



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:37 PM UTC

PDB ID : 7K17 / pdb_00007k17
Title : Re-refined crystal structure of DNA-dependent protein kinase catalytic subunit complexed with Ku80 C-terminal helix
Authors : Chen, X.; Gellert, M.; Yang, W.
Deposited on : 2020-09-07
Resolution : 4.30 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

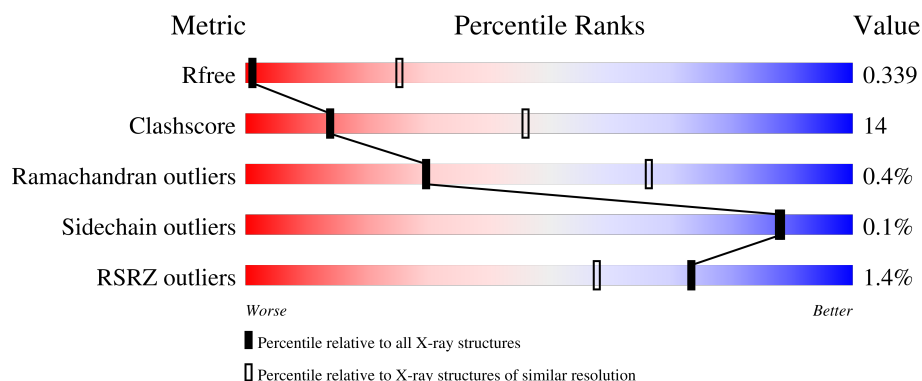
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

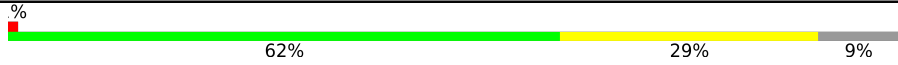
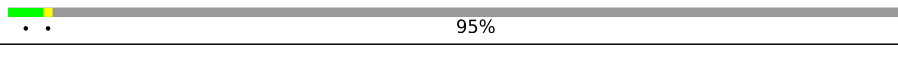
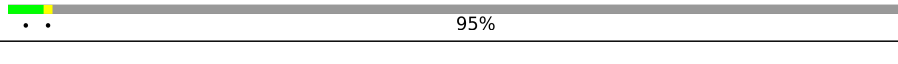
The reported resolution of this entry is 4.30 Å.

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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1052 (4.70-3.90)
Clashscore	190562	1097 (4.70-3.90)
Ramachandran outliers	187476	1001 (4.70-3.90)
Sidechain outliers	187428	1007 (4.72-3.88)
RSRZ outliers	180081	1049 (4.70-3.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	3986	
1	B	3986	
2	C	192	
2	D	192	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 56895 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called DNA-dependent protein kinase catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	3629	Total	C	N	O	S	0	0	0
			28238	18117	4751	5184	186			
1	B	3645	Total	C	N	O	S	0	0	0
			28521	18300	4815	5221	185			

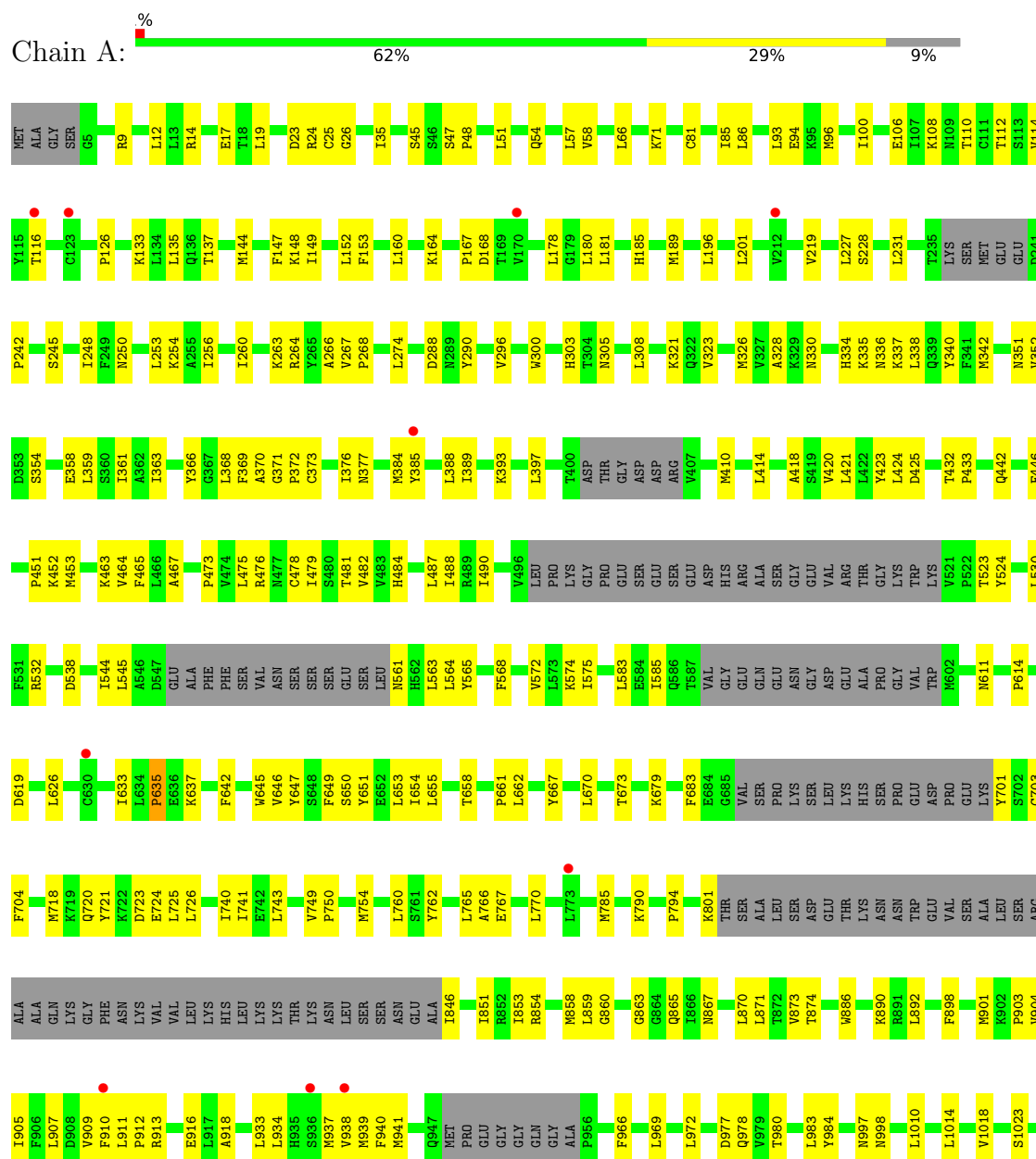
- Molecule 2 is a protein called X-ray repair cross-complementing protein 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	9	Total	C	N	O	S	0	0	0
			68	43	9	15	1			
2	C	9	Total	C	N	O	S	0	0	0
			68	43	9	15	1			

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: DNA-dependent protein kinase catalytic subunit

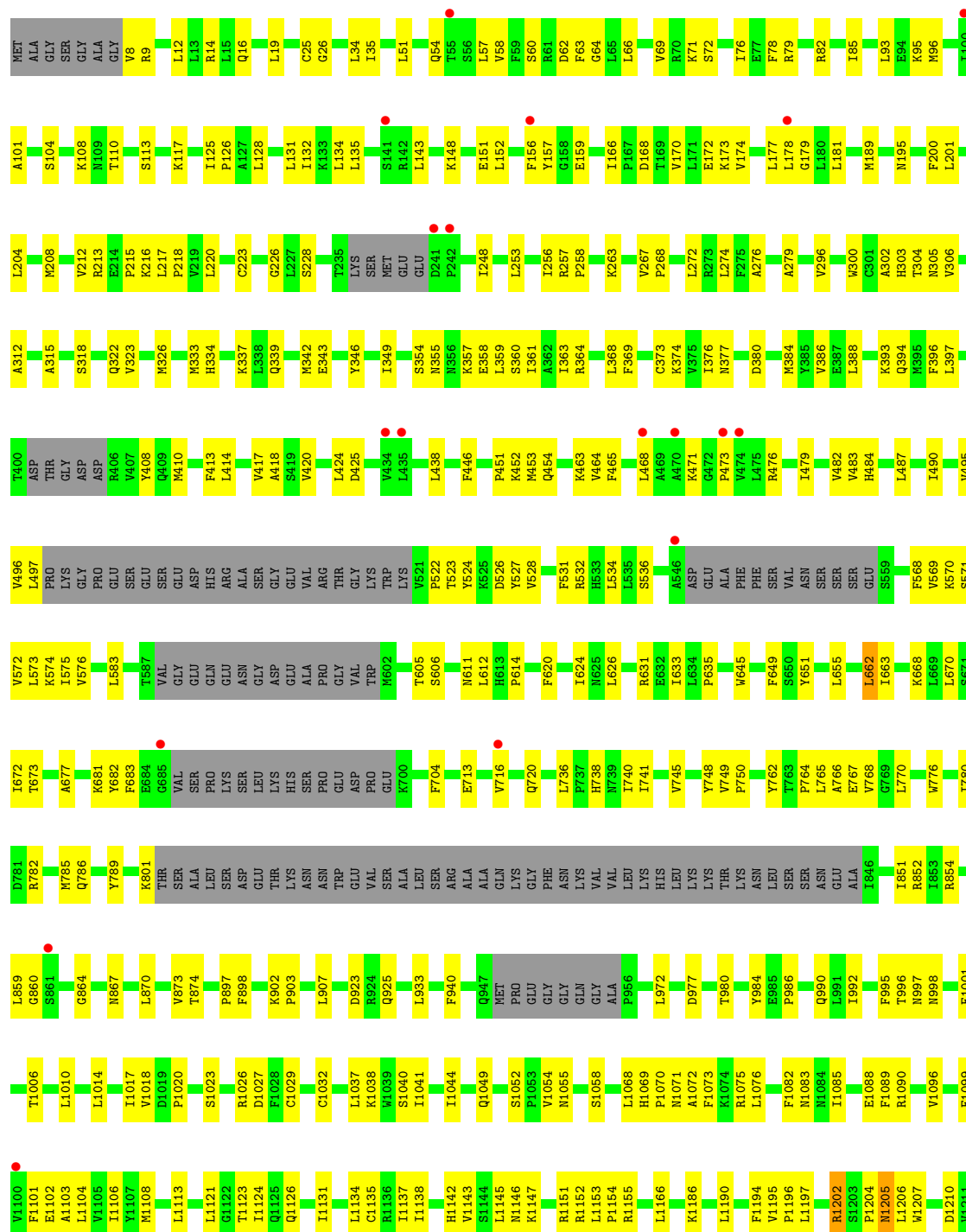




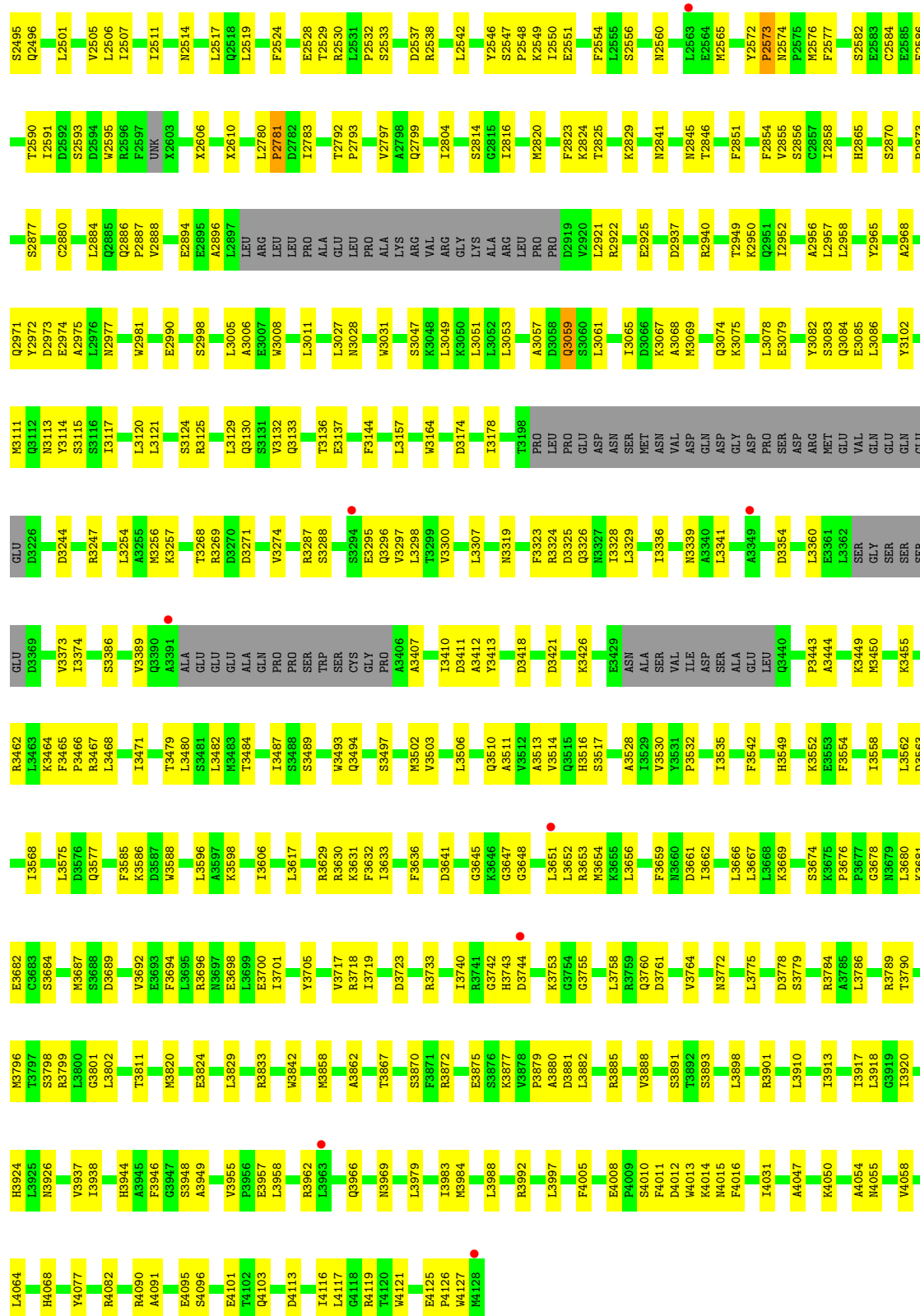
I3920	M3796	E3553	M3450	SER	Q3133	N3028	ALA	L2812	V2322
H3924	T3797	F3554	L3451	GLY	E3137	K3029	LYS	D2436	L2436
I3925	S3798	V3555	R3462	SER	I3138	I3030	ARG	D2437	D2437
M3929	R3799	L3463	K3463	SER	I3138	W3031	VAL	L2439	L2439
V3930	G3801	K3559	K3464	GLU	F3144	T3039	GLY	M2443	R2328
V3937	L3802	L3562	R3467	D3369	N3150	Y3043	LYS	E2338	Y2329
I3938	T3811	V3567	L3468	H3384	K3257	Y3043	ALA	L2446	E2338
G3939	L3812	K3585	L3468	L3385	L3258	K3248	ARG	K2447	L2446
I3940	D3814	L3575	I3471	S3386	L3259	L3049	LEU	P2448	L2341
F3946	S3674	D3576	P3476	V3389	K3260	K3050	PRO	V2449	P2449
G3947	L3480	Q3577	L3480	Q3390	E3261	L3053	D2919	E2450	L2344
A3949	F3585	F3585	S3481	A3391	T3268	A3057	V2920	L2451	L2344
V3955	D3587	K3588	L3482	GLU	R3269	Q3058	R2922	V2459	K2350
F3956	R3834	V3588	K3483	GLU	D3170	V3274	W2923	V2459	Q2351
E3957	L3687	S3589	I3487	ALA	A3171	S3275	E2925	H2464	T2355
R3962	E3698	N3590	S3488	GLN	D3174	L3061	E2925	P2465	M2356
K3975	L3699	R3593	S3489	PRO	D3181	L3062	L2926	C2469	K2359
E3976	V3700	L3596	V3490	PRO	R3186	F3064	R2931	Q2472	K2366
T3977	I3701	T3599	Q3494	TRP	F3189	I3077	G2934	M2473	T2368
I3983	G3707	T3599	S3497	SER	K3192	L3078	E2935	L2476	F2371
L3988	R3708	P3600	W3498	CYS	K3192	H3081	P2936	L2477	P2372
R3989	I3719	V3601	M3502	PRO	K3196	Y3082	R2940	M2478	P2373
R3992	T3727	L3606	V3503	ALA	T3198	S3083	I2942	W2479	L2374
S3993	R3733	E3607	L3506	D3411	PRO	Q3084	E2946	D2492	A2375
L3998	R3737	L3617	A3511	A3412	LEU	Q3085	I2952	S2495	F2378
T3999	I3740	D3619	V3514	F3419	GLU	L3088	L2957	I2498	F2389
F4005	R3759	A3622	Q3515	ASP	ASP	L3091	E2967	V2505	L2393
V4006	Q3760	P3623	H3516	ASN	SER	D3094	Q2971	L2506	K2394
K4007	D3761	R3629	S3517	C3420	MET	D3095	Y2972	N2514	T2396
E4008	V3764	K3631	T3522	Q3423	ASN	R3098	Q2885	L2397	L2396
P4009	M3771	F3632	Q3527	E3429	VAL	Q3326	Q2885	L2517	L2398
S4010	N3772	I3633	P3532	ASN	ASP	Q3108	E2974	I2785	L2398
F4011	I3775	Q3634	F3534	SER	GLN	S3109	A2975	P2887	L2402
M4015	D3778	F3636	I3534	VAL	ASP	F3110	L2976	H2787	C2403
E4017	R3779	L3640	F3535	TLE	SER	S3115	W2981	L2790	R2404
Q4018	S3779	L3651	F3542	ASP	ASP	D3118	L2892	I2791	L2415
K4019	C3781	L3652	K3543	SER	ARG	V3119	L2893	I2792	T2409
R3901	L3786	R3653	D3544	ALA	MET	L3120	E2894	Q2795	E2410
L3910	L3786	M3654	T3545	GLU	GLU	L3121	A2989	A2796	D2419
W4027	R3789	K3655	S3546	LEU	VAL	S3124	L2996	V2797	F2420
I4028	T3790	L3656	H3549	Q3440	GLN	K3128	LEU	Q2798	V2421
G3919	P3795	S3657	K3550	V3447	GLN	L3129	PRO	R2800	Q2422
		F3659	K3552	K3449	GLU	D3020	ALA	D2801	V2434
					D3226	V3132	LEU	I2804	C2435



● Molecule 1: DNA-dependent protein kinase catalytic subunit







• Molecule 2: X-ray repair cross-complementing protein 5

Chain D: . . .

95%

GLU
ALA
LYS
LYS
LYS
LYS
ASP
GLN
GLN
VAL
THR
GLN
ALA
ALA
GLU
ILE
PHE
GLN
ASP
ASN
HIS
GLU
GLU
ASP
GLY
PRO
THR
ALA
LYS
LYS
LEU
LYS
THR
GLU
GLN
GLY
GLY
HIS
PHE
SER
VAL
SER
SER
SER
LEU
ALA
ALA
GLU
GLY
SER
SER
VAL
THR
SER
VAL
GLY
SER
ASN
VAL
PRO
ALA
GLU
PHE
ASN
ARG
VAL

LEU	VAL	LYS	LYS	GLN	LYS	LYS	LYS	ALA	SER	PHE	GLU	GLU	ALA	SER	ASN	GLN	LEU	ILE	LEU	ASN	HIS	ILE	GLU	GLN	PHE	PHE	LEU	ASP	THR	THR	GLU	GLU	PRO	TYR	PHE	TYR	MET	LYS	SER	SER	ILE	ASP	CYS	ILE	ILE	ARG	ALA	PHE	ARG	GLU	GLU	ALA	ILE	PHE	LYS	PHE	SER	GLU	GLU	GLN	ARG	PHE	ASN	ASN	PHE	LEU	LYS
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ALA	LEU	GLN	LYS	VAL	GLU	ILE	LYS	GLN	LEU	ASN	HIS	PHE	TRP	THR	ILE	VAL	VAL	GLN	ASP	GLY	ILE	THR	LEU	ILE	THR	LYS	GLU	GLU	ALA	SER	GLY	SER	SER	SER	VAL	THR	THR	GLU	ALA	ALA	LYS	LYS	PHE	LEU	ALA	ALA	PRO	LYS	ASP	ASP	LYS	PRO	SER	SER	GLY	ASP	THR	ALA	ALA	VAL	VAL	PHE	THR
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GLU
GLY
GLY
D724
L728
M731
I732

- Molecule 2: X-ray repair cross-complementing protein 5

Chain C: 95%

GLU
ALA
LYS
LYS
LYS
LYS
ASP
GLN
VAL
THR
GLN
ALA
ALA
GLU
ILE
PHE
GLN
ASP
ASN
HIS
GLU
ASP
GLY
PRO
THR
ALA
LYS
LYS
LEU
LYS
THR
GLU
GLN
GLY
GLY
HIS
PHE
SER
VAL
SER
SER
LEU
ALA
ALA
GLY
GLY
VAL
VAL
THR
SER
VAL
GLY
SER
VAL
ASN
PRO
ALA
GLU
PHE
ASN
ARG
VAL

LEU	VAL	LYS	GLN	LYS	LYS	ALA	SER	GLU	GLU	ALA	SER	ASN	GLN	LEU	ILE	ASN	HIS	ILE	GLU	GLN	PHE	LEU	LEU	ASP	THR	ASN	GLU	THR	PRO	TYR	PHE	MET	LYS	SER	ILE	ASP	CYS	ILE	ILE	ALA	ARG	PHE	ARG	GLU	GLU	ALA	ILE	LYS	PHE	SER	GLU	GLU	GLN	ARG	PHE	ASN	ASN	PHE	LEU	LYS
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[illegible]

GLU
GLY
GLY
D724
L729
I732

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	169.12Å 132.64Å 296.59Å 90.00° 105.53° 90.00°	Depositor
Resolution (Å)	49.92 – 4.30 49.92 – 4.30	Depositor EDS
% Data completeness (in resolution range)	97.8 (49.92-4.30) 97.6 (49.92-4.30)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.33 (at 4.29Å)	Xtriage
Refinement program	PHENIX 1.14 _3260	Depositor
R, R_{free}	0.286 , 0.335 0.289 , 0.339	Depositor DCC
R_{free} test set	2009 reflections (2.32%)	wwPDB-VP
Wilson B-factor (Å ²)	184.6	Xtriage
Anisotropy	0.337	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 196.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.019 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	56895	wwPDB-VP
Average B, all atoms (Å ²)	217.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.76% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.20	0/28603	0.49	2/38757 (0.0%)
1	B	0.20	0/28898	0.49	3/39125 (0.0%)
2	C	0.16	0/67	0.36	0/90
2	D	0.23	0/67	0.40	0/90
All	All	0.20	0/57635	0.49	5/78062 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	1
All	All	0	3

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1846	ASP	N-CA-C	-7.62	103.05	113.18
1	A	2781	PRO	N-CA-CB	7.46	111.08	103.25
1	A	1995	GLU	N-CA-C	6.00	118.76	110.35
1	B	1611	GLN	CA-C-N	-5.27	111.47	121.54
1	B	1611	GLN	C-N-CA	-5.27	111.47	121.54

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1994	VAL	Peptide
1	A	2120	ARG	Peptide

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Mol	Chain	Res	Type	Group
1	B	1202	ARG	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	28238	0	27963	817	0
1	B	28521	0	28367	808	0
2	C	68	0	64	1	0
2	D	68	0	64	1	0
All	All	56895	0	56458	1627	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 14.

All (1627) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:ILE:HG22	1:A:300:TRP:CZ2	1.96	1.00
1:B:3701:ILE:HD12	1:B:3740:ILE:HD11	1.50	0.94
1:A:645:TRP:O	1:A:649:PHE:HB2	1.71	0.91
1:A:1406:LEU:HB3	1:A:1415:LEU:HD11	1.51	0.89
1:B:2459:VAL:HB	1:B:2505:VAL:HG21	1.55	0.88
1:A:3028:ASN:HA	1:A:3031:TRP:HD1	1.39	0.86
1:A:385:TYR:CE2	1:A:389:ILE:HD11	2.10	0.86
1:A:3662:ILE:HA	1:A:3665:MET:HE2	1.58	0.84
1:A:354:SER:HB3	1:A:358:GLU:HB2	1.62	0.82
1:B:1608:ARG:HA	1:B:1612:LYS:HB3	1.62	0.81
1:A:1676:ILE:O	1:A:1680:ALA:HB2	1.81	0.79
1:A:3545:THR:HG22	1:A:3546:SER:H	1.47	0.79
1:B:1615:GLY:HA3	1:B:1655:ILE:HG21	1.61	0.79
1:B:3325:ASP:HA	1:B:3328:ILE:HD12	1.65	0.79
1:B:3700:GLU:HA	1:B:3718:ARG:HA	1.64	0.78
1:A:260:ILE:HG22	1:A:300:TRP:CH2	2.19	0.78
1:A:1204:PRO:HB2	1:A:1275:THR:HG22	1.65	0.78
1:B:583:LEU:HA	1:B:614:PRO:HA	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1579:VAL:HG21	1:B:1621:THR:HG21	1.66	0.78
1:A:873:VAL:HG13	1:A:874:THR:H	1.48	0.77
1:B:135:LEU:HD12	1:B:177:LEU:HD11	1.67	0.77
1:B:1686:LEU:HD11	1:B:1721:HIS:HB3	1.66	0.76
1:A:3930:VAL:HG12	1:A:3937:VAL:HG12	1.67	0.76
1:A:1787:ARG:HB3	1:A:1831:CYS:HB3	1.66	0.76
1:B:873:VAL:HG13	1:B:874:THR:H	1.50	0.76
1:A:801:LYS:HA	1:A:3115:SER:HB2	1.68	0.76
1:A:2825:THR:HG22	1:A:2826:LEU:H	1.51	0.76
1:A:2216:LEU:HD11	1:A:2220:MET:HE3	1.67	0.75
1:B:3700:GLU:HG3	1:B:3718:ARG:HG2	1.66	0.75
1:A:1178:ARG:NH1	1:A:1183:CYS:SG	2.59	0.75
1:B:1068:LEU:HD11	1:B:1106:ILE:HG13	1.68	0.75
1:B:1076:LEU:HB2	1:B:1123:THR:HG22	1.68	0.75
1:B:1832:SER:H	1:B:1883:ARG:HH22	1.34	0.75
1:B:2851:PHE:HB3	1:B:2854:PHE:HB3	1.69	0.75
1:A:363:ILE:HG23	1:A:388:LEU:HD11	1.69	0.74
1:A:770:LEU:HD23	1:A:854:ARG:HD3	1.68	0.74
1:B:1090:ARG:HB2	1:B:1137:ILE:HG12	1.68	0.74
1:B:1406:LEU:HB3	1:B:1415:LEU:HD11	1.70	0.74
1:B:1727:ARG:HD2	1:B:1773:VAL:HG23	1.69	0.74
1:A:66:LEU:HD21	1:A:106:GLU:HB3	1.69	0.74
1:A:1082:PHE:HZ	1:A:1134:LEU:HG	1.53	0.73
1:B:1955:VAL:HG13	1:B:1956:PHE:H	1.52	0.73
1:A:14:ARG:HA	1:A:17:GLU:HG2	1.70	0.73
1:B:2965:TYR:HA	1:B:2968:ALA:HB3	1.70	0.73
1:A:35:ILE:HD12	1:A:81:CYS:HB2	1.70	0.73
1:A:3503:VAL:HG21	1:A:3532:PRO:HB2	1.71	0.73
1:A:300:TRP:CE3	1:A:308:LEU:HD21	2.24	0.73
1:B:2451:LEU:HD23	1:B:2484:TYR:HE2	1.54	0.73
1:A:1697:PRO:HB3	1:A:1753:SER:HB3	1.71	0.73
1:A:3515:GLN:NE2	1:A:3551:ASN:OD1	2.22	0.72
1:B:4011:PHE:HA	1:B:4015:ASN:HB2	1.70	0.72
1:A:3144:PHE:O	1:A:3150:ASN:ND2	2.22	0.72
1:B:1825:LEU:HD22	1:B:1879:VAL:HG21	1.70	0.72
1:A:1090:ARG:HB2	1:A:1137:ILE:HG12	1.70	0.72
1:A:2837:LEU:O	1:A:2841:ASN:ND2	2.21	0.72
1:A:260:ILE:HA	1:A:300:TRP:CH2	2.24	0.72
1:B:1991:PRO:HG2	1:B:2000:ARG:HH22	1.55	0.72
1:B:2823:PHE:HD1	1:B:2824:LYS:HG2	1.53	0.72
1:A:4011:PHE:HA	1:A:4015:ASN:HB2	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4042:GLN:NE2	1:A:4046:TYR:CE2	2.57	0.71
1:B:424:LEU:O	1:B:471:LYS:NZ	2.22	0.71
1:B:3137:GLU:OE1	1:B:3164:TRP:NE1	2.22	0.71
1:A:228:SER:HA	1:A:274:LEU:HD13	1.71	0.71
1:B:1892:LYS:H	1:B:1892:LYS:HD2	1.55	0.71
1:A:1845:VAL:HA	1:A:1848:ILE:HG22	1.72	0.71
1:A:3695:LEU:HD12	1:A:3698:GLU:HG2	1.71	0.71
1:B:394:GLN:HB3	1:B:1687:HIS:HB2	1.72	0.71
1:B:1817:GLN:NE2	1:B:1871:MET:SD	2.64	0.71
1:B:19:LEU:HD22	1:B:71:LYS:HG3	1.73	0.71
1:B:3833:ARG:HB3	1:B:3877:LYS:HE2	1.73	0.71
1:A:1373:VAL:HG11	1:A:1422:LYS:HE3	1.74	0.70
1:A:3667:LEU:HA	1:A:3670:MET:HE3	1.74	0.70
1:B:2148:LYS:O	1:B:2152:ASN:ND2	2.23	0.70
1:A:1955:VAL:HG23	1:A:1957:ASN:H	1.56	0.70
1:B:1257:LEU:HD22	1:B:1337:VAL:HG11	1.73	0.70
1:A:1406:LEU:HD13	1:A:1415:LEU:HD21	1.74	0.70
1:B:3549:HIS:HA	1:B:3552:LYS:HE2	1.72	0.70
1:A:762:TYR:HB3	1:A:765:LEU:HD22	1.72	0.69
1:A:3772:ASN:HA	1:A:3775:LEU:HB2	1.73	0.69
1:B:990:GLN:HG2	1:B:2780:LEU:O	1.90	0.69
1:B:1766:LEU:HG	1:B:1778:PHE:HD2	1.56	0.69
1:B:54:GLN:HA	1:B:57:LEU:HB3	1.73	0.69
1:B:228:SER:HA	1:B:274:LEU:HD13	1.74	0.69
1:B:2880:CYS:HB3	1:B:2886:GLN:HA	1.73	0.69
1:A:1850:VAL:O	1:A:1870:LYS:NZ	2.25	0.69
1:A:2887:PRO:HG2	1:A:3895:GLU:HG2	1.75	0.69
1:A:1257:LEU:HD22	1:A:1337:VAL:HG11	1.73	0.69
1:B:859:LEU:HG	1:B:867:ASN:HD21	1.56	0.69
1:A:148:LYS:HD3	1:A:148:LYS:H	1.57	0.69
1:A:4037:ASN:ND2	1:A:4066:LEU:O	2.25	0.69
1:A:160:LEU:HD21	1:A:178:LEU:HD12	1.76	0.68
1:A:1082:PHE:CZ	1:A:1134:LEU:HG	2.29	0.68
1:B:72:SER:O	1:B:82:ARG:NH1	2.26	0.68
1:B:323:VAL:HG13	1:B:369:PHE:HZ	1.59	0.68
1:B:992:ILE:O	1:B:996:THR:HG22	1.94	0.68
1:A:2290:PRO:HD3	1:A:2296:SER:HB3	1.76	0.68
1:B:2387:PRO:HG3	1:B:2418:LYS:HB3	1.74	0.68
1:A:1930:GLU:OE1	1:A:1937:ARG:NH2	2.26	0.68
1:A:2952:ILE:HD13	1:A:2975:ALA:HB2	1.75	0.68
1:B:3949:ALA:HB1	1:B:3957:GLU:HG3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2140:LEU:HD21	1:A:2178:GLY:HA2	1.76	0.68
1:B:1896:ILE:HD13	1:B:1906:THR:HB	1.74	0.68
1:A:2281:MET:HE2	1:A:2326:ILE:HA	1.75	0.67
1:A:3545:THR:HG22	1:A:3546:SER:N	2.09	0.67
1:B:2290:PRO:HD3	1:B:2296:SER:HB3	1.76	0.67
1:A:330:ASN:HB2	1:A:334:HIS:CD2	2.29	0.67
1:A:3577:GLN:HG3	1:A:3630:ARG:HD3	1.76	0.67
1:B:339:GLN:NE2	1:B:343:GLU:OE2	2.28	0.67
1:B:1406:LEU:HD13	1:B:1415:LEU:HD21	1.76	0.67
1:B:1147:LYS:O	1:B:1151:ARG:NH2	2.27	0.67
1:B:1398:VAL:HA	1:B:1401:ASN:HB2	1.75	0.67
1:A:1686:LEU:HD13	1:A:1721:HIS:HB3	1.77	0.67
1:A:1560:TYR:OH	1:A:1568:ASN:ND2	2.27	0.67
1:B:1440:ASP:HB2	1:B:1443:VAL:HG22	1.76	0.67
1:A:3775:LEU:HD11	1:A:3910:LEU:HD11	1.77	0.67
1:B:1828:LEU:O	1:B:1883:ARG:NH2	2.20	0.66
1:B:1483:LEU:HD22	1:B:1514:LEU:HD11	1.76	0.66
1:B:3775:LEU:HD11	1:B:3910:LEU:HD11	1.77	0.66
1:A:3462:ARG:NH1	1:A:3497:SER:OG	2.29	0.66
1:B:2194:LEU:HD11	1:B:2241:LEU:HD13	1.77	0.66
1:B:3503:VAL:HG21	1:B:3532:PRO:HB2	1.77	0.66
1:B:3585:PHE:HD2	1:B:3667:LEU:HD13	1.60	0.66
1:B:3758:LEU:HD12	1:B:3801:GLY:HA3	1.77	0.66
1:A:2148:LYS:O	1:A:2152:ASN:ND2	2.26	0.66
1:A:2312:TYR:HB3	1:A:2315:VAL:HG12	1.78	0.66
1:B:1626:TRP:CD1	1:B:1671:VAL:HG12	2.31	0.66
1:A:3339:ASN:ND2	1:A:3422:GLN:OE1	2.29	0.66
1:B:1612:LYS:C	1:B:1614:GLN:H	2.02	0.66
1:B:1984:LEU:HD11	1:B:2139:PRO:HG2	1.77	0.66
1:B:1361:LYS:HA	1:B:1364:CYS:HB2	1.78	0.65
1:B:272:LEU:HB3	1:B:315:ALA:HB2	1.77	0.65
1:A:903:PRO:HG3	1:A:2816:ILE:HG12	1.77	0.65
1:A:4083:GLY:HA3	1:A:4091:ALA:HB2	1.77	0.65
1:A:328:ALA:HA	1:A:372:PRO:HB3	1.79	0.65
1:A:1052:SER:HB2	1:A:1055:ASN:HB2	1.77	0.65
1:A:4064:LEU:HD13	1:A:4077:TYR:HB3	1.76	0.65
1:B:1038:LYS:NZ	1:B:1088:GLU:OE2	2.30	0.65
1:B:1750:LEU:HD13	1:B:1758:LEU:HB2	1.79	0.65
1:B:3946:PHE:O	1:B:3948:SER:N	2.27	0.65
1:B:1345:THR:HG21	1:B:1368:LEU:HD21	1.78	0.65
1:B:1750:LEU:HG	1:B:1785:ILE:HD11	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2448:PRO:HB3	1:A:2498:ILE:HD13	1.79	0.64
1:B:1612:LYS:O	1:B:1614:GLN:N	2.29	0.64
1:A:178:LEU:HB3	1:A:196:LEU:HD11	1.79	0.64
1:A:2286:PRO:HB3	1:A:2329:TYR:CE2	2.32	0.64
1:A:2458:VAL:HG11	1:A:2476:ILE:HD11	1.78	0.64
1:A:2856:SER:HA	1:A:2888:VAL:HG11	1.79	0.64
1:B:363:ILE:HG23	1:B:388:LEU:HD11	1.79	0.64
1:B:1108:MET:HG3	1:B:1131:ILE:HG21	1.80	0.64
1:B:1969:GLU:HB3	1:B:1977:ILE:HG13	1.79	0.64
1:B:2216:LEU:HD11	1:B:2220:MET:HE3	1.78	0.64
1:A:2181:GLY:O	1:A:2183:HIS:N	2.30	0.64
1:A:2409:THR:O	1:A:2411:LEU:N	2.31	0.64
1:B:2952:ILE:HD13	1:B:2975:ALA:HB2	1.80	0.64
1:B:3880:ALA:HB1	1:B:3969:ASN:HD22	1.62	0.64
1:A:160:LEU:O	1:A:164:LYS:NZ	2.22	0.64
1:B:66:LEU:HD11	1:B:110:THR:HG21	1.79	0.64
1:B:572:VAL:HG23	1:B:626:LEU:HD11	1.79	0.64
1:B:704:PHE:CE1	1:B:741:ILE:HG12	2.33	0.64
1:B:2011:ALA:HA	1:B:2195:SER:HA	1.80	0.64
1:A:2148:LYS:HA	1:A:2151:ILE:HD12	1.80	0.63
1:B:3005:LEU:HA	1:B:3254:LEU:HD13	1.80	0.63
1:B:35:ILE:HD13	1:B:85:ILE:HG13	1.79	0.63
1:B:373:CYS:SG	1:B:376:ILE:HG21	2.37	0.63
1:B:3468:LEU:HA	1:B:3471:ILE:HG22	1.79	0.63
1:A:3137:GLU:OE1	1:A:3164:TRP:NE1	2.32	0.63
1:B:1845:VAL:HA	1:B:1848:ILE:HG22	1.81	0.63
1:B:1877:LEU:O	1:B:1881:TYR:HB2	1.99	0.63
1:B:2133:LEU:HB2	1:B:2146:LEU:HD23	1.81	0.63
1:A:3587:ASP:OD2	1:A:3733:ARG:NH1	2.32	0.63
1:B:1623:LEU:HD22	1:B:1671:VAL:HG11	1.81	0.63
1:B:2148:LYS:HA	1:B:2151:ILE:HD12	1.80	0.63
1:B:359:LEU:O	1:B:363:ILE:HG12	1.99	0.63
1:B:3328:ILE:HD11	1:B:3412:ALA:HB2	1.81	0.63
1:A:93:LEU:HD12	1:A:100:ILE:HD13	1.81	0.62
1:B:1525:CYS:SG	1:B:1574:ASN:ND2	2.70	0.62
1:A:1825:LEU:O	1:A:1829:TRP:HB2	1.98	0.62
1:B:3027:LEU:HG	1:B:3067:LYS:HD2	1.81	0.62
1:A:2356:MET:HE3	1:A:2359:LYS:HD3	1.81	0.62
1:A:3813:LYS:HB2	1:A:3925:LEU:HB3	1.81	0.62
1:B:3879:PRO:O	1:B:3966:GLN:NE2	2.31	0.62
1:A:3468:LEU:HA	1:A:3471:ILE:HG22	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:148:LYS:HB3	1:B:151:GLU:HB2	1.80	0.62
1:A:1582:LEU:HG	1:A:1593:VAL:HG23	1.81	0.62
1:B:1992:VAL:HG12	1:B:2183:HIS:CD2	2.35	0.62
1:A:1346:THR:HG22	1:A:1402:LEU:HA	1.82	0.62
1:A:2375:ALA:HB3	1:A:2404:ARG:HG2	1.82	0.62
1:B:1658:SER:HB3	1:B:1661:PHE:HE1	1.64	0.62
1:B:2085:MET:HA	1:B:2089:ASN:HB2	1.82	0.62
1:B:451:PRO:O	1:B:452:LYS:HG2	1.99	0.62
1:B:704:PHE:HE1	1:B:741:ILE:HG12	1.64	0.62
1:B:4117:LEU:HB3	1:B:4126:PRO:HB2	1.80	0.62
1:B:2458:VAL:HG11	1:B:2476:ILE:HD11	1.81	0.61
1:B:1820:VAL:O	1:B:1825:LEU:HG	2.00	0.61
1:A:1833:LEU:HG	1:A:1835:ALA:H	1.65	0.61
1:B:2538:ARG:NE	1:B:2565:MET:SD	2.73	0.61
1:A:1181:THR:HG22	1:A:1184:ARG:HH12	1.66	0.61
1:B:16:GLN:NE2	1:B:62:ASP:O	2.33	0.61
1:A:1166:LEU:H	1:A:1166:LEU:HD12	1.65	0.61
1:A:1106:ILE:HD11	1:A:1155:ARG:H	1.65	0.61
1:B:1992:VAL:HG23	1:B:1993:GLU:H	1.65	0.61
1:B:3630:ARG:O	1:B:3633:ILE:HG12	2.01	0.61
1:B:333:MET:SD	1:B:333:MET:N	2.72	0.61
1:B:1121:LEU:HD22	1:B:1123:THR:HG23	1.81	0.61
1:A:1448:LEU:HD23	1:A:1510:LEU:HD21	1.81	0.61
1:B:770:LEU:HD23	1:B:854:ARG:HD2	1.82	0.61
1:B:1143:VAL:HA	1:B:1197:LEU:HD21	1.82	0.61
1:A:3174:ASP:O	1:A:3249:GLN:NE2	2.30	0.61
1:A:3417:ALA:HB1	1:A:3450:MET:HE2	1.83	0.61
1:A:4064:LEU:O	1:A:4068:HIS:HB2	2.01	0.61
1:A:1533:LEU:HD22	1:A:1589:ASN:HB2	1.83	0.60
1:B:376:ILE:HG13	1:B:377:ASN:H	1.65	0.60
1:B:2442:MET:HE2	1:B:2446:LEU:HD11	1.82	0.60
1:A:1733:THR:HB	1:A:1736:PHE:H	1.66	0.60
1:A:2588:GLU:HG3	1:A:2785:ILE:HD11	1.83	0.60
1:A:2940:ARG:HG3	1:A:2957:LEU:HD22	1.81	0.60
1:B:864:GLY:HA2	1:B:867:ASN:HB2	1.83	0.60
1:A:1579:VAL:HG21	1:A:1621:THR:HG21	1.82	0.60
1:B:12:LEU:HD23	1:B:64:GLY:HA2	1.83	0.60
1:B:358:GLU:O	1:B:361:ILE:HG12	2.01	0.60
1:B:2178:GLY:O	1:B:2182:ILE:HB	2.00	0.60
1:A:3955:VAL:HG11	1:A:4121:TRP:CE3	2.37	0.60
1:B:1425:ALA:O	1:B:1429:GLU:HG2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:394:GLN:HE22	1:B:1688:LEU:HD23	1.67	0.60
1:B:3031:TRP:HZ2	1:B:3068:ALA:HB1	1.66	0.60
1:A:704:PHE:CE1	1:A:741:ILE:HG12	2.37	0.60
1:B:1212:LEU:HD13	1:B:1220:LEU:HD22	1.84	0.60
1:B:2234:ASN:HA	1:B:2237:ILE:HD12	1.83	0.60
1:A:300:TRP:HE3	1:A:308:LEU:HD21	1.67	0.60
1:A:647:TYR:HD1	1:A:703:CYS:HB3	1.67	0.60
1:A:2546:TYR:CE2	1:A:2548:PRO:HB3	2.36	0.60
1:A:2575:PRO:HB3	1:A:2787:HIS:NE2	2.17	0.60
1:A:2841:ASN:O	1:A:2845:ASN:ND2	2.29	0.60
1:B:4058:VAL:HG21	1:B:4095:GLU:HB3	1.84	0.60
1:A:321:LYS:HA	1:A:368:LEU:HD21	1.83	0.59
1:A:1574:ASN:HB3	1:A:1577:LEU:HD21	1.83	0.59
1:B:1743:MET:HG3	1:B:1774:MET:HE1	1.84	0.59
1:B:3079:GLU:HB2	1:B:3102:TYR:HE1	1.67	0.59
1:B:3842:TRP:HH2	1:B:3867:THR:HG22	1.66	0.59
1:A:54:GLN:HA	1:A:57:LEU:HB3	1.85	0.59
1:A:1892:LYS:H	1:A:1892:LYS:HD3	1.67	0.59
1:B:3733:ARG:NH2	1:B:3755:GLY:O	2.35	0.59
1:B:3842:TRP:CD1	1:B:3870:SER:HG	2.19	0.59
1:B:3028:ASN:HA	1:B:3031:TRP:HD1	1.66	0.59
1:A:1255:CYS:SG	1:A:3695:LEU:HD23	2.42	0.59
1:A:1676:ILE:O	1:A:1680:ALA:CB	2.50	0.59
1:A:3309:GLU:HG2	1:A:3310:ASN:H	1.66	0.59
1:A:3789:ARG:HG2	1:A:3938:ILE:HD12	1.82	0.59
1:B:903:PRO:HG3	1:B:2816:ILE:HG12	1.84	0.59
1:B:1302:ALA:HA	1:B:1382:ILE:HA	1.83	0.59
1:B:1828:LEU:HB3	1:B:1879:VAL:HG11	1.84	0.59
1:B:3484:THR:HG22	1:B:3513:ALA:HA	1.83	0.59
1:A:487:LEU:HD21	1:A:568:PHE:HE1	1.68	0.59
1:A:3696:ARG:HD2	1:A:3697:ASN:H	1.67	0.59
1:B:156:PHE:HA	1:B:159:GLU:HB2	1.85	0.59
1:B:473:PRO:HA	1:B:476:ARG:HG2	1.83	0.59
1:A:366:TYR:CE2	1:A:384:MET:HG2	2.37	0.59
1:A:2373:PRO:HA	1:A:2404:ARG:HE	1.67	0.59
1:B:166:ILE:HG22	1:B:168:ASP:H	1.68	0.59
1:B:1612:LYS:HG3	1:B:1613:HIS:H	1.68	0.59
1:A:1686:LEU:H	1:A:1686:LEU:HD23	1.68	0.59
1:A:3795:PRO:HA	1:A:3801:GLY:HA2	1.85	0.59
1:A:572:VAL:HG23	1:A:626:LEU:HD21	1.83	0.59
1:B:522:PRO:HB3	1:B:526:ASP:CG	2.28	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:ILE:CG2	1:A:300:TRP:CZ2	2.81	0.58
1:B:1138:ILE:HG21	1:B:1194:PHE:CE1	2.39	0.58
1:B:1881:TYR:CE1	1:B:1889:VAL:HG21	2.38	0.58
1:B:3130:GLN:HB3	1:B:3178:ILE:HG12	1.84	0.58
1:A:1483:LEU:HD22	1:A:1514:LEU:HD11	1.85	0.58
1:A:3110:PHE:HD1	1:A:3128:LYS:HD2	1.68	0.58
1:B:1362:ASP:O	1:B:1367:HIS:ND1	2.21	0.58
1:A:1783:ARG:HB3	1:A:1830:HIS:CD2	2.38	0.58
1:B:1427:SER:HA	1:B:1430:GLU:HG2	1.84	0.58
1:B:1582:LEU:HG	1:B:1593:VAL:HG23	1.86	0.58
1:A:1675:TYR:O	1:A:1679:LEU:HD23	2.04	0.58
1:A:2249:LEU:O	1:A:2251:ILE:N	2.36	0.58
1:A:3121:LEU:O	1:A:3124:SER:OG	2.21	0.58
1:A:3962:ARG:NH1	1:A:4128:MET:O	2.35	0.58
1:B:3514:VAL:HG23	1:B:3517:SER:HB2	1.85	0.58
1:A:260:ILE:HG22	1:A:300:TRP:CE2	2.39	0.58
1:A:670:LEU:HA	1:A:673:THR:HG22	1.85	0.58
1:A:2522:ARG:HG3	1:A:2561:PHE:HE1	1.68	0.58
1:A:3630:ARG:O	1:A:3633:ILE:HG12	2.02	0.58
1:B:1801:VAL:HB	1:B:1824:LEU:HD12	1.86	0.58
1:A:4005:PHE:O	1:A:4011:PHE:HZ	1.86	0.58
1:A:3057:ALA:C	1:A:3059:GLN:H	2.12	0.58
1:A:3587:ASP:HB3	1:A:4022:LYS:HE2	1.85	0.58
1:A:4042:GLN:HE21	1:A:4046:TYR:HE2	1.50	0.58
1:B:859:LEU:O	1:B:867:ASN:ND2	2.36	0.58
1:B:1831:CYS:HA	1:B:1883:ARG:HH12	1.69	0.58
1:B:2490:GLU:OE1	1:B:2496:GLN:NE2	2.37	0.58
1:B:3421:ASP:OD1	1:B:3467:ARG:NE	2.37	0.58
1:A:260:ILE:HA	1:A:300:TRP:HH2	1.67	0.58
1:A:2234:ASN:HA	1:A:2237:ILE:HD12	1.86	0.58
1:B:2201:THR:HB	1:B:2205:VAL:H	1.68	0.58
1:B:3407:ALA:HA	1:B:3410:ILE:HG12	1.86	0.58
1:B:4055:ASN:HB2	1:B:4095:GLU:HA	1.86	0.58
1:A:3696:ARG:HD2	1:A:3697:ASN:N	2.18	0.57
1:B:2459:VAL:HG21	1:B:2501:LEU:HD11	1.86	0.57
1:B:3462:ARG:HG3	1:B:3494:GLN:HB3	1.85	0.57
1:A:2255:LEU:HD23	1:A:2256:ILE:H	1.69	0.57
1:B:2150:VAL:HG13	1:B:2157:PHE:CD2	2.39	0.57
1:A:901:MET:HE2	1:A:2819:GLU:HB3	1.86	0.57
1:B:1279:LEU:H	1:B:1279:LEU:HD23	1.69	0.57
1:B:1930:GLU:HB3	1:B:1937:ARG:HH12	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:25:CYS:SG	1:A:26:GLY:N	2.77	0.57
1:A:724:GLU:HG2	1:A:725:LEU:N	2.18	0.57
1:A:1023:SER:HA	1:A:1026:ARG:HE	1.69	0.57
1:A:1976:LEU:HD22	1:A:1979:GLU:HG3	1.87	0.57
1:A:3549:HIS:HA	1:A:3552:LYS:HE2	1.85	0.57
1:B:1605:PHE:CE1	1:B:1608:ARG:HD3	2.40	0.57
1:A:1103:ALA:HB1	1:A:1106:ILE:HB	1.86	0.57
1:A:2294:ILE:HG22	1:A:2295:GLN:H	1.70	0.57
1:A:3946:PHE:O	1:A:3948:SER:N	2.30	0.57
1:B:1619:ALA:HB1	1:B:1652:ILE:HG23	1.85	0.57
1:A:892:LEU:HB3	1:A:940:PHE:HE2	1.70	0.57
1:B:2119:PRO:N	1:B:2163:HIS:HE2	2.02	0.57
1:B:3789:ARG:HG2	1:B:3938:ILE:HD12	1.85	0.57
1:A:760:LEU:HD13	1:A:760:LEU:O	2.05	0.57
1:A:2084:GLU:O	1:A:2089:ASN:ND2	2.38	0.57
1:A:2610:UNK:O	1:A:2614:UNK:CB	2.52	0.57
1:A:2894:GLU:OE2	1:A:3901:ARG:NH2	2.37	0.57
1:B:1298:LEU:HB3	1:B:1367:HIS:HB3	1.86	0.57
1:B:1837:ARG:HH11	1:B:1884:LEU:HD21	1.69	0.57
1:B:3698:GLU:HG3	1:B:3718:ARG:HD2	1.87	0.57
1:A:1212:LEU:HD13	1:A:1220:LEU:HD22	1.86	0.57
1:B:583:LEU:HD12	1:B:611:ASN:ND2	2.20	0.57
1:A:3640:PHE:CZ	1:A:3670:MET:HG3	2.39	0.57
1:B:3684:SER:HB3	1:B:3687:MET:HE2	1.86	0.57
1:A:108:LYS:HE3	1:A:152:LEU:HD22	1.87	0.57
1:A:2591:ILE:HD13	1:A:2796:ALA:HB2	1.86	0.57
1:B:2528:GLU:O	1:B:2529:THR:HG22	2.05	0.57
1:B:3577:GLN:HG3	1:B:3630:ARG:HD3	1.85	0.57
1:A:662:LEU:HD23	1:A:662:LEU:H	1.70	0.56
1:A:1990:PHE:CZ	1:A:2144:LEU:HD21	2.40	0.56
1:A:3590:ASN:HA	1:A:3593:ARG:HG2	1.87	0.56
1:A:3820:MET:HB3	1:A:3824:GLU:HG3	1.86	0.56
1:B:3008:TRP:HB2	1:B:3051:LEU:HD13	1.87	0.56
1:B:3842:TRP:CH2	1:B:3867:THR:HG22	2.40	0.56
1:A:1076:LEU:HB2	1:A:1123:THR:HG22	1.88	0.56
1:A:1633:TRP:H	1:A:1633:TRP:CD1	2.22	0.56
1:A:2251:ILE:HD11	1:A:2288:TYR:CZ	2.40	0.56
1:A:2591:ILE:HD11	1:A:2792:THR:HB	1.88	0.56
1:A:3244:ASP:OD1	1:A:3247:ARG:NH1	2.37	0.56
1:A:3327:ASN:HB3	1:A:3384:HIS:O	2.06	0.56
1:B:414:LEU:HD12	1:B:464:VAL:HG21	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2359:LYS:H	1:B:2359:LYS:HD2	1.71	0.56
1:B:2797:VAL:HG13	1:B:2804:ILE:HG21	1.87	0.56
1:B:2877:SER:HB2	1:B:2925:GLU:HB3	1.86	0.56
1:B:3480:LEU:HD11	1:B:3510:GLN:OE1	2.05	0.56
1:B:3617:LEU:HD13	1:B:3636:PHE:CD2	2.41	0.56
1:B:3630:ARG:HG2	1:B:3632:PHE:H	1.70	0.56
1:A:2528:GLU:O	1:A:2529:THR:HG22	2.06	0.56
1:A:2826:LEU:HA	1:A:2829:LYS:HB2	1.87	0.56
1:A:2923:TRP:CE3	1:A:2946:GLU:HG3	2.41	0.56
1:B:3588:TRP:HH2	1:B:3651:LEU:HD21	1.70	0.56
1:B:3631:LYS:HD3	1:B:3682:GLU:HB3	1.87	0.56
1:A:2083:LEU:H	1:A:2083:LEU:HD12	1.70	0.56
1:A:3514:VAL:HG23	1:A:3517:SER:HB2	1.85	0.56
1:A:3918:LEU:O	1:A:3920:ILE:HG13	2.05	0.56
1:B:2409:THR:HG23	1:B:2410:GLU:H	1.71	0.56
1:A:1504:ASP:HB3	1:A:1507:CYS:HB3	1.87	0.56
1:B:2225:HIS:O	1:B:2227:LYS:N	2.39	0.56
1:B:2940:ARG:HG3	1:B:2957:LEU:HD22	1.86	0.56
1:B:3918:LEU:O	1:B:3920:ILE:HG13	2.06	0.56
1:A:724:GLU:HG3	1:A:2743:UNK:O	2.06	0.56
1:B:2281:MET:HE2	1:B:2326:ILE:HA	1.86	0.56
1:A:354:SER:CB	1:A:358:GLU:HB2	2.36	0.56
1:A:2137:ILE:HG13	1:A:2138:VAL:H	1.71	0.56
1:A:385:TYR:CZ	1:A:389:ILE:HD11	2.41	0.56
1:A:704:PHE:HE1	1:A:741:ILE:HG12	1.71	0.56
1:A:2446:LEU:O	1:A:2451:LEU:HB2	2.06	0.56
1:A:3278:GLN:HG2	1:A:3329:LEU:HD21	1.87	0.56
1:A:242:PRO:HA	1:A:245:SER:HB3	1.88	0.55
1:A:2131:GLY:O	1:A:2135:ASN:ND2	2.38	0.55
1:B:996:THR:OG1	1:B:1040:SER:HA	2.06	0.55
1:B:1155:ARG:HH21	1:B:3689:ASP:HB3	1.70	0.55
1:B:1686:LEU:HD11	1:B:1721:HIS:CB	2.36	0.55
1:B:2824:LYS:O	1:B:2829:LYS:HG3	2.05	0.55
1:B:3297:VAL:HA	1:B:3300:VAL:HG22	1.87	0.55
1:A:3138:ILE:HG12	1:A:3189:PHE:HZ	1.71	0.55
1:A:3463:LEU:HD13	1:A:3498:TRP:HZ2	1.71	0.55
1:B:864:GLY:HA2	1:B:867:ASN:CB	2.36	0.55
1:B:1271:ILE:HD13	1:B:1348:LEU:HD13	1.89	0.55
1:B:1993:GLU:OE2	1:B:2230:VAL:HB	2.06	0.55
1:B:2480:ILE:O	1:B:2484:TYR:HB2	2.06	0.55
1:A:4006:VAL:HG21	1:A:4044:ILE:HG12	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1096:VAL:HB	1:B:1101:PHE:HE2	1.69	0.55
1:B:1563:PHE:HB2	1:B:1567:ILE:HG13	1.88	0.55
1:B:2519:LEU:HD22	1:B:2606:UNK:O	2.07	0.55
1:A:305:ASN:HB2	1:A:308:LEU:HB3	1.87	0.55
1:A:1750:LEU:HD13	1:A:1758:LEU:HB2	1.87	0.55
1:B:1752:LEU:HD12	1:B:1753:SER:N	2.21	0.55
1:A:2088:LEU:HD11	1:A:2144:LEU:HD23	1.88	0.55
1:B:2547:SER:O	1:B:2549:LYS:N	2.40	0.55
1:B:3244:ASP:OD1	1:B:3247:ARG:NH1	2.39	0.55
1:A:478:CYS:HA	1:A:481:THR:HG22	1.88	0.55
1:A:1037:LEU:O	1:A:1040:SER:OG	2.21	0.55
1:A:2823:PHE:HD1	1:A:2824:LYS:HG2	1.71	0.55
1:A:2978:LYS:HG3	1:A:2981:TRP:CD2	2.41	0.55
1:B:446:PHE:CZ	1:B:454:GLN:HG2	2.41	0.55
1:A:3727:THR:OG1	1:A:3737:ARG:HB3	2.07	0.55
1:B:78:PHE:O	1:B:82:ARG:NH1	2.39	0.55
1:B:2949:THR:OG1	1:B:2990:GLU:OE2	2.23	0.55
1:A:1769:GLU:O	1:A:1822:ARG:NH1	2.40	0.55
1:B:483:VAL:HG23	1:B:571:SER:HB2	1.89	0.55
1:A:35:ILE:HD13	1:A:85:ILE:HG13	1.89	0.55
1:B:1040:SER:O	1:B:1049:GLN:NE2	2.39	0.55
1:A:2590:THR:HG22	1:A:2591:ILE:H	1.72	0.55
1:A:3888:VAL:HA	1:A:3891:SER:HB2	1.88	0.55
1:B:801:LYS:HA	1:B:3115:SER:HB2	1.88	0.55
1:B:1538:LEU:O	1:B:1553:PHE:N	2.40	0.55
1:B:1612:LYS:C	1:B:1614:GLN:N	2.65	0.55
1:B:1802:TYR:CZ	1:B:1843:ILE:HD11	2.42	0.55
1:B:2856:SER:HA	1:B:2888:VAL:HG11	1.89	0.55
1:B:3121:LEU:O	1:B:3124:SER:OG	2.25	0.55
1:A:1298:LEU:HB3	1:A:1367:HIS:HB3	1.88	0.54
1:A:1668:PHE:HZ	1:A:1702:LEU:HD22	1.72	0.54
1:B:2133:LEU:HD13	1:B:2146:LEU:HB3	1.88	0.54
1:A:351:ASN:OD1	1:A:352:VAL:N	2.39	0.54
1:A:1881:TYR:CE1	1:A:1951:VAL:HG23	2.42	0.54
1:A:3522:THR:HG23	1:A:3562:LEU:HD13	1.89	0.54
1:B:1090:ARG:HH11	1:B:1137:ILE:HD13	1.71	0.54
1:B:2255:LEU:HD23	1:B:2256:ILE:H	1.71	0.54
1:A:3527:GLN:HG2	1:A:3700:GLU:HB3	1.89	0.54
1:A:3760:GLN:OE1	1:A:4019:LYS:NZ	2.27	0.54
1:B:201:LEU:HD21	1:B:248:ILE:HG12	1.88	0.54
1:B:583:LEU:HD12	1:B:611:ASN:HD22	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:359:LEU:O	1:A:363:ILE:HG12	2.08	0.54
1:A:1147:LYS:O	1:A:1151:ARG:NH2	2.41	0.54
1:A:3811:THR:OG1	1:A:3814:ASP:OD1	2.25	0.54
1:B:1104:LEU:HD12	1:B:1134:LEU:HD23	1.89	0.54
1:B:1368:LEU:HA	1:B:1371:VAL:HG22	1.88	0.54
1:B:3692:VAL:HA	1:B:3696:ARG:NH1	2.22	0.54
1:A:651:TYR:CE1	1:A:655:LEU:HD21	2.43	0.54
1:A:2931:ARG:NH2	1:A:3043:TYR:OH	2.41	0.54
1:B:25:CYS:SG	1:B:26:GLY:N	2.81	0.54
1:B:1367:HIS:O	1:B:1371:VAL:HG13	2.08	0.54
1:B:2560:ASN:ND2	1:B:2799:GLN:OE1	2.35	0.54
1:B:2584:CYS:SG	1:B:2783:ILE:HG12	2.48	0.54
1:A:1228:GLY:HA3	1:A:1259:LEU:HD13	1.89	0.54
1:A:2614:UNK:HA	1:A:2795:GLN:OE1	2.08	0.54
1:A:3422:GLN:HE22	1:A:3423:GLN:HE21	1.55	0.54
1:A:4117:LEU:HB3	1:A:4126:PRO:HB2	1.90	0.54
1:B:334:HIS:HB3	1:B:337:LYS:HD2	1.89	0.54
1:B:1206:LEU:O	1:B:1210:ASP:HB2	2.08	0.54
1:B:2140:LEU:HD21	1:B:2178:GLY:HA2	1.90	0.54
1:B:2411:LEU:HB3	1:B:2442:MET:HE1	1.90	0.54
1:A:12:LEU:HD21	1:A:58:VAL:HG12	1.89	0.54
1:A:661:PRO:O	1:A:667:TYR:OH	2.25	0.54
1:A:1760:GLU:O	1:A:1764:GLU:HG2	2.07	0.54
1:A:1896:ILE:HG22	1:A:1911:LEU:H	1.71	0.54
1:B:346:TYR:HA	1:B:349:ILE:HG22	1.89	0.54
1:B:1967:PHE:CE1	1:B:2129:LEU:HD11	2.41	0.54
1:B:2409:THR:O	1:B:2411:LEU:N	2.40	0.54
1:B:3443:PRO:HA	1:B:3471:ILE:HD11	1.89	0.54
1:A:201:LEU:HD21	1:A:248:ILE:HG12	1.88	0.54
1:A:1101:PHE:CE1	1:A:1138:ILE:HG12	2.43	0.54
1:B:1802:TYR:CE1	1:B:1843:ILE:HD11	2.43	0.54
1:B:2582:SER:HB2	1:B:2781:PRO:HD2	1.90	0.54
1:A:2885:GLN:C	1:A:2887:PRO:HD3	2.33	0.54
1:A:3949:ALA:HB1	1:A:3957:GLU:HG3	1.89	0.54
1:B:860:GLY:HA3	1:B:3136:THR:OG1	2.08	0.54
1:B:1504:ASP:HB3	1:B:1507:CYS:HB3	1.89	0.54
1:B:1881:TYR:CE1	1:B:1951:VAL:HG23	2.43	0.54
1:B:3681:LYS:HD2	1:B:3687:MET:HE3	1.90	0.54
1:A:2165:LEU:HD21	1:A:2208:ASP:OD2	2.08	0.54
1:B:204:LEU:O	1:B:208:MET:HB2	2.08	0.54
1:B:662:LEU:H	1:B:662:LEU:HD23	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:860:GLY:HA2	1:A:3132:VAL:HG23	1.89	0.53
1:A:2091:HIS:O	1:A:2092:GLU:HG2	2.08	0.53
1:A:2188:GLU:O	1:A:2192:THR:HG22	2.08	0.53
1:B:645:TRP:O	1:B:649:PHE:HB2	2.08	0.53
1:A:2996:LEU:HD13	1:A:3039:THR:HB	1.90	0.53
1:A:3937:VAL:C	1:A:3938:ILE:HD13	2.32	0.53
1:B:1575:LEU:HD23	1:B:1617:LYS:HG2	1.91	0.53
1:B:1758:LEU:O	1:B:1762:MET:HB2	2.08	0.53
1:B:2546:TYR:CE2	1:B:2548:PRO:HB3	2.43	0.53
1:B:3133:GLN:O	1:B:3137:GLU:HG2	2.08	0.53
1:A:1090:ARG:HH11	1:A:1137:ILE:HD13	1.73	0.53
1:A:1633:TRP:CZ2	1:A:1674:THR:HG22	2.44	0.53
1:A:2464:HIS:ND1	1:A:2465:PRO:O	2.41	0.53
1:B:464:VAL:O	1:B:468:LEU:HD23	2.09	0.53
1:B:1825:LEU:HD11	1:B:1875:LYS:HB3	1.90	0.53
1:B:2190:VAL:HA	1:B:2193:ILE:HG22	1.90	0.53
1:B:2234:ASN:O	1:B:2238:ILE:HG13	2.08	0.53
1:A:1089:PHE:CE1	1:A:1096:VAL:HA	2.44	0.53
1:A:3243:ILE:HD13	1:A:3259:LEU:HD13	1.91	0.53
1:A:3328:ILE:HD11	1:A:3412:ALA:HB2	1.91	0.53
1:B:181:LEU:HB3	1:B:189:MET:HE1	1.91	0.53
1:B:859:LEU:HD21	1:B:870:LEU:HD13	1.91	0.53
1:B:1153:LEU:HD12	1:B:1154:PRO:HD2	1.90	0.53
1:B:1291:LEU:HD12	1:B:1291:LEU:H	1.74	0.53
1:B:1503:LEU:HD12	1:B:1508:LYS:HE2	1.89	0.53
1:B:2894:GLU:OE2	1:B:3901:ARG:NH2	2.31	0.53
1:B:3937:VAL:C	1:B:3938:ILE:HD13	2.33	0.53
1:A:544:ILE:HG13	1:A:545:LEU:HG	1.90	0.53
1:A:1718:ILE:HG23	1:A:1722:PHE:CD2	2.44	0.53
1:A:2877:SER:HB2	1:A:2925:GLU:HB3	1.91	0.53
1:A:3411:ASP:N	1:A:3411:ASP:OD1	2.41	0.53
1:B:8:VAL:HG12	1:B:9:ARG:H	1.73	0.53
1:B:1195:VAL:HG23	1:B:1196:PRO:HD3	1.89	0.53
1:B:1854:ARG:O	1:B:1866:GLN:NE2	2.41	0.53
1:A:418:ALA:HB2	1:A:464:VAL:HG23	1.91	0.53
1:A:451:PRO:O	1:A:452:LYS:HG2	2.09	0.53
1:A:654:ILE:O	1:A:658:THR:OG1	2.26	0.53
1:A:1743:MET:HG3	1:A:1774:MET:HE1	1.91	0.53
1:A:1195:VAL:HG23	1:A:1196:PRO:HD3	1.91	0.53
1:A:1297:PHE:CZ	1:A:1301:ILE:HD13	2.44	0.53
1:B:279:ALA:HB1	1:B:322:GLN:HG3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:966:PHE:CE1	1:A:969:LEU:HD12	2.43	0.53
1:A:1463:LEU:HG	1:A:1466:ASN:HB2	1.90	0.53
1:A:2492:ASP:HB3	1:A:2495:SER:H	1.74	0.53
1:B:2182:ILE:HD11	1:B:2185:MET:HB3	1.90	0.53
1:A:410:MET:HG2	1:A:442:GLN:HB2	1.90	0.53
1:B:1884:LEU:HD23	1:B:1885:PRO:HD2	1.91	0.53
1:B:2574:ASN:C	1:B:2576:MET:H	2.16	0.53
1:A:1343:GLU:O	1:A:1346:THR:OG1	2.26	0.52
1:A:1368:LEU:HA	1:A:1371:VAL:HG22	1.91	0.52
1:A:3975:LYS:HB2	1:A:3977:THR:HG22	1.91	0.52
1:A:2304:VAL:HG11	1:A:2344:LEU:HG	1.90	0.52
1:A:3325:ASP:HA	1:A:3328:ILE:HD12	1.91	0.52
1:B:157:TYR:OH	1:B:195:ASN:HB3	2.09	0.52
1:A:1955:VAL:O	1:A:1957:ASN:ND2	2.35	0.52
1:A:3786:LEU:HD21	1:A:3983:ILE:HD12	1.92	0.52
1:B:531:PHE:HA	1:B:534:LEU:HD12	1.90	0.52
1:B:1346:THR:HG23	1:B:1405:ALA:HB2	1.91	0.52
1:B:2532:PRO:HB2	1:B:2537:ASP:HB2	1.90	0.52
1:B:3360:LEU:HG	1:B:3373:VAL:HG21	1.91	0.52
1:B:3681:LYS:NZ	1:B:3723:ASP:O	2.28	0.52
1:A:1104:LEU:HD12	1:A:1134:LEU:HB3	1.92	0.52
1:A:1134:LEU:O	1:A:1138:ILE:HG13	2.10	0.52
1:A:1990:PHE:HE2	1:A:2144:LEU:HD11	1.74	0.52
1:A:3535:ILE:HD12	1:A:3759:ARG:CZ	2.40	0.52
1:B:1297:PHE:CZ	1:B:1301:ILE:HD13	2.45	0.52
1:B:3319:ASN:O	1:B:3323:PHE:HB2	2.10	0.52
1:A:765:LEU:HD23	1:A:766:ALA:H	1.73	0.52
1:A:1279:LEU:HD23	1:A:1279:LEU:H	1.74	0.52
1:B:1962:TYR:O	1:B:1967:PHE:HD2	1.92	0.52
1:B:2188:GLU:O	1:B:2191:ALA:HB3	2.08	0.52
1:B:113:SER:O	1:B:117:LYS:HG2	2.10	0.52
1:B:3341:LEU:HD13	1:B:3374:ILE:HG12	1.92	0.52
1:A:9:ARG:HB2	1:A:57:LEU:HD11	1.92	0.52
1:A:2246:LYS:NZ	1:A:2284:ASP:OD2	2.38	0.52
1:A:3330:LEU:HD13	1:A:3384:HIS:CE1	2.44	0.52
1:A:3654:MET:HG2	1:A:3656:LEU:HB2	1.92	0.52
1:A:96:MET:SD	1:A:96:MET:N	2.83	0.52
1:A:655:LEU:HD22	1:A:1389:VAL:HG12	1.91	0.52
1:A:2220:MET:HE2	1:A:2276:LEU:HD12	1.92	0.52
1:A:3761:ASP:HA	1:A:3764:VAL:HG22	1.92	0.52
1:B:1037:LEU:O	1:B:1040:SER:OG	2.26	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1765:VAL:HA	1:B:1768:ARG:HB2	1.91	0.52
1:A:646:VAL:O	1:A:650:SER:OG	2.28	0.52
1:B:1481:THR:HG22	1:B:1524:LEU:HD11	1.91	0.52
1:B:1948:ALA:O	1:B:1952:ILE:HG13	2.10	0.52
1:B:2402:LEU:O	1:B:2405:VAL:HG23	2.10	0.52
1:B:3913:ILE:HB	1:B:3984:MET:HG2	1.91	0.52
1:A:19:LEU:CD2	1:A:71:LYS:HG3	2.39	0.52
1:A:749:VAL:N	1:A:750:PRO:HD2	2.25	0.52
1:A:794:PRO:CG	1:A:873:VAL:HB	2.41	0.52
1:A:3028:ASN:HA	1:A:3031:TRP:CD1	2.31	0.52
1:A:3617:LEU:HD22	1:A:3636:PHE:CE2	2.45	0.52
1:B:3786:LEU:HD21	1:B:3983:ILE:HD12	1.91	0.52
1:A:898:PHE:HD2	1:A:903:PRO:HD2	1.75	0.51
1:A:1283:GLY:HA2	1:A:1358:LEU:CD1	2.40	0.51
1:A:1572:LEU:HD11	1:A:1604:SER:HB3	1.92	0.51
1:A:3567:VAL:HG11	1:A:3697:ASN:HB3	1.90	0.51
1:A:3588:TRP:HH2	1:A:3651:LEU:HD21	1.74	0.51
1:B:738:HIS:NE2	1:B:745:VAL:HG23	2.24	0.51
1:B:3586:LYS:HD3	1:B:3667:LEU:HD21	1.91	0.51
1:A:86:LEU:HB2	1:A:126:PRO:HB2	1.92	0.51
1:A:1071:ASN:HD21	1:A:1073:PHE:HB2	1.75	0.51
1:B:1142:HIS:CE1	1:B:1146:ASN:HA	2.45	0.51
1:B:2820:MET:HE3	1:B:2829:LYS:HG2	1.91	0.51
1:A:1427:SER:HA	1:A:1430:GLU:HG2	1.92	0.51
1:B:496:VAL:HG12	1:B:497:LEU:H	1.75	0.51
1:B:683:PHE:O	1:B:740:ILE:HG12	2.10	0.51
1:B:996:THR:HA	1:B:1001:PHE:HD1	1.74	0.51
1:A:323:VAL:HG13	1:A:369:PHE:HZ	1.75	0.51
1:A:414:LEU:HG	1:A:464:VAL:HG21	1.92	0.51
1:A:890:LYS:HD3	1:A:909:VAL:HG13	1.93	0.51
1:A:1724:MET:SD	1:A:1724:MET:N	2.81	0.51
1:A:1783:ARG:HD2	1:A:1830:HIS:ND1	2.24	0.51
1:A:1896:ILE:HD13	1:A:1906:THR:O	2.11	0.51
1:A:3144:PHE:HE1	1:A:3156:PRO:HB2	1.75	0.51
1:B:178:LEU:HD23	1:B:181:LEU:HD12	1.92	0.51
1:A:1082:PHE:HA	1:A:1085:ILE:HG12	1.93	0.51
1:B:1142:HIS:ND1	1:B:1145:LEU:O	2.44	0.51
1:B:1633:TRP:CZ2	1:B:1674:THR:HG22	2.46	0.51
1:B:2461:PHE:HB2	1:B:2473:MET:HG3	1.92	0.51
1:B:3506:LEU:HA	1:B:3511:ALA:HB1	1.91	0.51
1:A:2251:ILE:HD12	1:A:2253:TYR:CE2	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1686:LEU:HD22	1:A:1721:HIS:CD2	2.46	0.51
1:A:2886:GLN:N	1:A:2887:PRO:HD3	2.25	0.51
1:A:3258:LEU:HA	1:A:3261:GLU:HG2	1.91	0.51
1:B:1020:PRO:HA	1:B:1073:PHE:CE1	2.45	0.51
1:B:1102:GLU:O	1:B:1154:PRO:HB3	2.11	0.51
1:B:1575:LEU:HG	1:B:1576:ASP:H	1.76	0.51
1:A:2223:VAL:HG23	1:A:2234:ASN:HB3	1.93	0.51
1:A:2575:PRO:HB3	1:A:2787:HIS:CE1	2.46	0.51
1:B:256:ILE:C	1:B:258:PRO:HD3	2.36	0.51
1:B:1055:ASN:O	1:B:1058:SER:OG	2.22	0.51
1:B:2101:VAL:HG12	1:B:2156:VAL:HG21	1.92	0.51
1:B:3718:ARG:H	1:B:3743:HIS:CE1	2.28	0.51
1:A:1640:GLU:C	1:A:1642:LYS:H	2.19	0.51
1:B:354:SER:HB2	1:B:359:LEU:CB	2.41	0.51
1:B:1947:CYS:O	1:B:1951:VAL:HG12	2.11	0.51
1:B:4008:GLU:O	1:B:4010:SER:N	2.44	0.51
1:A:661:PRO:HD2	1:A:662:LEU:HD23	1.93	0.51
1:A:718:MET:HA	1:A:721:TYR:CD2	2.46	0.51
1:A:2288:TYR:HD1	1:A:2291:GLN:HB2	1.76	0.51
1:A:3506:LEU:HD22	1:A:3555:VAL:HG22	1.93	0.51
1:A:3545:THR:CG2	1:A:3546:SER:H	2.22	0.51
1:A:3585:PHE:HD2	1:A:3667:LEU:HD13	1.75	0.51
1:B:532:ARG:O	1:B:536:SER:HB3	2.10	0.51
1:B:3958:LEU:HB2	1:B:4116:ILE:HG23	1.93	0.51
1:A:1766:LEU:HG	1:A:1778:PHE:HD2	1.76	0.50
1:A:3842:TRP:CZ2	1:A:3867:THR:HG22	2.46	0.50
1:B:60:SER:HB2	1:B:63:PHE:O	2.11	0.50
1:B:782:ARG:O	1:B:786:GLN:HG3	2.11	0.50
1:B:1027:ASP:OD1	1:B:1027:ASP:N	2.43	0.50
1:B:3271:ASP:HA	1:B:3274:VAL:HG12	1.93	0.50
1:A:2472:GLN:O	1:A:2476:ILE:HG23	2.12	0.50
1:A:3354:ASP:O	1:A:3358:ARG:HG2	2.11	0.50
1:B:1766:LEU:HG	1:B:1778:PHE:CD2	2.44	0.50
1:B:3717:VAL:HA	1:B:3743:HIS:HE1	1.76	0.50
1:A:1038:LYS:HD3	1:A:1042:LYS:HE3	1.94	0.50
1:A:3630:ARG:HG2	1:A:3632:PHE:H	1.76	0.50
1:B:495:VAL:HG12	1:B:496:VAL:H	1.76	0.50
1:B:2004:TYR:CZ	1:B:2187:VAL:HG11	2.46	0.50
1:B:2249:LEU:HG	1:B:2285:LEU:HD13	1.94	0.50
1:B:3542:PHE:CG	1:B:3552:LYS:HG2	2.47	0.50
1:A:1104:LEU:HD13	1:A:1138:ILE:HD11	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1653:LEU:HB3	1:A:1698:PHE:CD1	2.47	0.50
1:A:2409:THR:O	1:A:2411:LEU:HB2	2.11	0.50
1:A:3619:ASP:HB2	1:A:3622:ALA:HB2	1.93	0.50
1:B:1693:VAL:O	1:B:1696:LEU:HD23	2.12	0.50
1:B:2887:PRO:HB3	1:B:3898:LEU:HD22	1.94	0.50
1:B:3065:ILE:HG23	1:B:3078:LEU:HD21	1.94	0.50
1:B:3648:GLY:O	1:B:3652:LEU:HD12	2.11	0.50
1:A:487:LEU:HA	1:A:490:ILE:HG12	1.94	0.50
1:A:1848:ILE:O	1:A:1852:LYS:HB2	2.12	0.50
1:A:1861:SER:O	1:A:1865:THR:OG1	2.24	0.50
1:A:2138:VAL:HG12	1:A:2143:ARG:HB2	1.92	0.50
1:B:479:ILE:HA	1:B:482:VAL:HG12	1.93	0.50
1:B:487:LEU:HD21	1:B:568:PHE:HE1	1.77	0.50
1:B:780:ILE:HG21	1:B:785:MET:SD	2.52	0.50
1:B:786:GLN:HA	1:B:789:TYR:CD2	2.46	0.50
1:B:2419:ASP:HB2	1:B:2422:GLN:HB2	1.94	0.50
1:B:3082:TYR:C	1:B:3084:GLN:H	2.19	0.50
1:A:2375:ALA:O	1:A:2379:MET:N	2.44	0.50
1:A:3772:ASN:HD21	1:A:3790:THR:HG23	1.76	0.50
1:A:3992:ARG:HD3	1:A:4100:GLU:HG3	1.93	0.50
1:B:200:PHE:HD1	1:B:223:CYS:SG	2.34	0.50
1:B:897:PRO:HA	1:B:902:LYS:HG3	1.93	0.50
1:B:898:PHE:HD2	1:B:903:PRO:HD2	1.75	0.50
1:B:1554:SER:OG	1:B:1557:GLU:HB2	2.12	0.50
1:B:1934:LEU:H	1:B:1934:LEU:HD23	1.75	0.50
1:B:2263:LYS:HA	1:B:2309:PHE:CE2	2.46	0.50
1:B:2420:PHE:CZ	1:B:2424:MET:HE3	2.46	0.50
1:B:3674:SER:O	1:B:3676:PRO:HD3	2.12	0.50
1:A:1681:ASP:O	1:A:1683:LYS:N	2.37	0.50
1:A:2281:MET:SD	1:A:2287:PRO:HD3	2.51	0.50
1:A:2402:LEU:HD13	1:A:2434:VAL:HG23	1.94	0.50
1:A:3533:PHE:HE2	1:A:3559:LYS:HD3	1.76	0.50
1:B:1335:CYS:HB3	1:B:1384:PHE:CE1	2.47	0.50
1:B:1566:THR:O	1:B:1570:GLU:HG2	2.12	0.50
1:B:1602:ASP:HA	1:B:2045:PHE:HE2	1.77	0.50
1:B:3462:ARG:NH1	1:B:3497:SER:OG	2.45	0.50
1:B:3881:ASP:OD1	1:B:3881:ASP:N	2.43	0.50
1:A:94:GLU:OE1	1:A:133:LYS:HD2	2.11	0.50
1:A:1154:PRO:HG2	1:A:1157:PHE:HB2	1.93	0.50
1:A:1579:VAL:O	1:A:1583:MET:HG2	2.12	0.50
1:B:388:LEU:HD23	1:B:420:VAL:HG11	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1837:ARG:HG3	1:B:1884:LEU:HD11	1.94	0.50
1:B:3992:ARG:NH1	1:B:4103:GLN:OE1	2.44	0.50
1:A:385:TYR:CZ	1:A:389:ILE:CD1	2.95	0.50
1:A:865:GLN:HG2	1:A:3170:ASP:HB3	1.94	0.50
1:A:2182:ILE:HG23	1:A:2186:VAL:HG21	1.93	0.50
1:A:2359:LYS:H	1:A:2359:LYS:HD2	1.77	0.50
1:B:108:LYS:HG2	1:B:131:LEU:HD11	1.94	0.50
1:B:670:LEU:HA	1:B:673:THR:HG22	1.93	0.50
1:B:1833:LEU:HG	1:B:1835:ALA:H	1.77	0.50
1:B:3057:ALA:C	1:B:3059:GLN:H	2.19	0.50
1:B:3586:LYS:HG2	1:B:3667:LEU:HD11	1.94	0.50
1:A:997:ASN:OD1	1:A:998:ASN:N	2.44	0.49
1:B:451:PRO:C	1:B:453:MET:H	2.19	0.49
1:B:933:LEU:HB2	1:B:2793:PRO:HB2	1.94	0.49
1:B:1082:PHE:HA	1:B:1085:ILE:HG12	1.92	0.49
1:B:3532:PRO:HA	1:B:3535:ILE:HG12	1.93	0.49
1:A:2393:LEU:HA	1:A:2396:LEU:HD12	1.94	0.49
1:A:3422:GLN:HE21	1:A:3423:GLN:HG2	1.77	0.49
1:B:898:PHE:CD2	1:B:903:PRO:HD2	2.47	0.49
1:B:1923:PHE:HA	1:B:1941:HIS:CG	2.46	0.49
1:A:393:LYS:HA	1:A:397:LEU:HD12	1.94	0.49
1:A:3421:ASP:OD1	1:A:3467:ARG:NE	2.45	0.49
1:B:1099:PHE:CZ	1:B:1152:ARG:HD2	2.47	0.49
1:B:1611:GLN:O	1:B:1611:GLN:HG2	2.12	0.49
1:B:3563:ASP:CG	1:B:3568:ILE:H	2.21	0.49
1:A:3049:LEU:HD22	1:A:3085:GLU:HG3	1.94	0.49
1:A:3259:LEU:HD12	1:A:3276:TRP:NE1	2.27	0.49
1:B:3798:SER:O	1:B:3799:ARG:HG2	2.12	0.49
1:A:135:LEU:HD22	1:A:144:MET:HE1	1.94	0.49
1:A:683:PHE:HB3	1:A:740:ILE:HG13	1.93	0.49
1:A:863:GLY:O	1:A:867:ASN:HB2	2.13	0.49
1:A:1783:ARG:HB3	1:A:1830:HIS:CG	2.47	0.49
1:B:1406:LEU:CB	1:B:1415:LEU:HD11	2.41	0.49
1:B:3867:THR:HG21	1:B:4119:ARG:CZ	2.43	0.49
1:A:476:ARG:NH2	1:A:1503:LEU:HD22	2.28	0.49
1:A:1342:MET:O	1:A:1346:THR:HG23	2.11	0.49
1:A:1612:LYS:O	1:A:1613:HIS:ND1	2.45	0.49
1:A:3065:ILE:HG23	1:A:3078:LEU:HD21	1.94	0.49
1:A:538:ASP:OD2	1:A:561:ASN:N	2.45	0.49
1:A:767:GLU:HG2	1:A:851:ILE:HD11	1.94	0.49
1:B:305:ASN:OD1	1:B:306:VAL:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2310:VAL:HG12	1:B:2316:TYR:CG	2.47	0.49
1:A:476:ARG:HH22	1:A:1503:LEU:HD22	1.78	0.49
1:A:619:ASP:OD2	1:A:2035:THR:HB	2.13	0.49
1:A:3082:TYR:HB3	1:A:3085:GLU:OE1	2.13	0.49
1:B:1206:LEU:O	1:B:1210:ASP:CB	2.59	0.49
1:A:532:ARG:HG2	1:A:637:LYS:HE2	1.94	0.49
1:A:1895:LYS:O	1:A:1899:VAL:HG23	2.12	0.49
1:A:2250:SER:O	1:A:2252:PRO:HD3	2.13	0.49
1:A:3095:ASP:OD1	1:A:3098:ARG:HB2	2.13	0.49
1:B:631:ARG:HH21	1:B:668:LYS:HD3	1.78	0.49
1:B:997:ASN:OD1	1:B:998:ASN:N	2.45	0.49
1:B:1334:LYS:O	1:B:1337:VAL:HG22	2.12	0.49
1:B:1747:LEU:HD12	1:B:1781:SER:HB2	1.95	0.49
1:B:1900:PHE:HB3	1:B:1904:CYS:SG	2.53	0.49
1:A:110:THR:O	1:A:114:VAL:HG23	2.13	0.49
1:A:1425:ALA:HA	1:A:1428:ILE:HD12	1.95	0.49
1:A:2219:LEU:O	1:A:2223:VAL:HB	2.13	0.49
1:A:2459:VAL:HB	1:A:2505:VAL:HG21	1.95	0.49
1:B:339:GLN:O	1:B:343:GLU:HG2	2.12	0.49
1:B:4054:ALA:HA	1:B:4096:SER:HA	1.95	0.49
1:A:370:ALA:HB1	1:A:420:VAL:HG23	1.94	0.48
1:A:938:VAL:HA	1:A:941:MET:HG2	1.95	0.48
1:A:2887:PRO:CG	1:A:3895:GLU:HG2	2.42	0.48
1:A:3120:LEU:HD11	1:A:3896:ALA:HA	1.95	0.48
1:B:1204:PRO:HG2	1:B:1205:ASN:ND2	2.28	0.48
1:B:1730:PRO:HG2	1:B:1733:THR:HG21	1.95	0.48
1:B:3444:ALA:HA	1:B:3479:THR:HG21	1.95	0.48
1:B:3858:MET:HE1	1:B:4119:ARG:HB3	1.95	0.48
1:A:264:ARG:O	1:A:266:ALA:N	2.46	0.48
1:A:538:ASP:HB2	1:A:561:ASN:OD1	2.14	0.48
1:A:1096:VAL:HB	1:A:1101:PHE:HE2	1.78	0.48
1:A:1362:ASP:OD1	1:A:1362:ASP:N	2.45	0.48
1:A:3778:ASP:OD1	1:A:3779:SER:N	2.46	0.48
1:B:1606:ARG:HG2	1:B:2042:GLN:OE1	2.12	0.48
1:B:1668:PHE:O	1:B:1671:VAL:HG22	2.13	0.48
1:B:2249:LEU:O	1:B:2251:ILE:N	2.46	0.48
2:D:728:LEU:O	2:D:731:MET:HB2	2.12	0.48
1:A:479:ILE:HA	1:A:482:VAL:HG12	1.96	0.48
1:B:267:VAL:HG23	1:B:268:PRO:HD3	1.94	0.48
1:B:1563:PHE:C	1:B:1565:GLU:H	2.21	0.48
1:B:1739:TYR:O	1:B:1743:MET:HG2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2294:ILE:HG22	1:B:2295:GLN:H	1.77	0.48
1:A:1853:SER:OG	1:A:1870:LYS:NZ	2.42	0.48
1:A:1984:LEU:HD11	1:A:2139:PRO:HG2	1.95	0.48
1:A:1992:VAL:HG23	1:A:1993:GLU:H	1.77	0.48
1:A:2182:ILE:HG12	1:A:2186:VAL:HG23	1.94	0.48
1:A:2411:LEU:HG	1:A:2415:LEU:HD13	1.94	0.48
1:B:620:PHE:O	1:B:624:ILE:HG12	2.14	0.48
1:B:972:LEU:HD13	1:B:984:TYR:CE2	2.49	0.48
1:B:1103:ALA:HB1	1:B:1106:ILE:HB	1.94	0.48
1:A:720:GLN:OE1	1:A:1026:ARG:NH2	2.47	0.48
1:A:1071:ASN:OD1	1:A:1072:ALA:N	2.47	0.48
1:A:1459:HIS:CG	1:A:1520:ALA:HB1	2.48	0.48
1:A:2085:MET:HA	1:A:2089:ASN:HB2	1.95	0.48
1:A:3448:GLU:HG2	1:A:3482:LEU:HD11	1.95	0.48
1:A:3760:GLN:O	1:A:3764:VAL:HG13	2.14	0.48
1:B:256:ILE:HB	1:B:300:TRP:HZ3	1.77	0.48
1:B:1328:GLU:N	1:B:1328:GLU:OE1	2.45	0.48
1:B:2301:GLN:HA	1:B:2344:LEU:HD21	1.95	0.48
1:B:3413:TYR:CD1	1:B:3449:LYS:HG3	2.49	0.48
1:A:421:LEU:HB3	1:A:467:ALA:HB1	1.95	0.48
1:A:421:LEU:HD22	1:A:424:LEU:HD23	1.96	0.48
1:A:1753:SER:O	1:A:1755:SER:N	2.46	0.48
1:A:3307:LEU:HD22	1:A:3330:LEU:HD21	1.96	0.48
1:B:570:LYS:O	1:B:574:LYS:HB2	2.12	0.48
1:B:1626:TRP:CE3	1:B:1674:THR:HG21	2.48	0.48
1:B:2245:TRP:O	1:B:2247:ASP:N	2.46	0.48
1:A:108:LYS:NZ	1:A:147:PHE:HB3	2.28	0.48
1:A:2257:PHE:HA	1:A:2260:PHE:CE2	2.49	0.48
1:B:272:LEU:HD13	1:B:312:ALA:HA	1.94	0.48
1:B:1124:ILE:HD12	1:B:1124:ILE:H	1.79	0.48
1:A:135:LEU:HB2	1:A:180:LEU:HD21	1.95	0.48
1:A:572:VAL:HA	1:A:575:ILE:HD12	1.96	0.48
1:A:2852:PRO:HG2	1:A:2853:PRO:HD3	1.96	0.48
1:A:3285:HIS:CE1	1:A:3333:THR:HG1	2.29	0.48
1:A:3701:ILE:HD12	1:A:3740:ILE:HD11	1.96	0.48
1:B:1926:ASN:HB3	1:B:1974:ASN:O	2.14	0.48
1:B:1956:PHE:HB2	1:B:1961:PHE:HE2	1.79	0.48
1:B:3069:MET:SD	1:B:3075:LYS:HG3	2.54	0.48
1:A:2934:GLY:HA2	1:A:2936:TYR:CE2	2.49	0.48
1:A:3778:ASP:HB3	1:A:3781:CYS:HB2	1.95	0.48
1:B:3300:VAL:HG11	1:B:3336:ILE:HG21	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:296:VAL:O	1:A:300:TRP:HD1	1.97	0.48
1:A:726:LEU:HD21	1:A:754:MET:HG2	1.95	0.48
1:A:1760:GLU:HG2	1:A:1804:MET:HE3	1.95	0.48
1:A:2168:LEU:HB3	1:A:2189:ILE:HG23	1.95	0.48
1:A:2277:LEU:HA	1:A:2280:VAL:HG12	1.96	0.48
1:B:2320:ALA:O	1:B:2367:VAL:HG22	2.14	0.48
1:B:3407:ALA:H	1:B:3410:ILE:HG23	1.78	0.48
1:A:342:MET:HE2	1:A:384:MET:SD	2.55	0.47
1:A:366:TYR:CZ	1:A:384:MET:HG2	2.49	0.47
1:A:977:ASP:OD1	1:A:978:GLN:N	2.47	0.47
1:A:2251:ILE:HD12	1:A:2253:TYR:HE2	1.79	0.47
1:A:3171:ALA:HB1	1:A:3248:LYS:HD2	1.96	0.47
1:A:3413:TYR:CE1	1:A:3449:LYS:HG3	2.48	0.47
1:B:1029:CYS:O	1:B:1032:CYS:HB2	2.14	0.47
1:B:1875:LYS:O	1:B:1878:ASP:HB2	2.14	0.47
1:B:3596:LEU:HD22	1:B:3606:ILE:HD12	1.96	0.47
1:A:1666:GLY:C	1:A:1669:PRO:HD2	2.39	0.47
1:A:2190:VAL:HA	1:A:2193:ILE:HG22	1.95	0.47
1:B:215:PRO:O	1:B:216:LYS:HG2	2.14	0.47
1:B:1586:SER:OG	1:B:1628:LYS:O	2.29	0.47
1:B:2572:TYR:N	1:B:2573:PRO:HD3	2.29	0.47
1:B:2937:ASP:OD1	1:B:3784:ARG:NH2	2.47	0.47
1:B:3772:ASN:HD21	1:B:3790:THR:HG23	1.78	0.47
1:A:153:PHE:HE1	1:A:196:LEU:HD13	1.79	0.47
1:A:565:TYR:HE1	1:A:642:PHE:HD1	1.61	0.47
1:A:633:ILE:C	1:A:635:PRO:HD3	2.39	0.47
1:A:1102:GLU:O	1:A:1105:VAL:HG22	2.14	0.47
1:A:1203:SER:HB3	1:A:1204:PRO:HD2	1.95	0.47
1:A:1977:ILE:O	1:A:1981:LEU:HB2	2.15	0.47
1:B:3083:SER:HA	1:B:3086:LEU:HD12	1.96	0.47
1:B:3742:GLY:C	1:B:3744:ASP:H	2.22	0.47
1:A:1361:LYS:O	1:A:1365:ASN:HB2	2.15	0.47
1:A:2393:LEU:H	1:A:2393:LEU:HD12	1.78	0.47
1:A:3599:THR:HG23	1:A:3601:VAL:HG12	1.96	0.47
1:B:446:PHE:CE1	1:B:454:GLN:HG2	2.49	0.47
1:B:2004:TYR:HB3	1:B:2233:HIS:CE1	2.49	0.47
1:B:3307:LEU:HD12	1:B:3307:LEU:HA	1.68	0.47
1:B:3487:ILE:HG23	1:B:3516:HIS:NE2	2.29	0.47
1:A:790:LYS:H	1:A:790:LYS:HD3	1.79	0.47
1:A:3049:LEU:HD21	1:A:3088:LEU:HD12	1.97	0.47
1:B:995:PHE:HB3	1:B:1006:THR:HG22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2106:ARG:NH2	1:B:2155:GLU:OE1	2.47	0.47
1:B:2873:PRO:HB3	1:B:2922:ARG:HA	1.97	0.47
1:A:1519:PHE:CZ	1:A:1528:LEU:HD22	2.49	0.47
1:A:1787:ARG:O	1:A:1787:ARG:HG2	2.15	0.47
1:A:3659:PHE:CE2	1:A:3661:ASP:HB3	2.50	0.47
1:B:606:SER:OG	1:B:1023:SER:HB2	2.15	0.47
1:B:1658:SER:HB3	1:B:1661:PHE:CE1	2.47	0.47
1:A:373:CYS:HA	1:A:376:ILE:CG2	2.45	0.47
1:A:1124:ILE:H	1:A:1124:ILE:HD12	1.79	0.47
1:A:1359:LEU:HB3	1:A:1363:LEU:HD11	1.96	0.47
1:A:1433:ALA:HB3	1:A:1436:LEU:HG	1.97	0.47
1:A:1725:GLN:O	1:A:1772:HIS:ND1	2.45	0.47
1:A:3544:ASP:OD1	1:A:3549:HIS:NE2	2.47	0.47
1:A:3693:GLU:HG2	1:A:3694:PHE:H	1.80	0.47
1:A:3860:LYS:HB3	1:A:4076:ASP:OD2	2.14	0.47
1:B:125:ILE:HB	1:B:126:PRO:HD3	1.96	0.47
1:B:786:GLN:HA	1:B:789:TYR:HD2	1.79	0.47
1:B:859:LEU:HG	1:B:867:ASN:ND2	2.25	0.47
1:B:986:PRO:O	1:B:990:GLN:HG3	2.14	0.47
1:B:1202:ARG:O	1:B:1207:TRP:HB2	2.15	0.47
1:B:1426:GLN:HG2	1:B:1427:SER:N	2.30	0.47
1:B:3955:VAL:HG11	1:B:4121:TRP:CE3	2.50	0.47
1:A:305:ASN:HB2	1:A:308:LEU:CB	2.45	0.47
1:A:1448:LEU:HG	1:A:1510:LEU:HD11	1.97	0.47
1:A:1765:VAL:HG23	1:A:1768:ARG:CZ	2.45	0.47
1:A:1949:ILE:HG12	1:A:2100:LEU:HD23	1.97	0.47
1:A:2036:LEU:HD23	1:A:2036:LEU:HA	1.67	0.47
1:B:14:ARG:HH12	1:B:34:LEU:HD21	1.80	0.47
1:B:620:PHE:HZ	1:B:663:ILE:HD12	1.80	0.47
1:B:1265:GLU:OE2	1:B:1340:ARG:HD2	2.15	0.47
1:B:1372:LEU:HD12	1:B:1402:LEU:HD23	1.97	0.47
1:B:1400:VAL:HG13	1:B:1461:ALA:HB2	1.96	0.47
1:B:2286:PRO:HB3	1:B:2329:TYR:CE2	2.50	0.47
1:B:3528:ALA:HB2	1:B:3705:TYR:CG	2.50	0.47
1:A:2184:TYR:H	1:A:2187:VAL:HG23	1.80	0.47
1:A:2556:SER:HB2	1:A:2799:GLN:HA	1.97	0.47
1:B:923:ASP:OD2	1:B:925:GLN:HB2	2.15	0.47
1:B:996:THR:HA	1:B:1001:PHE:CD1	2.49	0.47
1:B:1992:VAL:HG23	1:B:1994:VAL:HG23	1.97	0.47
1:B:3479:THR:HB	1:B:3482:LEU:HD23	1.97	0.47
1:B:4126:PRO:HD2	1:B:4127:TRP:CE3	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1934:LEU:HD23	1:A:1934:LEU:H	1.80	0.47
1:A:2893:LEU:HD13	1:A:2926:LEU:HB2	1.97	0.47
1:A:3418:ASP:OD2	1:A:3464:LYS:NZ	2.38	0.47
1:B:256:ILE:O	1:B:296:VAL:HG21	2.15	0.47
1:B:465:PHE:HE1	1:B:482:VAL:HG11	1.80	0.47
1:B:1135:CYS:O	1:B:1138:ILE:HG22	2.15	0.47
1:B:2556:SER:HB2	1:B:2799:GLN:HG2	1.97	0.47
1:B:3130:GLN:NE2	1:B:3174:ASP:OD1	2.48	0.47
1:B:3885:ARG:HA	1:B:3888:VAL:HG12	1.97	0.47
1:A:358:GLU:O	1:A:361:ILE:HG12	2.15	0.46
1:A:1121:LEU:HD22	1:A:1123:THR:HG23	1.97	0.46
1:A:1146:ASN:OD1	1:A:1164:CYS:HB3	2.14	0.46
1:A:2753:UNK:O	1:A:2757:UNK:CB	2.63	0.46
1:A:2967:GLU:O	1:A:2971:GLN:HG2	2.15	0.46
1:B:487:LEU:HD21	1:B:568:PHE:CE1	2.49	0.46
1:B:2409:THR:O	1:B:2411:LEU:HB2	2.14	0.46
1:B:2472:GLN:O	1:B:2476:ILE:HG23	2.14	0.46
1:B:2973:ASP:O	1:B:2977:ASN:ND2	2.48	0.46
1:A:933:LEU:HD22	1:A:2797:VAL:HG11	1.96	0.46
1:A:2194:LEU:HD11	1:A:2241:LEU:HD13	1.96	0.46
1:A:2563:LEU:HD21	1:A:2812:LEU:HD11	1.97	0.46
1:A:3085:GLU:OE1	1:A:3085:GLU:N	2.34	0.46
1:A:4042:GLN:NE2	1:A:4046:TYR:HE2	2.08	0.46
1:B:253:LEU:HD11	1:B:257:ARG:HD2	1.97	0.46
1:B:852:ARG:HD3	1:B:3111:MET:SD	2.55	0.46
1:B:1653:LEU:HB3	1:B:1698:PHE:CD1	2.50	0.46
1:B:2458:VAL:HG13	1:B:2473:MET:HG2	1.96	0.46
1:B:3120:LEU:HD23	1:B:3120:LEU:H	1.79	0.46
1:B:3129:LEU:O	1:B:3132:VAL:HG22	2.16	0.46
1:B:3389:VAL:HG21	1:B:3449:LYS:HE2	1.96	0.46
1:A:1890:HIS:ND1	1:A:1912:THR:HG21	2.30	0.46
1:B:1783:ARG:HD2	1:B:1830:HIS:ND1	2.30	0.46
1:B:3701:ILE:HD12	1:B:3740:ILE:CD1	2.34	0.46
1:A:2105:HIS:ND1	1:A:2156:VAL:HG13	2.30	0.46
1:B:2971:GLN:HA	1:B:2974:GLU:HB2	1.96	0.46
1:B:3913:ILE:O	1:B:3917:ILE:HG12	2.16	0.46
1:A:335:LYS:HB2	1:A:376:ILE:HD11	1.98	0.46
1:A:1416:GLU:O	1:A:1420:ARG:HG3	2.16	0.46
1:A:3050:LYS:NZ	1:A:3181:ASP:OD1	2.34	0.46
1:B:396:PHE:CE1	1:B:410:MET:HE2	2.50	0.46
1:B:767:GLU:HG2	1:B:851:ILE:HD11	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1562:LEU:HD23	1:B:1562:LEU:HA	1.75	0.46
1:B:2169:LEU:HD11	1:B:2212:ALA:HA	1.98	0.46
1:B:2591:ILE:HD11	1:B:2792:THR:CB	2.45	0.46
1:B:3256:MET:HE2	1:B:3287:ARG:HH12	1.81	0.46
1:A:133:LYS:O	1:A:137:THR:HG22	2.15	0.46
1:A:3324:ARG:O	1:A:3328:ILE:HG13	2.16	0.46
1:B:425:ASP:OD1	1:B:425:ASP:N	2.46	0.46
1:B:677:ALA:HB1	1:B:683:PHE:HE2	1.80	0.46
1:B:1224:PHE:HD1	1:B:1266:CYS:SG	2.39	0.46
1:B:2482:ASP:OD2	1:B:2530:ARG:NH1	2.49	0.46
1:B:2950:LYS:HA	1:B:2950:LYS:HD3	1.64	0.46
1:B:3554:PHE:CE2	1:B:3558:ILE:HD11	2.51	0.46
1:B:3879:PRO:HG2	1:B:3882:LEU:HD22	1.98	0.46
1:B:4054:ALA:H	1:B:4103:GLN:NE2	2.14	0.46
1:A:418:ALA:HB1	1:A:463:LYS:HG3	1.96	0.46
1:A:2921:LEU:H	1:A:2921:LEU:HD23	1.81	0.46
1:A:3487:ILE:HG23	1:A:3516:HIS:NE2	2.31	0.46
1:A:3545:THR:CG2	1:A:3546:SER:N	2.78	0.46
1:B:749:VAL:N	1:B:750:PRO:HD2	2.30	0.46
1:B:1601:LEU:HD22	1:B:1618:LEU:HD21	1.96	0.46
1:B:2288:TYR:CD2	1:B:2291:GLN:HB2	2.51	0.46
1:B:2412:TYR:OH	1:B:2453:GLU:HG2	2.16	0.46
1:A:1713:VAL:O	1:A:1716:GLN:HB2	2.14	0.46
1:B:131:LEU:HD22	1:B:177:LEU:HD21	1.97	0.46
1:B:1166:LEU:HD12	1:B:1166:LEU:H	1.81	0.46
1:B:1697:PRO:HG2	1:B:1752:LEU:HD11	1.98	0.46
1:B:2402:LEU:HD13	1:B:2434:VAL:HG23	1.97	0.46
1:B:2591:ILE:HD12	1:B:2591:ILE:H	1.81	0.46
1:B:3502:MET:SD	1:B:3514:VAL:HG21	2.56	0.46
1:A:3419:PHE:O	1:A:3422:GLN:HG3	2.16	0.46
1:B:323:VAL:HG13	1:B:369:PHE:CZ	2.46	0.46
1:B:364:ARG:HH21	1:B:368:LEU:HB2	1.80	0.46
1:B:1733:THR:O	1:B:1737:ASN:HB2	2.16	0.46
1:B:2393:LEU:HD12	1:B:2393:LEU:H	1.81	0.46
1:A:338:LEU:HD21	1:A:376:ILE:HG21	1.98	0.46
1:A:647:TYR:O	1:A:651:TYR:HB2	2.16	0.46
1:A:1075:ARG:NH2	1:A:1117:ASP:OD1	2.49	0.46
1:A:1100:VAL:HG12	1:A:1134:LEU:HD11	1.98	0.46
1:A:1139:GLU:OE1	1:A:1193:LYS:HE2	2.16	0.46
1:A:1352:SER:O	1:A:1354:GLU:N	2.42	0.46
1:A:1754:GLN:HB2	1:A:1797:LEU:HD11	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1981:LEU:O	1:A:1981:LEU:HD23	2.16	0.46
1:A:2551:GLU:HG3	1:A:2849:SER:HB2	1.99	0.46
1:B:96:MET:SD	1:B:96:MET:N	2.89	0.46
1:B:762:TYR:CE1	1:B:764:PRO:HD2	2.51	0.46
1:B:1797:LEU:O	1:B:1801:VAL:HG23	2.16	0.46
1:A:977:ASP:HB3	1:A:980:THR:HG22	1.98	0.45
1:A:1425:ALA:O	1:A:1429:GLU:HG2	2.16	0.45
1:A:2165:LEU:HD12	1:A:2200:ALA:HB1	1.97	0.45
1:A:3295:GLU:HA	1:A:3298:LEU:HD12	1.99	0.45
1:A:3607:GLU:OE2	1:A:3655:LYS:NZ	2.48	0.45
1:A:3694:PHE:O	1:A:3696:ARG:N	2.47	0.45
1:B:1479:VAL:O	1:B:1483:LEU:HG	2.16	0.45
1:B:1684:LEU:HD23	1:B:1684:LEU:HA	1.77	0.45
1:B:2224:PHE:CE2	1:B:2226:PRO:HG3	2.51	0.45
1:B:4090:ARG:NH1	1:B:4113:ASP:OD2	2.39	0.45
1:A:451:PRO:C	1:A:453:MET:H	2.24	0.45
1:A:918:ALA:O	1:A:972:LEU:HD21	2.16	0.45
1:A:2394:LYS:O	1:A:2398:LEU:HG	2.16	0.45
1:A:3658:ASP:OD1	1:A:3659:PHE:N	2.49	0.45
1:B:216:LYS:O	1:B:220:LEU:HD13	2.16	0.45
1:B:397:LEU:HD11	1:B:438:LEU:HD13	1.97	0.45
1:B:1779:GLN:NE2	1:B:1822:ARG:O	2.47	0.45
1:A:651:TYR:O	1:A:655:LEU:HG	2.17	0.45
1:A:785:MET:HE2	1:A:785:MET:HB3	1.78	0.45
1:A:907:LEU:HA	1:A:910:PHE:CZ	2.51	0.45
1:A:1881:TYR:CD1	1:A:1951:VAL:HG23	2.51	0.45
1:A:3133:GLN:O	1:A:3137:GLU:HG2	2.17	0.45
1:A:4006:VAL:HB	1:A:4040:PRO:HB3	1.99	0.45
1:A:4008:GLU:O	1:A:4010:SER:N	2.48	0.45
1:B:1423:ILE:HD12	1:B:1458:LEU:HD11	1.99	0.45
1:B:1529:VAL:HA	1:B:1532:LEU:HD12	1.97	0.45
1:B:1840:PHE:O	1:B:1843:ILE:HG22	2.16	0.45
1:B:2524:PHE:O	1:B:2530:ARG:HG2	2.16	0.45
1:B:2841:ASN:O	1:B:2845:ASN:ND2	2.37	0.45
1:B:3694:PHE:O	1:B:3696:ARG:HG3	2.15	0.45
2:C:729:LEU:O	2:C:732:ILE:HB	2.16	0.45
1:A:425:ASP:OD1	1:A:425:ASP:N	2.48	0.45
1:A:574:LYS:HA	1:A:574:LYS:HD2	1.71	0.45
1:A:1224:PHE:HD1	1:A:1266:CYS:SG	2.39	0.45
1:A:3575:LEU:HB3	1:A:3800:LEU:HD21	1.98	0.45
1:B:907:LEU:CD2	1:B:940:PHE:CD2	2.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2486:ASP:O	1:B:2488:GLU:N	2.50	0.45
1:B:3659:PHE:HD2	1:B:3662:ILE:HG12	1.80	0.45
1:B:3891:SER:C	1:B:3893:SER:H	2.22	0.45
1:B:4013:TRP:HA	1:B:4016:PHE:HB3	1.98	0.45
1:A:743:LEU:HD12	1:A:743:LEU:O	2.16	0.45
1:A:1669:PRO:C	1:A:1671:VAL:H	2.24	0.45
1:A:2973:ASP:O	1:A:2977:ASN:ND2	2.47	0.45
1:A:3335:ARG:NH1	1:A:3422:GLN:HG2	2.31	0.45
1:B:148:LYS:O	1:B:152:LEU:HB2	2.16	0.45
1:B:1633:TRP:H	1:B:1633:TRP:CD1	2.34	0.45
1:B:1832:SER:OG	1:B:1833:LEU:N	2.50	0.45
1:B:3288:SER:HB2	1:B:3296:GLN:HG3	1.99	0.45
1:B:3354:ASP:OD1	1:B:3354:ASP:N	2.46	0.45
1:B:3862:ALA:HB3	1:B:4119:ARG:HH12	1.81	0.45
1:B:4047:ALA:HA	1:B:4050:LYS:HG2	1.98	0.45
1:A:1920:TYR:HA	1:A:1923:PHE:CZ	2.52	0.45
1:A:2787:HIS:O	1:A:2790:LEU:HG	2.17	0.45
1:A:3506:LEU:HA	1:A:3511:ALA:HB1	1.98	0.45
1:B:3455:LYS:HE2	1:B:3489:SER:O	2.17	0.45
1:A:19:LEU:O	1:A:24:ARG:NH1	2.50	0.45
1:A:253:LEU:HA	1:A:256:ILE:HG12	1.98	0.45
1:A:1427:SER:O	1:A:1431:LEU:HG	2.16	0.45
1:A:1646:LEU:HD13	1:A:1692:ALA:HB2	1.98	0.45
1:B:2004:TYR:O	1:B:2007:ILE:HB	2.17	0.45
1:A:376:ILE:HG23	1:A:377:ASN:H	1.82	0.45
1:A:1117:ASP:OD2	1:A:1123:THR:OG1	2.25	0.45
1:A:1181:THR:HG22	1:A:1184:ARG:NH1	2.30	0.45
1:A:1580:LEU:HG	1:A:1625:HIS:NE2	2.31	0.45
1:A:2538:ARG:O	1:A:2542:LEU:HG	2.17	0.45
1:A:3120:LEU:H	1:A:3120:LEU:HD23	1.81	0.45
1:A:3885:ARG:HA	1:A:3888:VAL:HG12	1.99	0.45
1:B:384:MET:C	1:B:386:VAL:H	2.24	0.45
1:B:408:TYR:CE1	1:B:453:MET:HE2	2.52	0.45
1:B:3061:LEU:O	1:B:3065:ILE:HG12	2.16	0.45
1:A:288:ASP:OD1	1:A:288:ASP:N	2.50	0.45
1:A:371:GLY:HA2	1:A:423:TYR:CD2	2.52	0.45
1:A:1143:VAL:HG23	1:A:1197:LEU:HD22	1.98	0.45
1:A:3858:MET:HE1	1:A:4119:ARG:HB3	1.98	0.45
1:A:3948:SER:HB3	1:A:4016:PHE:HZ	1.82	0.45
1:B:1205:ASN:HA	1:B:1275:THR:HA	1.99	0.45
1:B:1941:HIS:HB3	1:B:1981:LEU:HD23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2277:LEU:HD21	1:B:2326:ILE:HD11	1.99	0.45
1:B:2593:SER:C	1:B:2595:TRP:H	2.25	0.45
1:B:3493:TRP:CE3	1:B:3494:GLN:HG3	2.52	0.45
1:B:3988:LEU:O	1:B:3992:ARG:HG2	2.17	0.45
1:A:583:LEU:HA	1:A:614:PRO:HA	1.99	0.45
1:A:2137:ILE:O	1:A:2138:VAL:C	2.59	0.45
1:A:2420:PHE:HE1	1:A:2435:CYS:HB2	1.82	0.45
1:A:2572:TYR:HA	1:A:2787:HIS:CD2	2.52	0.45
1:A:3476:PRO:HA	1:A:3480:LEU:HD13	1.99	0.45
1:B:12:LEU:HD21	1:B:58:VAL:HA	1.99	0.45
1:B:1872:GLY:O	1:B:1876:ILE:HG13	2.17	0.45
1:B:1877:LEU:HD13	1:B:1915:LEU:HD11	1.98	0.45
1:B:1906:THR:HG22	1:B:1906:THR:O	2.16	0.45
1:B:2172:ALA:HB2	1:B:2189:ILE:HG21	1.99	0.45
1:B:4005:PHE:O	1:B:4011:PHE:HZ	1.99	0.45
1:A:3813:LYS:HB2	1:A:3925:LEU:CB	2.47	0.44
1:B:487:LEU:HA	1:B:490:ILE:HG12	2.00	0.44
1:B:1006:THR:OG1	1:B:1054:VAL:HG21	2.17	0.44
1:B:1069:HIS:C	1:B:1071:ASN:H	2.25	0.44
1:B:1190:LEU:HD23	1:B:1190:LEU:HA	1.80	0.44
1:B:2183:HIS:C	1:B:2185:MET:H	2.25	0.44
1:B:3082:TYR:HB3	1:B:3085:GLU:OE1	2.17	0.44
1:B:3962:ARG:NH1	1:B:4125:GLU:O	2.29	0.44
1:A:1878:ASP:OD2	1:A:1946:ASN:HB3	2.17	0.44
1:A:2249:LEU:O	1:A:2251:ILE:HG23	2.17	0.44
1:A:3091:LEU:O	1:A:3192:LYS:HE2	2.16	0.44
1:A:3257:LYS:HG3	1:A:3258:LEU:N	2.31	0.44
1:B:569:VAL:HG12	1:B:573:LEU:HD23	1.99	0.44
1:B:1072:ALA:HA	1:B:1075:ARG:NH2	2.32	0.44
1:B:1727:ARG:HH21	1:B:1773:VAL:HG23	1.83	0.44
1:B:3113:ASN:O	1:B:3117:ILE:HG13	2.17	0.44
1:B:3450:MET:HB3	1:B:3468:LEU:HD11	1.98	0.44
1:B:3733:ARG:HD3	1:B:3753:LYS:HG2	1.98	0.44
1:B:3811:THR:HG21	1:B:3926:ASN:ND2	2.32	0.44
1:B:4064:LEU:HD13	1:B:4077:TYR:HB3	1.98	0.44
1:A:701:TYR:C	1:A:703:CYS:H	2.25	0.44
1:A:1633:TRP:CD1	1:A:1633:TRP:N	2.85	0.44
1:A:2379:MET:HE1	1:A:2404:ARG:HB3	2.00	0.44
1:B:303:HIS:O	1:B:305:ASN:N	2.44	0.44
1:B:1143:VAL:HG23	1:B:1197:LEU:HG	1.99	0.44
1:B:2168:LEU:HB2	1:B:2193:ILE:HD12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2436:LEU:HD23	1:B:2472:GLN:HB3	1.99	0.44
1:B:3295:GLU:HA	1:B:3298:LEU:HD12	1.99	0.44
1:A:19:LEU:HD21	1:A:71:LYS:HG3	1.98	0.44
1:A:635:PRO:O	1:A:679:LYS:NZ	2.44	0.44
1:A:870:LEU:HB3	1:A:3129:LEU:HD11	1.99	0.44
1:A:1730:PRO:HG2	1:A:1733:THR:OG1	2.16	0.44
1:A:2531:LEU:HD22	1:A:2541:ALA:HB1	2.00	0.44
1:A:2801:ASP:HB3	1:A:2804:ILE:HG22	1.99	0.44
1:A:3385:LEU:HD22	1:A:3416:LEU:HB2	2.00	0.44
1:B:326:MET:HE3	1:B:326:MET:HB2	1.82	0.44
1:B:377:ASN:HB3	1:B:380:ASP:H	1.83	0.44
1:B:1298:LEU:CB	1:B:1367:HIS:HB3	2.47	0.44
1:B:2894:GLU:O	1:B:2896:ALA:N	2.44	0.44
1:B:3659:PHE:CE2	1:B:3662:ILE:HG23	2.53	0.44
1:A:1583:MET:HE2	1:A:1625:HIS:HB2	1.99	0.44
1:A:2473:MET:O	1:A:2476:ILE:HG12	2.17	0.44
1:A:2813:PHE:CD2	1:A:2861:ILE:HB	2.53	0.44
1:A:2870:SER:HB2	1:A:2922:ARG:HH22	1.81	0.44
1:B:720:GLN:OE1	1:B:1026:ARG:NH2	2.50	0.44
1:B:1690:GLY:O	1:B:1693:VAL:HG12	2.18	0.44
1:A:267:VAL:HG23	1:A:268:PRO:HD3	2.00	0.44
1:A:718:MET:HE2	1:A:718:MET:HB2	1.80	0.44
1:A:859:LEU:HD21	1:A:870:LEU:HD13	1.99	0.44
1:A:2389:PHE:CE1	1:A:2393:LEU:HD22	2.53	0.44
1:A:3833:ARG:HB3	1:A:3877:LYS:HE2	2.00	0.44
1:B:605:THR:OG1	1:B:1027:ASP:HB3	2.18	0.44
1:B:1070:PRO:HA	1:B:1113:LEU:HD21	1.99	0.44
1:B:1508:LYS:HZ2	1:B:1562:LEU:HD22	1.82	0.44
1:B:1900:PHE:CE2	1:B:1906:THR:OG1	2.71	0.44
1:B:2125:TRP:CZ3	1:B:2126:MET:HE3	2.53	0.44
1:B:2404:ARG:HD2	1:B:2404:ARG:HA	1.64	0.44
1:A:359:LEU:HD23	1:A:359:LEU:H	1.81	0.44
1:A:563:LEU:HD13	1:A:563:LEU:HA	1.84	0.44
1:A:1010:LEU:O	1:A:1014:LEU:HD13	2.18	0.44
1:A:2122:LEU:HA	1:A:2122:LEU:HD23	1.66	0.44
1:A:2572:TYR:N	1:A:2573:PRO:HD3	2.32	0.44
1:A:3891:SER:C	1:A:3893:SER:H	2.24	0.44
1:B:364:ARG:HH22	1:B:368:LEU:HD13	1.81	0.44
1:B:1041:ILE:HG22	1:B:1049:GLN:HE22	1.83	0.44
1:B:2972:TYR:HB3	1:B:2998:SER:OG	2.17	0.44
1:B:3326:GLN:O	1:B:3329:LEU:HG	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:ASN:O	1:A:254:LYS:HE2	2.17	0.44
1:A:336:ASN:OD1	1:A:337:LYS:HD2	2.18	0.44
1:A:1633:TRP:CH2	1:A:1674:THR:HG22	2.53	0.44
1:A:1951:VAL:O	1:A:1955:VAL:HG13	2.18	0.44
1:A:1990:PHE:HZ	1:A:2144:LEU:HD21	1.83	0.44
1:A:2785:ILE:HG12	1:A:2786:LYS:HB2	1.99	0.44
1:A:3094:ASP:OD1	1:A:3196:LYS:NZ	2.43	0.44
1:A:3846:MET:HG2	1:A:3862:ALA:HB2	2.00	0.44
1:B:263:LYS:HA	1:B:263:LYS:HD3	1.82	0.44
1:B:1089:PHE:CE1	1:B:1096:VAL:HA	2.53	0.44
1:B:1787:ARG:HB3	1:B:1831:CYS:HB3	1.98	0.44
1:B:3629:ARG:HD2	1:B:3633:ILE:HD11	2.00	0.44
1:B:3666:LEU:HA	1:B:3669:LYS:HG2	2.00	0.44
1:A:1483:LEU:O	1:A:1487:VAL:HG23	2.18	0.44
1:A:1712:ARG:O	1:A:1716:GLN:HG2	2.18	0.44
1:A:3422:GLN:HE22	1:A:3423:GLN:NE2	2.15	0.44
1:A:3858:MET:HE3	1:A:3858:MET:HB3	1.75	0.44
1:B:1813:SER:HB3	1:B:1936:ARG:NH2	2.32	0.44
1:B:1861:SER:O	1:B:1865:THR:OG1	2.25	0.44
1:B:2870:SER:HB2	1:B:2922:ARG:HH22	1.83	0.44
1:B:3085:GLU:OE1	1:B:3085:GLU:N	2.40	0.44
1:B:3307:LEU:HD21	1:B:3326:GLN:OE1	2.17	0.44
1:A:388:LEU:HD12	1:A:388:LEU:HA	1.86	0.43
1:A:765:LEU:HD23	1:A:766:ALA:N	2.32	0.43
1:A:1948:ALA:O	1:A:1952:ILE:HG13	2.18	0.43
1:A:2572:TYR:CD2	1:A:2787:HIS:HB2	2.53	0.43
1:A:2863:CYS:HB2	1:A:2892:LEU:HD13	1.99	0.43
1:A:3285:HIS:NE2	1:A:3333:THR:OG1	2.35	0.43
1:B:16:GLN:NE2	1:B:63:PHE:HA	2.33	0.43
1:B:1563:PHE:HD1	1:B:1567:ILE:HD11	1.83	0.43
1:B:2146:LEU:HD12	1:B:2146:LEU:HA	1.87	0.43
1:B:2538:ARG:O	1:B:2542:LEU:HG	2.17	0.43
1:B:3575:LEU:HD13	1:B:3796:MET:HE1	1.99	0.43
1:A:651:TYR:OH	1:A:1392:MET:HE1	2.18	0.43
1:A:1029:CYS:O	1:A:1032:CYS:HB2	2.18	0.43
1:A:1067:ALA:O	1:A:1075:ARG:HB2	2.18	0.43
1:A:1075:ARG:NE	1:A:1114:ALA:HB2	2.34	0.43
1:A:1282:LEU:HD13	1:A:1291:LEU:HD21	1.99	0.43
1:A:1361:LYS:HA	1:A:1364:CYS:HB2	2.00	0.43
1:A:1802:TYR:CZ	1:A:1843:ILE:HD11	2.53	0.43
1:A:3082:TYR:C	1:A:3084:GLN:H	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3835:PRO:O	1:A:3839:TYR:HB2	2.17	0.43
1:B:713:GLU:O	1:B:716:VAL:HG12	2.19	0.43
1:B:1787:ARG:O	1:B:1787:ARG:HG2	2.18	0.43
1:B:1851:LEU:O	1:B:1870:LYS:NZ	2.38	0.43
1:B:2084:GLU:O	1:B:2089:ASN:ND2	2.49	0.43
1:B:2239:LYS:HG3	1:B:2279:ILE:HG23	2.00	0.43
1:B:2264:ASP:O	1:B:2266:ASN:N	2.49	0.43
1:A:1723:PRO:HD2	1:A:1739:TYR:CD1	2.53	0.43
1:A:1790:SER:O	1:A:1793:THR:HG22	2.18	0.43
1:B:1672:PHE:HE2	1:B:1702:LEU:HD21	1.84	0.43
1:B:1848:ILE:HD12	1:B:1848:ILE:HA	1.85	0.43
1:B:2958:LEU:HG	1:B:4101:GLU:HG2	2.00	0.43
1:B:3386:SER:O	1:B:3389:VAL:HG22	2.18	0.43
1:B:3778:ASP:OD1	1:B:3779:SER:N	2.50	0.43
1:A:583:LEU:HD23	1:A:583:LEU:H	1.83	0.43
1:A:585:ILE:HA	1:A:611:ASN:OD1	2.18	0.43
1:A:4099:SER:O	1:A:4103:GLN:HB2	2.18	0.43
1:B:414:LEU:HD13	1:B:414:LEU:HA	1.87	0.43
1:B:1186:LYS:HA	1:B:1186:LYS:HD3	1.82	0.43
1:B:1463:LEU:HG	1:B:1466:ASN:HB2	2.00	0.43
1:B:2372:PRO:HG2	1:B:2373:PRO:HD3	2.01	0.43
1:B:3659:PHE:CE2	1:B:3661:ASP:HB3	2.53	0.43
1:B:3910:LEU:HD12	1:B:3910:LEU:HA	1.84	0.43
1:A:227:LEU:O	1:A:231:LEU:HB2	2.18	0.43
1:A:432:THR:N	1:A:433:PRO:HD2	2.33	0.43
1:A:473:PRO:C	1:A:475:LEU:H	2.25	0.43
1:A:561:ASN:HA	1:A:564:LEU:HD12	2.00	0.43
1:A:1294:VAL:O	1:A:1298:LEU:HD13	2.18	0.43
1:A:1479:VAL:O	1:A:1483:LEU:HG	2.17	0.43
1:A:2091:HIS:O	1:A:2093:CYS:N	2.52	0.43
1:A:2281:MET:HG2	1:A:2326:ILE:HG12	2.01	0.43
1:A:2443:MET:HE1	1:A:2479:TRP:HB3	1.99	0.43
1:A:3623:PRO:HG2	1:A:3633:ILE:HD12	2.00	0.43
1:B:1017:ILE:HG23	1:B:1018:VAL:HG13	2.01	0.43
1:B:1023:SER:HA	1:B:1026:ARG:HE	1.83	0.43
1:B:1747:LEU:HD12	1:B:1781:SER:CB	2.48	0.43
1:B:1790:SER:O	1:B:1793:THR:HG22	2.18	0.43
1:B:1832:SER:N	1:B:1883:ARG:HH22	2.11	0.43
1:B:2375:ALA:O	1:B:2379:MET:N	2.51	0.43
1:B:2439:ILE:O	1:B:2443:MET:HG3	2.19	0.43
1:B:2547:SER:C	1:B:2549:LYS:H	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2950:LYS:HE3	1:B:2981:TRP:CE3	2.54	0.43
1:B:3068:ALA:O	1:B:3074:GLN:HB3	2.19	0.43
1:B:3979:LEU:O	1:B:3983:ILE:HG12	2.19	0.43
1:A:1208:LEU:HD12	1:A:1208:LEU:HA	1.81	0.43
1:A:1575:LEU:HD23	1:A:1617:LYS:HG2	2.00	0.43
1:A:3077:ILE:HG23	1:A:3081:HIS:CE1	2.52	0.43
1:A:3992:ARG:NH1	1:A:4103:GLN:OE1	2.51	0.43
1:A:3999:THR:HA	1:A:4002:MET:CE	2.49	0.43
1:B:765:LEU:HA	1:B:768:VAL:HG12	2.01	0.43
1:B:1361:LYS:HA	1:B:1361:LYS:HD2	1.88	0.43
1:B:1626:TRP:CZ3	1:B:1674:THR:HG21	2.54	0.43
1:B:2398:LEU:O	1:B:2401:VAL:HG12	2.19	0.43
1:A:939:MET:HE2	1:A:2784:GLN:HA	2.01	0.43
1:A:1718:ILE:HG12	1:A:1722:PHE:CE2	2.54	0.43
1:A:2327:LEU:HD13	1:A:2371:PHE:CD2	2.54	0.43
1:A:2419:ASP:HB2	1:A:2422:GLN:HB2	2.00	0.43
1:A:3268:THR:HG23	1:A:3269:ARG:H	1.84	0.43
1:B:418:ALA:CB	1:B:463:LYS:HG3	2.49	0.43
1:B:977:ASP:O	1:B:980:THR:HG22	2.18	0.43
1:B:1839:PHE:HA	1:B:1842:THR:HG22	2.00	0.43
1:B:2551:GLU:HA	1:B:2554:PHE:HB2	2.00	0.43
1:B:3829:LEU:HD23	1:B:3829:LEU:HA	1.87	0.43
1:B:3988:LEU:HD21	1:B:4103:GLN:OE1	2.19	0.43
1:B:4126:PRO:HD2	1:B:4127:TRP:CZ3	2.53	0.43
1:A:3596:LEU:HD22	1:A:3606:ILE:HD12	2.01	0.43
1:A:3798:SER:O	1:A:3799:ARG:HG2	2.19	0.43
1:A:3867:THR:HG21	1:A:4119:ARG:CZ	2.49	0.43
1:B:484:HIS:CE1	1:B:575:ILE:HG13	2.53	0.43
1:B:2511:ILE:HG12	1:B:2550:ILE:HG22	2.01	0.43
1:B:2548:PRO:HG3	1:B:2846:THR:HB	2.01	0.43
1:B:3418:ASP:OD2	1:B:3464:LYS:NZ	2.31	0.43
1:A:647:TYR:CD1	1:A:703:CYS:HB3	2.51	0.43
1:A:873:VAL:HG13	1:A:874:THR:N	2.26	0.43
1:A:3019:ILE:HG21	1:A:3029:LYS:HB3	2.01	0.43
1:A:3301:LEU:HD11	1:A:3359:ILE:HD11	2.01	0.43
1:A:3669:LYS:HE2	1:A:3669:LYS:HB2	1.92	0.43
1:B:276:ALA:HA	1:B:318:SER:CB	2.49	0.43
1:B:633:ILE:C	1:B:635:PRO:HD3	2.43	0.43
1:B:1346:THR:HG23	1:B:1405:ALA:CB	2.49	0.43
1:B:2451:LEU:HD12	1:B:2451:LEU:HA	1.78	0.43
1:B:2492:ASP:HB3	1:B:2495:SER:H	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3411:ASP:OD1	1:B:3411:ASP:N	2.46	0.43
1:B:4012:ASP:C	1:B:4014:LYS:H	2.27	0.43
1:A:112:THR:O	1:A:116:THR:OG1	2.32	0.43
1:A:149:ILE:HB	1:A:185:HIS:ND1	2.34	0.43
1:A:723:ASP:OD1	1:A:723:ASP:N	2.52	0.43
1:A:912:PRO:O	1:A:916:GLU:HB2	2.19	0.43
1:A:1122:GLY:HA2	1:A:1125:GLN:OE1	2.19	0.43
1:A:1962:TYR:O	1:A:1967:PHE:HD2	2.02	0.43
1:A:2225:HIS:CE1	1:A:2230:VAL:HG21	2.54	0.43
1:A:3489:SER:O	1:A:3490:VAL:HG23	2.19	0.43
1:A:3771:MET:HE3	1:A:3771:MET:HB2	1.90	0.43
1:A:4044:ILE:HD13	1:A:4044:ILE:HA	1.72	0.43
1:A:4054:ALA:H	1:A:4103:GLN:NE2	2.16	0.43
1:B:1001:PHE:CE1	1:B:1044:ILE:HD11	2.54	0.43
1:B:1859:ASN:HB3	1:B:1862:THR:HG22	2.01	0.43
1:B:3820:MET:HB3	1:B:3824:GLU:HG3	2.00	0.43
1:A:326:MET:HE3	1:A:326:MET:HB2	1.83	0.42
1:A:1348:LEU:HG	1:A:1359:LEU:HD21	2.01	0.42
1:A:1411:TYR:O	1:A:1415:LEU:HG	2.19	0.42
1:A:1440:ASP:OD1	1:A:1440:ASP:N	2.52	0.42
1:A:1858:LEU:HD23	1:A:1858:LEU:HA	1.88	0.42
1:A:3661:ASP:O	1:A:3665:MET:HG3	2.18	0.42
1:A:3929:MET:HE3	1:A:3940:ILE:HD13	2.01	0.42
1:B:487:LEU:HD22	1:B:571:SER:OG	2.19	0.42
1:B:523:THR:OG1	1:B:524:TYR:N	2.52	0.42
1:B:2219:LEU:O	1:B:2223:VAL:HB	2.19	0.42
1:B:3324:ARG:O	1:B:3328:ILE:HG13	2.18	0.42
1:B:3678:GLY:C	1:B:3680:LEU:H	2.25	0.42
1:B:3872:ARG:HA	1:B:3875:GLU:HG2	2.01	0.42
1:A:465:PHE:HE1	1:A:482:VAL:HG11	1.84	0.42
1:A:969:LEU:HD23	1:A:969:LEU:HA	1.79	0.42
1:A:1057:LYS:HE3	1:A:1099:PHE:HB2	2.01	0.42
1:A:1134:LEU:HD23	1:A:1134:LEU:HA	1.83	0.42
1:A:1930:GLU:CD	1:A:1937:ARG:HH22	2.25	0.42
1:A:2896:ALA:O	1:A:2899:ARG:NE	2.47	0.42
1:B:527:TYR:O	1:B:531:PHE:HD1	2.02	0.42
1:B:1579:VAL:O	1:B:1583:MET:HG2	2.19	0.42
1:B:1648:LEU:O	1:B:1652:ILE:HG12	2.20	0.42
1:B:1984:LEU:O	1:B:1984:LEU:HD23	2.19	0.42
1:B:2440:TYR:HA	1:B:2443:MET:HE2	2.01	0.42
1:B:3114:TYR:CE2	1:B:3125:ARG:HB3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:ASP:OD1	1:A:219:VAL:HG23	2.19	0.42
1:A:767:GLU:OE1	1:A:854:ARG:NH1	2.52	0.42
1:A:1801:VAL:HB	1:A:1824:LEU:HD12	2.01	0.42
1:A:1856:THR:HG22	1:A:1858:LEU:HB2	2.00	0.42
1:A:1861:SER:C	1:A:1863:PHE:H	2.27	0.42
1:A:2181:GLY:C	1:A:2183:HIS:H	2.27	0.42
1:A:2477:LEU:HB3	1:A:2506:LEU:HG	2.02	0.42
1:A:2881:LEU:HD23	1:A:2886:GLN:HE21	1.84	0.42
1:A:3118:ASP:OD2	1:A:3895:GLU:HB3	2.19	0.42
1:A:4027:TRP:O	1:A:4028:ILE:HG23	2.18	0.42
1:A:4085:LYS:H	1:A:4091:ALA:HB3	1.84	0.42
1:B:128:LEU:HD23	1:B:128:LEU:HA	1.86	0.42
1:A:858:MET:HE3	1:A:858:MET:HB3	1.86	0.42
1:A:1333:SER:O	1:A:1336:THR:HG22	2.20	0.42
1:A:1342:MET:HA	1:A:1345:THR:HG22	2.02	0.42
1:A:1515:LEU:HD21	1:A:1519:PHE:CE2	2.54	0.42
1:A:1532:LEU:O	1:A:1592:MET:HE2	2.19	0.42
1:A:1820:VAL:O	1:A:1825:LEU:HG	2.19	0.42
1:A:1851:LEU:HB3	1:A:1918:LEU:HD13	2.01	0.42
1:A:2225:HIS:O	1:A:2227:LYS:N	2.52	0.42
1:A:2288:TYR:CD1	1:A:2291:GLN:HB2	2.54	0.42
1:A:2368:THR:HA	1:A:2371:PHE:O	2.20	0.42
1:A:3020:ASP:O	1:A:3024:PRO:HB3	2.18	0.42
1:A:3274:VAL:O	1:A:3278:GLN:HG3	2.19	0.42
1:A:4055:ASN:HB3	1:A:4058:VAL:HG23	2.00	0.42
1:B:51:LEU:HD11	1:B:95:LYS:HD3	2.01	0.42
1:B:101:ALA:HB1	1:B:143:LEU:HD11	2.02	0.42
1:B:104:SER:HB3	1:B:134:LEU:HD11	2.01	0.42
1:B:302:ALA:HB2	1:B:358:GLU:OE2	2.20	0.42
1:B:651:TYR:CE1	1:B:655:LEU:HD11	2.53	0.42
1:A:767:GLU:HG3	1:A:846:ILE:HD13	2.01	0.42
1:A:983:LEU:O	1:A:984:TYR:HB2	2.19	0.42
1:A:1352:SER:C	1:A:1354:GLU:H	2.26	0.42
1:A:1873:TYR:HD1	1:A:1873:TYR:HA	1.78	0.42
1:A:1990:PHE:HB2	1:A:2179:GLY:HA3	2.01	0.42
1:A:2350:LYS:HG2	1:A:2378:PHE:HE1	1.84	0.42
1:A:3535:ILE:HD12	1:A:3759:ARG:NH1	2.33	0.42
1:B:354:SER:HA	1:B:358:GLU:HB2	2.00	0.42
1:B:1433:ALA:C	1:B:1435:ASN:H	2.27	0.42
1:B:3049:LEU:O	1:B:3053:LEU:HG	2.18	0.42
1:B:3654:MET:HG2	1:B:3656:LEU:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1788:ARG:H	1:A:1794:GLN:HE21	1.67	0.42
1:A:1840:PHE:O	1:A:1843:ILE:HG22	2.19	0.42
1:A:2193:ILE:O	1:A:2196:TRP:NE1	2.52	0.42
1:A:2514:ASN:O	1:A:2517:LEU:HB3	2.18	0.42
1:A:3998:LEU:O	1:A:4002:MET:HG3	2.19	0.42
1:B:342:MET:HA	1:B:342:MET:HE3	2.01	0.42
1:B:413:PHE:O	1:B:417:VAL:HG23	2.19	0.42
1:B:1254:LEU:H	1:B:1254:LEU:HD22	1.84	0.42
1:B:1264:LEU:HD21	1:B:1341:ILE:HG13	2.01	0.42
1:B:2556:SER:HB2	1:B:2799:GLN:HA	2.01	0.42
1:B:3558:ILE:O	1:B:3562:LEU:HB2	2.20	0.42
1:A:71:LYS:O	1:A:71:LYS:HD3	2.20	0.42
1:A:1615:GLY:C	1:A:1655:ILE:HG21	2.45	0.42
1:A:1909:ASN:HB2	1:A:1913:LYS:HB2	2.01	0.42
1:A:2101:VAL:HG12	1:A:2156:VAL:HG21	2.01	0.42
1:A:2125:TRP:CZ3	1:A:2126:MET:HE3	2.54	0.42
1:A:2436:LEU:O	1:A:2439:ILE:HG22	2.19	0.42
1:A:3144:PHE:CE2	1:A:3157:LEU:HD13	2.55	0.42
1:B:1010:LEU:O	1:B:1014:LEU:HD13	2.20	0.42
1:B:1519:PHE:CE2	1:B:1528:LEU:HD22	2.54	0.42
1:B:2312:TYR:O	1:B:2315:VAL:HG12	2.19	0.42
1:B:2921:LEU:O	1:B:2925:GLU:HG2	2.20	0.42
1:A:178:LEU:HD23	1:A:181:LEU:HD12	2.01	0.42
1:A:1395:LEU:HB3	1:A:1396:PRO:HD3	2.02	0.42
1:A:1703:THR:O	1:A:1707:LEU:HB2	2.19	0.42
1:A:2105:HIS:CG	1:A:2156:VAL:HG13	2.55	0.42
1:A:2281:MET:HE1	1:A:2287:PRO:HD3	2.01	0.42
1:A:3502:MET:SD	1:A:3514:VAL:HG21	2.59	0.42
1:B:93:LEU:HD21	1:B:134:LEU:HD12	2.01	0.42
1:B:528:VAL:HA	1:B:633:ILE:HD11	2.02	0.42
1:B:2288:TYR:HD2	1:B:2291:GLN:HB2	1.85	0.42
1:B:2528:GLU:C	1:B:2530:ARG:H	2.27	0.42
1:B:2586:PHE:N	1:B:2783:ILE:HD11	2.34	0.42
1:B:3006:ALA:O	1:B:3257:LYS:HE3	2.20	0.42
1:B:3760:GLN:O	1:B:3764:VAL:HG13	2.20	0.42
1:A:268:PRO:HB2	1:A:308:LEU:HD11	2.01	0.42
1:A:484:HIS:CE1	1:A:488:ILE:HD11	2.55	0.42
1:A:1601:LEU:HD22	1:A:1618:LEU:HD21	2.02	0.42
1:A:1743:MET:HE2	1:A:1774:MET:HE1	2.01	0.42
1:A:1952:ILE:O	1:A:1955:VAL:HG22	2.20	0.42
1:A:2255:LEU:HD23	1:A:2256:ILE:HG13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:736:LEU:HD22	1:B:741:ILE:HD12	2.01	0.42
1:B:2128:PHE:CZ	1:B:2132:LYS:HD2	2.55	0.42
1:B:2251:ILE:HD12	1:B:2253:TYR:CE2	2.55	0.42
1:B:3464:LYS:HE3	1:B:3997:LEU:HD23	2.01	0.42
1:A:465:PHE:CE1	1:A:482:VAL:HG11	2.55	0.42
1:A:966:PHE:HE1	1:A:969:LEU:HD12	1.83	0.42
1:A:1018:VAL:CG1	1:A:1074:LYS:HA	2.50	0.42
1:A:1283:GLY:HA2	1:A:1358:LEU:HD11	2.02	0.42
1:A:1991:PRO:O	1:A:2184:TYR:HB2	2.20	0.42
1:A:3110:PHE:CD1	1:A:3128:LYS:HD2	2.52	0.42
1:A:3511:ALA:HB3	1:A:3551:ASN:ND2	2.34	0.42
1:A:3554:PHE:CE2	1:A:3558:ILE:HD11	2.54	0.42
1:A:3629:ARG:NH2	1:A:3634:GLN:HB2	2.35	0.42
1:A:3868:VAL:O	1:A:3872:ARG:HG2	2.19	0.42
1:B:573:LEU:HA	1:B:576:VAL:HG12	2.01	0.42
1:B:631:ARG:HG3	1:B:672:ILE:HD11	2.01	0.42
1:B:2255:LEU:HD23	1:B:2256:ILE:HG13	2.02	0.42
1:B:2304:VAL:HG21	1:B:2344:LEU:HG	2.02	0.42
1:B:2334:LYS:HE3	1:B:2334:LYS:HB2	1.90	0.42
1:B:2458:VAL:CG1	1:B:2476:ILE:HD11	2.50	0.42
1:B:2855:VAL:HA	1:B:2858:ILE:HG12	2.02	0.42
1:A:227:LEU:HD21	1:A:248:ILE:HD13	2.01	0.41
1:A:937:MET:HE3	1:A:937:MET:HB2	1.91	0.41
1:A:1474:ASP:C	1:A:1476:HIS:H	2.28	0.41
1:A:1575:LEU:C	1:A:1577:LEU:H	2.28	0.41
1:A:1982:ILE:HG22	1:A:1983:ASP:H	1.85	0.41
1:A:2801:ASP:O	1:A:2804:ILE:HG22	2.20	0.41
1:A:3326:GLN:O	1:A:3329:LEU:HG	2.20	0.41
1:B:1455:CYS:HA	1:B:1458:LEU:HD12	2.01	0.41
1:B:1623:LEU:HD23	1:B:1623:LEU:HA	1.87	0.41
1:B:1630:ASP:C	1:B:1632:TRP:H	2.27	0.41
1:B:1752:LEU:HD12	1:B:1752:LEU:C	2.44	0.41
1:B:1828:LEU:HD23	1:B:1828:LEU:HA	1.90	0.41
1:B:1920:TYR:O	1:B:1924:THR:OG1	2.38	0.41
1:B:3144:PHE:CZ	1:B:3157:LEU:HD13	2.55	0.41
1:B:4055:ASN:HB3	1:B:4058:VAL:HG23	2.02	0.41
1:B:4082:ARG:HH12	1:B:4091:ALA:HA	1.85	0.41
1:A:23:ASP:C	1:A:25:CYS:H	2.28	0.41
1:A:934:LEU:HB3	1:A:984:TYR:OH	2.20	0.41
1:A:1916:ILE:HD13	1:A:1916:ILE:HA	1.91	0.41
1:A:1947:CYS:O	1:A:1951:VAL:HG12	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2389:PHE:HB3	1:A:2393:LEU:HB2	2.02	0.41
1:B:69:VAL:HG22	1:B:82:ARG:HG3	2.02	0.41
1:B:132:ILE:HD12	1:B:173:LYS:HD2	2.01	0.41
1:B:217:LEU:HB3	1:B:218:PRO:HD3	2.02	0.41
1:B:873:VAL:HG13	1:B:874:THR:N	2.28	0.41
1:B:1083:ASN:OD1	1:B:1126:GLN:HG3	2.19	0.41
1:B:1361:LYS:O	1:B:1365:ASN:HB2	2.20	0.41
1:B:1837:ARG:HD3	1:B:1837:ARG:N	2.34	0.41
1:B:1956:PHE:O	1:B:1958:GLU:HG3	2.20	0.41
1:B:2151:ILE:HD13	1:B:2188:GLU:HB3	2.01	0.41
1:B:3268:THR:HG23	1:B:3269:ARG:H	1.85	0.41
1:B:3339:ASN:OD1	1:B:3426:LYS:NZ	2.37	0.41
1:B:3413:TYR:HB3	1:B:3449:LYS:O	2.21	0.41
1:B:3761:ASP:HA	1:B:3764:VAL:HG22	2.02	0.41
1:A:303:HIS:ND1	1:A:305:ASN:OD1	2.41	0.41
1:A:1579:VAL:H	1:A:1579:VAL:HG22	1.66	0.41
1:A:2220:MET:HG2	1:A:2276:LEU:HD11	2.02	0.41
1:A:2274:ILE:HD12	1:A:2318:ALA:HB3	2.02	0.41
1:A:2402:LEU:CD1	1:A:2437:ASP:HB3	2.50	0.41
1:A:2887:PRO:HD2	1:A:2888:VAL:H	1.84	0.41
1:A:2923:TRP:CD2	1:A:2946:GLU:HG3	2.55	0.41
1:B:1225:GLU:OE2	1:B:1288:SER:OG	2.38	0.41
1:B:1362:ASP:OD1	1:B:1362:ASP:N	2.50	0.41
1:B:2003:LYS:HD3	1:B:2184:TYR:HE1	1.85	0.41
1:B:2519:LEU:HD13	1:B:2610:UNK:CA	2.50	0.41
1:B:2528:GLU:OE2	1:B:2533:SER:HB3	2.21	0.41
1:A:1096:VAL:HB	1:A:1101:PHE:CE2	2.55	0.41
1:A:1599:GLY:HA2	1:A:1602:ASP:OD1	2.21	0.41
1:A:2338:GLU:HA	1:A:2341:LEU:HD21	2.02	0.41
1:A:3463:LEU:HD13	1:A:3498:TRP:CZ2	2.52	0.41
1:A:3652:LEU:HB3	1:A:3653:ARG:HE	1.86	0.41
1:A:3708:ARG:HA	1:A:3708:ARG:HD2	1.85	0.41
1:B:374:LYS:C	1:B:376:ILE:H	2.27	0.41
1:B:1096:VAL:HB	1:B:1101:PHE:CE2	2.53	0.41
1:B:1261:LEU:HD21	1:B:1337:VAL:HA	2.02	0.41
1:B:1825:LEU:O	1:B:1829:TRP:HB2	2.21	0.41
1:B:2590:THR:OG1	1:B:2591:ILE:N	2.53	0.41
1:B:3701:ILE:HB	1:B:3719:ILE:HB	2.02	0.41
1:B:3924:HIS:CD2	1:B:3924:HIS:H	2.37	0.41
1:A:263:LYS:O	1:A:264:ARG:HG2	2.21	0.41
1:A:1141:LYS:HA	1:A:1141:LYS:HD2	1.80	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1389:VAL:O	1:A:1393:ALA:HB3	2.21	0.41
1:A:1440:ASP:HB2	1:A:1443:VAL:HG22	2.02	0.41
1:A:1646:LEU:HD23	1:A:1646:LEU:HA	1.87	0.41
1:B:170:VAL:O	1:B:174:VAL:HG23	2.19	0.41
1:B:2379:MET:HG3	1:B:2383:PHE:CE2	2.55	0.41
1:B:3562:LEU:HD12	1:B:3562:LEU:HA	1.88	0.41
1:B:3652:LEU:HB3	1:B:3653:ARG:HE	1.86	0.41
1:B:3802:LEU:HD12	1:B:3802:LEU:HA	1.96	0.41
1:B:3944:HIS:HB3	1:B:3948:SER:HB2	2.02	0.41
1:A:342:MET:HE3	1:A:342:MET:HA	2.03	0.41
1:A:653:LEU:HD13	1:A:670:LEU:HG	2.03	0.41
1:A:983:LEU:HD12	1:A:983:LEU:HA	1.90	0.41
1:A:1117:ASP:O	1:A:1118:GLU:HG2	2.20	0.41
1:A:1747:LEU:HD21	1:A:1778:PHE:CE1	2.55	0.41
1:A:3881:ASP:OD1	1:A:3881:ASP:N	2.48	0.41
1:B:569:VAL:HA	1:B:572:VAL:HG12	2.01	0.41
1:B:1448:LEU:HD23	1:B:1510:LEU:HD11	2.02	0.41
1:B:1949:ILE:HD11	1:B:2097:LEU:HD23	2.02	0.41
1:B:2477:LEU:HB3	1:B:2506:LEU:HG	2.02	0.41
1:B:2507:ILE:HG22	1:B:2550:ILE:HD11	2.02	0.41
1:B:3082:TYR:O	1:B:3084:GLN:N	2.54	0.41
1:B:3554:PHE:O	1:B:3558:ILE:HG13	2.20	0.41
1:B:3647:GLY:O	1:B:3651:LEU:HB3	2.20	0.41
1:A:385:TYR:CD2	1:A:389:ILE:HD11	2.50	0.41
1:A:446:PHE:CD1	1:A:530:LEU:HD22	2.55	0.41
1:A:871:LEU:H	1:A:871:LEU:HD23	1.84	0.41
1:A:913:ARG:HA	1:A:913:ARG:HD2	1.88	0.41
1:A:1349:LEU:HD21	1:A:1356:TRP:HA	2.02	0.41
1:A:1717:LEU:O	1:A:1721:HIS:HB2	2.20	0.41
1:A:2289:ASP:O	1:A:2291:GLN:N	2.53	0.41
1:A:2436:LEU:HD22	1:A:2469:CYS:SG	2.61	0.41
1:A:3167:ARG:O	1:A:3186:ARG:NH2	2.52	0.41
1:A:3462:ARG:NH1	1:A:3707:GLY:HA3	2.35	0.41
1:A:3802:LEU:HA	1:A:3802:LEU:HD12	1.86	0.41
1:B:1052:SER:HB3	1:B:1055:ASN:HB2	2.02	0.41
1:B:1601:LEU:HD13	1:B:1601:LEU:HA	1.95	0.41
1:B:2256:ILE:H	1:B:2256:ILE:HG13	1.56	0.41
1:B:2366:LYS:HA	1:B:2366:LYS:HD3	1.84	0.41
1:B:2591:ILE:HD11	1:B:2792:THR:OG1	2.21	0.41
1:B:3465:PHE:HB3	1:B:3466:PRO:HD3	2.03	0.41
1:B:3598:LYS:NZ	1:B:4031:ILE:HD13	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:414:LEU:HG	1:A:464:VAL:CG2	2.51	0.41
1:A:1134:LEU:O	1:A:1137:ILE:HG22	2.19	0.41
1:A:1334:LYS:O	1:A:1337:VAL:HG22	2.21	0.41
1:A:1969:GLU:HB3	1:A:1977:ILE:HG13	2.03	0.41
1:A:3061:LEU:HD12	1:A:3061:LEU:HA	1.88	0.41
1:B:354:SER:O	1:B:355:ASN:C	2.63	0.41
1:B:453:MET:HE3	1:B:453:MET:HB3	1.88	0.41
1:B:738:HIS:ND1	1:B:741:ILE:O	2.54	0.41
1:B:1586:SER:HA	1:B:1593:VAL:HG11	2.01	0.41
1:B:1969:GLU:HB2	1:B:1975:LEU:O	2.21	0.41
1:B:2825:THR:O	1:B:2829:LYS:N	2.40	0.41
1:B:3641:ASP:O	1:B:3645:GLY:N	2.53	0.41
1:A:385:TYR:O	1:A:389:ILE:HG13	2.21	0.41
1:A:904:VAL:O	1:A:905:ILE:HD13	2.21	0.41
1:A:1534:ASN:HA	1:A:1535:PRO:HD3	1.87	0.41
1:A:1733:THR:HG22	1:A:1735:ARG:H	1.84	0.41
1:A:1779:GLN:O	1:A:1783:ARG:HG3	2.20	0.41
1:A:1832:SER:OG	1:A:1833:LEU:N	2.52	0.41
1:A:1982:ILE:HG22	1:A:1983:ASP:N	2.36	0.41
1:A:1990:PHE:CE2	1:A:2144:LEU:HD11	2.55	0.41
1:A:2203:THR:OG1	1:A:2247:ASP:HB2	2.21	0.41
1:A:2284:ASP:HB3	1:A:2285:LEU:HG	2.03	0.41
1:A:2322:VAL:O	1:A:2326:ILE:HG13	2.20	0.41
1:A:2447:LYS:O	1:A:2449:VAL:N	2.50	0.41
1:A:2792:THR:N	1:A:2793:PRO:HD2	2.36	0.41
1:A:3542:PHE:HZ	1:A:3555:VAL:HG21	1.86	0.41
1:A:3924:HIS:H	1:A:3924:HIS:CD2	2.39	0.41
1:B:212:VAL:HG22	1:B:213:ARG:H	1.86	0.41
1:B:354:SER:CB	1:B:359:LEU:H	2.33	0.41
1:B:393:LYS:HA	1:B:397:LEU:HD13	2.03	0.41
1:B:612:LEU:HA	1:B:612:LEU:HD23	1.82	0.41
1:B:683:PHE:HB3	1:B:740:ILE:HD13	2.03	0.41
1:B:776:TRP:O	1:B:780:ILE:HG22	2.20	0.41
1:B:1433:ALA:O	1:B:1436:LEU:HD23	2.21	0.41
1:B:1617:LYS:HB2	1:B:1617:LYS:HE3	1.89	0.41
1:B:1696:LEU:N	1:B:1697:PRO:CD	2.84	0.41
1:B:1848:ILE:HD11	1:B:1918:LEU:HD21	2.01	0.41
1:B:1930:GLU:HB3	1:B:1937:ARG:NH1	2.36	0.41
1:B:2268:LYS:HD3	1:B:2314:GLU:OE2	2.21	0.41
1:B:2586:PHE:H	1:B:2783:ILE:HD11	1.85	0.41
1:B:2814:SER:HA	1:B:2865:HIS:NE2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3577:GLN:HA	1:B:3630:ARG:HH11	1.85	0.41
1:B:4064:LEU:O	1:B:4068:HIS:HB2	2.21	0.41
1:A:290:TYR:HE2	1:A:340:TYR:CD2	2.39	0.41
1:A:655:LEU:HD22	1:A:1389:VAL:CG1	2.51	0.41
1:A:873:VAL:CG1	1:A:874:THR:H	2.27	0.41
1:A:1564:SER:O	1:A:1603:GLN:HG3	2.21	0.41
1:A:1700:THR:HG23	1:A:1757:MET:HE3	2.03	0.41
1:A:1914:THR:O	1:A:1918:LEU:HG	2.20	0.41
1:A:1978:PHE:O	1:A:1982:ILE:HG12	2.21	0.41
1:A:2351:GLN:O	1:A:2355:THR:HG22	2.21	0.41
1:A:2942:ILE:H	1:A:2942:ILE:HG12	1.75	0.41
1:A:2987:THR:C	1:A:2989:ALA:H	2.28	0.41
1:A:3386:SER:O	1:A:3389:VAL:HG22	2.21	0.41
1:A:3988:LEU:O	1:A:3992:ARG:HG2	2.21	0.41
1:A:4031:ILE:HG13	1:A:4035:GLU:HB2	2.03	0.41
1:B:1267:TYR:HB3	1:B:1344:PHE:CE1	2.56	0.41
1:B:1419:LEU:HD13	1:B:1467:ILE:HD11	2.03	0.41
1:B:2091:HIS:O	1:B:2093:CYS:N	2.54	0.41
1:B:2140:LEU:HD21	1:B:2179:GLY:H	1.84	0.41
1:B:3480:LEU:HD12	1:B:3480:LEU:HA	1.86	0.41
1:A:9:ARG:HA	1:A:12:LEU:HD13	2.04	0.40
1:A:523:THR:OG1	1:A:524:TYR:N	2.53	0.40
1:A:1938:ARG:HH21	1:A:1983:ASP:HA	1.86	0.40
1:A:2366:LYS:HD3	1:A:2366:LYS:HA	1.86	0.40
1:A:3666:LEU:HA	1:A:3669:LYS:HG2	2.03	0.40
1:A:3719:ILE:HD12	1:A:3740:ILE:HD12	2.02	0.40
1:B:620:PHE:CZ	1:B:663:ILE:HD12	2.56	0.40
1:B:1197:LEU:O	1:B:1197:LEU:HD23	2.21	0.40
1:B:1334:LYS:NZ	1:B:1383:GLY:HA3	2.35	0.40
1:B:1344:PHE:O	1:B:1347:THR:HG22	2.21	0.40
1:B:1372:LEU:O	1:B:1375:THR:OG1	2.32	0.40
1:B:2097:LEU:HB3	1:B:2149:LEU:HD11	2.03	0.40
1:B:2164:TRP:O	1:B:2196:TRP:HZ3	2.04	0.40
1:B:2263:LYS:HA	1:B:2309:PHE:HE2	1.86	0.40
1:B:3129:LEU:HD23	1:B:3129:LEU:HA	1.92	0.40
1:A:1372:LEU:HD12	1:A:1402:LEU:HD23	2.02	0.40
1:A:1474:ASP:OD1	1:A:1474:ASP:N	2.54	0.40
1:A:1749:ALA:O	1:A:1753:SER:OG	2.34	0.40
1:A:2253:TYR:HD2	1:A:2292:CYS:HB2	1.87	0.40
1:A:2306:ASN:O	1:A:2309:PHE:HB2	2.21	0.40
1:B:1263:ALA:HA	1:B:1266:CYS:SG	2.62	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1627:LYS:HE2	1:B:1627:LYS:HB2	1.80	0.40
1:B:1832:SER:H	1:B:1883:ARG:NH2	2.10	0.40
1:B:1894:SER:HA	1:B:1897:ASN:HB2	2.03	0.40
1:B:2514:ASN:O	1:B:2517:LEU:HB3	2.21	0.40
1:B:2884:LEU:HD23	1:B:2884:LEU:HA	1.97	0.40
1:A:853:ILE:HD11	1:A:3108:GLN:OE1	2.21	0.40
1:A:1178:ARG:HG2	1:A:1180:GLN:H	1.86	0.40
1:A:2294:ILE:HG22	1:A:2295:GLN:N	2.35	0.40
1:A:2551:GLU:HG3	1:A:2849:SER:CB	2.50	0.40
1:A:3053:LEU:HD11	1:A:3088:LEU:HD13	2.03	0.40
1:A:3674:SER:O	1:A:3676:PRO:HD3	2.21	0.40
1:B:179:GLY:HA3	1:B:226:GLY:HA2	2.04	0.40
1:B:357:LYS:O	1:B:360:SER:HB3	2.21	0.40
1:B:681:LYS:O	1:B:683:PHE:N	2.54	0.40
1:B:738:HIS:HE1	1:B:748:TYR:CE1	2.39	0.40
1:B:765:LEU:HD23	1:B:766:ALA:H	1.85	0.40
1:B:1101:PHE:CE1	1:B:1138:ILE:HD13	2.56	0.40
1:B:1423:ILE:HD11	1:B:1467:ILE:HD13	2.03	0.40
1:B:1831:CYS:HA	1:B:1883:ARG:NH1	2.36	0.40
1:B:2956:ALA:HB1	1:B:2972:TYR:CZ	2.56	0.40
1:B:3011:LEU:HD23	1:B:3047:SER:HB3	2.03	0.40
1:B:3389:VAL:HB	1:B:3413:TYR:HE1	1.85	0.40
1:A:47:SER:N	1:A:48:PRO:HD2	2.36	0.40
1:A:1503:LEU:HD12	1:A:1508:LYS:HE2	2.03	0.40
1:A:1515:LEU:CD2	1:A:1519:PHE:CE2	3.04	0.40
1:A:3059:GLN:HE21	1:A:3063:THR:HG23	1.86	0.40
1:A:3896:ALA:O	1:A:3900:LEU:HD13	2.22	0.40
1:A:3989:ARG:O	1:A:3993:SER:OG	2.30	0.40
1:B:1301:ILE:C	1:B:1303:MET:H	2.29	0.40
1:B:1436:LEU:HD13	1:B:1444:ASP:HB3	2.03	0.40
1:B:1832:SER:O	1:B:1833:LEU:HB2	2.21	0.40
1:B:3530:VAL:HA	1:B:3562:LEU:HD21	2.04	0.40
1:A:45:SER:HB3	1:A:51:LEU:HD22	2.04	0.40
1:A:189:MET:HE2	1:A:189:MET:HB2	1.74	0.40
1:A:886:TRP:CZ3	1:A:911:LEU:HG	2.56	0.40
1:A:941:MET:HE3	1:A:941:MET:HB2	2.00	0.40
1:A:1078:ALA:O	1:A:1107:TYR:OH	2.38	0.40
1:A:1261:LEU:HD21	1:A:1337:VAL:HG12	2.03	0.40
1:A:1643:MET:HE2	1:A:1643:MET:HB2	1.99	0.40
1:A:2549:LYS:HD3	1:A:2549:LYS:HA	1.96	0.40
1:A:3462:ARG:HG3	1:A:3494:GLN:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3796:MET:HE3	1:A:3796:MET:HB2	2.00	0.40
1:B:9:ARG:HA	1:B:12:LEU:HD13	2.03	0.40
1:B:76:ILE:O	1:B:79:ARG:NH1	2.54	0.40
1:B:172:GLU:HB2	1:B:218:PRO:O	2.21	0.40
1:B:476:ARG:NH2	1:B:1503:LEU:HD22	2.36	0.40
1:B:1333:SER:O	1:B:1337:VAL:HG13	2.21	0.40
1:B:1754:GLN:HB2	1:B:1797:LEU:HD11	2.03	0.40
1:B:1804:MET:HE3	1:B:1804:MET:HB2	1.92	0.40
1:B:1982:ILE:HG22	1:B:1983:ASP:N	2.36	0.40
1:B:2310:VAL:HG12	1:B:2316:TYR:CD2	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	3544/3986 (89%)	3047 (86%)	482 (14%)	15 (0%)	30	66
1	B	3559/3986 (89%)	3069 (86%)	475 (13%)	15 (0%)	30	66
2	C	7/192 (4%)	7 (100%)	0	0	100	100
2	D	7/192 (4%)	7 (100%)	0	0	100	100
All	All	7117/8356 (85%)	6130 (86%)	957 (13%)	30 (0%)	30	66

All (30) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2182	ILE
1	A	2250	SER
1	A	2410	GLU
1	A	2781	PRO
1	B	1613	HIS

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Mol	Chain	Res	Type
1	B	2250	SER
1	B	2410	GLU
1	A	1681	ASP
1	B	2246	LYS
1	B	3059	GLN
1	B	2206	PRO
1	B	2406	GLU
1	B	2407	GLY
1	A	167	PRO
1	A	2577	PHE
1	A	3059	GLN
1	A	1682	THR
1	A	1956	PHE
1	A	2886	GLN
1	A	2121	ASP
1	A	2177	ASN
1	B	304	THR
1	B	682	TYR
1	B	2577	PHE
1	A	635	PRO
1	A	2783	ILE
1	B	1992	VAL
1	B	2226	PRO
1	B	2573	PRO
1	B	2781	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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	3046/3515 (87%)	3046 (100%)	0	100	100
1	B	3093/3515 (88%)	3089 (100%)	4 (0%)	88	88
2	C	8/165 (5%)	8 (100%)	0	100	100
2	D	8/165 (5%)	8 (100%)	0	100	100
All	All	6155/7360 (84%)	6151 (100%)	4 (0%)	88	88

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	662	LEU
1	B	1205	ASN
1	B	1727	ARG
1	B	2489	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (61) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	322	GLN
1	A	344	GLN
1	A	399	GLN
1	A	1126	GLN
1	A	1476	HIS
1	A	1725	GLN
1	A	1909	ASN
1	A	2217	ASN
1	A	2283	ASN
1	A	2305	ASN
1	A	2353	GLN
1	A	2483	ASN
1	A	2587	GLN
1	A	2787	HIS
1	A	2834	GLN
1	A	3059	GLN
1	A	3251	ASN
1	A	3379	GLN
1	A	3383	GLN
1	A	3423	GLN
1	A	3494	GLN
1	A	3602	ASN
1	A	3664	ASN
1	A	3679	ASN
1	A	3697	ASN
1	A	3766	GLN
1	A	3808	ASN
1	A	3924	HIS
1	A	4015	ASN
1	A	4087	HIS
1	A	4088	ASN
1	B	355	ASN
1	B	415	GLN

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Mol	Chain	Res	Type
1	B	484	HIS
1	B	786	GLN
1	B	869	ASN
1	B	925	GLN
1	B	1048	GLN
1	B	1049	GLN
1	B	1126	GLN
1	B	1589	ASN
1	B	1817	GLN
1	B	1909	ASN
1	B	1957	ASN
1	B	2233	HIS
1	B	2283	ASN
1	B	2305	ASN
1	B	2553	HIS
1	B	2784	GLN
1	B	2977	ASN
1	B	3130	GLN
1	B	3251	ASN
1	B	3278	GLN
1	B	3423	GLN
1	B	3664	ASN
1	B	3743	HIS
1	B	3969	ASN
1	B	4015	ASN
1	B	4087	HIS
1	B	4088	ASN
1	B	4110	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	B	2
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	2614:UNK	C	2740:UNK	N	43.02
1	A	2614:UNK	C	2739:UNK	N	37.67
1	B	2765:UNK	C	2779:ASP	N	14.02
1	A	2765:UNK	C	2779:ASP	N	13.16

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	3590/3986 (90%)	0.21	48 (1%) 75 59	144, 217, 281, 339	0
1	B	3607/3986 (90%)	0.23	52 (1%) 73 58	148, 210, 309, 413	0
2	C	9/192 (4%)	0.13	0 100 100	217, 221, 227, 228	0
2	D	9/192 (4%)	0.53	0 100 100	160, 169, 180, 182	0
All	All	7215/8356 (86%)	0.22	100 (1%) 73 58	144, 213, 288, 413	0

All (100) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1560	TYR	4.8
1	A	3301	LEU	4.3
1	A	1993	GLU	3.9
1	A	116	THR	3.8
1	B	1391	VAL	3.7
1	A	4063	GLU	3.7
1	B	4128	MET	3.5
1	B	178	LEU	3.4
1	A	1559	PHE	3.4
1	A	1227	GLY	3.4
1	B	685	GLY	3.2
1	B	156	PHE	3.2
1	B	3391	ALA	3.2
1	B	1251	GLN	3.2
1	B	546	ALA	3.1
1	B	1993	GLU	3.1
1	B	3651	LEU	3.0
1	B	1686	LEU	3.0
1	A	1339	VAL	3.0
1	B	2249	LEU	2.9
1	A	936	SER	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	1395	LEU	2.8
1	B	1494	GLY	2.8
1	B	435	LEU	2.8
1	A	4018	GLN	2.8
1	B	55	THR	2.8
1	B	1979	GLU	2.8
1	A	123	CYS	2.8
1	B	1303	MET	2.8
1	B	473	PRO	2.7
1	B	241	ASP	2.6
1	A	1100	VAL	2.6
1	A	630	CYS	2.6
1	A	170	VAL	2.6
1	A	3277	VAL	2.6
1	A	3699	LEU	2.6
1	A	3311	ASN	2.6
1	B	1980	ASN	2.6
1	B	1590	THR	2.6
1	B	1700	THR	2.6
1	A	3451	LEU	2.5
1	A	1060	PHE	2.5
1	A	1880	MET	2.5
1	A	910	PHE	2.5
1	A	1230	GLY	2.5
1	B	434	VAL	2.5
1	A	3651	LEU	2.5
1	A	212	VAL	2.5
1	B	1581	GLU	2.4
1	B	2325	LEU	2.4
1	A	1057	LYS	2.4
1	B	2278	GLY	2.4
1	B	1256	TRP	2.4
1	B	1359	LEU	2.4
1	A	3391	ALA	2.4
1	A	2781	PRO	2.3
1	A	3316	LEU	2.3
1	B	3294	SER	2.3
1	A	3527	GLN	2.3
1	B	474	VAL	2.3
1	A	3286	CYS	2.3
1	B	2563	LEU	2.3
1	A	1133	HIS	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	242	PRO	2.3
1	B	1387	GLY	2.3
1	B	3349	ALA	2.3
1	B	3744	ASP	2.3
1	B	1482	GLU	2.2
1	A	1251	GLN	2.2
1	A	2554	PHE	2.2
1	A	1873	TYR	2.2
1	B	2004	TYR	2.2
1	B	100	ILE	2.2
1	A	2868	LEU	2.2
1	A	1537	VAL	2.2
1	B	2048	GLY	2.2
1	B	861	SER	2.2
1	A	3447	VAL	2.2
1	B	470	ALA	2.1
1	A	773	LEU	2.1
1	A	938	VAL	2.1
1	B	716	VAL	2.1
1	B	1432	CYS	2.1
1	A	3483	MET	2.1
1	A	385	TYR	2.1
1	B	141	SER	2.1
1	A	2374	LEU	2.1
1	B	468	LEU	2.1
1	B	1100	VAL	2.1
1	B	1541	ALA	2.1
1	B	1227	GLY	2.1
1	B	3963	LEU	2.1
1	A	2882	ALA	2.0
1	B	1302	ALA	2.0
1	B	2277	LEU	2.0
1	B	2469	CYS	2.0
1	A	1226	GLY	2.0
1	A	2784	GLN	2.0
1	A	1884	LEU	2.0
1	A	3700	GLU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.