HA	1:G:4232:GLU:HB3	1.89	0.55
1:B:580:GLU:HG3	1:B:620:LEU:HD22	1.88	0.54
1:G:887:ILE:HG21	1:G:959:TYR:HA	1.88	0.54
1:G:1970:GLN:NE2	1:G:3646:THR:OG1	2.40	0.54
1:G:2803:GLU:OE2	1:G:2806:ARG:NH1	2.40	0.54
1:E:887:ILE:HG21	1:E:959:TYR:HA	1.89	0.54
1:E:1232:ARG:HD2	1:E:1702:HIS:HB3	1.89	0.54
1:E:2758:PHE:O	1:E:2762:THR:N	2.39	0.54
1:G:55:ALA:O	1:G:281:ARG:NH1	2.35	0.54
1:G:2368:LEU:HB2	1:G:2376:LEU:HD23	1.88	0.54
1:B:1232:ARG:HD2	1:B:1702:HIS:HB3	1.89	0.54
1:E:2042:CYS:SG	1:E:2043:GLY:N	2.80	0.54
1:E:4581:LYS:HB2	1:E:4632:LEU:HB2	1.88	0.54
1:I:3762:ARG:HG2	1:I:4756:ARG:HA	1.88	0.54
1:I:3971:GLY:H	1:I:5005:GLY:HA3	1.71	0.54
1:I:4125:PHE:HA	1:I:4128:PHE:HB3	1.89	0.54
1:I:4229:GLU:HA	1:I:4232:GLU:HB3	1.89	0.54
1:B:469:ARG:HH21	1:B:3712:GLU:HB3	1.72	0.54
1:E:18:ASP:H	1:E:69:LEU:HB2	1.73	0.54
1:E:1970:GLN:NE2	1:E:3646:THR:OG1	2.40	0.54
1:I:744:VAL:HG22	1:I:759:ILE:HG12	1.88	0.54
1:G:469:ARG:HH21	1:G:3712:GLU:HB3	1.72	0.54
1:G:3762:ARG:HG2	1:G:4756:ARG:HA	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:293:LEU:HB2	1:B:378:LEU:HD12	1.90	0.54
1:B:475:GLN:NE2	1:B:528:SER:O	2.38	0.54
1:B:2803:GLU:OE2	1:B:2806:ARG:NH1	2.40	0.54
1:B:4998:LYS:NZ	1:B:5007:GLU:OE1	2.39	0.54
1:G:683:ARG:NH1	1:G:707:VAL:O	2.38	0.54
1:G:2042:CYS:SG	1:G:2043:GLY:N	2.80	0.54
1:I:463:GLU:OE2	1:I:467:LYS:NZ	2.41	0.54
1:I:2318:TYR:OH	1:I:2414:ASN:N	2.41	0.54
1:G:463:GLU:OE2	1:G:467:LYS:NZ	2.41	0.54
1:B:695:TYR:OH	1:B:1073:ARG:NH1	2.39	0.54
1:B:1812:LEU:HD21	1:B:1861:GLN:HG2	1.90	0.54
1:E:293:LEU:HB2	1:E:378:LEU:HD12	1.90	0.54
1:E:469:ARG:HH21	1:E:3712:GLU:HB3	1.73	0.54
1:I:580:GLU:HG3	1:I:620:LEU:HD22	1.88	0.54
1:I:1970:GLN:NE2	1:I:3646:THR:OG1	2.40	0.54
1:G:2318:TYR:OH	1:G:2414:ASN:N	2.41	0.54
1:E:1812:LEU:HD21	1:E:1861:GLN:HG2	1.90	0.54
1:E:4885:PHE:HE2	1:E:4901:ILE:HD11	1.73	0.54
1:I:469:ARG:HH21	1:I:3712:GLU:HB3	1.72	0.54
1:G:1865:MET:HB3	1:G:1926:LEU:HB2	1.90	0.54
1:E:3762:ARG:HG2	1:E:4756:ARG:HA	1.88	0.54
1:I:293:LEU:HB2	1:I:378:LEU:HD12	1.90	0.54
1:G:580:GLU:HG3	1:G:620:LEU:HD22	1.88	0.54
1:E:776:LEU:HG	1:E:848:HIS:HA	1.90	0.54
1:E:4125:PHE:HA	1:E:4128:PHE:HB3	1.90	0.54
1:E:4229:GLU:HA	1:E:4232:GLU:HB3	1.89	0.54
1:I:1812:LEU:HD21	1:I:1861:GLN:HG2	1.90	0.54
1:I:3752:SER:O	1:I:3756:LYS:N	2.38	0.54
1:G:709:ASP:O	1:G:725:HIS:ND1	2.40	0.54
1:B:776:LEU:HG	1:B:848:HIS:HA	1.90	0.53
1:B:1679:ASN:ND2	1:B:1798:LEU:O	2.41	0.53
1:B:1865:MET:HB3	1:B:1926:LEU:HB2	1.90	0.53
1:B:2770:LYS:HB3	1:B:2775:TRP:HB2	1.90	0.53
1:B:4229:GLU:HA	1:B:4232:GLU:HB3	1.89	0.53
1:I:2803:GLU:OE2	1:I:2806:ARG:NH1	2.40	0.53
1:G:293:LEU:HB2	1:G:378:LEU:HD12	1.90	0.53
1:G:4125:PHE:HA	1:G:4128:PHE:HB3	1.89	0.53
1:I:488:LEU:O	1:I:492:ASP:N	2.36	0.53
1:I:776:LEU:HG	1:I:848:HIS:HA	1.90	0.53
1:I:2042:CYS:SG	1:I:2043:GLY:N	2.80	0.53
1:G:18:ASP:HB2	1:G:69:LEU:HD12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:2770:LYS:HB3	1:G:2775:TRP:HB2	1.90	0.53
1:B:1841:VAL:HA	1:B:1844:LEU:HB3	1.91	0.53
1:B:1970:GLN:NE2	1:B:3646:THR:OG1	2.40	0.53
1:B:4885:PHE:HE2	1:B:4901:ILE:HD11	1.73	0.53
1:E:1679:ASN:ND2	1:E:1798:LEU:O	2.41	0.53
1:I:1865:MET:HB3	1:I:1926:LEU:HB2	1.90	0.53
1:I:2927:LEU:HD23	1:I:2930:LEU:HD12	1.90	0.53
1:G:18:ASP:H	1:G:69:LEU:HB2	1.73	0.53
1:B:2318:TYR:OH	1:B:2414:ASN:N	2.41	0.53
1:E:2770:LYS:HB3	1:E:2775:TRP:HB2	1.91	0.53
1:I:1841:VAL:HA	1:I:1844:LEU:HB3	1.91	0.53
1:I:2770:LYS:HB3	1:I:2775:TRP:HB2	1.91	0.53
1:G:776:LEU:HG	1:G:848:HIS:HA	1.90	0.53
1:G:1679:ASN:ND2	1:G:1798:LEU:O	2.41	0.53
1:G:1778:SER:N	1:G:1799:SER:O	2.41	0.53
1:B:463:GLU:OE2	1:B:467:LYS:NZ	2.41	0.53
1:E:463:GLU:OE2	1:E:467:LYS:NZ	2.41	0.53
1:E:1841:VAL:HA	1:E:1844:LEU:HB3	1.91	0.53
1:G:1841:VAL:HA	1:G:1844:LEU:HB3	1.91	0.53
1:E:1865:MET:HB3	1:E:1926:LEU:HB2	1.90	0.53
1:I:485:SER:O	1:I:489:ASN:N	2.41	0.53
1:I:4763:GLY:O	1:I:4766:THR:OG1	2.24	0.53
1:G:241:GLN:O	1:G:289:ARG:NH1	2.37	0.53
1:G:1812:LEU:HD21	1:G:1861:GLN:HG2	1.90	0.53
1:B:3762:ARG:HG2	1:B:4756:ARG:HA	1.88	0.53
1:B:4687:TYR:OH	1:B:4699:GLY:O	2.26	0.53
1:E:168:ASP:HB3	1:E:199:LEU:HD22	1.91	0.53
1:I:426:ARG:HB2	1:I:506:TYR:HA	1.90	0.53
1:G:168:ASP:HB3	1:G:199:LEU:HD22	1.91	0.53
1:G:4885:PHE:HE2	1:G:4901:ILE:HD11	1.73	0.53
1:B:18:ASP:H	1:B:69:LEU:HB2	1.73	0.53
1:B:1778:SER:N	1:B:1799:SER:O	2.41	0.53
1:I:1679:ASN:ND2	1:I:1798:LEU:O	2.41	0.53
1:I:4138:ASP:O	1:I:4142:ASN:ND2	2.42	0.53
1:G:1232:ARG:HD2	1:G:1702:HIS:HB3	1.89	0.53
1:G:4138:ASP:O	1:G:4142:ASN:ND2	2.42	0.53
1:B:426:ARG:HB2	1:B:506:TYR:HA	1.91	0.53
1:E:1727:ARG:HH12	1:E:1772:ARG:HB3	1.74	0.53
1:E:2318:TYR:OH	1:E:2414:ASN:N	2.41	0.53
1:G:485:SER:O	1:G:489:ASN:N	2.41	0.53
1:G:1931:LEU:HB3	1:G:1935:VAL:HB	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:4746:ALA:O	1:G:4750:ILE:N	2.42	0.53
1:B:488:LEU:HA	1:B:491:ILE:HB	1.91	0.53
1:B:621:ILE:O	1:B:625:LEU:N	2.38	0.53
1:E:4138:ASP:O	1:E:4142:ASN:ND2	2.42	0.53
1:I:257:ARG:O	1:I:284:HIS:NE2	2.37	0.53
1:I:4746:ALA:O	1:I:4750:ILE:N	2.42	0.53
1:G:4687:TYR:OH	1:G:4699:GLY:O	2.26	0.53
1:B:168:ASP:HB3	1:B:199:LEU:HD22	1.91	0.52
1:E:18:ASP:HB2	1:E:69:LEU:HD12	1.90	0.52
1:E:978:THR:HB	1:E:980:ALA:H	1.74	0.52
1:I:1931:LEU:HB3	1:I:1935:VAL:HB	1.91	0.52
1:B:647:ASN:ND2	1:B:820:ARG:O	2.42	0.52
1:B:1931:LEU:HB3	1:B:1935:VAL:HB	1.91	0.52
1:B:4172:GLU:HA	1:B:4175:ARG:HE	1.74	0.52
1:I:18:ASP:H	1:I:69:LEU:HB2	1.73	0.52
1:I:360:ALA:N	1:I:375:LYS:O	2.38	0.52
1:I:1152:MET:HB2	1:I:1161:ILE:HB	1.91	0.52
1:I:4687:TYR:OH	1:I:4699:GLY:O	2.26	0.52
1:G:2927:LEU:HD23	1:G:2930:LEU:HD12	1.90	0.52
1:B:1727:ARG:HH12	1:B:1772:ARG:HB3	1.74	0.52
1:E:1931:LEU:HB3	1:E:1935:VAL:HB	1.91	0.52
1:E:4172:GLU:HA	1:E:4175:ARG:HE	1.74	0.52
1:E:4687:TYR:OH	1:E:4699:GLY:O	2.26	0.52
1:I:168:ASP:HB3	1:I:199:LEU:HD22	1.91	0.52
1:G:4928:LEU:HA	1:G:4931:ILE:HD12	1.91	0.52
1:I:3832:ILE:O	1:I:3836:MET:N	2.42	0.52
1:I:4681:LEU:HD21	1:I:4687:TYR:HD2	1.75	0.52
1:I:4928:LEU:HA	1:I:4931:ILE:HD12	1.91	0.52
1:B:18:ASP:HB2	1:B:69:LEU:HD12	1.90	0.52
1:B:1764:GLY:HA3	1:B:1859:VAL:HG11	1.91	0.52
1:B:4928:LEU:HA	1:B:4931:ILE:HD12	1.91	0.52
1:I:4822:THR:OG1	1:G:4839:MET:SD	2.63	0.52
1:G:1764:GLY:HA3	1:G:1859:VAL:HG11	1.91	0.52
1:G:2758:PHE:O	1:G:2762:THR:N	2.39	0.52
1:E:360:ALA:N	1:E:375:LYS:O	2.38	0.52
1:I:488:LEU:HA	1:I:491:ILE:HB	1.91	0.52
1:I:4957:LYS:HG2	1:I:4964:GLY:HA2	1.92	0.52
1:G:4172:GLU:HA	1:G:4175:ARG:HE	1.74	0.52
1:B:395:GLN:NE2	1:B:397:GLU:OE1	2.43	0.52
1:E:1764:GLY:HA3	1:E:1859:VAL:HG11	1.91	0.52
1:I:1764:GLY:HA3	1:I:1859:VAL:HG11	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:4957:LYS:HG2	1:G:4964:GLY:HA2	1.92	0.52
1:B:45:ARG:NH2	1:B:447:ASP:OD1	2.37	0.52
1:B:2927:LEU:HD23	1:B:2930:LEU:HD12	1.90	0.52
1:B:4681:LEU:HD21	1:B:4687:TYR:HD2	1.75	0.52
1:B:4957:LYS:HG2	1:B:4964:GLY:HA2	1.92	0.52
1:E:2927:LEU:HD23	1:E:2930:LEU:HD12	1.90	0.52
1:E:4957:LYS:HG2	1:E:4964:GLY:HA2	1.92	0.52
1:I:1727:ARG:HH12	1:I:1772:ARG:HB3	1.74	0.52
1:I:4069:LYS:HB2	1:I:4133:GLN:HG3	1.92	0.52
1:G:426:ARG:HB2	1:G:506:TYR:HA	1.90	0.52
1:G:1152:MET:HB2	1:G:1161:ILE:HB	1.91	0.52
1:G:3752:SER:O	1:G:3756:LYS:N	2.38	0.52
1:G:4005:GLN:HE21	1:G:4110:PHE:HE1	1.57	0.52
1:B:40:GLU:HB3	1:B:44:ASN:HB3	1.92	0.52
1:B:877:ASN:HD22	1:B:1045:THR:HG23	1.75	0.52
1:B:978:THR:HB	1:B:980:ALA:H	1.75	0.52
1:B:1978:ALA:O	1:B:1983:ALA:N	2.40	0.52
1:B:2002:PRO:HA	1:B:2005:GLN:HB3	1.92	0.52
1:E:485:SER:O	1:E:489:ASN:N	2.41	0.52
1:I:395:GLN:NE2	1:I:397:GLU:OE1	2.43	0.52
1:G:488:LEU:HA	1:G:491:ILE:HB	1.91	0.52
1:G:1727:ARG:HH12	1:G:1772:ARG:HB3	1.74	0.52
1:G:4572:ALA:HA	1:G:4575:PHE:HB3	1.92	0.52
1:B:457:GLU:OE1	1:B:464:LYS:NZ	2.40	0.52
1:E:184:THR:HA	1:E:189:LEU:HA	1.92	0.52
1:E:426:ARG:HB2	1:E:506:TYR:HA	1.91	0.52
1:E:4681:LEU:HD21	1:E:4687:TYR:HD2	1.75	0.52
1:I:40:GLU:HB3	1:I:44:ASN:HB3	1.92	0.52
1:I:1713:ASP:O	1:I:1717:SER:N	2.39	0.52
1:I:4998:LYS:NZ	1:I:5007:GLU:OE1	2.39	0.52
1:G:45:ARG:NH2	1:G:447:ASP:OD1	2.37	0.52
1:B:55:ALA:O	1:B:281:ARG:NH1	2.35	0.51
1:B:4069:LYS:HB2	1:B:4133:GLN:HG3	1.92	0.51
1:B:4763:GLY:O	1:B:4766:THR:OG1	2.24	0.51
1:E:1659:LEU:O	1:E:1663:HIS:N	2.37	0.51
1:E:4069:LYS:HB2	1:E:4133:GLN:HG3	1.92	0.51
1:I:18:ASP:HB2	1:I:69:LEU:HD12	1.90	0.51
1:I:978:THR:HB	1:I:980:ALA:H	1.75	0.51
1:I:4885:PHE:HE2	1:I:4901:ILE:HD11	1.73	0.51
1:G:719:LEU:HD22	1:G:735:GLN:HG2	1.92	0.51
1:B:629:ARG:HB3	1:B:634:GLN:HE21	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1970:GLN:HA	1:B:3641:LEU:HG	1.92	0.51
1:B:3898:ASP:O	1:B:3902:TYR:N	2.43	0.51
1:B:4138:ASP:O	1:B:4142:ASN:ND2	2.42	0.51
1:B:4697:VAL:O	1:B:4701:TRP:N	2.42	0.51
1:E:488:LEU:HA	1:E:491:ILE:HB	1.91	0.51
1:E:647:ASN:ND2	1:E:820:ARG:O	2.42	0.51
1:E:877:ASN:HD22	1:E:1045:THR:HG23	1.75	0.51
1:E:1978:ALA:O	1:E:1983:ALA:N	2.40	0.51
1:E:4062:PHE:HA	1:E:4132:PHE:HZ	1.76	0.51
1:I:4572:ALA:HA	1:I:4575:PHE:HB3	1.92	0.51
1:G:978:THR:HB	1:G:980:ALA:H	1.75	0.51
1:G:4095:LYS:O	1:G:4099:SER:N	2.43	0.51
1:B:2116:LEU:O	1:B:2120:MET:N	2.43	0.51
1:I:719:LEU:HD22	1:I:735:GLN:HG2	1.92	0.51
1:I:3898:ASP:O	1:I:3902:TYR:N	2.43	0.51
1:G:184:THR:HA	1:G:189:LEU:HA	1.93	0.51
1:G:221:ARG:NE	1:G:258:SER:OG	2.44	0.51
1:G:1970:GLN:HA	1:G:3641:LEU:HG	1.92	0.51
1:G:3885:PHE:O	1:G:3889:GLN:N	2.41	0.51
1:B:3885:PHE:O	1:B:3889:GLN:N	2.41	0.51
1:B:4107:GLU:O	1:B:4111:LEU:N	2.40	0.51
1:E:1694:LEU:O	1:E:1712:TYR:OH	2.22	0.51
1:I:4095:LYS:O	1:I:4099:SER:N	2.43	0.51
1:G:4069:LYS:HB2	1:G:4133:GLN:HG3	1.92	0.51
1:B:184:THR:HA	1:B:189:LEU:HA	1.93	0.51
1:E:3927:GLN:O	1:E:3931:SER:N	2.42	0.51
1:I:629:ARG:O	1:I:634:GLN:NE2	2.44	0.51
1:I:3840:SER:OG	1:I:3875:MET:O	2.26	0.51
1:G:457:GLU:OE1	1:G:464:LYS:NZ	2.40	0.51
1:G:1659:LEU:O	1:G:1663:HIS:N	2.37	0.51
1:G:3927:GLN:O	1:G:3931:SER:N	2.42	0.51
1:B:1152:MET:HB2	1:B:1161:ILE:HB	1.91	0.51
1:I:1089:TYR:N	1:I:1224:GLU:O	2.41	0.51
1:I:1111:PRO:HD3	1:I:1605:TRP:HE1	1.76	0.51
1:I:4172:GLU:HA	1:I:4175:ARG:HE	1.74	0.51
1:G:989:ALA:O	1:G:1035:ASN:ND2	2.44	0.51
1:B:3832:ILE:O	1:B:3836:MET:N	2.42	0.51
1:E:4857:ASN:HB2	1:G:4807:PHE:HZ	1.74	0.51
1:E:4928:LEU:HA	1:E:4931:ILE:HD12	1.91	0.51
1:I:877:ASN:HD22	1:I:1045:THR:HG23	1.75	0.51
1:I:1970:GLN:HA	1:I:3641:LEU:HG	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:488:LEU:O	1:G:492:ASP:N	2.36	0.51
1:G:621:ILE:O	1:G:625:LEU:N	2.38	0.51
1:G:877:ASN:HD22	1:G:1045:THR:HG23	1.75	0.51
1:G:1111:PRO:HD3	1:G:1605:TRP:HE1	1.76	0.51
1:B:2758:PHE:O	1:B:2762:THR:N	2.39	0.51
1:B:4572:ALA:HA	1:B:4575:PHE:HB3	1.91	0.51
1:E:1152:MET:HB2	1:E:1161:ILE:HB	1.91	0.51
1:E:3898:ASP:O	1:E:3902:TYR:N	2.43	0.51
1:I:1778:SER:N	1:I:1799:SER:O	2.42	0.51
1:I:2272:PRO:HA	1:I:2275:VAL:HG12	1.93	0.51
1:G:3832:ILE:O	1:G:3836:MET:N	2.42	0.51
1:I:173:SER:OG	1:I:174:VAL:N	2.44	0.51
1:I:184:THR:HA	1:I:189:LEU:HA	1.93	0.51
1:B:4095:LYS:O	1:B:4099:SER:N	2.44	0.51
1:E:719:LEU:HD22	1:E:735:GLN:HG2	1.92	0.51
1:E:793:LEU:HG	1:E:1625:GLY:HA2	1.93	0.51
1:E:1970:GLN:HA	1:E:3641:LEU:HG	1.92	0.51
1:E:2326:CYS:SG	1:E:2327:GLY:N	2.84	0.51
1:E:4572:ALA:HA	1:E:4575:PHE:HB3	1.92	0.51
1:I:629:ARG:HB3	1:I:634:GLN:HE21	1.76	0.51
1:I:2002:PRO:HA	1:I:2005:GLN:HB3	1.92	0.51
1:I:4081:VAL:HB	1:I:4088:ILE:HD12	1.92	0.51
1:G:4081:VAL:HB	1:G:4088:ILE:HD12	1.92	0.51
1:G:5012:LYS:O	1:G:5016:GLU:N	2.42	0.51
1:B:2326:CYS:SG	1:B:2327:GLY:N	2.84	0.50
1:E:395:GLN:NE2	1:E:397:GLU:OE1	2.43	0.50
1:E:1032:LYS:O	1:E:1036:ARG:N	2.39	0.50
1:I:4005:GLN:HE21	1:I:4110:PHE:HE1	1.57	0.50
1:G:629:ARG:O	1:G:634:GLN:NE2	2.44	0.50
1:G:2272:PRO:HA	1:G:2275:VAL:HG12	1.93	0.50
1:B:629:ARG:O	1:B:634:GLN:NE2	2.44	0.50
1:B:864:PRO:HD2	1:B:867:LEU:HD12	1.93	0.50
1:E:173:SER:OG	1:E:174:VAL:N	2.44	0.50
1:E:629:ARG:HB3	1:E:634:GLN:HE21	1.75	0.50
1:I:45:ARG:NH2	1:I:447:ASP:OD1	2.37	0.50
1:G:2002:PRO:HA	1:G:2005:GLN:HB3	1.92	0.50
1:G:4062:PHE:HA	1:G:4132:PHE:HZ	1.76	0.50
1:B:2272:PRO:HA	1:B:2275:VAL:HG12	1.93	0.50
1:E:3885:PHE:O	1:E:3889:GLN:N	2.41	0.50
1:E:4937:ILE:O	1:E:4941:GLY:N	2.41	0.50
1:I:2326:CYS:SG	1:I:2327:GLY:N	2.84	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:4820:VAL:HB	1:I:4823:LEU:HD23	1.94	0.50
1:G:4681:LEU:HD21	1:G:4687:TYR:HD2	1.75	0.50
1:G:4820:VAL:HB	1:G:4823:LEU:HD23	1.94	0.50
1:B:221:ARG:NE	1:B:258:SER:OG	2.44	0.50
1:B:1111:PRO:HD3	1:B:1605:TRP:HE1	1.76	0.50
1:B:4860:ARG:HG3	1:B:4876:CYS:HB3	1.94	0.50
1:E:40:GLU:HB3	1:E:44:ASN:HB3	1.92	0.50
1:E:989:ALA:O	1:E:1035:ASN:ND2	2.44	0.50
1:E:2002:PRO:HA	1:E:2005:GLN:HB3	1.92	0.50
1:E:4024:VAL:HG23	1:E:4027:LEU:HD12	1.94	0.50
1:E:4820:VAL:HB	1:E:4823:LEU:HD23	1.94	0.50
1:I:221:ARG:NE	1:I:258:SER:OG	2.44	0.50
1:I:989:ALA:O	1:I:1035:ASN:ND2	2.44	0.50
1:I:4062:PHE:HA	1:I:4132:PHE:HZ	1.76	0.50
1:G:40:GLU:HB3	1:G:44:ASN:HB3	1.92	0.50
1:G:245:VAL:HG21	1:G:299:LEU:HG	1.93	0.50
1:G:629:ARG:HB3	1:G:634:GLN:HE21	1.75	0.50
1:G:685:GLY:N	1:G:780:VAL:O	2.35	0.50
1:G:793:LEU:HG	1:G:1625:GLY:HA2	1.93	0.50
1:G:864:PRO:HD2	1:G:867:LEU:HD12	1.93	0.50
1:G:3840:SER:OG	1:G:3875:MET:O	2.26	0.50
1:B:4824:ARG:HA	1:B:4827:LEU:HB2	1.94	0.50
1:E:4005:GLN:HE21	1:E:4110:PHE:HE1	1.57	0.50
1:E:4081:VAL:HB	1:E:4088:ILE:HD12	1.92	0.50
1:E:4152:GLU:OE1	1:E:4194:TYR:OH	2.29	0.50
1:E:4860:ARG:HG3	1:E:4876:CYS:HB3	1.94	0.50
1:I:1163:THR:HA	1:I:1168:VAL:HA	1.94	0.50
1:G:647:ASN:ND2	1:G:820:ARG:O	2.42	0.50
1:G:2326:CYS:SG	1:G:2327:GLY:N	2.84	0.50
1:E:4651:THR:HA	1:E:4799:SER:HB3	1.92	0.50
1:I:4169:SER:O	1:I:4173:TYR:N	2.45	0.50
1:G:173:SER:OG	1:G:174:VAL:N	2.44	0.50
1:G:596:ASN:HB3	1:G:599:VAL:HG22	1.94	0.50
1:G:736:HIS:HB3	2:H:8:SER:H	1.77	0.50
1:G:2116:LEU:O	1:G:2120:MET:N	2.43	0.50
1:G:3898:ASP:O	1:G:3902:TYR:N	2.43	0.50
1:B:245:VAL:HG21	1:B:299:LEU:HG	1.93	0.50
1:B:596:ASN:HB3	1:B:599:VAL:HG22	1.94	0.50
1:B:1931:LEU:HD22	1:B:1935:VAL:HG11	1.94	0.50
1:B:4005:GLN:HE21	1:B:4110:PHE:HE1	1.57	0.50
1:B:4081:VAL:HB	1:B:4088:ILE:HD12	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4169:SER:O	1:B:4173:TYR:N	2.45	0.50
1:B:4820:VAL:HB	1:B:4823:LEU:HD23	1.94	0.50
1:E:221:ARG:NE	1:E:258:SER:OG	2.44	0.50
1:E:621:ILE:O	1:E:625:LEU:N	2.39	0.50
1:E:2116:LEU:O	1:E:2120:MET:N	2.43	0.50
1:E:4746:ALA:O	1:E:4750:ILE:N	2.42	0.50
1:G:3781:GLN:O	1:G:3785:ALA:N	2.45	0.50
1:G:4860:ARG:HG3	1:G:4876:CYS:HB3	1.94	0.50
1:B:932:LEU:HD23	1:B:935:LEU:HD12	1.94	0.50
1:B:2823:ILE:HG12	1:B:2937:VAL:HG22	1.94	0.50
1:B:3927:GLN:O	1:B:3931:SER:N	2.42	0.50
1:E:269:TRP:HB3	1:E:272:SER:HB3	1.94	0.50
1:E:629:ARG:O	1:E:634:GLN:NE2	2.44	0.50
1:E:2457:LEU:HD23	1:E:2460:LEU:HD12	1.94	0.50
1:E:4697:VAL:O	1:E:4701:TRP:N	2.42	0.50
1:I:551:LEU:HD21	1:I:589:LEU:HB2	1.94	0.50
1:I:596:ASN:HB3	1:I:599:VAL:HG22	1.94	0.50
1:I:3676:ASP:N	1:I:3676:ASP:OD1	2.45	0.50
1:G:4824:ARG:HA	1:G:4827:LEU:HB2	1.94	0.50
1:B:4822:THR:O	1:B:4825:THR:OG1	2.29	0.50
1:E:1778:SER:N	1:E:1799:SER:O	2.41	0.50
1:E:2272:PRO:HA	1:E:2275:VAL:HG12	1.93	0.50
1:I:793:LEU:HG	1:I:1625:GLY:HA2	1.93	0.50
1:I:1721:GLU:OE2	1:I:1725:ARG:NH2	2.39	0.50
1:G:1978:ALA:O	1:G:1983:ALA:N	2.40	0.50
1:B:173:SER:OG	1:B:174:VAL:N	2.44	0.49
1:B:1032:LYS:O	1:B:1036:ARG:N	2.39	0.49
1:B:3676:ASP:OD1	1:B:3676:ASP:N	2.45	0.49
1:B:4024:VAL:HG23	1:B:4027:LEU:HD12	1.94	0.49
1:E:448:LEU:HA	1:E:451:TYR:HB3	1.94	0.49
1:E:864:PRO:HD2	1:E:867:LEU:HD12	1.93	0.49
1:I:1931:LEU:HD22	1:I:1935:VAL:HG11	1.94	0.49
1:I:2342:ASN:OD1	1:I:2342:ASN:N	2.45	0.49
1:I:4651:THR:HA	1:I:4799:SER:HB3	1.93	0.49
1:G:1032:LYS:O	1:G:1036:ARG:N	2.39	0.49
1:G:2868:SER:O	1:G:2872:GLN:N	2.45	0.49
1:G:4169:SER:O	1:G:4173:TYR:N	2.45	0.49
1:B:719:LEU:HD22	1:B:735:GLN:HG2	1.92	0.49
1:B:793:LEU:HG	1:B:1625:GLY:HA2	1.93	0.49
1:B:989:ALA:O	1:B:1035:ASN:ND2	2.44	0.49
1:B:4062:PHE:HA	1:B:4132:PHE:HZ	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1950:GLU:O	1:E:1954:ARG:N	2.45	0.49
1:E:4095:LYS:O	1:E:4099:SER:N	2.44	0.49
1:E:4822:THR:O	1:E:4825:THR:OG1	2.28	0.49
1:E:5012:LYS:O	1:E:5016:GLU:N	2.42	0.49
1:I:245:VAL:HG21	1:I:299:LEU:HG	1.93	0.49
1:B:1163:THR:HA	1:B:1168:VAL:HA	1.94	0.49
1:E:2823:ILE:HG12	1:E:2937:VAL:HG22	1.94	0.49
1:G:269:TRP:HB3	1:G:272:SER:HB3	1.94	0.49
1:G:1163:THR:HA	1:G:1168:VAL:HA	1.94	0.49
1:G:4152:GLU:OE1	1:G:4194:TYR:OH	2.29	0.49
1:B:1679:ASN:HA	1:B:1682:ALA:HB3	1.94	0.49
1:B:2737:PRO:O	1:B:2888:ARG:NH2	2.46	0.49
1:E:596:ASN:HB3	1:E:599:VAL:HG22	1.94	0.49
1:I:911:HIS:O	1:I:918:ARG:NH2	2.45	0.49
1:I:2457:LEU:HD23	1:I:2460:LEU:HD12	1.94	0.49
1:G:72:SER:HB2	1:G:107:ILE:HG13	1.95	0.49
1:G:551:LEU:HD21	1:G:589:LEU:HB2	1.94	0.49
1:B:911:HIS:O	1:B:918:ARG:NH2	2.45	0.49
1:B:1698:LEU:N	1:B:1712:TYR:OH	2.46	0.49
1:E:1111:PRO:HD3	1:E:1605:TRP:HE1	1.76	0.49
1:E:2006:ILE:O	1:E:2010:LEU:N	2.43	0.49
1:E:2868:SER:O	1:E:2872:GLN:N	2.45	0.49
1:E:3781:GLN:O	1:E:3785:ALA:N	2.45	0.49
1:I:864:PRO:HD2	1:I:867:LEU:HD12	1.93	0.49
1:I:932:LEU:HD23	1:I:935:LEU:HD12	1.94	0.49
1:I:2823:ILE:HG12	1:I:2937:VAL:HG22	1.94	0.49
1:I:2880:GLU:O	1:I:2884:ASN:N	2.42	0.49
1:I:3885:PHE:O	1:I:3889:GLN:N	2.41	0.49
1:I:4822:THR:O	1:I:4825:THR:OG1	2.29	0.49
1:G:3676:ASP:OD1	1:G:3676:ASP:N	2.45	0.49
1:G:4024:VAL:HG23	1:G:4027:LEU:HD12	1.94	0.49
1:B:4152:GLU:OE1	1:B:4194:TYR:OH	2.29	0.49
1:B:4651:THR:HA	1:B:4799:SER:HB3	1.93	0.49
1:E:245:VAL:HG21	1:E:299:LEU:HG	1.93	0.49
1:E:395:GLN:HG3	1:E:397:GLU:H	1.78	0.49
1:E:551:LEU:HD21	1:E:589:LEU:HB2	1.94	0.49
1:E:4702:ASP:OD1	1:E:4778:TRP:NE1	2.44	0.49
1:I:1679:ASN:HA	1:I:1682:ALA:HB3	1.94	0.49
1:I:2176:ASN:O	1:I:2180:GLN:N	2.42	0.49
1:I:2346:VAL:HG22	1:I:2348:GLU:H	1.78	0.49
1:I:4860:ARG:HG3	1:I:4876:CYS:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:395:GLN:HG3	1:G:397:GLU:H	1.78	0.49
1:G:3707:ARG:HA	1:G:3710:LEU:HD23	1.94	0.49
1:B:3752:SER:O	1:B:3756:LYS:N	2.38	0.49
1:B:3780:LEU:HD11	1:B:3816:MET:HG3	1.95	0.49
1:E:838:HIS:HA	1:E:1201:HIS:HB3	1.94	0.49
1:E:1698:LEU:N	1:E:1712:TYR:OH	2.46	0.49
1:E:1713:ASP:O	1:E:1717:SER:N	2.39	0.49
1:E:4107:GLU:O	1:E:4111:LEU:N	2.40	0.49
1:I:580:GLU:OE2	1:I:624:ASN:ND2	2.46	0.49
1:I:1698:LEU:N	1:I:1712:TYR:OH	2.46	0.49
1:I:3927:GLN:O	1:I:3931:SER:N	2.42	0.49
1:I:4824:ARG:HA	1:I:4827:LEU:HB2	1.94	0.49
1:G:717:ASP:OD1	1:G:720:HIS:ND1	2.46	0.49
1:G:2346:VAL:HG22	1:G:2348:GLU:H	1.78	0.49
1:G:3897:ASN:O	1:G:3901:ASN:ND2	2.46	0.49
1:G:4201:ASN:HA	1:G:4204:GLN:HB3	1.95	0.49
1:G:4651:THR:HA	1:G:4799:SER:HB3	1.93	0.49
1:B:2176:ASN:O	1:B:2180:GLN:N	2.42	0.49
1:B:2880:GLU:O	1:B:2884:ASN:N	2.42	0.49
1:B:3840:SER:OG	1:B:3875:MET:O	2.26	0.49
1:E:45:ARG:NH2	1:E:447:ASP:OD1	2.37	0.49
1:E:3897:ASN:O	1:E:3901:ASN:ND2	2.46	0.49
1:I:395:GLN:HG3	1:I:397:GLU:H	1.78	0.49
1:I:838:HIS:HA	1:I:1201:HIS:HB3	1.94	0.49
1:I:3707:ARG:HA	1:I:3710:LEU:HD23	1.94	0.49
1:I:4697:VAL:O	1:I:4701:TRP:N	2.42	0.49
1:G:1516:UNK:N	1:G:1529:UNK:O	2.45	0.49
1:G:1931:LEU:HD22	1:G:1935:VAL:HG11	1.94	0.49
1:G:2737:PRO:O	1:G:2888:ARG:NH2	2.46	0.49
1:G:3946:GLN:OE1	1:G:3950:ASN:ND2	2.46	0.49
1:B:580:GLU:OE2	1:B:624:ASN:ND2	2.46	0.49
1:B:1089:TYR:N	1:B:1224:GLU:O	2.41	0.49
1:B:2346:VAL:HG22	1:B:2348:GLU:H	1.78	0.49
1:B:3842:LEU:O	1:B:3929:SER:OG	2.31	0.49
1:B:4066:LEU:HA	1:B:4133:GLN:HE22	1.78	0.49
1:E:1931:LEU:HD22	1:E:1935:VAL:HG11	1.94	0.49
1:E:3780:LEU:HD11	1:E:3816:MET:HG3	1.95	0.49
1:I:269:TRP:HB3	1:I:272:SER:HB3	1.94	0.49
1:I:952:LYS:HB3	1:I:968:ALA:HB1	1.95	0.49
1:I:4107:GLU:O	1:I:4111:LEU:N	2.40	0.49
1:G:111:HIS:N	1:G:116:MET:O	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:395:GLN:NE2	1:G:397:GLU:OE1	2.43	0.49
1:G:838:HIS:HA	1:G:1201:HIS:HB3	1.94	0.49
1:B:838:HIS:HA	1:B:1201:HIS:HB3	1.94	0.49
1:B:1516:UNK:N	1:B:1529:UNK:O	2.46	0.49
1:B:2751:LEU:HD11	1:B:2823:ILE:HG21	1.95	0.49
1:E:23:GLN:OE1	1:E:203:ASN:ND2	2.46	0.49
1:E:619:ASP:OD1	1:E:1680:ARG:NH1	2.46	0.49
1:E:2737:PRO:O	1:E:2888:ARG:NH2	2.46	0.49
1:E:4832:HIS:NE2	1:E:4942:GLU:OE1	2.46	0.49
1:I:647:ASN:ND2	1:I:820:ARG:O	2.42	0.49
1:I:2009:LEU:HD23	1:I:2012:PHE:HE2	1.78	0.49
1:I:3781:GLN:O	1:I:3785:ALA:N	2.45	0.49
1:I:3897:ASN:O	1:I:3901:ASN:ND2	2.46	0.49
1:I:4024:VAL:HG23	1:I:4027:LEU:HD12	1.94	0.49
1:I:4702:ASP:OD1	1:I:4778:TRP:NE1	2.44	0.49
1:G:3780:LEU:HD11	1:G:3816:MET:HG3	1.95	0.49
1:B:23:GLN:HE21	1:B:34:LYS:HB3	1.78	0.48
1:B:395:GLN:HG3	1:B:397:GLU:H	1.78	0.48
1:B:551:LEU:HD21	1:B:589:LEU:HB2	1.94	0.48
1:B:583:ILE:HA	1:B:586:ILE:HD12	1.95	0.48
1:B:717:ASP:OD1	1:B:720:HIS:ND1	2.46	0.48
1:B:2868:SER:O	1:B:2872:GLN:N	2.45	0.48
1:B:3781:GLN:O	1:B:3785:ALA:N	2.45	0.48
1:E:932:LEU:HD23	1:E:935:LEU:HD12	1.94	0.48
1:I:72:SER:HB2	1:I:107:ILE:HG13	1.95	0.48
1:I:717:ASP:OD1	1:I:720:HIS:ND1	2.46	0.48
1:I:1770:SER:OG	1:I:1772:ARG:NE	2.46	0.48
1:I:1863:LEU:HB3	1:I:1870:VAL:HG11	1.95	0.48
1:I:2432:LEU:O	1:I:2436:CYS:N	2.46	0.48
1:G:23:GLN:HE21	1:G:34:LYS:HB3	1.77	0.48
1:G:1093:GLU:OE1	1:G:1201:HIS:NE2	2.46	0.48
1:G:2823:ILE:HG12	1:G:2937:VAL:HG22	1.94	0.48
1:B:269:TRP:HB3	1:B:272:SER:HB3	1.94	0.48
1:B:870:ILE:HD11	1:B:1049:TYR:CG	2.48	0.48
1:B:983:THR:O	1:B:987:ARG:N	2.45	0.48
1:B:1154:ASP:O	1:B:1158:ASN:N	2.46	0.48
1:B:1671:ARG:HE	1:B:1713:ASP:HB3	1.79	0.48
1:B:2006:ILE:O	1:B:2010:LEU:N	2.43	0.48
1:B:2009:LEU:HD23	1:B:2012:PHE:HE2	1.78	0.48
1:E:870:ILE:HD11	1:E:1049:TYR:CG	2.48	0.48
1:E:1163:THR:HA	1:E:1168:VAL:HA	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:3832:ILE:O	1:E:3836:MET:N	2.42	0.48
1:I:243:ARG:NH2	1:I:303:ASP:OD1	2.29	0.48
1:I:396:GLU:HG2	1:I:399:GLN:HB3	1.95	0.48
1:I:540:PHE:HD2	1:I:567:VAL:HG11	1.78	0.48
1:I:3946:GLN:OE1	1:I:3950:ASN:ND2	2.46	0.48
1:G:23:GLN:OE1	1:G:203:ASN:ND2	2.46	0.48
1:B:485:SER:O	1:B:489:ASN:N	2.41	0.48
1:E:4022:ASP:HA	1:E:4025:VAL:HG22	1.95	0.48
1:E:4201:ASN:HA	1:E:4204:GLN:HB3	1.95	0.48
1:E:4824:ARG:HA	1:E:4827:LEU:HB2	1.94	0.48
1:I:2737:PRO:O	1:I:2888:ARG:NH2	2.46	0.48
1:I:3365:UNK:O	1:I:3369:UNK:N	2.45	0.48
1:I:3780:LEU:HD11	1:I:3816:MET:HG3	1.95	0.48
1:G:15:ARG:HG2	1:G:100:THR:HA	1.96	0.48
1:G:396:GLU:HG2	1:G:399:GLN:HB3	1.95	0.48
1:G:1271:ARG:HA	1:G:1471:UNK:HA	1.95	0.48
1:G:2302:LEU:O	1:G:2306:GLY:N	2.46	0.48
1:G:2457:LEU:HD23	1:G:2460:LEU:HD12	1.94	0.48
1:G:3365:UNK:O	1:G:3369:UNK:N	2.46	0.48
1:B:3946:GLN:OE1	1:B:3950:ASN:ND2	2.46	0.48
1:B:4180:ARG:O	1:B:4987:ASN:ND2	2.47	0.48
1:E:580:GLU:OE2	1:E:624:ASN:ND2	2.46	0.48
1:E:1154:ASP:O	1:E:1158:ASN:N	2.46	0.48
1:E:1671:ARG:HE	1:E:1713:ASP:HB3	1.78	0.48
1:E:4169:SER:O	1:E:4173:TYR:N	2.45	0.48
1:G:1698:LEU:N	1:G:1712:TYR:OH	2.46	0.48
1:G:4822:THR:O	1:G:4825:THR:OG1	2.28	0.48
1:B:3897:ASN:O	1:B:3901:ASN:ND2	2.46	0.48
1:B:4807:PHE:HZ	1:I:4857:ASN:HB2	1.79	0.48
1:E:396:GLU:HG2	1:E:399:GLN:HB3	1.95	0.48
1:E:1679:ASN:HA	1:E:1682:ALA:HB3	1.94	0.48
1:E:3365:UNK:O	1:E:3369:UNK:N	2.46	0.48
1:E:3707:ARG:HA	1:E:3710:LEU:HD23	1.94	0.48
1:E:3946:GLN:OE1	1:E:3950:ASN:ND2	2.46	0.48
1:E:4028:LEU:HD11	1:E:4142:ASN:HB3	1.96	0.48
1:E:4702:ASP:HA	1:E:4778:TRP:HE1	1.78	0.48
1:I:57:ASN:HD22	1:I:308:HIS:HB2	1.79	0.48
1:I:442:ILE:HG23	1:I:521:LEU:HD11	1.96	0.48
1:I:2751:LEU:HD11	1:I:2823:ILE:HG21	1.95	0.48
1:I:2868:SER:O	1:I:2872:GLN:N	2.45	0.48
1:I:4832:HIS:NE2	1:I:4942:GLU:OE1	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:448:LEU:HA	1:G:451:TYR:HB3	1.94	0.48
1:G:580:GLU:OE2	1:G:624:ASN:ND2	2.46	0.48
1:G:619:ASP:OD1	1:G:1680:ARG:NH1	2.47	0.48
1:G:731:THR:OG1	1:G:1519:UNK:O	2.32	0.48
1:G:932:LEU:HD23	1:G:935:LEU:HD12	1.94	0.48
1:G:2342:ASN:N	1:G:2342:ASN:OD1	2.45	0.48
1:G:4091:LYS:HA	1:G:4094:GLN:HB3	1.96	0.48
1:G:4702:ASP:HA	1:G:4778:TRP:HE1	1.78	0.48
1:B:111:HIS:HD2	1:B:114:SER:H	1.62	0.48
1:B:2128:TYR:HB3	1:B:3669:PHE:HB3	1.95	0.48
1:B:3945:GLU:O	1:B:3949:ARG:N	2.45	0.48
1:B:4091:LYS:HA	1:B:4094:GLN:HB3	1.96	0.48
1:B:4201:ASN:HA	1:B:4204:GLN:HB3	1.95	0.48
1:E:15:ARG:HG2	1:E:100:THR:HA	1.96	0.48
1:E:72:SER:HB2	1:E:107:ILE:HG13	1.95	0.48
1:E:4091:LYS:HA	1:E:4094:GLN:HB3	1.96	0.48
1:I:621:ILE:O	1:I:625:LEU:N	2.38	0.48
1:I:870:ILE:HD11	1:I:1049:TYR:CG	2.48	0.48
1:I:4022:ASP:HA	1:I:4025:VAL:HG22	1.95	0.48
1:I:4152:GLU:OE1	1:I:4194:TYR:OH	2.29	0.48
1:G:1089:TYR:N	1:G:1224:GLU:O	2.41	0.48
1:G:1950:GLU:O	1:G:1954:ARG:N	2.45	0.48
1:B:2342:ASN:N	1:B:2342:ASN:OD1	2.45	0.48
1:B:5012:LYS:O	1:B:5016:GLU:N	2.42	0.48
1:E:540:PHE:HD2	1:E:567:VAL:HG11	1.78	0.48
1:E:717:ASP:OD1	1:E:720:HIS:ND1	2.46	0.48
1:E:2751:LEU:HD11	1:E:2823:ILE:HG21	1.95	0.48
1:I:241:GLN:O	1:I:289:ARG:NH1	2.37	0.48
1:I:2758:PHE:O	1:I:2762:THR:N	2.39	0.48
1:I:3889:GLN:OE1	1:I:3960:GLN:NE2	2.47	0.48
1:I:4091:LYS:HA	1:I:4094:GLN:HB3	1.96	0.48
1:I:4201:ASN:HA	1:I:4204:GLN:HB3	1.95	0.48
1:G:111:HIS:HD2	1:G:114:SER:H	1.62	0.48
1:G:870:ILE:HD11	1:G:1049:TYR:CG	2.48	0.48
1:G:2009:LEU:HD23	1:G:2012:PHE:HE2	1.78	0.48
1:G:2128:TYR:HB3	1:G:3669:PHE:HB3	1.95	0.48
1:G:3945:GLU:O	1:G:3949:ARG:N	2.45	0.48
1:G:4236:SER:O	1:G:4240:ASP:N	2.43	0.48
1:G:4697:VAL:O	1:G:4701:TRP:N	2.42	0.48
1:B:236:ALA:HA	1:B:242:ARG:HD2	1.95	0.48
1:B:1863:LEU:HB3	1:B:1870:VAL:HG11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2432:LEU:O	1:B:2436:CYS:N	2.46	0.48
1:B:4832:HIS:NE2	1:B:4942:GLU:OE1	2.46	0.48
1:E:23:GLN:HE21	1:E:34:LYS:HB3	1.78	0.48
1:E:3752:SER:O	1:E:3756:LYS:N	2.38	0.48
1:E:3842:LEU:O	1:E:3929:SER:OG	2.30	0.48
1:E:4180:ARG:O	1:E:4987:ASN:ND2	2.47	0.48
1:I:111:HIS:HD2	1:I:114:SER:H	1.62	0.48
1:I:448:LEU:HA	1:I:451:TYR:HB3	1.94	0.48
1:I:2302:LEU:O	1:I:2306:GLY:N	2.46	0.48
1:I:4180:ARG:O	1:I:4987:ASN:ND2	2.47	0.48
1:G:1863:LEU:HB3	1:G:1870:VAL:HG11	1.95	0.48
2:F:7:ILE:HG22	2:F:9:PRO:HD2	1.96	0.48
1:B:540:PHE:HD2	1:B:567:VAL:HG11	1.78	0.48
1:B:2457:LEU:HD23	1:B:2460:LEU:HD12	1.94	0.48
1:E:952:LYS:HB3	1:E:968:ALA:HB1	1.95	0.48
1:E:2302:LEU:O	1:E:2306:GLY:N	2.46	0.48
1:I:1671:ARG:HE	1:I:1713:ASP:HB3	1.78	0.48
1:I:1965:TYR:OH	1:I:2027:ILE:O	2.27	0.48
1:G:236:ALA:HA	1:G:242:ARG:HD2	1.95	0.48
1:G:1713:ASP:O	1:G:1717:SER:N	2.39	0.48
1:G:2432:LEU:O	1:G:2436:CYS:N	2.46	0.48
2:A:7:ILE:HG22	2:A:9:PRO:HD2	1.96	0.48
1:B:15:ARG:HG2	1:B:100:THR:HA	1.96	0.48
1:B:1770:SER:OG	1:B:1772:ARG:NE	2.46	0.48
1:B:3707:ARG:HA	1:B:3710:LEU:HD23	1.94	0.48
1:B:4567:LEU:HD12	1:B:4816:ILE:HD12	1.96	0.48
1:E:2009:LEU:HD23	1:E:2012:PHE:HE2	1.78	0.48
1:I:23:GLN:HE21	1:I:34:LYS:HB3	1.78	0.48
1:I:410:LEU:HD21	1:I:441:VAL:HA	1.96	0.48
1:I:619:ASP:OD1	1:I:1680:ARG:NH1	2.47	0.48
1:I:2452:ARG:NH1	1:G:175:SER:O	2.44	0.48
1:I:4066:LEU:HA	1:I:4133:GLN:HE22	1.78	0.48
1:G:1770:SER:OG	1:G:1772:ARG:NE	2.46	0.48
1:G:2451:LEU:O	1:G:2455:ALA:N	2.42	0.48
1:G:2751:LEU:HD11	1:G:2823:ILE:HG21	1.95	0.48
1:G:4022:ASP:HA	1:G:4025:VAL:HG22	1.95	0.48
2:H:7:ILE:HG22	2:H:9:PRO:HD2	1.96	0.48
1:B:410:LEU:HD21	1:B:441:VAL:HA	1.96	0.47
1:B:682:LEU:HD13	1:B:787:VAL:HG11	1.96	0.47
1:B:913:LEU:HD13	1:B:918:ARG:HA	1.96	0.47
1:B:3365:UNK:O	1:B:3369:UNK:N	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4022:ASP:HA	1:B:4025:VAL:HG22	1.95	0.47
1:E:241:GLN:O	1:E:289:ARG:NH1	2.37	0.47
1:E:2342:ASN:N	1:E:2342:ASN:OD1	2.45	0.47
1:E:4200:THR:O	1:E:4204:GLN:N	2.37	0.47
1:I:23:GLN:OE1	1:I:203:ASN:ND2	2.46	0.47
1:I:4567:LEU:HD12	1:I:4816:ILE:HD12	1.96	0.47
1:I:4584:ASP:HA	1:I:4627:MET:HA	1.96	0.47
1:G:1679:ASN:HA	1:G:1682:ALA:HB3	1.94	0.47
1:G:2281:ILE:HA	1:G:2341:VAL:HG11	1.96	0.47
1:G:3829:PHE:HA	1:G:3832:ILE:HD12	1.96	0.47
1:G:4028:LEU:HD11	1:G:4142:ASN:HB3	1.96	0.47
1:G:4832:HIS:NE2	1:G:4942:GLU:OE1	2.46	0.47
1:B:72:SER:HB2	1:B:107:ILE:HG13	1.95	0.47
1:B:448:LEU:HA	1:B:451:TYR:HB3	1.94	0.47
1:B:619:ASP:OD1	1:B:1680:ARG:NH1	2.47	0.47
1:E:236:ALA:HA	1:E:242:ARG:HD2	1.95	0.47
1:E:736:HIS:HB2	2:F:7:ILE:HG23	1.95	0.47
1:E:1863:LEU:HB3	1:E:1870:VAL:HG11	1.95	0.47
1:I:3994:HIS:O	1:I:3998:HIS:ND1	2.42	0.47
1:G:57:ASN:HD22	1:G:308:HIS:HB2	1.79	0.47
1:G:451:TYR:O	1:G:474:ARG:NH1	2.44	0.47
1:G:583:ILE:HA	1:G:586:ILE:HD12	1.95	0.47
1:G:4180:ARG:O	1:G:4987:ASN:ND2	2.47	0.47
2:J:7:ILE:HG22	2:J:9:PRO:HD2	1.96	0.47
1:B:396:GLU:HG2	1:B:399:GLN:HB3	1.95	0.47
1:B:891:TRP:HA	1:B:902:ARG:HB3	1.96	0.47
1:B:4746:ALA:O	1:B:4750:ILE:N	2.42	0.47
1:B:4942:GLU:O	1:B:4946:GLN:N	2.47	0.47
1:E:583:ILE:HA	1:E:586:ILE:HD12	1.95	0.47
1:E:3840:SER:OG	1:E:3875:MET:O	2.27	0.47
1:I:15:ARG:HG2	1:I:100:THR:HA	1.96	0.47
1:I:236:ALA:HA	1:I:242:ARG:HD2	1.95	0.47
1:I:583:ILE:HA	1:I:586:ILE:HD12	1.95	0.47
1:I:1516:UNK:N	1:I:1529:UNK:O	2.46	0.47
1:I:4937:ILE:O	1:I:4941:GLY:N	2.41	0.47
1:G:4937:ILE:O	1:G:4941:GLY:N	2.41	0.47
2:A:39:SER:HB2	2:A:45:PRO:HA	1.96	0.47
1:B:23:GLN:OE1	1:B:203:ASN:ND2	2.46	0.47
1:B:3994:HIS:O	1:B:3998:HIS:ND1	2.43	0.47
1:B:4560:TYR:O	1:B:4564:PHE:N	2.44	0.47
1:E:2128:TYR:HB3	1:E:3669:PHE:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:2346:VAL:HG22	1:E:2348:GLU:H	1.78	0.47
1:I:1848:LEU:HB3	1:I:1853:ILE:HB	1.97	0.47
1:G:442:ILE:HG23	1:G:521:LEU:HD11	1.96	0.47
1:G:540:PHE:HD2	1:G:567:VAL:HG11	1.78	0.47
1:G:1867:GLU:HA	1:G:1870:VAL:HB	1.96	0.47
1:B:111:HIS:N	1:B:116:MET:O	2.46	0.47
1:B:350:HIS:N	1:B:355:LEU:O	2.48	0.47
1:B:360:ALA:N	1:B:375:LYS:O	2.38	0.47
1:B:1950:GLU:O	1:B:1954:ARG:N	2.45	0.47
1:E:410:LEU:HD21	1:E:441:VAL:HA	1.96	0.47
1:I:682:LEU:HD13	1:I:787:VAL:HG11	1.96	0.47
1:G:3889:GLN:OE1	1:G:3960:GLN:NE2	2.47	0.47
1:B:3889:GLN:OE1	1:B:3960:GLN:NE2	2.47	0.47
1:B:4204:GLN:NE2	1:B:4245:MET:SD	2.70	0.47
1:B:4236:SER:O	1:B:4240:ASP:N	2.43	0.47
1:B:4702:ASP:HA	1:B:4778:TRP:HE1	1.78	0.47
1:E:57:ASN:HD22	1:E:308:HIS:HB2	1.79	0.47
1:E:891:TRP:HA	1:E:902:ARG:HB3	1.97	0.47
1:E:2281:ILE:HA	1:E:2341:VAL:HG11	1.96	0.47
1:E:3676:ASP:OD1	1:E:3676:ASP:N	2.45	0.47
1:I:1032:LYS:O	1:I:1036:ARG:N	2.39	0.47
1:I:1950:GLU:O	1:I:1954:ARG:N	2.45	0.47
1:I:4702:ASP:HA	1:I:4778:TRP:HE1	1.78	0.47
1:G:342:GLY:HA2	1:G:389:PHE:HD2	1.80	0.47
1:G:410:LEU:HD21	1:G:441:VAL:HA	1.96	0.47
1:G:1671:ARG:HE	1:G:1713:ASP:HB3	1.79	0.47
1:G:4066:LEU:HA	1:G:4133:GLN:HE22	1.78	0.47
1:B:57:ASN:HD22	1:B:308:HIS:HB2	1.79	0.47
1:B:442:ILE:HG23	1:B:521:LEU:HD11	1.96	0.47
1:B:886:ARG:HB2	1:B:907:LEU:HD21	1.97	0.47
1:B:952:LYS:HB3	1:B:968:ALA:HB1	1.95	0.47
1:B:1093:GLU:OE1	1:B:1201:HIS:NE2	2.46	0.47
1:B:1848:LEU:HB3	1:B:1853:ILE:HB	1.97	0.47
1:B:2302:LEU:O	1:B:2306:GLY:N	2.46	0.47
1:B:3552:UNK:O	1:B:3556:UNK:N	2.48	0.47
1:B:4028:LEU:HD11	1:B:4142:ASN:HB3	1.96	0.47
1:E:442:ILE:HG23	1:E:521:LEU:HD11	1.96	0.47
1:E:886:ARG:HB2	1:E:907:LEU:HD21	1.97	0.47
1:E:911:HIS:O	1:E:918:ARG:NH2	2.45	0.47
1:E:983:THR:O	1:E:987:ARG:N	2.45	0.47
1:E:1516:UNK:N	1:E:1529:UNK:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:4066:LEU:HA	1:E:4133:GLN:HE22	1.78	0.47
1:E:4584:ASP:HA	1:E:4627:MET:HA	1.96	0.47
1:I:2116:LEU:O	1:I:2120:MET:N	2.43	0.47
1:I:2128:TYR:HB3	1:I:3669:PHE:HB3	1.95	0.47
1:I:3552:UNK:O	1:I:3556:UNK:N	2.48	0.47
1:I:3702:VAL:O	1:I:3706:SER:N	2.43	0.47
1:G:886:ARG:HB2	1:G:907:LEU:HD21	1.97	0.47
1:G:911:HIS:O	1:G:918:ARG:NH2	2.45	0.47
1:G:983:THR:O	1:G:987:ARG:N	2.45	0.47
1:G:1848:LEU:HB3	1:G:1853:ILE:HB	1.97	0.47
1:G:2176:ASN:O	1:G:2180:GLN:N	2.42	0.47
1:G:4584:ASP:HA	1:G:4627:MET:HA	1.96	0.47
1:B:709:ASP:HB3	1:B:725:HIS:CE1	2.50	0.47
1:B:4584:ASP:HA	1:B:4627:MET:HA	1.96	0.47
1:E:560:ILE:HA	1:E:563:VAL:HG12	1.97	0.47
1:E:4567:LEU:HD12	1:E:4816:ILE:HD12	1.96	0.47
1:I:342:GLY:HA2	1:I:389:PHE:HD2	1.80	0.47
1:I:1093:GLU:OE1	1:I:1201:HIS:NE2	2.46	0.47
1:G:560:ILE:HA	1:G:563:VAL:HG12	1.97	0.47
1:G:1154:ASP:O	1:G:1158:ASN:N	2.46	0.47
1:G:4763:GLY:O	1:G:4766:THR:OG1	2.24	0.47
2:H:69:GLY:N	2:H:103:LEU:O	2.47	0.47
1:E:1867:GLU:HA	1:E:1870:VAL:HB	1.96	0.47
1:E:2739:PRO:HB3	1:E:2884:ASN:HB3	1.97	0.47
1:E:3829:PHE:HA	1:E:3832:ILE:HD12	1.96	0.47
1:I:3829:PHE:HA	1:I:3832:ILE:HD12	1.96	0.47
1:I:4028:LEU:HD11	1:I:4142:ASN:HB3	1.96	0.47
1:G:2739:PRO:HB3	1:G:2884:ASN:HB3	1.97	0.47
1:G:3842:LEU:O	1:G:3929:SER:OG	2.30	0.47
1:G:4567:LEU:HD12	1:G:4816:ILE:HD12	1.96	0.47
2:H:39:SER:HB2	2:H:45:PRO:HA	1.96	0.47
1:B:342:GLY:HA2	1:B:389:PHE:HD2	1.80	0.47
1:B:1076:ARG:NH2	1:B:1107:PRO:O	2.40	0.47
1:E:709:ASP:HB3	1:E:725:HIS:CE1	2.50	0.47
1:E:1952:GLN:HA	1:E:1955:VAL:HG12	1.97	0.47
1:I:2420:HIS:ND1	1:I:2493:UNK:O	2.30	0.47
1:I:4236:SER:O	1:I:4240:ASP:N	2.43	0.47
1:G:876:GLU:O	1:G:880:GLU:N	2.42	0.47
1:G:952:LYS:HB3	1:G:968:ALA:HB1	1.95	0.47
1:G:1952:GLN:HA	1:G:1955:VAL:HG12	1.97	0.47
1:G:3781:GLN:HA	1:G:3784:SER:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:39:SER:HB2	2:F:45:PRO:HA	1.96	0.47
2:J:39:SER:HB2	2:J:45:PRO:HA	1.96	0.47
1:B:614:VAL:HG22	1:B:616:SER:H	1.80	0.46
1:B:1713:ASP:O	1:B:1717:SER:N	2.39	0.46
1:E:111:HIS:HD2	1:E:114:SER:H	1.62	0.46
1:E:342:GLY:HA2	1:E:389:PHE:HD2	1.80	0.46
1:E:4090:LYS:HD3	1:E:4112:LEU:HD13	1.96	0.46
1:I:895:PRO:HA	1:I:905:PRO:HB3	1.97	0.46
1:I:2281:ILE:HA	1:I:2341:VAL:HG11	1.96	0.46
1:I:4101:LYS:HG3	1:G:4731:ILE:HA	1.96	0.46
1:G:891:TRP:HA	1:G:902:ARG:HB3	1.96	0.46
1:G:913:LEU:HD13	1:G:918:ARG:HA	1.96	0.46
1:B:731:THR:OG1	1:B:1519:UNK:O	2.33	0.46
1:B:3829:PHE:HA	1:B:3832:ILE:HD12	1.96	0.46
1:E:895:PRO:HA	1:E:905:PRO:HB3	1.97	0.46
1:E:1770:SER:OG	1:E:1772:ARG:NE	2.46	0.46
1:I:886:ARG:HB2	1:I:907:LEU:HD21	1.97	0.46
1:I:2739:PRO:HB3	1:I:2884:ASN:HB3	1.97	0.46
1:G:4942:GLU:O	1:G:4946:GLN:N	2.47	0.46
1:B:2281:ILE:HA	1:B:2341:VAL:HG11	1.96	0.46
1:E:1089:TYR:N	1:E:1224:GLU:O	2.41	0.46
1:E:3986:TRP:NE1	1:E:4043:GLN:OE1	2.48	0.46
1:E:4560:TYR:O	1:E:4564:PHE:N	2.44	0.46
1:I:709:ASP:HB3	1:I:725:HIS:CE1	2.50	0.46
1:I:3781:GLN:HA	1:I:3784:SER:HB3	1.97	0.46
1:I:3891:LEU:HB3	1:I:3899:PHE:CE2	2.51	0.46
1:G:709:ASP:HB3	1:G:725:HIS:CE1	2.50	0.46
1:G:3986:TRP:NE1	1:G:4043:GLN:OE1	2.48	0.46
1:B:1211:LEU:HD11	1:B:1225:PRO:HB3	1.97	0.46
1:B:1867:GLU:HA	1:B:1870:VAL:HB	1.96	0.46
1:E:55:ALA:O	1:E:281:ARG:NH1	2.35	0.46
1:E:1093:GLU:OE1	1:E:1201:HIS:NE2	2.46	0.46
1:E:1211:LEU:HD11	1:E:1225:PRO:HB3	1.97	0.46
1:E:2432:LEU:O	1:E:2436:CYS:N	2.46	0.46
1:I:350:HIS:N	1:I:355:LEU:O	2.48	0.46
1:I:356:TRP:O	1:I:379:HIS:N	2.43	0.46
1:I:451:TYR:O	1:I:474:ARG:NH1	2.44	0.46
1:I:891:TRP:HA	1:I:902:ARG:HB3	1.97	0.46
1:I:983:THR:O	1:I:987:ARG:N	2.45	0.46
1:I:1090:PHE:HD2	1:I:1202:LEU:HD11	1.81	0.46
1:I:3770:LEU:HD13	1:I:3770:LEU:HA	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:356:TRP:O	1:G:379:HIS:N	2.43	0.46
1:G:1284:UNK:HA	1:G:1463:UNK:HA	1.98	0.46
1:G:4204:GLN:NE2	1:G:4245:MET:SD	2.70	0.46
2:F:59:PHE:HD1	2:F:74:LEU:HD11	1.81	0.46
1:B:497:TYR:HB3	1:B:500:ALA:HB2	1.98	0.46
1:B:895:PRO:HA	1:B:905:PRO:HB3	1.98	0.46
1:B:3986:TRP:NE1	1:B:4043:GLN:OE1	2.48	0.46
1:B:4090:LYS:HD3	1:B:4112:LEU:HD13	1.96	0.46
1:E:1848:LEU:HB3	1:E:1853:ILE:HB	1.97	0.46
1:E:3645:PRO:O	1:E:3649:ALA:N	2.46	0.46
1:E:3994:HIS:O	1:E:3998:HIS:ND1	2.42	0.46
1:I:1211:LEU:HD11	1:I:1225:PRO:HB3	1.97	0.46
1:I:1867:GLU:HA	1:I:1870:VAL:HB	1.96	0.46
1:I:2440:MET:O	1:I:2444:GLN:N	2.39	0.46
1:G:682:LEU:HD13	1:G:787:VAL:HG11	1.96	0.46
1:G:1090:PHE:HD2	1:G:1202:LEU:HD11	1.81	0.46
1:G:3891:LEU:HB3	1:G:3899:PHE:CE2	2.51	0.46
1:B:25:SER:HA	1:B:34:LYS:HA	1.98	0.46
1:B:179:TYR:OH	1:E:2359:ARG:NH1	2.49	0.46
1:E:485:SER:HA	1:E:488:LEU:HB2	1.98	0.46
1:E:1271:ARG:HA	1:E:1471:UNK:HA	1.97	0.46
1:E:3945:GLU:O	1:E:3949:ARG:N	2.45	0.46
1:I:3658:LYS:HA	1:I:3661:TRP:CD2	2.51	0.46
1:I:3986:TRP:NE1	1:I:4043:GLN:OE1	2.48	0.46
1:G:113:HIS:CE1	1:G:399:GLN:HA	2.51	0.46
1:G:617:ASN:HA	1:G:620:LEU:HB2	1.98	0.46
1:G:2880:GLU:O	1:G:2884:ASN:N	2.42	0.46
1:G:4060:LYS:HE3	1:G:4064:MET:HB2	1.97	0.46
1:G:4090:LYS:HD3	1:G:4112:LEU:HD13	1.96	0.46
1:B:3702:VAL:O	1:B:3706:SER:N	2.43	0.46
1:E:614:VAL:HG22	1:E:616:SER:H	1.80	0.46
1:E:617:ASN:HA	1:E:620:LEU:HB2	1.98	0.46
1:E:4041:ALA:HA	1:E:4044:MET:HB2	1.98	0.46
1:I:497:TYR:HB3	1:I:500:ALA:HB2	1.98	0.46
1:G:1211:LEU:HD11	1:G:1225:PRO:HB3	1.97	0.46
1:G:3552:UNK:O	1:G:3556:UNK:N	2.48	0.46
2:H:59:PHE:HD1	2:H:74:LEU:HD11	1.81	0.46
1:B:224:HIS:N	1:B:229:GLU:O	2.42	0.46
1:B:3891:LEU:HB3	1:B:3899:PHE:CE2	2.51	0.46
1:E:913:LEU:HD13	1:E:918:ARG:HA	1.96	0.46
1:E:3781:GLN:HA	1:E:3784:SER:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:25:SER:HA	1:I:34:LYS:HA	1.98	0.46
1:I:113:HIS:CE1	1:I:399:GLN:HA	2.51	0.46
1:I:485:SER:HA	1:I:488:LEU:HB2	1.98	0.46
1:I:1154:ASP:O	1:I:1158:ASN:N	2.46	0.46
1:I:1284:UNK:HA	1:I:1463:UNK:HA	1.98	0.46
1:B:485:SER:HA	1:B:488:LEU:HB2	1.98	0.46
1:B:1952:GLN:HA	1:B:1955:VAL:HG12	1.97	0.46
1:B:2297:LYS:O	1:B:2301:TYR:N	2.44	0.46
1:B:4060:LYS:HE3	1:B:4064:MET:HB2	1.97	0.46
1:E:451:TYR:O	1:E:474:ARG:NH1	2.44	0.46
1:E:633:LEU:HB3	1:E:1639:LEU:HD22	1.98	0.46
1:E:4942:GLU:O	1:E:4946:GLN:N	2.47	0.46
1:I:218:HIS:HB3	1:I:392:ARG:HD3	1.98	0.46
1:I:1952:GLN:HA	1:I:1955:VAL:HG12	1.97	0.46
1:I:4060:LYS:HE3	1:I:4064:MET:HB2	1.97	0.46
1:I:4864:ASN:H	1:I:4874:MET:HG2	1.81	0.46
1:G:1269:CYS:HA	1:G:1473:UNK:HA	1.98	0.46
1:B:560:ILE:HA	1:B:563:VAL:HG12	1.97	0.46
1:B:876:GLU:O	1:B:880:GLU:N	2.42	0.46
1:B:2739:PRO:HB3	1:B:2884:ASN:HB3	1.97	0.46
1:B:3781:GLN:HA	1:B:3784:SER:HB3	1.97	0.46
1:E:1721:GLU:OE2	1:E:1725:ARG:NH2	2.39	0.46
1:E:2297:LYS:O	1:E:2301:TYR:N	2.44	0.46
1:E:3552:UNK:O	1:E:3556:UNK:N	2.49	0.46
1:E:3889:GLN:OE1	1:E:3960:GLN:NE2	2.47	0.46
1:I:633:LEU:HB3	1:I:1639:LEU:HD22	1.98	0.46
1:I:913:LEU:HD13	1:I:918:ARG:HA	1.96	0.46
1:I:2212:VAL:O	1:I:2216:GLY:N	2.44	0.46
1:I:5012:LYS:O	1:I:5016:GLU:N	2.42	0.46
1:G:218:HIS:HB3	1:G:392:ARG:HD3	1.98	0.46
1:G:360:ALA:N	1:G:375:LYS:O	2.38	0.46
1:G:2155:LEU:HD21	1:G:2188:ASN:HD22	1.81	0.46
1:G:4041:ALA:HA	1:G:4044:MET:HB2	1.98	0.46
1:G:4864:ASN:H	1:G:4874:MET:HG2	1.81	0.46
2:A:59:PHE:HD1	2:A:74:LEU:HD11	1.81	0.46
1:B:3658:LYS:HA	1:B:3661:TRP:CD2	2.51	0.45
1:E:2176:ASN:O	1:E:2180:GLN:N	2.42	0.45
1:E:2764:GLU:HG3	1:E:2857:PRO:HB2	1.98	0.45
1:E:2878:LEU:HD13	1:E:2926:LEU:HD23	1.98	0.45
1:I:2327:GLY:HA2	1:I:2330:ARG:HD3	1.98	0.45
1:I:2451:LEU:O	1:I:2455:ALA:N	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:3461:UNK:O	1:G:3465:UNK:N	2.49	0.45
1:G:4937:ILE:HA	1:G:4940:PHE:HD2	1.81	0.45
2:J:59:PHE:HD1	2:J:74:LEU:HD11	1.81	0.45
1:B:134:ASP:HA	1:B:192:ASP:HA	1.98	0.45
1:B:2102:VAL:HB	1:B:2124:LEU:HD12	1.99	0.45
1:B:2420:HIS:ND1	1:B:2493:UNK:O	2.30	0.45
1:E:25:SER:HA	1:E:34:LYS:HA	1.98	0.45
1:E:111:HIS:N	1:E:116:MET:O	2.46	0.45
1:E:682:LEU:HD13	1:E:787:VAL:HG11	1.96	0.45
1:E:1243:PRO:HB2	1:E:1600:LEU:HD13	1.98	0.45
1:E:1965:TYR:HE1	1:E:2027:ILE:HB	1.82	0.45
1:E:3730:ALA:O	1:E:3734:HIS:N	2.50	0.45
1:I:55:ALA:O	1:I:281:ARG:NH1	2.35	0.45
1:I:560:ILE:HA	1:I:563:VAL:HG12	1.97	0.45
1:I:614:VAL:HG22	1:I:616:SER:H	1.80	0.45
1:I:617:ASN:HA	1:I:620:LEU:HB2	1.98	0.45
1:I:4090:LYS:HD3	1:I:4112:LEU:HD13	1.96	0.45
1:G:134:ASP:HA	1:G:192:ASP:HA	1.98	0.45
1:G:485:SER:HA	1:G:488:LEU:HB2	1.98	0.45
1:G:664:PHE:HB2	1:G:746:CYS:HB2	1.98	0.45
1:G:895:PRO:HA	1:G:905:PRO:HB3	1.97	0.45
1:G:1095:VAL:HB	1:G:1199:VAL:HG23	1.98	0.45
1:G:1456:UNK:HA	1:G:1498:UNK:HA	1.98	0.45
1:G:2121:PHE:O	1:G:3725:TYR:OH	2.33	0.45
1:G:2327:GLY:HA2	1:G:2330:ARG:HD3	1.98	0.45
1:G:4006:ASP:HB3	1:G:4009:GLN:HB2	1.98	0.45
1:G:4200:THR:O	1:G:4204:GLN:N	2.37	0.45
1:B:2384:ILE:O	1:B:2388:GLU:N	2.49	0.45
1:B:2878:LEU:HD13	1:B:2926:LEU:HD23	1.98	0.45
1:E:1076:ARG:NH2	1:E:1107:PRO:O	2.40	0.45
1:E:3658:LYS:HA	1:E:3661:TRP:CD2	2.51	0.45
1:E:3885:PHE:HA	1:E:3888:LEU:HB2	1.98	0.45
1:E:4236:SER:O	1:E:4240:ASP:N	2.43	0.45
1:I:793:LEU:HD12	1:I:797:HIS:HB2	1.99	0.45
1:I:2878:LEU:HD13	1:I:2926:LEU:HD23	1.98	0.45
1:G:790:ARG:HG2	1:G:1627:ALA:HA	1.98	0.45
1:G:4561:THR:O	1:G:4565:LEU:N	2.50	0.45
1:B:633:LEU:HB3	1:B:1639:LEU:HD22	1.98	0.45
1:B:1716:ILE:HD11	1:B:1844:LEU:HD13	1.99	0.45
1:B:2155:LEU:HD21	1:B:2188:ASN:HD22	1.81	0.45
1:B:4041:ALA:HA	1:B:4044:MET:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4702:ASP:OD1	1:B:4778:TRP:NE1	2.44	0.45
1:B:4864:ASN:H	1:B:4874:MET:HG2	1.81	0.45
1:E:113:HIS:CE1	1:E:399:GLN:HA	2.51	0.45
1:E:790:ARG:HG2	1:E:1627:ALA:HA	1.99	0.45
1:E:4006:ASP:HB3	1:E:4009:GLN:HB2	1.98	0.45
1:E:4060:LYS:HE3	1:E:4064:MET:HB2	1.97	0.45
1:I:1076:ARG:NH2	1:I:1107:PRO:O	2.40	0.45
1:I:2102:VAL:HB	1:I:2124:LEU:HD12	1.99	0.45
1:I:4745:LEU:O	1:I:4749:GLU:N	2.50	0.45
1:I:4937:ILE:HA	1:I:4940:PHE:HD2	1.81	0.45
1:G:25:SER:HA	1:G:34:LYS:HA	1.98	0.45
1:G:633:LEU:HB3	1:G:1639:LEU:HD22	1.98	0.45
1:G:2517:UNK:O	1:G:2521:UNK:N	2.50	0.45
1:G:4107:GLU:O	1:G:4111:LEU:N	2.40	0.45
1:B:2451:LEU:O	1:B:2455:ALA:N	2.42	0.45
1:E:1284:UNK:HA	1:E:1463:UNK:HA	1.98	0.45
1:E:4215:ARG:HA	1:E:4218:ILE:HD12	1.99	0.45
1:I:3959:LYS:O	1:I:3963:ASN:N	2.48	0.45
1:B:1090:PHE:HD2	1:B:1202:LEU:HD11	1.81	0.45
1:B:1965:TYR:HE1	1:B:2027:ILE:HB	1.82	0.45
1:B:2764:GLU:HG3	1:B:2857:PRO:HB2	1.98	0.45
1:B:4200:THR:O	1:B:4204:GLN:N	2.37	0.45
1:B:4243:PHE:HE2	1:B:4668:LEU:HA	1.82	0.45
1:E:1090:PHE:HD2	1:E:1202:LEU:HD11	1.81	0.45
1:E:1095:VAL:HB	1:E:1199:VAL:HG23	1.98	0.45
1:E:2880:GLU:O	1:E:2884:ASN:N	2.42	0.45
1:E:3891:LEU:HB3	1:E:3899:PHE:HE2	1.81	0.45
1:I:870:ILE:HA	1:I:870:ILE:HD12	1.79	0.45
1:I:4561:THR:O	1:I:4565:LEU:N	2.50	0.45
1:G:317:ARG:N	1:G:347:PHE:O	2.48	0.45
1:G:1721:GLU:OE2	1:G:1725:ARG:NH2	2.39	0.45
1:G:3658:LYS:HA	1:G:3661:TRP:CD2	2.51	0.45
1:G:4215:ARG:HA	1:G:4218:ILE:HD12	1.99	0.45
1:E:497:TYR:HB3	1:E:500:ALA:HB2	1.98	0.45
1:E:4232:GLU:OE2	1:E:5017:ARG:NH1	2.50	0.45
1:E:4864:ASN:H	1:E:4874:MET:HG2	1.81	0.45
1:I:3885:PHE:HA	1:I:3888:LEU:HB2	1.98	0.45
1:G:242:ARG:NH1	1:G:481:GLU:OE1	2.44	0.45
1:B:664:PHE:HB2	1:B:746:CYS:HB2	1.98	0.45
1:B:1284:UNK:HA	1:B:1463:UNK:HA	1.98	0.45
1:E:218:HIS:HB3	1:E:392:ARG:HD3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:2517:UNK:O	1:E:2521:UNK:N	2.50	0.45
1:I:111:HIS:N	1:I:116:MET:O	2.46	0.45
1:I:134:ASP:HA	1:I:192:ASP:HA	1.98	0.45
1:I:1965:TYR:HE1	1:I:2027:ILE:HB	1.82	0.45
1:G:2775:TRP:HZ3	1:G:2783:GLU:HA	1.82	0.45
1:G:2813:LEU:HD21	1:G:2926:LEU:HD11	1.99	0.45
2:A:69:GLY:N	2:A:103:LEU:O	2.48	0.45
1:B:113:HIS:CE1	1:B:399:GLN:HA	2.51	0.45
1:B:264:PRO:HG2	1:B:270:SER:HB2	1.99	0.45
1:B:617:ASN:HA	1:B:620:LEU:HB2	1.98	0.45
1:B:790:ARG:HG2	1:B:1627:ALA:HA	1.99	0.45
1:B:4147:LEU:HD23	1:B:4150:LEU:HD12	1.99	0.45
1:E:134:ASP:HA	1:E:192:ASP:HA	1.98	0.45
1:E:1716:ILE:HD11	1:E:1844:LEU:HD13	1.99	0.45
1:E:2775:TRP:HZ3	1:E:2783:GLU:HA	1.82	0.45
1:E:2813:LEU:HD21	1:E:2926:LEU:HD11	1.99	0.45
1:I:1290:UNK:HA	1:I:1598:GLN:HE22	1.81	0.45
1:I:2236:LEU:HD23	1:I:2275:VAL:HG21	1.98	0.45
1:I:2813:LEU:HD21	1:I:2926:LEU:HD11	1.99	0.45
1:I:3713:LYS:HG2	1:I:3715:LYS:H	1.82	0.45
1:G:1046:LEU:HD12	1:G:1053:ILE:HD11	1.99	0.45
1:G:2039:LEU:HA	1:G:2042:CYS:HB3	1.99	0.45
1:G:2212:VAL:O	1:G:2216:GLY:N	2.44	0.45
1:G:4147:LEU:HD23	1:G:4150:LEU:HD12	1.99	0.45
1:B:243:ARG:NH2	1:B:303:ASP:OD1	2.29	0.45
1:B:1243:PRO:HB2	1:B:1600:LEU:HD13	1.98	0.45
1:B:3730:ALA:O	1:B:3734:HIS:N	2.50	0.45
1:B:4215:ARG:HA	1:B:4218:ILE:HD12	1.99	0.45
1:E:1269:CYS:HA	1:E:1473:UNK:HA	1.97	0.45
1:E:3770:LEU:HD13	1:E:3770:LEU:HA	1.81	0.45
1:E:4745:LEU:O	1:E:4749:GLU:N	2.50	0.45
1:I:1978:ALA:O	1:I:1983:ALA:N	2.40	0.45
1:I:2384:ILE:O	1:I:2388:GLU:N	2.49	0.45
1:I:2517:UNK:O	1:I:2521:UNK:N	2.50	0.45
1:G:1258:ALA:HB3	1:G:1271:ARG:HB3	1.99	0.45
1:G:1653:LEU:HB3	1:G:1660:GLN:HB2	1.99	0.45
1:G:3663:LEU:H	1:G:3663:LEU:HG	1.57	0.45
1:G:3713:LYS:HG2	1:G:3715:LYS:H	1.82	0.45
1:G:3730:ALA:O	1:G:3734:HIS:N	2.50	0.45
1:B:2236:LEU:HD23	1:B:2275:VAL:HG21	1.99	0.44
1:B:2247:GLN:O	1:B:2279:SER:OG	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3770:LEU:HD13	1:B:3770:LEU:HA	1.81	0.44
1:B:4568:PHE:HA	1:B:4571:PHE:HD2	1.83	0.44
1:E:2102:VAL:HB	1:E:2124:LEU:HD12	1.99	0.44
1:E:2155:LEU:HD21	1:E:2188:ASN:HD22	1.81	0.44
1:E:3891:LEU:HB3	1:E:3899:PHE:CE2	2.51	0.44
1:E:4568:PHE:HA	1:E:4571:PHE:HD2	1.83	0.44
1:E:4937:ILE:HA	1:E:4940:PHE:HD2	1.81	0.44
1:I:264:PRO:HG2	1:I:270:SER:HB2	1.99	0.44
1:I:664:PHE:HB2	1:I:746:CYS:HB2	1.98	0.44
1:I:1258:ALA:HB3	1:I:1271:ARG:HB3	1.99	0.44
1:I:2155:LEU:HD21	1:I:2188:ASN:HD22	1.81	0.44
1:I:4041:ALA:HA	1:I:4044:MET:HB2	1.98	0.44
1:I:4147:LEU:HD23	1:I:4150:LEU:HD12	1.99	0.44
1:I:4204:GLN:NE2	1:I:4245:MET:SD	2.70	0.44
1:I:4215:ARG:HA	1:I:4218:ILE:HD12	1.99	0.44
1:G:243:ARG:NH2	1:G:303:ASP:OD1	2.29	0.44
1:G:350:HIS:N	1:G:355:LEU:O	2.48	0.44
1:G:793:LEU:HD12	1:G:797:HIS:HB2	1.99	0.44
1:G:2764:GLU:HG3	1:G:2857:PRO:HB2	1.98	0.44
2:F:69:GLY:HA2	2:F:104:LEU:HD23	1.99	0.44
1:B:218:HIS:HB3	1:B:392:ARG:HD3	1.99	0.44
1:B:2039:LEU:HA	1:B:2042:CYS:HB3	1.99	0.44
1:B:2212:VAL:O	1:B:2216:GLY:N	2.44	0.44
1:B:2813:LEU:HD21	1:B:2926:LEU:HD11	1.99	0.44
1:B:4745:LEU:O	1:B:4749:GLU:N	2.50	0.44
1:E:2327:GLY:HA2	1:E:2330:ARG:HD3	1.98	0.44
1:E:2466:LEU:HA	1:E:2469:ILE:HD12	2.00	0.44
1:E:3713:LYS:HG2	1:E:3715:LYS:H	1.82	0.44
1:E:4147:LEU:HD23	1:E:4150:LEU:HD12	1.99	0.44
1:E:4243:PHE:HE2	1:E:4668:LEU:HA	1.82	0.44
1:E:4687:TYR:HE1	1:E:4703:ARG:HG2	1.82	0.44
1:I:2039:LEU:HA	1:I:2042:CYS:HB3	1.99	0.44
1:I:2121:PHE:O	1:I:3725:TYR:OH	2.33	0.44
1:I:2764:GLU:HG3	1:I:2857:PRO:HB2	1.97	0.44
1:I:4006:ASP:HB3	1:I:4009:GLN:HB2	1.98	0.44
1:I:4243:PHE:HE2	1:I:4668:LEU:HA	1.82	0.44
1:G:497:TYR:HB3	1:G:500:ALA:HB2	1.98	0.44
1:G:614:VAL:HG22	1:G:616:SER:H	1.80	0.44
1:G:1243:PRO:HB2	1:G:1600:LEU:HD13	1.98	0.44
1:G:4243:PHE:HE2	1:G:4668:LEU:HA	1.82	0.44
1:B:241:GLN:O	1:B:289:ARG:NH1	2.37	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1685:LEU:HD22	1:B:1718:ILE:HD13	1.99	0.44
1:B:2327:GLY:HA2	1:B:2330:ARG:HD3	1.98	0.44
1:B:4006:ASP:HB3	1:B:4009:GLN:HB2	1.98	0.44
1:E:664:PHE:HB2	1:E:746:CYS:HB2	1.98	0.44
1:E:731:THR:OG1	1:E:1519:UNK:O	2.26	0.44
1:E:1258:ALA:HB3	1:E:1271:ARG:HB3	1.99	0.44
1:E:2236:LEU:HD23	1:E:2275:VAL:HG21	1.98	0.44
1:E:3930:ILE:HG23	1:E:3951:PHE:HE1	1.83	0.44
1:I:1095:VAL:HB	1:I:1199:VAL:HG23	1.98	0.44
1:I:2466:LEU:HA	1:I:2469:ILE:HD12	2.00	0.44
1:G:2878:LEU:HD13	1:G:2926:LEU:HD23	1.98	0.44
1:G:4702:ASP:OD1	1:G:4778:TRP:NE1	2.44	0.44
1:B:1258:ALA:HB3	1:B:1271:ARG:HB3	1.99	0.44
1:B:1721:GLU:OE2	1:B:1725:ARG:NH2	2.39	0.44
1:B:4687:TYR:HE1	1:B:4703:ARG:HG2	1.82	0.44
1:B:4837:LEU:O	1:B:4840:THR:OG1	2.31	0.44
1:E:356:TRP:O	1:E:379:HIS:N	2.43	0.44
1:I:317:ARG:N	1:I:347:PHE:O	2.48	0.44
1:I:3730:ALA:O	1:I:3734:HIS:N	2.50	0.44
1:I:4155:PRO:HB2	1:I:4156:HIS:CD2	2.53	0.44
1:I:4560:TYR:O	1:I:4564:PHE:N	2.44	0.44
1:B:793:LEU:HD12	1:B:797:HIS:HB2	1.99	0.44
1:B:2274:ASP:O	1:B:2278:ALA:N	2.50	0.44
1:B:4114:CYS:HB3	1:B:4131:ARG:HH22	1.82	0.44
1:B:4155:PRO:HB2	1:B:4156:HIS:CD2	2.53	0.44
1:B:4232:GLU:OE2	1:B:5017:ARG:NH1	2.50	0.44
1:B:5018:CYS:SG	1:B:5019:TRP:N	2.91	0.44
1:E:876:GLU:O	1:E:880:GLU:N	2.42	0.44
1:E:1838:PHE:HB3	1:E:1842:LEU:HD11	2.00	0.44
1:E:2451:LEU:O	1:E:2455:ALA:N	2.42	0.44
1:I:790:ARG:HG2	1:I:1627:ALA:HA	1.99	0.44
1:I:1269:CYS:HA	1:I:1473:UNK:HA	1.99	0.44
1:I:1970:GLN:HB2	1:I:3642:TYR:HA	2.00	0.44
1:I:5018:CYS:SG	1:I:5019:TRP:N	2.91	0.44
1:G:2102:VAL:HB	1:G:2124:LEU:HD12	1.98	0.44
1:G:2466:LEU:HA	1:G:2469:ILE:HD12	2.00	0.44
1:G:3885:PHE:HA	1:G:3888:LEU:HB2	1.98	0.44
1:G:4745:LEU:O	1:G:4749:GLU:N	2.50	0.44
1:G:5018:CYS:SG	1:G:5019:TRP:N	2.91	0.44
2:A:69:GLY:HA2	2:A:104:LEU:HD23	1.99	0.44
1:B:4987:ASN:HA	1:B:4990:PHE:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1685:LEU:HD22	1:E:1718:ILE:HD13	1.99	0.44
1:E:1973:GLN:HA	1:E:1976:ARG:HB3	2.00	0.44
1:E:2039:LEU:HA	1:E:2042:CYS:HB3	1.99	0.44
1:E:5018:CYS:SG	1:E:5019:TRP:N	2.91	0.44
1:I:876:GLU:O	1:I:880:GLU:N	2.42	0.44
1:I:1046:LEU:HD12	1:I:1053:ILE:HD11	1.99	0.44
1:I:1716:ILE:HD11	1:I:1844:LEU:HD13	1.99	0.44
1:I:2274:ASP:O	1:I:2278:ALA:N	2.50	0.44
1:I:2793:PRO:HG3	1:I:2855:TYR:CZ	2.53	0.44
1:G:1838:PHE:HB3	1:G:1842:LEU:HD11	2.00	0.44
1:G:2006:ILE:O	1:G:2010:LEU:N	2.43	0.44
1:G:2236:LEU:HD23	1:G:2275:VAL:HG21	1.98	0.44
1:G:2793:PRO:HG3	1:G:2855:TYR:CZ	2.53	0.44
1:G:4568:PHE:HA	1:G:4571:PHE:HD2	1.82	0.44
1:B:1046:LEU:HD12	1:B:1053:ILE:HD11	1.99	0.44
1:B:1838:PHE:HB3	1:B:1842:LEU:HD11	2.00	0.44
1:E:793:LEU:HD12	1:E:797:HIS:HB2	1.99	0.44
1:E:2212:VAL:O	1:E:2216:GLY:N	2.44	0.44
1:E:4108:ILE:HA	1:E:4111:LEU:HD12	1.99	0.44
1:I:224:HIS:N	1:I:229:GLU:O	2.42	0.44
1:I:733:PRO:HD2	1:I:763:PRO:HD2	2.00	0.44
1:I:3930:ILE:HG23	1:I:3951:PHE:HE1	1.83	0.44
1:G:1293:UNK:N	1:G:1456:UNK:O	2.50	0.44
1:G:3960:GLN:HA	1:G:3963:ASN:HD22	1.83	0.44
2:J:29:MET:HB3	2:J:98:ILE:HB	2.00	0.44
1:B:685:GLY:N	1:B:780:VAL:O	2.35	0.44
1:B:1095:VAL:HB	1:B:1199:VAL:HG23	1.99	0.44
1:B:2517:UNK:O	1:B:2521:UNK:N	2.51	0.44
1:B:2760:GLU:O	1:B:2764:GLU:N	2.48	0.44
1:B:2788:HIS:CE1	1:B:2790:MET:HB2	2.53	0.44
1:B:3885:PHE:HA	1:B:3888:LEU:HB2	1.99	0.44
1:B:4657:CYS:O	1:B:4661:TYR:N	2.49	0.44
1:E:2793:PRO:HG3	1:E:2855:TYR:CZ	2.53	0.44
1:E:3461:UNK:O	1:E:3465:UNK:N	2.51	0.44
1:E:4155:PRO:HB2	1:E:4156:HIS:CD2	2.53	0.44
1:I:2788:HIS:CE1	1:I:2790:MET:HB2	2.53	0.44
1:G:4108:ILE:HA	1:G:4111:LEU:HD12	1.99	0.44
1:G:4232:GLU:OE2	1:G:5017:ARG:NH1	2.50	0.44
1:G:4687:TYR:HE1	1:G:4703:ARG:HG2	1.82	0.44
1:B:733:PRO:HD2	1:B:763:PRO:HD2	2.00	0.44
1:B:1653:LEU:HB3	1:B:1660:GLN:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1704:PRO:HG2	1:B:1707:LEU:HB2	2.00	0.44
1:B:1970:GLN:HB2	1:B:3642:TYR:HA	2.00	0.44
1:B:1973:GLN:HA	1:B:1976:ARG:HB3	2.00	0.44
1:B:2452:ARG:NH1	1:I:175:SER:O	2.45	0.44
1:B:2466:LEU:HA	1:B:2469:ILE:HD12	2.00	0.44
1:B:3891:LEU:HB3	1:B:3899:PHE:HE2	1.82	0.44
1:E:1735:ILE:HG23	1:E:1771:LEU:HD23	2.00	0.44
1:E:4987:ASN:HA	1:E:4990:PHE:HB2	2.00	0.44
1:I:1653:LEU:HB3	1:I:1660:GLN:HB2	1.99	0.44
1:I:1973:GLN:HA	1:I:1976:ARG:HB3	2.00	0.44
1:I:4687:TYR:HE1	1:I:4703:ARG:HG2	1.82	0.44
1:G:45:ARG:HD2	1:G:138:GLN:HB2	2.00	0.44
1:G:1023:PRO:O	1:G:1027:LEU:N	2.51	0.44
1:G:1965:TYR:HE1	1:G:2027:ILE:HB	1.82	0.44
1:G:1973:GLN:HA	1:G:1976:ARG:HB3	2.00	0.44
1:B:1234:VAL:HG12	1:B:1236:THR:H	1.83	0.43
1:E:4561:THR:O	1:E:4565:LEU:N	2.50	0.43
1:I:1234:VAL:HG12	1:I:1236:THR:H	1.83	0.43
1:I:1293:UNK:N	1:I:1456:UNK:O	2.50	0.43
1:I:3361:UNK:O	1:I:3365:UNK:N	2.51	0.43
1:I:3461:UNK:O	1:I:3465:UNK:N	2.51	0.43
1:I:3891:LEU:HB3	1:I:3899:PHE:HE2	1.81	0.43
1:I:4114:CYS:HB3	1:I:4131:ARG:HH22	1.82	0.43
1:G:264:PRO:HG2	1:G:270:SER:HB2	1.99	0.43
1:G:668:VAL:O	1:G:741:GLU:N	2.50	0.43
1:G:1716:ILE:HD11	1:G:1844:LEU:HD13	1.99	0.43
1:G:2788:HIS:CE1	1:G:2790:MET:HB2	2.53	0.43
1:G:3891:LEU:HB3	1:G:3899:PHE:HE2	1.82	0.43
1:G:3994:HIS:O	1:G:3998:HIS:ND1	2.42	0.43
1:G:4987:ASN:HA	1:G:4990:PHE:HB2	2.00	0.43
2:J:7:ILE:N	2:J:71:ARG:O	2.47	0.43
2:J:69:GLY:N	2:J:103:LEU:O	2.48	0.43
1:B:1082:THR:HG21	1:B:1107:PRO:HG3	1.99	0.43
1:B:1735:ILE:HG23	1:B:1771:LEU:HD23	2.01	0.43
1:B:2765:LYS:HA	1:B:2859:PRO:HG3	2.00	0.43
1:B:3713:LYS:HG2	1:B:3715:LYS:H	1.82	0.43
1:B:4101:LYS:HG3	1:I:4731:ILE:HA	2.00	0.43
1:E:2247:GLN:O	1:E:2279:SER:OG	2.35	0.43
1:E:4114:CYS:HB3	1:E:4131:ARG:HH22	1.82	0.43
1:E:4187:SER:OG	1:E:4191:GLU:OE2	2.36	0.43
1:I:242:ARG:NH1	1:I:481:GLU:OE1	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:1023:PRO:O	1:I:1027:LEU:N	2.51	0.43
1:I:1704:PRO:HG2	1:I:1707:LEU:HB2	2.00	0.43
1:I:2247:GLN:O	1:I:2279:SER:OG	2.35	0.43
1:I:2775:TRP:HZ3	1:I:2783:GLU:HA	1.82	0.43
1:I:3645:PRO:O	1:I:3649:ALA:N	2.46	0.43
1:I:3960:GLN:HA	1:I:3963:ASN:HD22	1.83	0.43
1:I:4201:ASN:ND2	1:I:4993:MET:SD	2.92	0.43
1:I:4568:PHE:HA	1:I:4571:PHE:HD2	1.83	0.43
1:G:2247:GLN:O	1:G:2279:SER:OG	2.35	0.43
1:G:3930:ILE:HG23	1:G:3951:PHE:HE1	1.83	0.43
1:G:4142:ASN:HA	1:G:4145:VAL:HG12	2.01	0.43
1:G:4187:SER:OG	1:G:4191:GLU:OE2	2.36	0.43
1:B:345:LEU:HD23	1:B:389:PHE:HB3	2.01	0.43
1:B:894:GLY:HA3	1:B:903:LEU:HD22	2.00	0.43
1:B:4108:ILE:HA	1:B:4111:LEU:HD12	1.99	0.43
1:B:4142:ASN:HA	1:B:4145:VAL:HG12	2.01	0.43
1:E:264:PRO:HG2	1:E:270:SER:HB2	1.99	0.43
1:E:2121:PHE:O	1:E:3725:TYR:OH	2.33	0.43
1:E:2440:MET:O	1:E:2444:GLN:N	2.40	0.43
1:E:2869:ARG:HA	1:E:2872:GLN:HB3	2.01	0.43
1:I:45:ARG:HD2	1:I:138:GLN:HB2	2.00	0.43
1:I:1838:PHE:HB3	1:I:1842:LEU:HD11	2.00	0.43
1:G:950:LEU:HD22	1:G:970:LEU:HB3	2.00	0.43
1:G:1970:GLN:HB2	1:G:3642:TYR:HA	2.00	0.43
1:G:2384:ILE:O	1:G:2388:GLU:N	2.49	0.43
2:F:29:MET:HB3	2:F:98:ILE:HB	2.00	0.43
1:B:356:TRP:O	1:B:379:HIS:N	2.43	0.43
1:B:1023:PRO:O	1:B:1027:LEU:N	2.51	0.43
1:B:2332:LEU:HA	1:B:2335:LEU:HB2	2.00	0.43
1:B:4930:ALA:O	1:B:4934:GLY:N	2.48	0.43
1:E:1970:GLN:HB2	1:E:3642:TYR:HA	2.00	0.43
1:E:4763:GLY:O	1:E:4766:THR:OG1	2.25	0.43
1:I:4987:ASN:HA	1:I:4990:PHE:HB2	2.00	0.43
1:G:1082:THR:HG21	1:G:1107:PRO:HG3	1.99	0.43
1:G:1685:LEU:HD22	1:G:1718:ILE:HD13	1.99	0.43
1:G:4114:CYS:HB3	1:G:4131:ARG:HH22	1.83	0.43
1:G:4155:PRO:HB2	1:G:4156:HIS:CD2	2.53	0.43
2:A:29:MET:HB3	2:A:98:ILE:HB	2.00	0.43
2:J:69:GLY:HA2	2:J:104:LEU:HD23	1.99	0.43
1:B:242:ARG:NH1	1:B:481:GLU:OE1	2.44	0.43
1:B:4937:ILE:HA	1:B:4940:PHE:HD2	1.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:733:PRO:HD2	1:E:763:PRO:HD2	2.00	0.43
1:E:870:ILE:HD12	1:E:870:ILE:HA	1.80	0.43
1:E:894:GLY:HA3	1:E:903:LEU:HD22	2.00	0.43
1:E:950:LEU:HD22	1:E:970:LEU:HB3	2.00	0.43
1:E:1653:LEU:HB3	1:E:1660:GLN:HB2	1.99	0.43
1:E:1704:PRO:HG2	1:E:1707:LEU:HB2	2.00	0.43
1:E:2332:LEU:HA	1:E:2335:LEU:HB2	2.00	0.43
1:I:313:SER:HB3	1:I:351:VAL:HB	2.01	0.43
1:I:1243:PRO:HB2	1:I:1600:LEU:HD13	1.98	0.43
1:I:4142:ASN:HA	1:I:4145:VAL:HG12	2.01	0.43
1:I:4232:GLU:OE2	1:I:5017:ARG:NH1	2.50	0.43
1:G:733:PRO:HD2	1:G:763:PRO:HD2	2.00	0.43
1:B:950:LEU:HD22	1:B:970:LEU:HB3	2.00	0.43
1:B:1269:CYS:HA	1:B:1473:UNK:HA	1.99	0.43
1:B:2775:TRP:HZ3	1:B:2783:GLU:HA	1.82	0.43
1:B:2793:PRO:HG3	1:B:2855:TYR:CZ	2.53	0.43
1:E:313:SER:HB3	1:E:351:VAL:HB	2.01	0.43
1:E:345:LEU:HD23	1:E:389:PHE:HB3	2.01	0.43
1:E:2788:HIS:CE1	1:E:2790:MET:HB2	2.53	0.43
1:E:3960:GLN:HA	1:E:3963:ASN:HD22	1.83	0.43
1:I:583:ILE:HD13	1:I:621:ILE:HD13	2.01	0.43
1:I:788:LYS:HG2	1:I:1630:CYS:N	2.32	0.43
1:I:2760:GLU:O	1:I:2764:GLU:N	2.48	0.43
1:G:988:LEU:O	1:G:992:GLY:N	2.45	0.43
1:G:1747:LEU:HD13	1:G:1760:HIS:CE1	2.54	0.43
1:G:2765:LYS:HA	1:G:2859:PRO:HG3	2.00	0.43
1:G:2869:ARG:HA	1:G:2872:GLN:HB3	2.01	0.43
1:G:4048:LEU:HD23	1:G:4048:LEU:HA	1.85	0.43
1:G:4657:CYS:O	1:G:4661:TYR:N	2.49	0.43
1:E:1046:LEU:HD12	1:E:1053:ILE:HD11	1.99	0.43
1:E:2765:LYS:HA	1:E:2859:PRO:HG3	2.00	0.43
1:E:4142:ASN:HA	1:E:4145:VAL:HG12	2.01	0.43
1:E:4201:ASN:ND2	1:E:4993:MET:SD	2.92	0.43
1:I:2765:LYS:HA	1:I:2859:PRO:HG3	2.00	0.43
1:I:3818:ASP:O	1:I:3822:ASP:N	2.52	0.43
1:G:1665:HIS:HA	1:G:1668:ARG:HG2	2.01	0.43
1:G:4560:TYR:O	1:G:4564:PHE:N	2.44	0.43
2:F:69:GLY:N	2:F:103:LEU:O	2.48	0.43
1:B:550:LYS:HD3	1:B:550:LYS:HA	1.87	0.43
1:B:668:VAL:O	1:B:741:GLU:N	2.50	0.43
1:B:3754:GLU:O	1:B:3758:MET:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3959:LYS:O	1:B:3963:ASN:N	2.47	0.43
1:B:3960:GLN:HA	1:B:3963:ASN:HD22	1.83	0.43
1:B:4201:ASN:ND2	1:B:4993:MET:SD	2.92	0.43
1:E:457:GLU:OE1	1:E:464:LYS:NZ	2.40	0.43
1:E:988:LEU:O	1:E:992:GLY:N	2.45	0.43
1:E:3646:THR:O	1:E:3650:CYS:N	2.49	0.43
1:I:345:LEU:HD23	1:I:389:PHE:HB3	2.01	0.43
1:I:1685:LEU:HD22	1:I:1718:ILE:HD13	1.99	0.43
1:I:2006:ILE:O	1:I:2010:LEU:N	2.43	0.43
1:I:2332:LEU:HA	1:I:2335:LEU:HB2	2.00	0.43
1:G:1735:ILE:HG23	1:G:1771:LEU:HD23	2.01	0.43
1:G:2332:LEU:HA	1:G:2335:LEU:HB2	2.00	0.43
1:G:4828:SER:O	1:G:4832:HIS:N	2.51	0.43
1:B:1747:LEU:HD13	1:B:1760:HIS:CE1	2.54	0.43
1:B:2869:ARG:HA	1:B:2872:GLN:HB3	2.01	0.43
1:E:1234:VAL:HG12	1:E:1236:THR:H	1.83	0.43
1:E:3663:LEU:H	1:E:3663:LEU:HG	1.57	0.43
1:I:3842:LEU:O	1:I:3929:SER:OG	2.31	0.43
1:G:450:GLY:HA2	1:G:453:GLU:HB2	2.01	0.43
1:G:1094:ALA:HB3	1:G:1147:ASP:HB3	2.00	0.43
1:B:313:SER:HB3	1:B:351:VAL:HB	2.01	0.43
1:B:2969:UNK:O	1:B:2973:UNK:N	2.52	0.43
1:B:3930:ILE:HG23	1:B:3951:PHE:HE1	1.83	0.43
1:B:4019:LEU:O	1:B:4023:MET:N	2.46	0.43
1:B:4804:TYR:HB3	1:B:4806:ASN:HD22	1.84	0.43
1:E:1082:THR:HG21	1:E:1107:PRO:HG3	1.99	0.43
1:E:4780:PHE:HA	1:E:4783:ILE:HD12	2.01	0.43
1:I:950:LEU:HD22	1:I:970:LEU:HB3	2.00	0.43
1:I:1082:THR:HG21	1:I:1107:PRO:HG3	1.99	0.43
1:I:3754:GLU:O	1:I:3758:MET:N	2.52	0.43
1:G:1130:GLN:HG2	1:G:1138:PRO:HA	2.01	0.43
1:G:2132:GLY:O	1:G:2136:ARG:N	2.52	0.43
1:G:4780:PHE:HA	1:G:4783:ILE:HD12	2.01	0.43
1:B:21:VAL:HG22	1:B:203:ASN:HB2	2.01	0.42
1:B:45:ARG:HD2	1:B:138:GLN:HB2	2.00	0.42
1:B:450:GLY:HA2	1:B:453:GLU:HB2	2.01	0.42
1:B:534:ARG:NH2	1:B:573:GLU:OE2	2.51	0.42
1:E:102:LEU:HB2	1:E:105:HIS:CE1	2.54	0.42
1:E:668:VAL:O	1:E:741:GLU:N	2.50	0.42
1:E:1094:ALA:HB3	1:E:1147:ASP:HB3	2.00	0.42
1:E:1665:HIS:HA	1:E:1668:ARG:HG2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:4048:LEU:HD23	1:E:4048:LEU:HA	1.85	0.42
1:I:662:TRP:HH2	1:I:814:ALA:H	1.67	0.42
1:I:1735:ILE:HG23	1:I:1771:LEU:HD23	2.01	0.42
1:I:2297:LYS:O	1:I:2301:TYR:N	2.44	0.42
1:I:4804:TYR:HB3	1:I:4806:ASN:HD22	1.84	0.42
1:G:313:SER:HB3	1:G:351:VAL:HB	2.01	0.42
1:G:1704:PRO:HG2	1:G:1707:LEU:HB2	2.00	0.42
1:G:2297:LYS:O	1:G:2301:TYR:N	2.44	0.42
1:G:4982:GLU:OE1	1:G:4982:GLU:N	2.52	0.42
2:H:69:GLY:HA2	2:H:104:LEU:HD23	1.99	0.42
1:B:583:ILE:HD13	1:B:621:ILE:HD13	2.01	0.42
1:B:1665:HIS:HA	1:B:1668:ARG:HG2	2.01	0.42
1:B:4780:PHE:HA	1:B:4783:ILE:HD12	2.01	0.42
1:E:1023:PRO:O	1:E:1027:LEU:N	2.51	0.42
1:E:2384:ILE:O	1:E:2388:GLU:N	2.49	0.42
1:I:1130:GLN:HG2	1:I:1138:PRO:HA	2.01	0.42
1:I:1747:LEU:HD13	1:I:1760:HIS:CE1	2.54	0.42
1:I:3755:GLU:HA	1:I:3758:MET:HB3	2.02	0.42
1:I:4108:ILE:HA	1:I:4111:LEU:HD12	1.99	0.42
1:G:345:LEU:HD23	1:G:389:PHE:HB3	2.01	0.42
1:G:788:LYS:HG2	1:G:1630:CYS:N	2.32	0.42
1:G:1234:VAL:HG12	1:G:1236:THR:H	1.83	0.42
1:G:4019:LEU:O	1:G:4023:MET:N	2.45	0.42
1:G:4201:ASN:ND2	1:G:4993:MET:SD	2.92	0.42
2:H:12:GLY:HA2	2:H:70:GLN:HE21	1.84	0.42
1:B:681:HIS:HB3	1:B:784:SER:HB3	2.01	0.42
1:B:3812:VAL:O	1:B:3816:MET:N	2.46	0.42
1:E:21:VAL:HG22	1:E:203:ASN:HB2	2.01	0.42
1:E:1072:VAL:HG22	1:E:1195:GLY:HA2	2.01	0.42
1:E:2274:ASP:O	1:E:2278:ALA:N	2.50	0.42
1:E:4657:CYS:O	1:E:4661:TYR:N	2.49	0.42
1:E:4982:GLU:OE1	1:E:4982:GLU:N	2.52	0.42
1:I:3906:GLN:H	1:I:3912:THR:HG23	1.85	0.42
1:G:583:ILE:HD13	1:G:621:ILE:HD13	2.01	0.42
1:G:893:TYR:HD1	1:G:907:LEU:HB2	1.84	0.42
1:G:2004:GLU:O	1:G:2008:MET:N	2.50	0.42
1:G:3818:ASP:O	1:G:3822:ASP:N	2.52	0.42
1:B:111:HIS:CD2	1:B:114:SER:H	2.38	0.42
1:B:662:TRP:HH2	1:B:814:ALA:H	1.68	0.42
1:B:1574:PRO:HB3	1:B:1589:PRO:HA	2.01	0.42
1:B:1679:ASN:O	1:B:1683:HIS:ND1	2.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4577:LEU:HG	1:B:4580:TYR:HE2	1.85	0.42
1:E:77:ALA:O	1:E:81:MET:N	2.49	0.42
1:E:111:HIS:CD2	1:E:114:SER:H	2.38	0.42
1:E:350:HIS:N	1:E:355:LEU:O	2.48	0.42
1:E:1130:GLN:HG2	1:E:1138:PRO:HA	2.01	0.42
1:E:1574:PRO:HB3	1:E:1589:PRO:HA	2.01	0.42
1:I:102:LEU:HB2	1:I:105:HIS:CE1	2.54	0.42
1:I:894:GLY:HA3	1:I:903:LEU:HD22	2.00	0.42
1:I:4577:LEU:HG	1:I:4580:TYR:HE2	1.85	0.42
1:I:4780:PHE:HA	1:I:4783:ILE:HD12	2.01	0.42
1:I:4828:SER:O	1:I:4832:HIS:N	2.51	0.42
1:G:111:HIS:CD2	1:G:114:SER:H	2.38	0.42
1:G:1290:UNK:HA	1:G:1598:GLN:HE22	1.84	0.42
1:G:3906:GLN:H	1:G:3912:THR:HG23	1.84	0.42
1:G:4837:LEU:O	1:G:4840:THR:OG1	2.31	0.42
1:B:1130:GLN:HG2	1:B:1138:PRO:HA	2.01	0.42
1:B:3461:UNK:O	1:B:3465:UNK:N	2.52	0.42
1:B:4974:GLY:O	1:B:4978:HIS:N	2.46	0.42
1:E:224:HIS:N	1:E:229:GLU:O	2.42	0.42
1:E:379:HIS:HD2	1:E:382:GLY:H	1.68	0.42
1:E:450:GLY:HA2	1:E:453:GLU:HB2	2.01	0.42
1:E:1747:LEU:HD13	1:E:1760:HIS:CE1	2.54	0.42
1:I:534:ARG:NH2	1:I:573:GLU:OE2	2.51	0.42
1:I:1665:HIS:HA	1:I:1668:ARG:HG2	2.01	0.42
1:I:2132:GLY:O	1:I:2136:ARG:N	2.51	0.42
1:I:2869:ARG:HA	1:I:2872:GLN:HB3	2.01	0.42
1:I:4187:SER:OG	1:I:4191:GLU:OE2	2.36	0.42
1:I:4930:ALA:O	1:I:4934:GLY:N	2.48	0.42
1:I:4982:GLU:N	1:I:4982:GLU:OE1	2.52	0.42
1:G:102:LEU:HB2	1:G:105:HIS:CE1	2.54	0.42
2:A:12:GLY:HA2	2:A:70:GLN:HE21	1.84	0.42
1:B:893:TYR:HD1	1:B:907:LEU:HB2	1.84	0.42
1:B:1094:ALA:HB3	1:B:1147:ASP:HB3	2.00	0.42
1:B:4561:THR:O	1:B:4565:LEU:N	2.50	0.42
1:I:450:GLY:HA2	1:I:453:GLU:HB2	2.01	0.42
1:I:681:HIS:HB3	1:I:784:SER:HB3	2.01	0.42
1:I:893:TYR:HD1	1:I:907:LEU:HB2	1.84	0.42
1:I:2908:TYR:CZ	1:I:2916:LYS:HG2	2.55	0.42
1:G:2760:GLU:O	1:G:2764:GLU:N	2.48	0.42
1:G:4804:TYR:HB3	1:G:4806:ASN:HD22	1.84	0.42
1:G:5022:PHE:HA	1:G:5023:PRO:HD3	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:2:VAL:HG21	2:J:61:GLU:HB2	2.02	0.42
2:J:12:GLY:HA2	2:J:70:GLN:HE21	1.84	0.42
1:B:102:LEU:HB2	1:B:105:HIS:CE1	2.54	0.42
1:B:1293:UNK:N	1:B:1456:UNK:O	2.52	0.42
1:B:2191:PHE:HD1	1:B:2198:MET:HG3	1.84	0.42
1:B:4937:ILE:O	1:B:4941:GLY:N	2.41	0.42
1:E:45:ARG:HD2	1:E:138:GLN:HB2	2.01	0.42
1:E:4204:GLN:NE2	1:E:4245:MET:SD	2.70	0.42
1:I:838:HIS:CE1	1:I:1201:HIS:HD2	2.38	0.42
1:I:1094:ALA:HB3	1:I:1147:ASP:HB3	2.00	0.42
1:I:2009:LEU:HA	1:I:2012:PHE:CE2	2.55	0.42
1:I:4671:PHE:HA	1:I:4674:GLU:HB2	2.02	0.42
1:I:5022:PHE:HA	1:I:5023:PRO:HD3	1.82	0.42
1:G:243:ARG:HA	1:G:301:VAL:HB	2.02	0.42
1:G:894:GLY:HA3	1:G:903:LEU:HD22	2.00	0.42
1:G:2274:ASP:O	1:G:2278:ALA:N	2.50	0.42
1:G:4549:VAL:HA	1:G:4552:LEU:HB3	2.01	0.42
1:G:4577:LEU:HG	1:G:4580:TYR:HE2	1.85	0.42
2:F:12:GLY:HA2	2:F:70:GLN:HE21	1.84	0.42
2:H:2:VAL:HG21	2:H:61:GLU:HB2	2.02	0.42
2:H:29:MET:HB3	2:H:98:ILE:HB	2.00	0.42
1:B:2009:LEU:HA	1:B:2012:PHE:CE2	2.55	0.42
1:B:4671:PHE:HA	1:B:4674:GLU:HB2	2.02	0.42
1:B:4828:SER:O	1:B:4832:HIS:N	2.51	0.42
1:B:5022:PHE:HA	1:B:5023:PRO:HD3	1.83	0.42
1:E:583:ILE:HD13	1:E:621:ILE:HD13	2.01	0.42
1:E:1679:ASN:O	1:E:1683:HIS:ND1	2.40	0.42
1:E:3959:LYS:O	1:E:3963:ASN:N	2.47	0.42
1:E:4804:TYR:HB3	1:E:4806:ASN:HD22	1.84	0.42
1:I:181:HIS:ND1	1:I:195:PHE:HB2	2.35	0.42
1:I:243:ARG:HA	1:I:301:VAL:HB	2.02	0.42
1:I:2191:PHE:HD1	1:I:2198:MET:HG3	1.84	0.42
1:G:111:HIS:HB2	1:G:137:LEU:HD11	2.02	0.42
1:G:3992:PHE:O	1:G:3996:PHE:N	2.43	0.42
2:A:2:VAL:HG21	2:A:61:GLU:HB2	2.02	0.42
1:B:1290:UNK:HA	1:B:1598:GLN:HE22	1.85	0.42
1:B:2908:TYR:CZ	1:B:2916:LYS:HG2	2.55	0.42
1:B:4899:ASP:OD1	1:E:4892:ARG:NH2	2.49	0.42
1:B:4982:GLU:OE1	1:B:4982:GLU:N	2.52	0.42
1:E:662:TRP:HH2	1:E:814:ALA:H	1.68	0.42
1:E:3812:VAL:O	1:E:3816:MET:N	2.46	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:21:VAL:HG22	1:I:203:ASN:HB2	2.01	0.42
1:I:111:HIS:CD2	1:I:114:SER:H	2.38	0.42
1:I:1072:VAL:HG22	1:I:1195:GLY:HA2	2.01	0.42
1:I:4834:GLY:HA2	1:I:4837:LEU:HB2	2.02	0.42
1:G:1164:LEU:N	1:G:1167:GLU:O	2.50	0.42
1:G:4767:TRP:HE3	1:G:4770:SER:HB2	1.85	0.42
2:H:55:VAL:HG23	2:H:60:GLU:HB2	2.02	0.42
1:B:1072:VAL:HG22	1:B:1195:GLY:HA2	2.01	0.42
1:B:3755:GLU:HA	1:B:3758:MET:HB3	2.02	0.42
1:E:111:HIS:HB2	1:E:137:LEU:HD11	2.02	0.42
1:E:1164:LEU:N	1:E:1167:GLU:O	2.50	0.42
1:E:3906:GLN:H	1:E:3912:THR:HG23	1.85	0.42
1:G:21:VAL:HG22	1:G:203:ASN:HB2	2.01	0.42
1:G:838:HIS:CE1	1:G:1201:HIS:HD2	2.38	0.42
1:B:181:HIS:ND1	1:B:195:PHE:HB2	2.35	0.41
1:B:214:VAL:HB	1:B:339:ILE:HB	2.02	0.41
1:B:3646:THR:O	1:B:3650:CYS:N	2.49	0.41
1:E:119:SER:HA	1:E:146:CYS:HA	2.02	0.41
1:E:2009:LEU:HA	1:E:2012:PHE:CE2	2.55	0.41
1:E:4019:LEU:O	1:E:4023:MET:N	2.45	0.41
1:E:4671:PHE:HA	1:E:4674:GLU:HB2	2.02	0.41
1:E:4767:TRP:HE3	1:E:4770:SER:HB2	1.85	0.41
1:E:4860:ARG:NH2	1:G:4582:VAL:HG21	2.34	0.41
1:I:1574:PRO:HB3	1:I:1589:PRO:HA	2.01	0.41
1:I:4220:ASP:O	1:I:4224:GLU:N	2.49	0.41
1:G:181:HIS:ND1	1:G:195:PHE:HB2	2.35	0.41
1:G:232:THR:OG1	1:G:233:ILE:N	2.53	0.41
1:G:379:HIS:HD2	1:G:382:GLY:H	1.68	0.41
1:G:534:ARG:NH2	1:G:573:GLU:OE2	2.51	0.41
1:G:662:TRP:HH2	1:G:814:ALA:H	1.68	0.41
2:J:55:VAL:HG23	2:J:60:GLU:HB2	2.02	0.41
1:B:379:HIS:HD2	1:B:382:GLY:H	1.68	0.41
1:B:3645:PRO:O	1:B:3649:ALA:N	2.46	0.41
1:E:139:GLU:O	1:E:141:ALA:N	2.53	0.41
1:E:3755:GLU:HA	1:E:3758:MET:HB3	2.02	0.41
1:I:886:ARG:HB3	1:I:891:TRP:HB2	2.02	0.41
1:I:4767:TRP:HE3	1:I:4770:SER:HB2	1.85	0.41
1:G:119:SER:HA	1:G:146:CYS:HA	2.02	0.41
1:G:1072:VAL:HG22	1:G:1195:GLY:HA2	2.01	0.41
1:G:1574:PRO:HB3	1:G:1589:PRO:HA	2.01	0.41
1:G:2908:TYR:CZ	1:G:2916:LYS:HG2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3818:ASP:O	1:B:3822:ASP:N	2.52	0.41
1:B:4677:LEU:HD13	1:B:4677:LEU:HA	1.91	0.41
1:E:232:THR:OG1	1:E:233:ILE:N	2.54	0.41
1:E:1259:ARG:NH2	1:E:1595:LEU:O	2.54	0.41
1:E:2908:TYR:CZ	1:E:2916:LYS:HG2	2.54	0.41
1:I:214:VAL:HB	1:I:339:ILE:HB	2.03	0.41
1:I:4200:THR:O	1:I:4204:GLN:N	2.37	0.41
1:B:232:THR:OG1	1:B:233:ILE:N	2.54	0.41
1:B:243:ARG:HA	1:B:301:VAL:HB	2.02	0.41
1:E:214:VAL:HB	1:E:339:ILE:HB	2.02	0.41
1:E:2191:PHE:HD1	1:E:2198:MET:HG3	1.85	0.41
1:E:3754:GLU:O	1:E:3758:MET:N	2.51	0.41
1:E:3850:GLN:HA	1:E:3853:ALA:HB3	2.03	0.41
1:E:4110:PHE:HA	1:E:4113:SER:HB3	2.03	0.41
1:I:139:GLU:O	1:I:141:ALA:N	2.54	0.41
1:I:2878:LEU:HD23	1:I:2878:LEU:HA	1.91	0.41
1:I:4710:SER:OG	1:I:4772:ASP:OD2	2.25	0.41
1:I:4942:GLU:O	1:I:4946:GLN:N	2.47	0.41
1:G:139:GLU:O	1:G:141:ALA:N	2.53	0.41
1:G:886:ARG:HB3	1:G:891:TRP:HB2	2.02	0.41
1:G:2007:ASN:OD1	1:G:3656:SER:OG	2.33	0.41
1:G:4671:PHE:HA	1:G:4674:GLU:HB2	2.02	0.41
2:J:14:THR:N	2:J:67:SER:OG	2.54	0.41
1:B:290:TYR:O	1:B:302:VAL:N	2.42	0.41
1:B:3361:UNK:O	1:B:3365:UNK:N	2.54	0.41
1:E:4577:LEU:HG	1:E:4580:TYR:HE2	1.84	0.41
1:I:685:GLY:N	1:I:780:VAL:O	2.35	0.41
1:I:1096:THR:HG23	1:I:1199:VAL:HG22	2.03	0.41
1:I:4549:VAL:HA	1:I:4552:LEU:HB3	2.01	0.41
1:I:4583:SER:O	1:I:4628:VAL:N	2.49	0.41
1:G:681:HIS:HB3	1:G:784:SER:HB3	2.01	0.41
1:G:3361:UNK:O	1:G:3365:UNK:N	2.53	0.41
2:H:14:THR:N	2:H:67:SER:OG	2.54	0.41
1:B:139:GLU:O	1:B:141:ALA:N	2.53	0.41
1:B:838:HIS:CE1	1:B:1201:HIS:HD2	2.38	0.41
1:B:3906:GLN:H	1:B:3912:THR:HG23	1.84	0.41
1:B:4110:PHE:HA	1:B:4113:SER:HB3	2.03	0.41
1:B:4767:TRP:HE3	1:B:4770:SER:HB2	1.85	0.41
1:E:181:HIS:ND1	1:E:195:PHE:HB2	2.35	0.41
1:E:886:ARG:HB3	1:E:891:TRP:HB2	2.02	0.41
1:E:1639:LEU:N	1:E:1648:MET:O	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1687:SER:OG	2:F:90:VAL:HG22	2.20	0.41
1:E:4549:VAL:HA	1:E:4552:LEU:HB3	2.01	0.41
1:G:4930:ALA:O	1:G:4934:GLY:N	2.48	0.41
1:B:77:ALA:O	1:B:81:MET:N	2.49	0.41
1:B:1774:PRO:HG2	1:B:1776:HIS:CE1	2.56	0.41
1:B:2121:PHE:O	1:B:3725:TYR:OH	2.33	0.41
1:B:3850:GLN:HA	1:B:3853:ALA:HB3	2.03	0.41
1:E:243:ARG:HA	1:E:301:VAL:HB	2.02	0.41
1:E:1286:UNK:HA	1:E:1461:UNK:HA	2.03	0.41
1:E:2132:GLY:O	1:E:2136:ARG:N	2.52	0.41
1:E:4062:PHE:O	1:E:4066:LEU:N	2.54	0.41
1:I:111:HIS:HB2	1:I:137:LEU:HD11	2.02	0.41
1:I:4242:ILE:O	1:I:4246:GLN:N	2.53	0.41
1:I:5026:ASP:OD1	1:I:5027:CYS:N	2.54	0.41
1:G:2009:LEU:HA	1:G:2012:PHE:CE2	2.55	0.41
1:B:317:ARG:N	1:B:347:PHE:O	2.48	0.41
1:B:2265:LEU:HD22	1:B:2330:ARG:HB3	2.03	0.41
1:B:4990:PHE:O	1:B:4994:TYR:N	2.44	0.41
1:E:587:ILE:O	1:E:591:ASP:N	2.54	0.41
1:E:893:TYR:HD1	1:E:907:LEU:HB2	1.84	0.41
1:E:4834:GLY:HA2	1:E:4837:LEU:HB2	2.02	0.41
1:E:5022:PHE:HA	1:E:5023:PRO:HD3	1.82	0.41
1:I:379:HIS:HD2	1:I:382:GLY:H	1.68	0.41
1:I:649:PHE:HB3	1:I:776:LEU:HD13	2.03	0.41
1:I:1259:ARG:NH2	1:I:1595:LEU:O	2.54	0.41
1:I:3850:GLN:HA	1:I:3853:ALA:HB3	2.03	0.41
1:I:4062:PHE:O	1:I:4066:LEU:N	2.54	0.41
1:I:4657:CYS:O	1:I:4661:TYR:N	2.49	0.41
1:G:214:VAL:HB	1:G:339:ILE:HB	2.02	0.41
1:G:2199:ARG:NE	1:G:2246:ASN:OD1	2.54	0.41
1:G:3922:TYR:O	1:G:3926:LEU:N	2.47	0.41
2:A:14:THR:N	2:A:67:SER:OG	2.54	0.41
2:A:55:VAL:HG23	2:A:60:GLU:HB2	2.02	0.41
2:H:7:ILE:N	2:H:71:ARG:O	2.47	0.41
1:B:111:HIS:HB2	1:B:137:LEU:HD11	2.02	0.41
1:B:288:GLY:HA3	1:B:405:HIS:CE1	2.56	0.41
1:B:886:ARG:HB3	1:B:891:TRP:HB2	2.03	0.41
1:B:1096:THR:HG23	1:B:1199:VAL:HG22	2.02	0.41
1:B:1105:ALA:O	1:B:1189:LEU:N	2.54	0.41
1:B:1164:LEU:N	1:B:1167:GLU:O	2.50	0.41
1:B:2199:ARG:NE	1:B:2246:ASN:OD1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2674:UNK:O	1:B:2676:UNK:N	2.54	0.41
1:B:4549:VAL:HA	1:B:4552:LEU:HB3	2.01	0.41
1:B:4834:GLY:HA2	1:B:4837:LEU:HB2	2.02	0.41
1:B:5026:ASP:OD1	1:B:5027:CYS:N	2.54	0.41
1:B:5033:GLU:O	1:B:5037:SER:N	2.54	0.41
1:E:288:GLY:HA3	1:E:405:HIS:CE1	2.56	0.41
1:E:681:HIS:HB3	1:E:784:SER:HB3	2.01	0.41
1:E:3361:UNK:O	1:E:3365:UNK:N	2.54	0.41
1:E:3662:ILE:H	1:E:3662:ILE:HG13	1.79	0.41
1:E:3694:LYS:HA	1:E:3695:PRO:HD3	1.87	0.41
1:E:3818:ASP:O	1:E:3822:ASP:N	2.52	0.41
1:E:3896:ASN:ND2	1:E:3898:ASP:OD1	2.54	0.41
1:I:283:ARG:HH21	1:I:402:ARG:HH12	1.68	0.41
1:I:3945:GLU:O	1:I:3949:ARG:N	2.45	0.41
1:I:4110:PHE:HA	1:I:4113:SER:HB3	2.03	0.41
1:I:4728:HIS:HD2	1:I:4731:ILE:HD11	1.86	0.41
1:I:4987:ASN:OD1	1:I:4987:ASN:N	2.54	0.41
1:I:5033:GLU:O	1:I:5037:SER:N	2.54	0.41
1:G:222:LEU:HG	1:G:390:LEU:HD22	2.03	0.41
1:G:288:GLY:HA3	1:G:405:HIS:CE1	2.56	0.41
1:G:710:ASP:OD1	1:G:710:ASP:N	2.48	0.41
1:G:898:ASP:HB3	1:G:901:LYS:HB2	2.02	0.41
1:G:1259:ARG:NH2	1:G:1595:LEU:O	2.54	0.41
1:G:1639:LEU:N	1:G:1648:MET:O	2.54	0.41
1:G:2191:PHE:HD1	1:G:2198:MET:HG3	1.84	0.41
1:G:3542:UNK:O	1:G:3546:UNK:N	2.54	0.41
1:G:3754:GLU:O	1:G:3758:MET:N	2.51	0.41
1:G:4834:GLY:HA2	1:G:4837:LEU:HB2	2.02	0.41
2:F:2:VAL:HG21	2:F:61:GLU:HB2	2.02	0.41
2:F:14:THR:N	2:F:67:SER:OG	2.54	0.41
2:J:77:THR:OG1	2:J:79:ASP:OD1	2.34	0.41
1:B:451:TYR:O	1:B:474:ARG:NH1	2.44	0.41
1:B:1259:ARG:NH2	1:B:1595:LEU:O	2.54	0.41
1:B:3896:ASN:ND2	1:B:3898:ASP:OD1	2.54	0.41
1:B:4062:PHE:O	1:B:4066:LEU:N	2.54	0.41
1:B:4728:HIS:HD2	1:B:4731:ILE:HD11	1.86	0.41
1:E:243:ARG:NH2	1:E:303:ASP:OD1	2.29	0.41
1:E:838:HIS:CE1	1:E:1201:HIS:HD2	2.38	0.41
1:E:898:ASP:HB3	1:E:901:LYS:HB2	2.02	0.41
1:E:1150:GLY:O	1:E:1163:THR:OG1	2.34	0.41
1:E:2004:GLU:O	1:E:2008:MET:N	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:2969:UNK:O	1:E:2973:UNK:N	2.54	0.41
1:E:5033:GLU:O	1:E:5037:SER:N	2.54	0.41
1:I:77:ALA:O	1:I:81:MET:N	2.49	0.41
1:I:288:GLY:HA3	1:I:405:HIS:CE1	2.56	0.41
1:I:1077:ALA:HB3	1:I:1189:LEU:HD11	2.03	0.41
1:I:1774:PRO:HG2	1:I:1776:HIS:CE1	2.56	0.41
1:I:2158:CYS:HB2	1:I:2184:ASN:HD22	1.86	0.41
1:I:3892:CYS:HB2	1:I:3900:GLN:HG2	2.03	0.41
1:I:4578:LEU:O	1:G:4880:MET:HG3	2.21	0.41
1:I:4974:GLY:O	1:I:4978:HIS:N	2.46	0.41
1:G:283:ARG:HH21	1:G:402:ARG:HH12	1.68	0.41
1:G:2158:CYS:HB2	1:G:2184:ASN:HD22	1.86	0.41
1:B:119:SER:HA	1:B:146:CYS:HA	2.02	0.40
1:B:2158:CYS:HB2	1:B:2184:ASN:HD22	1.86	0.40
1:B:4227:GLU:HG3	1:B:4228:ALA:H	1.85	0.40
1:E:359:TYR:HA	1:E:376:ALA:HA	2.03	0.40
1:E:1096:THR:HG23	1:E:1199:VAL:HG22	2.02	0.40
1:E:2158:CYS:HB2	1:E:2184:ASN:HD22	1.86	0.40
1:I:2199:ARG:NE	1:I:2246:ASN:OD1	2.54	0.40
1:I:4227:GLU:HG3	1:I:4228:ALA:H	1.85	0.40
1:G:870:ILE:HD12	1:G:870:ILE:HA	1.79	0.40
1:G:1077:ALA:HB3	1:G:1189:LEU:HD11	2.03	0.40
1:G:1105:ALA:O	1:G:1189:LEU:N	2.54	0.40
1:G:3812:VAL:O	1:G:3816:MET:N	2.46	0.40
1:G:3850:GLN:HA	1:G:3853:ALA:HB3	2.03	0.40
1:G:4062:PHE:O	1:G:4066:LEU:N	2.54	0.40
2:A:7:ILE:N	2:A:71:ARG:O	2.47	0.40
1:B:283:ARG:HH21	1:B:402:ARG:HH12	1.68	0.40
1:B:731:THR:OG1	1:B:1520:UNK:O	2.36	0.40
1:B:988:LEU:O	1:B:992:GLY:N	2.45	0.40
1:B:2132:GLY:O	1:B:2136:ARG:N	2.52	0.40
1:E:534:ARG:NH2	1:E:573:GLU:OE2	2.51	0.40
1:E:2007:ASN:OD1	1:E:3656:SER:OG	2.33	0.40
1:E:2587:UNK:O	1:E:2591:UNK:N	2.54	0.40
1:E:4028:LEU:HD23	1:E:4146:LEU:HD13	2.04	0.40
1:E:4687:TYR:CE1	1:E:4692:PRO:HG3	2.56	0.40
1:I:736:HIS:HB3	2:J:8:SER:H	1.85	0.40
1:I:1708:ARG:HG2	1:I:1711:TYR:CE2	2.57	0.40
1:I:2265:LEU:HD22	1:I:2330:ARG:HB3	2.03	0.40
1:I:2298:VAL:HA	1:I:2301:TYR:HB2	2.04	0.40
1:I:3663:LEU:H	1:I:3663:LEU:HG	1.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1720:LEU:HB2	1:G:1847:THR:HG23	2.03	0.40
1:G:3755:GLU:HA	1:G:3758:MET:HB3	2.02	0.40
1:G:3892:CYS:HB2	1:G:3900:GLN:HG2	2.03	0.40
1:G:3959:LYS:O	1:G:3963:ASN:N	2.47	0.40
1:G:4031:LEU:HD22	1:G:4149:ASN:ND2	2.36	0.40
2:F:55:VAL:HG23	2:F:60:GLU:HB2	2.02	0.40
1:B:736:HIS:HB3	2:A:8:SER:H	1.85	0.40
1:B:2025:GLU:HA	1:B:2028:ARG:NE	2.37	0.40
1:B:2298:VAL:HA	1:B:2301:TYR:HB2	2.04	0.40
1:B:4943:LEU:HA	1:B:4946:GLN:HB2	2.03	0.40
1:E:1774:PRO:HG2	1:E:1776:HIS:CE1	2.56	0.40
1:E:5000:GLU:HA	1:E:5003:HIS:NE2	2.37	0.40
1:E:5026:ASP:OD1	1:E:5027:CYS:N	2.54	0.40
1:I:119:SER:HA	1:I:146:CYS:HA	2.02	0.40
1:I:898:ASP:HB3	1:I:901:LYS:HB2	2.03	0.40
1:I:2674:UNK:O	1:I:2676:UNK:N	2.53	0.40
1:I:3896:ASN:ND2	1:I:3898:ASP:OD1	2.54	0.40
1:I:3915:ILE:H	1:I:3915:ILE:HG13	1.67	0.40
1:I:4031:LEU:HD22	1:I:4149:ASN:ND2	2.36	0.40
1:I:4687:TYR:CE1	1:I:4692:PRO:HG3	2.56	0.40
1:G:473:ASN:O	1:G:477:LEU:N	2.53	0.40
1:G:1727:ARG:HH21	1:G:1775:HIS:CE1	2.40	0.40
1:G:1774:PRO:HG2	1:G:1776:HIS:CE1	2.56	0.40
1:G:4227:GLU:HG3	1:G:4228:ALA:H	1.85	0.40
1:G:4728:HIS:HD2	1:G:4731:ILE:HD11	1.86	0.40
1:G:4943:LEU:HA	1:G:4946:GLN:HB2	2.03	0.40
1:G:5033:GLU:O	1:G:5037:SER:N	2.54	0.40
1:B:101:LEU:HB3	1:B:150:MET:HE3	2.02	0.40
1:B:788:LYS:HG2	1:B:1630:CYS:N	2.32	0.40
1:B:946:ALA:HA	1:B:949:ASN:HB2	2.04	0.40
1:B:2021:CYS:HA	1:B:2022:PRO:HD3	1.95	0.40
1:B:3922:TYR:O	1:B:3926:LEU:N	2.47	0.40
1:E:27:THR:OG1	1:E:31:GLU:N	2.55	0.40
1:E:1256:GLU:HG2	1:E:1273:ALA:HB3	2.04	0.40
1:E:1708:ARG:HG2	1:E:1711:TYR:CE2	2.57	0.40
1:E:1965:TYR:OH	1:E:2027:ILE:O	2.27	0.40
1:E:4031:LEU:HD22	1:E:4149:ASN:ND2	2.36	0.40
1:I:222:LEU:HG	1:I:390:LEU:HD22	2.03	0.40
1:I:4677:LEU:HD13	1:I:4677:LEU:HA	1.91	0.40
1:G:359:TYR:HA	1:G:376:ALA:HA	2.03	0.40
1:G:649:PHE:HB3	1:G:776:LEU:HD13	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:4110:PHE:HA	1:G:4113:SER:HB3	2.03	0.40
1:B:222:LEU:HG	1:B:390:LEU:HD22	2.03	0.40
1:B:1141:ARG:H	1:B:1141:ARG:HD2	1.87	0.40
1:B:2587:UNK:O	1:B:2591:UNK:N	2.54	0.40
1:E:473:ASN:O	1:E:477:LEU:N	2.53	0.40
1:E:1105:ALA:O	1:E:1189:LEU:N	2.54	0.40
1:E:2674:UNK:O	1:E:2676:UNK:N	2.54	0.40
1:E:2797:PHE:HB3	1:E:2801:ASP:HB2	2.03	0.40
1:G:114:SER:HA	1:G:399:GLN:HE21	1.87	0.40
1:G:564:LEU:HA	1:G:567:VAL:HG22	2.03	0.40
1:G:1096:THR:HG23	1:G:1199:VAL:HG22	2.02	0.40
1:G:2025:GLU:HA	1:G:2028:ARG:NE	2.37	0.40
1:G:3462:UNK:O	1:G:3466:UNK:N	2.55	0.40
1:G:3770:LEU:HA	1:G:3770:LEU:HD13	1.80	0.40
1:G:4220:ASP:O	1:G:4224:GLU:N	2.49	0.40
1:G:4987:ASN:N	1:G:4987:ASN:OD1	2.54	0.40
1:G:5026:ASP:OD1	1:G:5027:CYS:N	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	3235/4687 (69%)	2875 (89%)	355 (11%)	5 (0%)	47	81
1	E	3235/4687 (69%)	2874 (89%)	356 (11%)	5 (0%)	47	81
1	G	3235/4687 (69%)	2876 (89%)	354 (11%)	5 (0%)	47	81
1	I	3235/4687 (69%)	2876 (89%)	354 (11%)	5 (0%)	47	81
2	A	105/108 (97%)	94 (90%)	11 (10%)	0	100	100
2	F	105/108 (97%)	94 (90%)	11 (10%)	0	100	100
2	H	105/108 (97%)	94 (90%)	11 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	J	105/108 (97%)	94 (90%)	11 (10%)	0	100	100
All	All	13360/19180 (70%)	11877 (89%)	1463 (11%)	20 (0%)	54	85

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1708	ARG
1	E	1708	ARG
1	I	1708	ARG
1	G	1708	ARG
1	B	1932	PRO
1	E	1932	PRO
1	I	1932	PRO
1	G	1932	PRO
1	B	1840	PRO
1	E	1840	PRO
1	I	1840	PRO
1	G	1840	PRO
1	B	5023	PRO
1	E	5023	PRO
1	I	5023	PRO
1	G	5023	PRO
1	B	4641	PRO
1	E	4641	PRO
1	I	4641	PRO
1	G	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	B	2493/3209 (78%)	2478 (99%)	15 (1%)	86	92
1	E	2493/3209 (78%)	2478 (99%)	15 (1%)	86	92
1	G	2493/3209 (78%)	2478 (99%)	15 (1%)	86	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	2493/3209 (78%)	2478 (99%)	15 (1%)	86	92
2	A	88/89 (99%)	88 (100%)	0	100	100
2	F	88/89 (99%)	88 (100%)	0	100	100
2	H	88/89 (99%)	88 (100%)	0	100	100
2	J	88/89 (99%)	88 (100%)	0	100	100
All	All	10324/13192 (78%)	10264 (99%)	60 (1%)	86	92

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	534	ARG
1	B	553	ARG
1	B	978	THR
1	B	1076	ARG
1	B	1141	ARG
1	B	1964	ARG
1	B	3663	LEU
1	B	3770	LEU
1	B	3787	LYS
1	B	3896	ASN
1	B	4034	ASN
1	B	4085	ARG
1	B	4120	ASN
1	B	4137	ARG
1	B	4985	LEU
1	E	534	ARG
1	E	553	ARG
1	E	978	THR
1	E	1076	ARG
1	E	1141	ARG
1	E	1964	ARG
1	E	3663	LEU
1	E	3770	LEU
1	E	3787	LYS
1	E	3896	ASN
1	E	4034	ASN
1	E	4085	ARG
1	E	4120	ASN
1	E	4137	ARG
1	E	4985	LEU

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Mol	Chain	Res	Type
1	I	534	ARG
1	I	553	ARG
1	I	978	THR
1	I	1076	ARG
1	I	1141	ARG
1	I	1964	ARG
1	I	3663	LEU
1	I	3770	LEU
1	I	3787	LYS
1	I	3896	ASN
1	I	4034	ASN
1	I	4085	ARG
1	I	4120	ASN
1	I	4137	ARG
1	I	4985	LEU
1	G	534	ARG
1	G	553	ARG
1	G	978	THR
1	G	1076	ARG
1	G	1141	ARG
1	G	1964	ARG
1	G	3663	LEU
1	G	3770	LEU
1	G	3787	LYS
1	G	3896	ASN
1	G	4034	ASN
1	G	4085	ARG
1	G	4120	ASN
1	G	4137	ARG
1	G	4985	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (165) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	23	GLN
1	B	57	ASN
1	B	105	HIS
1	B	111	HIS
1	B	203	ASN
1	B	379	HIS
1	B	383	HIS
1	B	405	HIS

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Mol	Chain	Res	Type
1	B	479	GLN
1	B	582	HIS
1	B	838	HIS
1	B	1158	ASN
1	B	1598	GLN
1	B	1679	ASN
1	B	1702	HIS
1	B	1719	HIS
1	B	1775	HIS
1	B	1941	ASN
1	B	1970	GLN
1	B	1973	GLN
1	B	2005	GLN
1	B	2127	GLN
1	B	2184	ASN
1	B	3766	GLN
1	B	3771	HIS
1	B	3809	ASN
1	B	3896	ASN
1	B	3946	GLN
1	B	3950	ASN
1	B	3963	ASN
1	B	3976	ASN
1	B	4005	GLN
1	B	4054	ASN
1	B	4102	GLN
1	B	4120	ASN
1	B	4133	GLN
1	B	4142	ASN
1	B	4156	HIS
1	B	4714	ASN
1	B	4728	HIS
1	B	4806	ASN
1	E	23	GLN
1	E	57	ASN
1	E	105	HIS
1	E	111	HIS
1	E	203	ASN
1	E	379	HIS
1	E	383	HIS
1	E	405	HIS
1	E	479	GLN

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Mol	Chain	Res	Type
1	E	838	HIS
1	E	1158	ASN
1	E	1598	GLN
1	E	1679	ASN
1	E	1693	GLN
1	E	1702	HIS
1	E	1719	HIS
1	E	1775	HIS
1	E	1941	ASN
1	E	1970	GLN
1	E	1973	GLN
1	E	2005	GLN
1	E	2127	GLN
1	E	2184	ASN
1	E	3766	GLN
1	E	3771	HIS
1	E	3809	ASN
1	E	3896	ASN
1	E	3946	GLN
1	E	3950	ASN
1	E	3963	ASN
1	E	3976	ASN
1	E	4005	GLN
1	E	4054	ASN
1	E	4102	GLN
1	E	4120	ASN
1	E	4133	GLN
1	E	4142	ASN
1	E	4156	HIS
1	E	4714	ASN
1	E	4728	HIS
1	E	4806	ASN
1	E	5031	GLN
1	I	23	GLN
1	I	57	ASN
1	I	105	HIS
1	I	111	HIS
1	I	203	ASN
1	I	379	HIS
1	I	383	HIS
1	I	405	HIS
1	I	479	GLN

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Mol	Chain	Res	Type
1	I	582	HIS
1	I	838	HIS
1	I	1158	ASN
1	I	1598	GLN
1	I	1679	ASN
1	I	1702	HIS
1	I	1719	HIS
1	I	1775	HIS
1	I	1941	ASN
1	I	1970	GLN
1	I	1973	GLN
1	I	2005	GLN
1	I	2127	GLN
1	I	2184	ASN
1	I	3771	HIS
1	I	3809	ASN
1	I	3896	ASN
1	I	3946	GLN
1	I	3950	ASN
1	I	3963	ASN
1	I	3976	ASN
1	I	4005	GLN
1	I	4054	ASN
1	I	4102	GLN
1	I	4120	ASN
1	I	4133	GLN
1	I	4142	ASN
1	I	4156	HIS
1	I	4714	ASN
1	I	4728	HIS
1	I	4806	ASN
1	G	23	GLN
1	G	57	ASN
1	G	105	HIS
1	G	111	HIS
1	G	203	ASN
1	G	379	HIS
1	G	383	HIS
1	G	405	HIS
1	G	479	GLN
1	G	582	HIS
1	G	838	HIS

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Mol	Chain	Res	Type
1	G	1158	ASN
1	G	1598	GLN
1	G	1679	ASN
1	G	1693	GLN
1	G	1702	HIS
1	G	1719	HIS
1	G	1775	HIS
1	G	1941	ASN
1	G	1970	GLN
1	G	1973	GLN
1	G	2005	GLN
1	G	2127	GLN
1	G	2184	ASN
1	G	3771	HIS
1	G	3809	ASN
1	G	3896	ASN
1	G	3946	GLN
1	G	3950	ASN
1	G	3963	ASN
1	G	3976	ASN
1	G	4005	GLN
1	G	4054	ASN
1	G	4102	GLN
1	G	4120	ASN
1	G	4133	GLN
1	G	4142	ASN
1	G	4156	HIS
1	G	4714	ASN
1	G	4728	HIS
1	G	4806	ASN
1	G	5031	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides 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
1	E	12
1	B	12
1	I	12
1	G	12

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	3613:UNK	C	3639:THR	N	45.91
1	B	3613:UNK	C	3639:THR	N	45.70
1	I	3613:UNK	C	3639:THR	N	45.65
1	G	3613:UNK	C	3639:THR	N	45.46
1	I	3163:UNK	C	3170:UNK	N	16.67
1	B	3163:UNK	C	3170:UNK	N	16.62
1	G	3163:UNK	C	3170:UNK	N	16.55
1	E	3163:UNK	C	3170:UNK	N	16.51
1	G	3063:UNK	C	3134:UNK	N	14.87

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	3063:UNK	C	3134:UNK	N	14.83
1	I	3063:UNK	C	3134:UNK	N	14.78
1	B	3063:UNK	C	3134:UNK	N	14.77
1	E	2703:UNK	C	2734:ASN	N	14.08
1	G	2703:UNK	C	2734:ASN	N	14.07
1	I	2703:UNK	C	2734:ASN	N	14.05
1	E	3468:UNK	C	3511:UNK	N	14.02
1	B	2703:UNK	C	2734:ASN	N	13.99
1	B	3468:UNK	C	3511:UNK	N	13.95
1	I	3468:UNK	C	3511:UNK	N	13.78
1	G	3468:UNK	C	3511:UNK	N	13.75
1	E	3236:UNK	C	3241:UNK	N	12.64
1	E	1564:UNK	C	1573:MET	N	12.60
1	G	3236:UNK	C	3241:UNK	N	12.60
1	B	3236:UNK	C	3241:UNK	N	12.55
1	B	1564:UNK	C	1573:MET	N	12.50
1	I	3236:UNK	C	3241:UNK	N	12.47
1	B	2976:UNK	C	2995:UNK	N	12.32
1	I	2976:UNK	C	2995:UNK	N	12.32
1	G	1564:UNK	C	1573:MET	N	12.32
1	I	1564:UNK	C	1573:MET	N	12.31
1	E	2976:UNK	C	2995:UNK	N	12.29
1	G	2976:UNK	C	2995:UNK	N	12.29
1	E	3254:UNK	C	3261:UNK	N	8.51
1	G	3254:UNK	C	3261:UNK	N	8.49
1	B	3254:UNK	C	3261:UNK	N	8.43
1	I	3254:UNK	C	3261:UNK	N	8.39
1	I	1297:UNK	C	1430:UNK	N	5.75
1	G	1297:UNK	C	1430:UNK	N	5.72
1	B	1297:UNK	C	1430:UNK	N	5.70
1	E	1297:UNK	C	1430:UNK	N	5.49
1	I	2939:ARG	C	2942:UNK	N	4.57
1	B	2939:ARG	C	2942:UNK	N	4.45
1	G	2939:ARG	C	2942:UNK	N	4.45
1	E	2939:ARG	C	2942:UNK	N	4.41
1	I	2479:LEU	C	2487:UNK	N	4.05
1	G	2479:LEU	C	2487:UNK	N	4.02
1	B	2479:LEU	C	2487:UNK	N	4.01
1	E	2479:LEU	C	2487:UNK	N	4.00

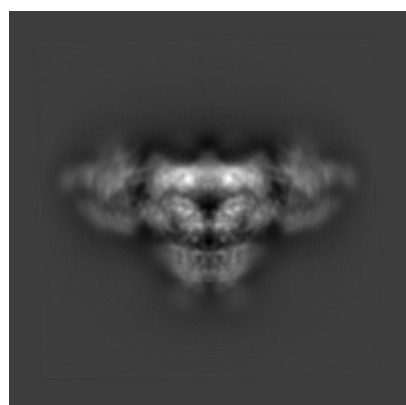
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20486. These allow visual inspection of the internal detail of the map and identification of artifacts.

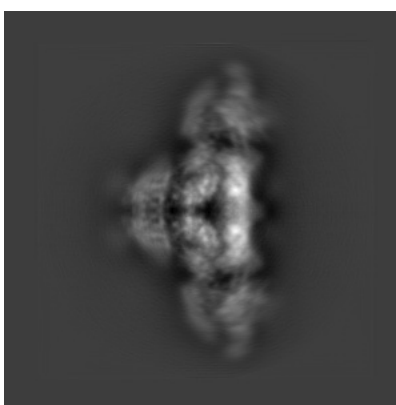
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

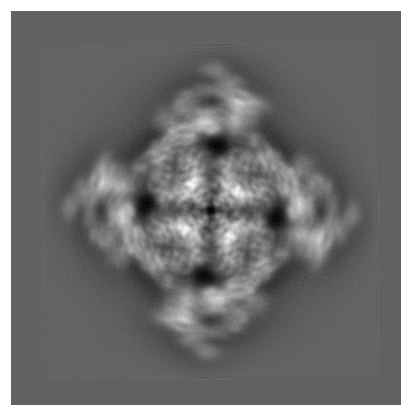
6.1.1 Primary map



X



Y

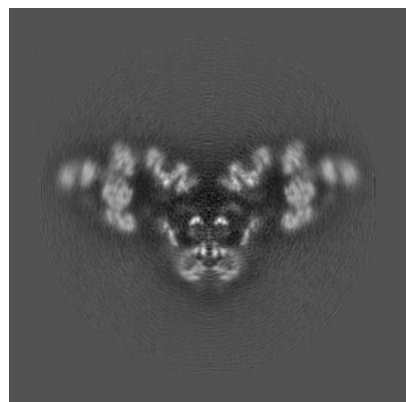


Z

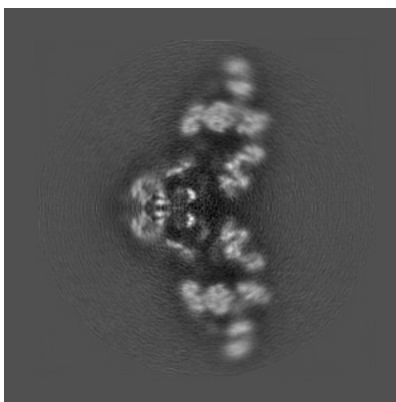
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

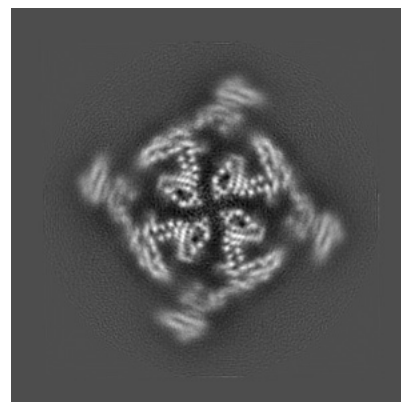
6.2.1 Primary map



X Index: 200



Y Index: 200

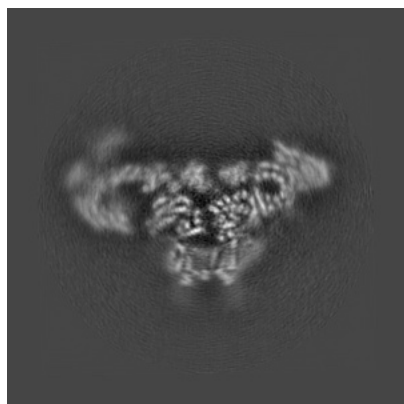


Z Index: 200

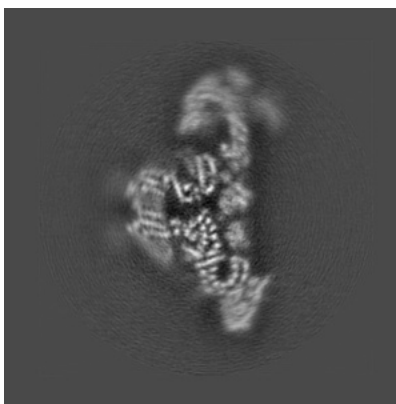
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

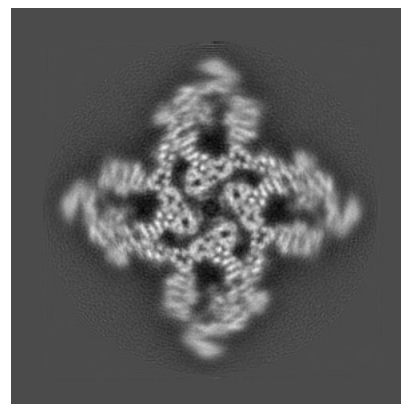
6.3.1 Primary map



X Index: 179



Y Index: 177



Z Index: 231

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.166. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

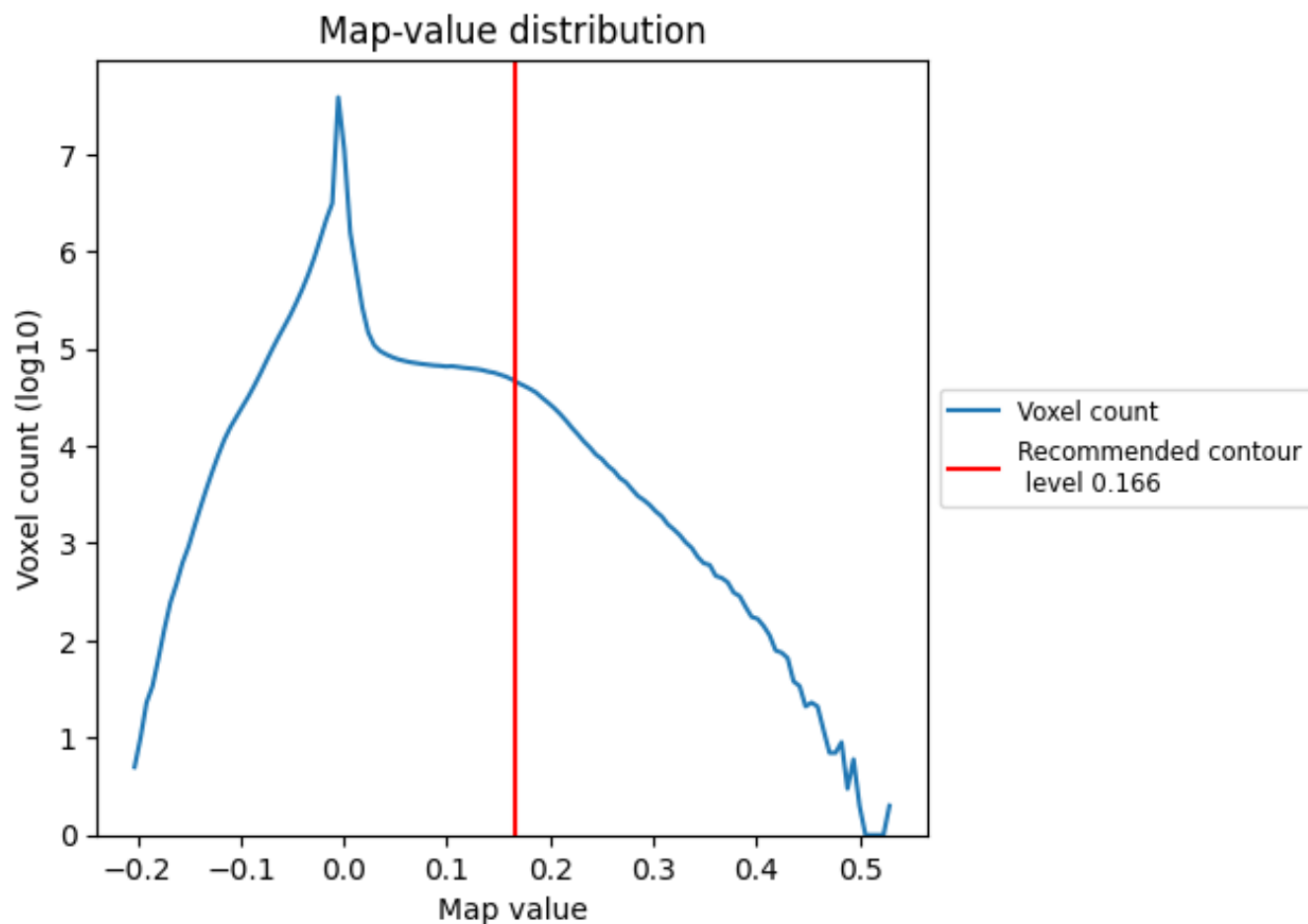
6.5 Mask visualisation

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

7 Map analysis [i](#)

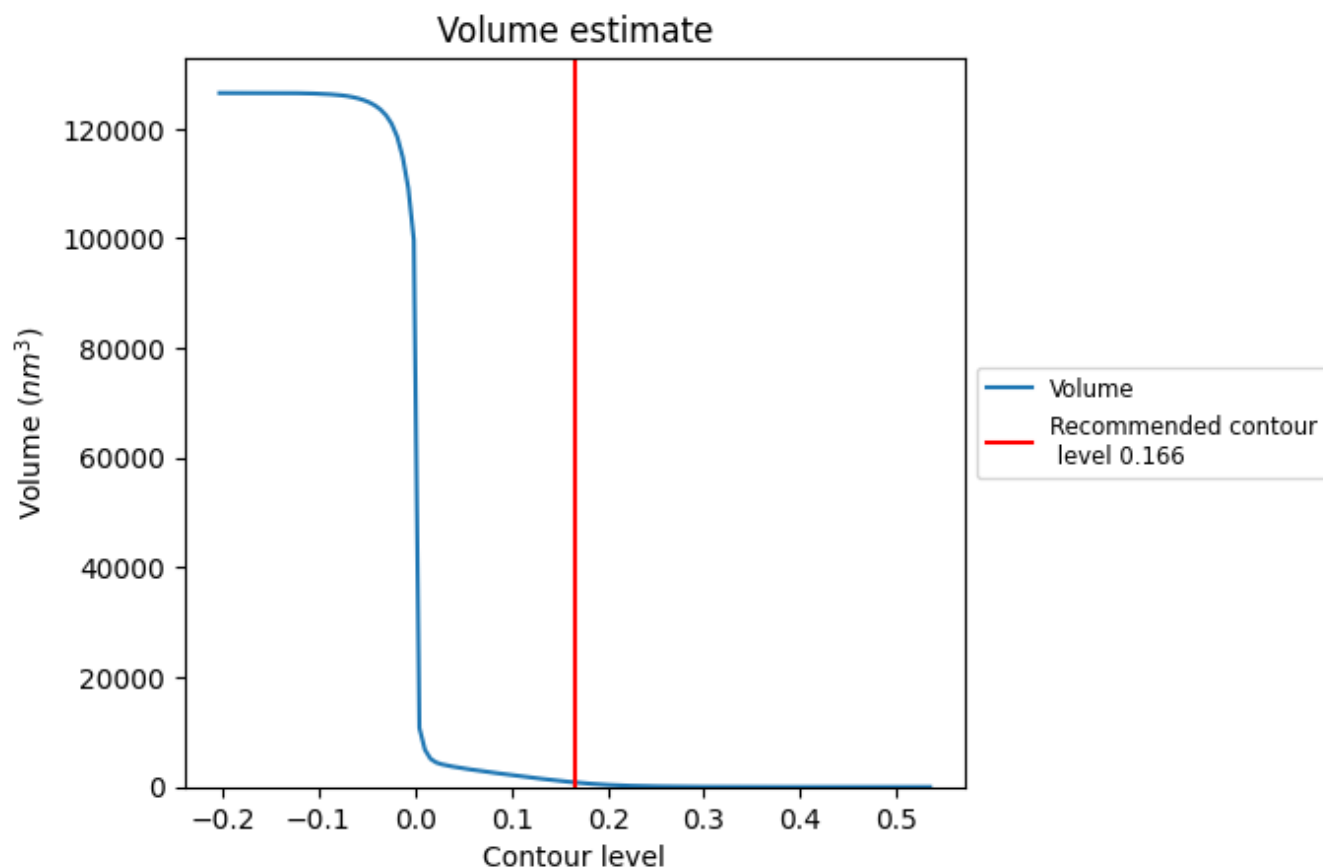
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

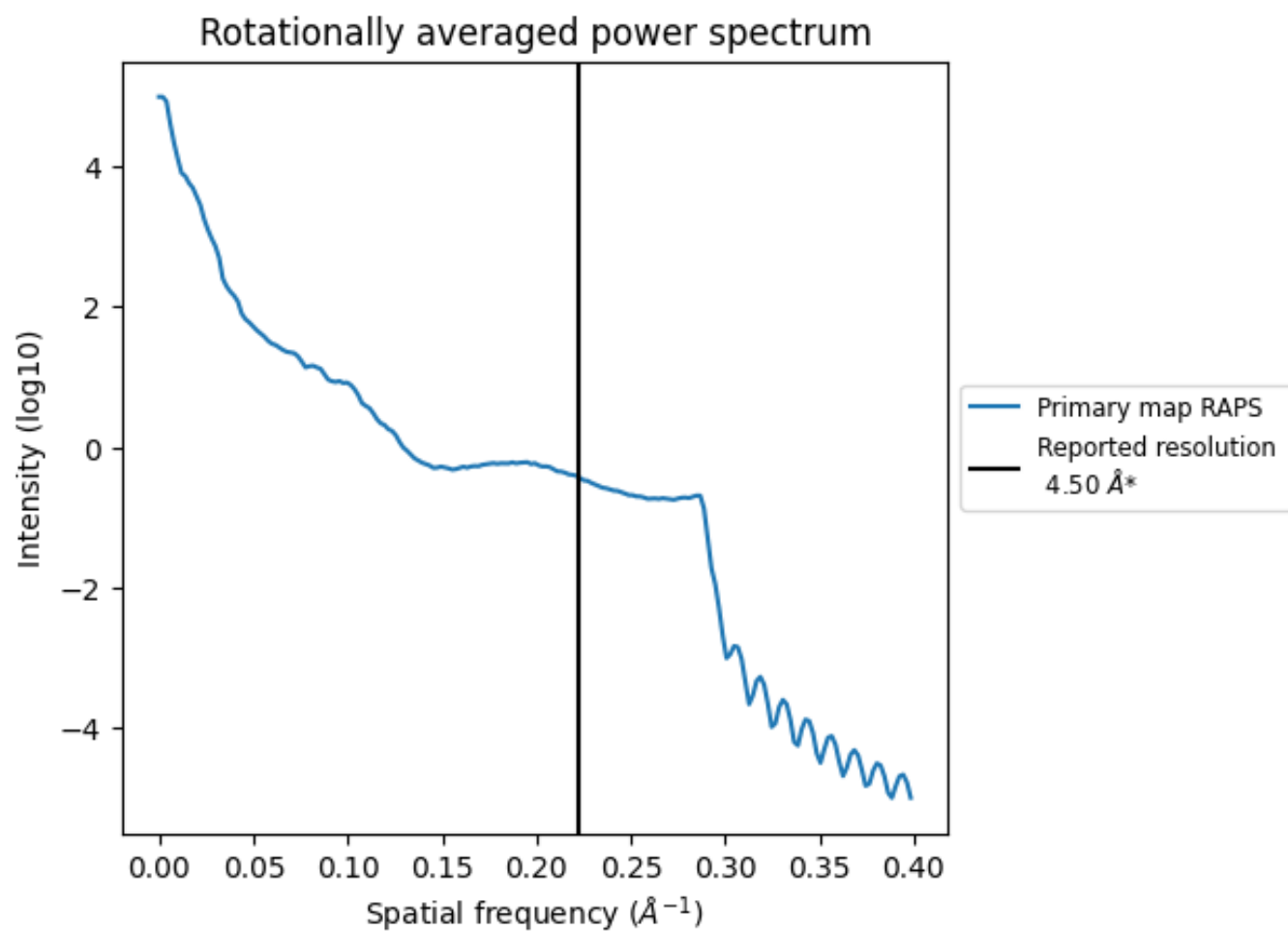
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 830 nm³; this corresponds to an approximate mass of 750 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

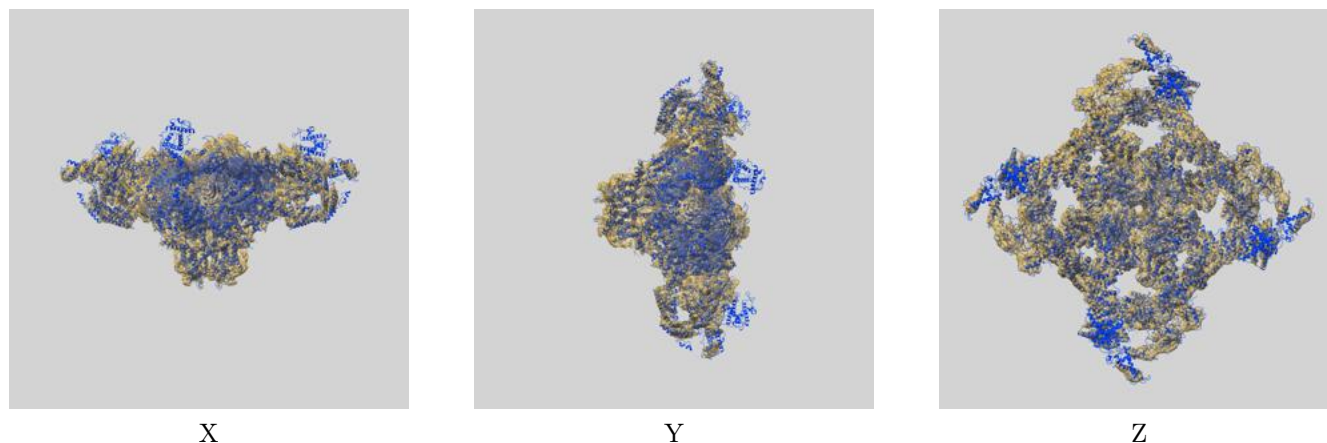
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

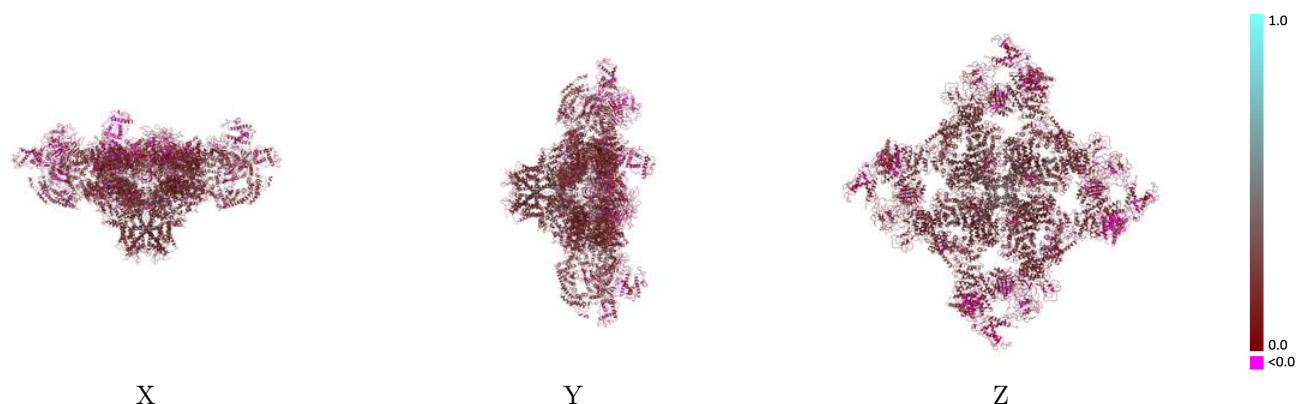
This section contains information regarding the fit between EMDB map EMD-20486 and PDB model 6PV6. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



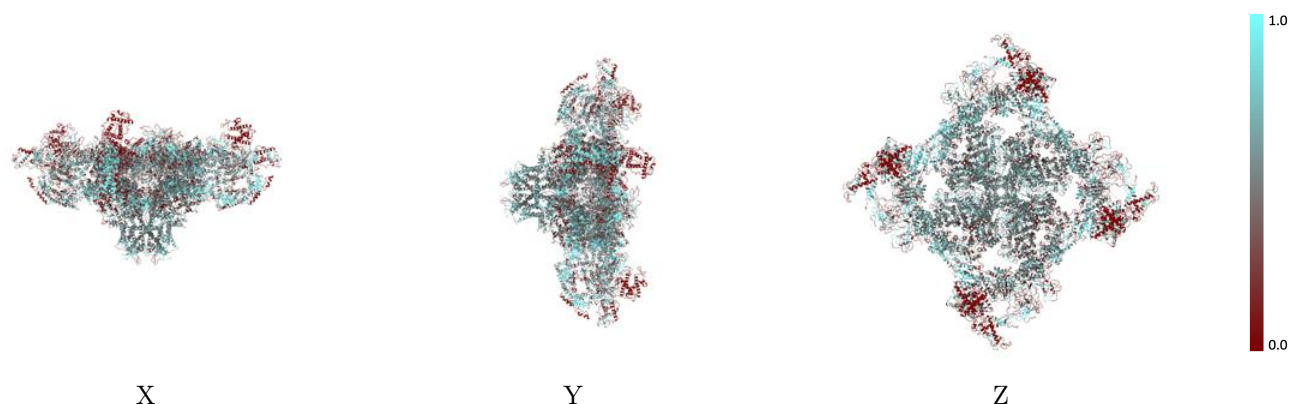
The images above show the 3D surface view of the map at the recommended contour level 0.166 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



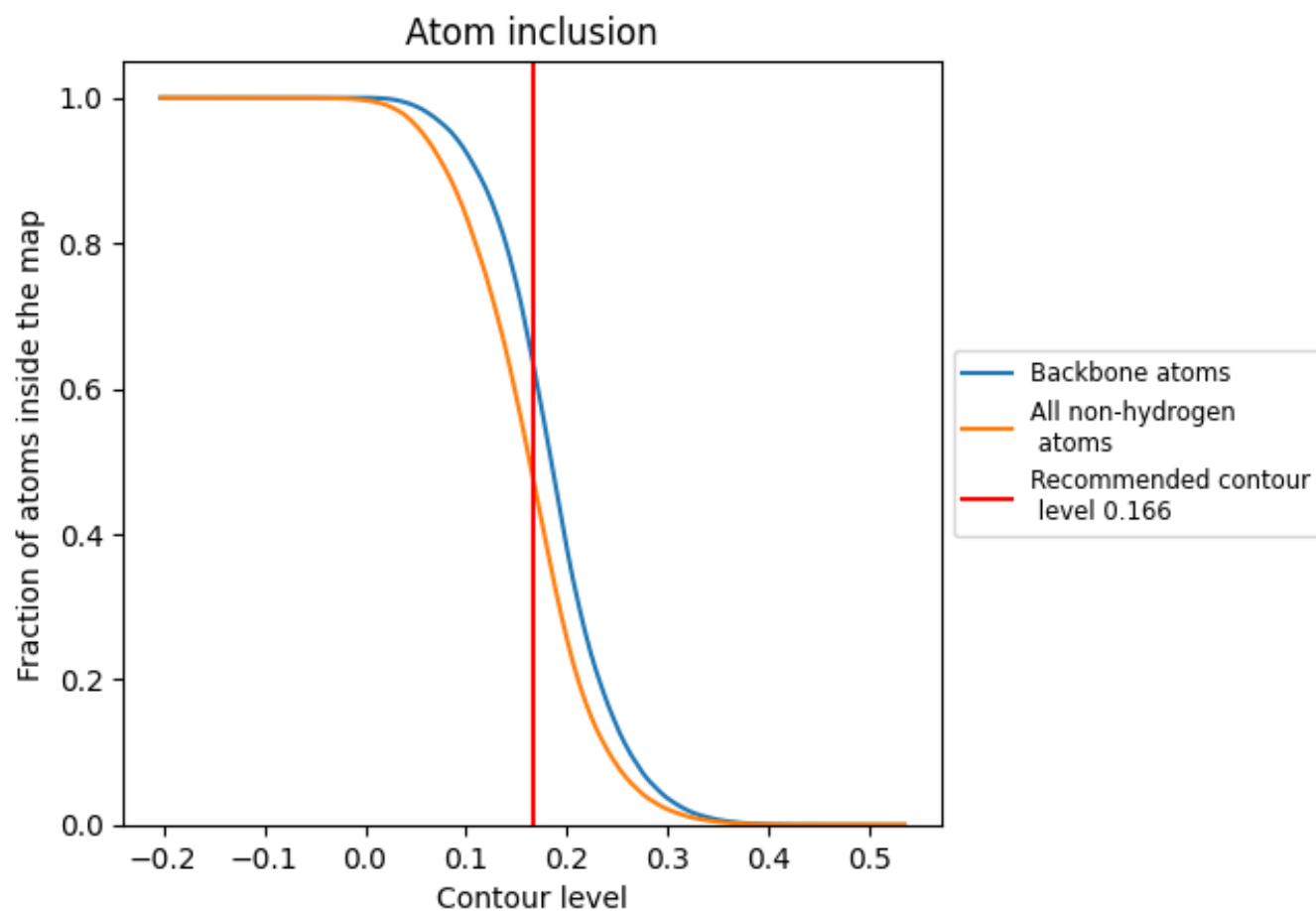
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.166).

9.4 Atom inclusion [i](#)



At the recommended contour level, 64% 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 (0.166) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.4791	<div></div> 0.1800
A	<div></div> 0.4851	<div></div> 0.1850
B	<div></div> 0.4972	<div></div> 0.1950
E	<div></div> 0.4766	<div></div> 0.1780
F	<div></div> 0.4268	<div></div> 0.1320
G	<div></div> 0.4624	<div></div> 0.1660
H	<div></div> 0.4107	<div></div> 0.1400
I	<div></div> 0.4837	<div></div> 0.1860
J	<div></div> 0.4702	<div></div> 0.1810

